Online Data Supplements

Supplemental Methods

Bioinformatic Analysis of Gene Expression Profile.

Biological networks of the differentially expressed genes were generated with Ingenuity pathway analysis (IPA) tools (Ingenuity Systems Inc.). The list of differentially expressed genes from Polony Multiplex Analysis of Gene Expression (PMAGE) was imported into Ingenuity and each gene identifier was overlaid onto a global molecular network developed from information contained in the Ingenuity Pathways Knowledge Base. Networks of these genes were then generated based on their connectivity.

Proteomic Screening with Protein Interaction Pull-down Assay.

The Txnip coding sequence was subcloned into pCDH-CMV-MCS-EF1-Puro (System Biosciences, Mountain View, CA) with a glutathione S-transferase (GST) tag and transduced into HEK293F cells. Cells expressing GST alone were used as a negative control. Cells were lysed in 0.5% Triton X-100, 150 mM NaCl, 50 mM Tris, 1 mM phenylmethanesulfonylfluoride, and protease inhibitors (Sigma-Aldrich, St. Louis, MO), pH 7.4. Txnip pulldown was performed using magnetic glutathione beads (Thermo Fisher Scientific, Rockford, IL) according to the manufacturer’s instructions. Pulled down proteins were subjected to SDS-PAGE and analyzed by mass spectrometry.

Assays for Oxidative Phosphorylation (OXPHOS) Complexes.

Protein levels of total oxidative phosphorylation (OXPHOS) complexes were detected with immunoblotting analysis using the monoclonal antibody cocktail from MitoProfile Rodent Total OXPHOS Complexes Detection Kit (MitoSciences Inc., Eugene, OR). Mouse heart mitochondria were also separated by blue native gel electrophoresis and stained with Coomassie blue to visualize respiratory complexes. Quantitative analyses of complex III and IV activities were performed using MitoTox OXPHOS Complex III Activity Kit and MitoProfile Rapid Microplate Assay Kit for Mouse Complex IV Activity (MitoSciences Inc., Eugene, OR), respectively. It should be noted that, in this Complex III assay, the enzymatic reaction is partially affected by the activity of complex II.

Mitochondrial Permeability Transition Pore Opening.

Mitochondrial permeability transition pore opening was determined by mitochondrial swelling (1). Osmotic swelling was induced by addition of 250 μM $CaCl_2$, and measured by decrease in absorbance at 540 nm using 96-well plate reader (Molecular Devices Inc., Sunnyvale, CA). Glutathione-induced mitochondrial swelling was also assessed by addition of 10 mM reduced glutathione (2).

Binding Assay of Thioredoxin-2 to Txnip.

The binding assay was performed as described (3). Briefly, mitochondrial thioredoxin-2 cDNA was subcloned into pGEX-4T3 (Amersham Biosciences), carboxyl-terminal to glutathione S-transferase (GST). GST fusion proteins were induced in *E.coli* BL21 cells and cellular lysates were incubated with glutathione-Sepharose 4B beads (Bio-World, Dublin, OH). Txnip was overexpressed in HEK 293 cells using a mammalian overexpression vector (pcDNA3.1/V5/His, Invitrogen) and FuGENE (Roche Applied Science) transfection reagent. For GST binding, HEK 293 cells lysates were incubated with beads containing equal amounts of GST protein. Binding proceeded overnight and bound proteins were released by boiling in gel-loading sample buffer. Protein samples were electrophoresed and the immune-complex between Txnip and thioredoxin-2 was detected using our monoclonal Txnip antibody JY2 (available from MLB International, Woburn, MA).

Supplemental Results and Discussion

Ingenuity Pathway Analysis Reveals Putative Downstream Targets Responding to Cardiometabolic Effects by Txnip.

The results of the network reconstruction by Ingenuity and connectivity map of the responses are shown in Supplemental Figure 1. Ingenuity network analysis found two significant networks (Supplemental Figure 1A and 1B). The p statistics for significance were $1x10^{-50}$ and $1x10^{-38}$, respectively. In the networks, red and green indicate up- and down-regulation of gene expression, respectively, while grey indicates no information or no change. As shown in network 1, the downstream partner genes include retinoid X receptor α (RXRA), which has been shown to interact with peroxisome proliferator-activated receptor gamma coactivator 1-α (PGC-1α) that regulates the genes involved in energy metabolism and mitochondrial biogenesis. Recently, it has been reported that Txnip binds Myb-binding protein 1a (Mybbp1a) which inhibits PGC-1α function (4). Thus, down-regulation of PGC-1α might be a mechanism through which deletion of Txnip leads to decreased levels of multiple molecules participating in several central metabolic pathways. Among the other fundamental cardiac components, p38 MAPK and peroxisome proliferator-activated receptor gamma coactivator 1-β (PPARGC1B) may be the interface components associated with mitochondrial metabolism in network 2. Glycogen synthase was also among the genes constituting network 2 and was significantly down-regulated by deletion of Txnip at the level of transcription. Thus, the Ingenuity Pathway analysis suggested putative downstream targets responding to potential cardiometabolic effects by Txnip, although the precise molecular mechanism of how deletion of Txnip controls these multiple networks remains unclear.

Txnip-KO Mitochondria Have Comparable Calcium Capacity with Wild Type Mitochondria.

The import of Ca^{2+} from cytosol into cardiac mitochondria is an important regulatory event in cell signaling. Calcium efflux occurs with mitochondrial permeability transition pore opening, and the activation of the permeability transition pore with mitochondrial calcium flux plays a role in early myocardial ischemia-reperfusion injury (5). We directly compared the effects of exposure to Ca^{2+} in mitochondria between isolated from Txnip-KO and wild type hearts. Supplemental Figure 2E shows absorbance changes after the addition of 250 μM $CaCl_2$ to mitochondria. Exposure to Ca^{2+} led to a large decrease in the absorbance to the same extent in wild type and Txnip-KO mitochondria, indicating that Txnip-KO and wild type mitochondria have comparable calcium capacities. We also compared the effects of exposure to glutathione. As shown in Supplemental Figure 2F, glutathione-dependent swelling of mitochondria was comparable between Txnip-KO mice and wild type mice. Thus, Txnip-KO mitochondria show no difference in the sensitivity of mitochondrial permeability transition pore opening compared to wild type mitochondria.

Supplemental Figure Legends

Supplemental Figure 1. Ingenuity pathway analysis (IPA) gene networks. Biological networks of the differentially expressed genes were generated in Ingenuity pathway analysis tools (Ingenuity Systems Inc.). The intensity of colors indicates the degree of up-regulation (red) or down-regulation (green), and grey indicates no information or no change. Node (gene) symbols are described. The p statistics for significance of Network 1 (**A**) and Network 2 (**B**) were 1×10^{-50} and 1×10^{-38}, respectively. The networks contain genes such as retinoid X receptor α (RXRA), peroxisome proliferator-activated receptor gamma coactivator 1-β (PPARGC1B) and other signaling molecules.

Supplemental Figure 2. (**A**) Complex III activity was measured by monitoring the conversion of cytochrome *c* in its oxidized form to its reduced form, as a linear increase in absorbance at 550 nm. (**B**) Complex IV activity was determined by the oxidation of reduced cytochrome *c* in isolated mitochondria (n=6 each). Values are mean±SEM. (**C**) Immunoblotting analysis was performed using a monoclonal antibody cocktail for the OXPHOS complex. (**D**) Multiprotein complexes from mouse heart mitochondria were separated by blue-native PAGE, and probed with a monoclonal antibody cocktail for the OXPHOS complex. (**E**) Calcium-sensitive osmotic swelling was induced by 250 μM $CaCl_2$ and measured by decrease in absorbance at 540 nm using 96-well plate reader (Molecular

Device Inc., Sunnyvale, CA). (**F**) Glutathione-induced mitochondrial swelling was also assessed by addition of 10 mM reduced glutathione. (**G**) Binding assay confirmed that Txnip can interact with thioredoxin-2. Txnip protein was overexpressed in HEK293 cells by transfection, and the cell lysates were incubated with thioredoxin-2-GST beads. After washing, beads were incubated in sample buffer and the supernatant was probed with anti-Txnip antibody. Protein expression of thioredoxin-2 was confirmed by Coomassie Blue Stain. Cells without Txnip overexpression were used as a control.

Supplemental References

1. Zhao K, et al. Cell-permeable peptide antioxidants targeted to inner mitochondrial membrane inhibit mitochondrial swelling, oxidative cell death, and reperfusion injury. *J Biol Chem*. 2004;279(33):34682-34690.
2. Lehninger AL, Schneider M. Mitochondrial swelling induced by glutathione. *J Biophys Biochem Cytol*. 1959;5(1):109-116.
3. Patwari P, Higgins LJ, Chutkow WA, Yoshioka J, Lee RT. The interaction of thioredoxin with Txnip. Evidence for formation of a mixed disulfide by disulfide exchange. *J Biol Chem*. 2006;281(31):21884-21891.
4. Yoshihara E, et al. Disruption of TBP-2 ameliorates insulin sensitivity and secretion without affecting obesity. *Nat Commun*. 2010;1:127.
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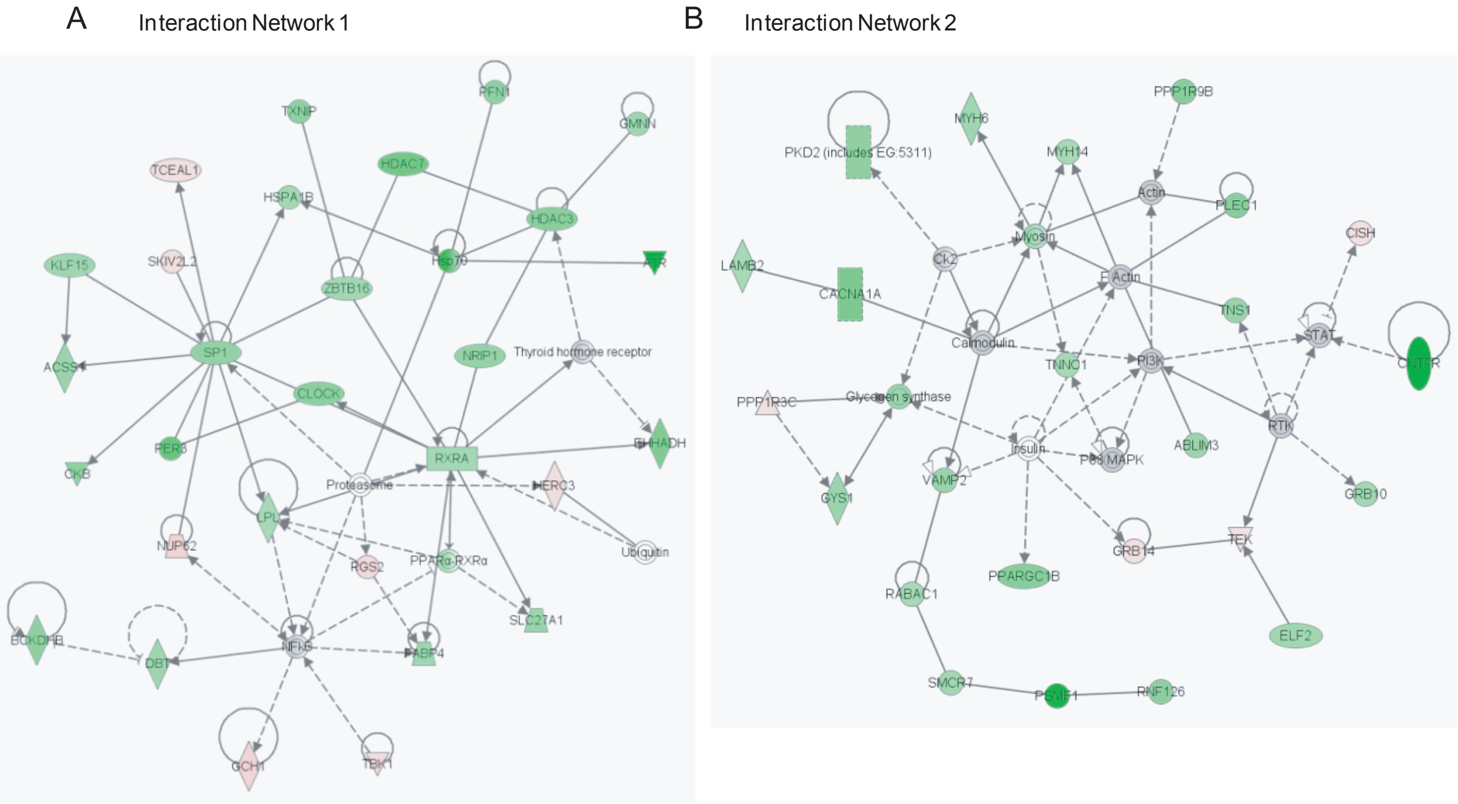
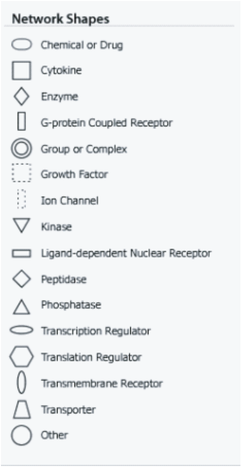
Supplemental Figure 1





Symbol	Gene
Ablim3	Actin binding LIM protein family, member 3
Acss1	Acyl-CoA synthetase short-chain family member 1
Atr	Ataxia telangiectasia and Rad3 related
Bckdhb	Branched chain ketoacid dehydrogenase E1, beta polypeptide
Cacna1a	cDNA sequence BY080835
Cish	Cytokine inducible SH2-containing protein
Ck2	Creatine kinase, mitochondrial 2
Ckb	Creatine kinase, brain
Clock	Circadian locomoter output cycles kaput
Cntfr	Ciliary neurotrophic factor receptor
Dbt	Dihydrolipoamide branched chain transacylase E2
Ehhadh	Enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase
Elf2	E74-like factor 2
Fabp4	Fatty acid binding protein 4, adipocyte
Gch1	GTP cyclohydrolase 1
Gmnn	Geminin
Grb10	Growth factor receptor bound protein 10
Grb14	Growth factor receptor bound protein 14
Gys1	Glycogen synthase 1, muscle
Hdac3	Histone deacetylase 3
Hdac7a	Histone deacetylase 7A
Herc3	Hect domain and RLD 3
Hspa1b	Heat shock 70kDa protein 1B
Klf15	Kruppel-like factor 15
Lamb2	Laminin, beta 2
Lpl	Lipoprotein lipase
Myh14	Myosin, heavy polypeptide 14
Myh6	Myosin, heavy polypeptide 6, cardiac muscle, alpha
Nrip1	Nuclear receptor interacting protein 1
Nup62	Nucleoporin 62
Per3	Period homolog 3 (Drosophila)
Pfn1	Profilin 1
Pkd2	Polycystic kidney disease 2
Plec1	Plectin 1
Ppargc1b	Peroxisome proliferative activated receptor, gamma, coactivator 1 beta
Ppp1r3c	Protein phosphatase 1, regulatory (inhibitor) subunit 3C
Ppp1r9b	Protein phosphatase 1, regulatory subunit 9B
Psmf1	Proteasome (prosome, macropain) inhibitor subunit 1 (PI31)
Rabac1	Rab acceptor 1 (prenylated)
Rgs2	Regulator of G-protein signaling 2
Rnf126	Ring finger protein 126
Rxra	Retinoid X receptor alpha
Skiv2l2	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)
Slc27a1	Solute carrier family 27 (fatty acid transporter), member 1
Smcr7	Smith-Magenis syndrome chromosome region, candidate 7 homolog (human)
Sp1	Trans-acting transcription factor 1
Tbk1	TANK-binding kinase 1
Tceal1	Transcription elongation factor A (SII)-like 1
Tek	Endothelial-specific receptor tyrosine kinase
Tnnc1	Troponin C, cardiac/slow skeletal
Tns1	Tensin 1
Vamp2	Vesicle-associated membrane protein 2
Zbtb16	Zinc finger and BTB domain containing 16

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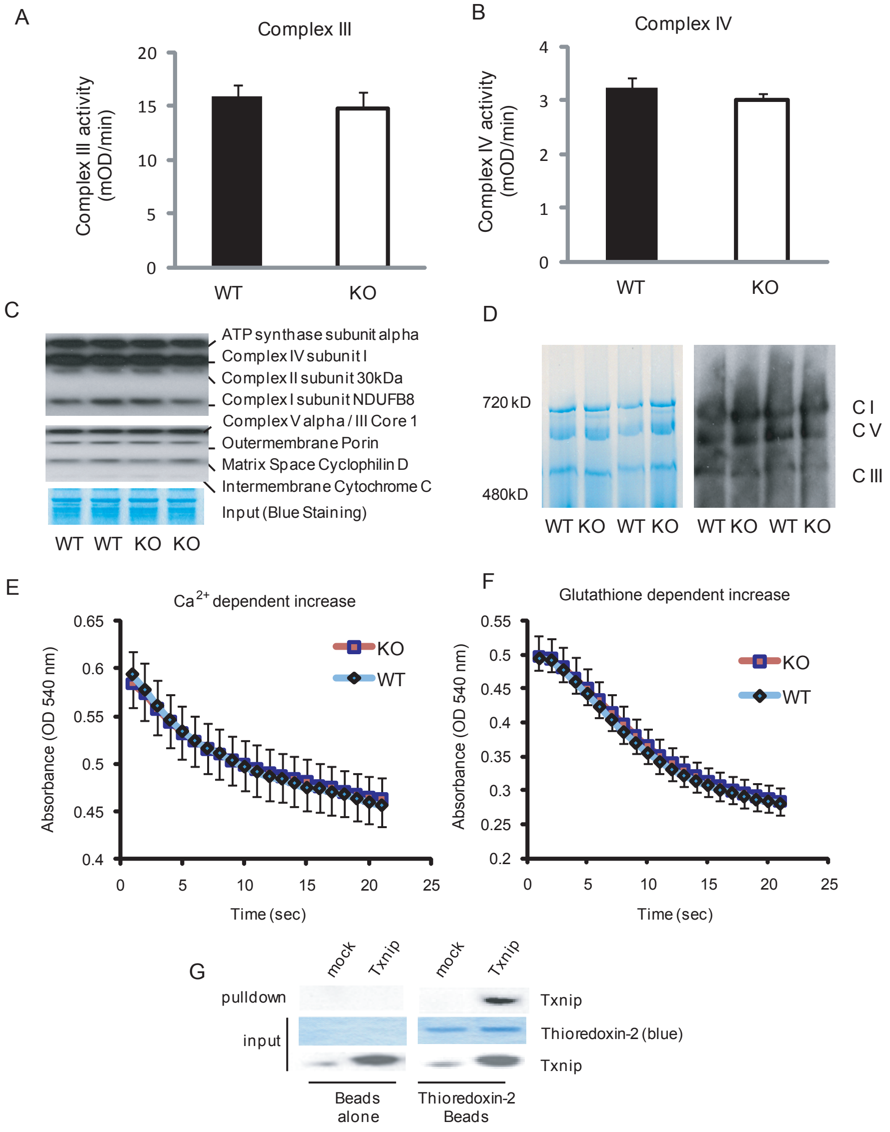
Supplemental Figure 2



Supplemental Figure 2. (**A**) Complex III activity was measured by monitoring the conversion of cytochrome *c* in its oxidized form to its reduced form, as a linear increase in absorbance at 550 nm. (**B**) Complex IV activity was determined by the oxidation of reduced cytochrome *c* in isolated mitochondria (n=6 each). Values are mean±SEM. (**C**) Immunoblotting analysis was performed using a monoclonal antibody cocktail for the OXPHOS complex. (**D**) Multiprotein complexes from mouse heart mitochondria were separated by blue-native PAGE, and probed with a monoclonal antibody cocktail for the OXPHOS complex. (**E**) Calcium-sensitive osmotic swelling was induced by 250 μM $CaCl_2$ and measured by decrease in absorbance at 540 nm using 96-well plate reader (Molecular Device Inc., Sunnyvale, CA). (**F**) Glutathione-induced mitochondrial swelling was also assessed by addition of 10 mM reduced glutathione. (**G**) Binding assay confirmed that Txnip can interact with thioredoxin-2. Txnip protein was overexpressed in HEK293 cells by transfection, and the cell lysates were incubated with thioredoxin-2-GST beads. After washing, beads were incubated in sample buffer and the supernatant was probed with anti-Txnip antibody. Protein expression of thioredoxin-2 was confirmed by Coomassie Blue Stain. Cells without Txnip overexpression were used as a control.

Supplemental Table 1

Differentially-regulated genes for dehydrogenases, oxidoreductases, and enzymes controlling oxidative phosphorylation/electron transport are highlighted in red.

		Normalized Tag Count			KO/WT	
NCBI Unigene Symbol	Gene Name	WT	Txnip-KO	Total	Fold Change	P-value
Pars2	prolyl-tRNA synthetase 2, mitochondrial (putative)	12	1	13	-12	0.0000135
Zfp385b	zinc finger protein 385B	11	1	12	-11	0.0001676
4833426J09Rik	RIKEN cDNA 4833426J09 gene	10	1	11	-10	0.0003808
C1qtnf1	C1q and tumor necrosis factor related protein 1	10	1	11	-10	0.0003808
Cnr1	Cannabinoid receptor 1 (brain)	19	2	21	-9.5	0.0000008
Bdh1	3-hydroxybutyrate dehydrogenase, type 1	148	16	164	-9.25	0.0000000
Dcp1b	DCP1 decapping enzyme homolog b (S. cerevisiae)	9	1	10	-9	0.0008580
Mm.400598	Transcribed locus	8	1	9	-8	0.0004556
Itga3	Integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	8	1	9	-8	0.0010832
Lonrf2	LON peptidase N-terminal domain and ring finger 2	8	1	9	-8	0.0010832
Hfe2	Hemochromatosis type 2 (juvenile) (human homolog)	256	40	296	-6.4	0.0000000
Adamts15	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 15	15	3	18	-5	0.0003413
Pdia5	Protein disulfide isomerase associated 5	10	2	12	-5	0.0013050
Cntfr	Ciliary neurotrophic factor receptor	28	6	34	-4.66	0.0000011
Mm.367626	Transcribed locus	32	7	39	-4.57	0.0000002
Abat	4-aminobutyrate aminotransferase	22	5	27	-4.4	0.0000215
Ssh3	Slingshot homolog 3 (Drosophila)	16	4	20	-4	0.0009254
Atr	Ataxia telangiectasia and Rad3 related	12	3	15	-4	0.0021816
Zfp697	Zinc finger protein 697	23	6	29	-3.83	0.0001223
Ei24	Etoposide induced 2.4 mRNA	87	23	110	-3.78	0.0000000
Psmf1	Proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	15	4	19	-3.75	0.0017306
Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	29	8	37	-3.62	0.0000297
Ctso	Cathepsin O	21	6	27	-3.5	0.0004045
Sergef	Secretion regulating guanine nucleotide exchange factor	21	6	27	-3.5	0.0004045
Evc2	Ellis van Creveld syndrome 2 homolog (human)	14	4	18	-3.5	0.0015405
Armc2	armadillo repeat containing 2	38	11	49	-3.45	0.0000007
Hook1	Hook homolog 1 (Drosophila)	34	10	44	-3.4	0.0000066
Dis3	DIS3 mitotic control homolog (S. cerevisiae)	17	5	22	-3.4	0.0020353
BY080835	cDNA sequence BY080835	20	6	26	-3.33	0.0003716
Hspa1a	Heat shock protein 1A	73	22	95	-3.31	0.0000000
Jup	Junction plakoglobin	255	78	333	-3.26	0.0000000
2410001C21Rik	RIKEN cDNA 2410001C21 gene	29	9	38	-3.22	0.0000570
Slc39a13	Solute carrier family 39 (metal ion transporter), member 13	29	9	38	-3.22	0.0000570
Eif3s9	eukaryotic translation initiation factor 3. subunit 9	32	10	42	-3.2	0.0000209
Pex12	Peroxisomal biogenesis factor 12	16	5	21	-3.2	0.0018957
Fah	Fumarylacetoacetate hydrolase	185	58	243	-3.18	0.0000000
Bbx	Bobby sox homolog (Drosophila)	28	9	37	-3.11	0.0001002
Gdpd3	Glycerophosphodiester phosphodiesterase domain containing 3	28	9	37	-3.11	0.0001002
Ccbl2	Cysteine conjugate-beta lyase 2	66	22	88	-3	0.0000000
Crip1	Cysteine-rich protein 1 (intestinal)	51	17	68	-3	0.0000005
Scd1	Stearoyl-Coenzyme A desaturase 1	27	9	36	-3	0.0001745
Ddt	D-dopachrome tautomerase	27	9	36	-3	0.0003107
Caskin2	Cask-interacting protein 2	24	8	32	-3	0.0008536
Zrsr2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	24	8	32	-3	0.0008536
Zcchc17	Zinc finger, CCHC domain containing 17	32	11	43	-2.9	0.0000385
Cpsf4	Cleavage and polyadenylation specific factor 4	29	10	39	-2.9	0.0001879
BC020535	CDNA sequence BC020535	20	7	27	-2.85	0.0013389
Mll1	Myeloid/lymphoid or mixed-lineage leukemia 1	34	12	46	-2.83	0.0000728
Dnajc15	DnaJ (Hsp40) homolog, subfamily C, member 15	25	9	34	-2.77	0.0008823
Myo1d	Myosin ID	38	14	52	-2.71	0.0000276
Frap1	FK506 binding protein 12-rapamycin associated protein 1	38	14	52	-2.71	0.0000467
Magix	MAGI family member, X-linked	38	14	52	-2.71	0.0000467
Slfn5	Schlafen 5	46	17	63	-2.7	0.0000111

Tbc1d17	TBC1 domain family, member 17	40	15	55	-2.66	0.0000474
Mm.393986	Transcribed locus	24	9	33	-2.66	0.0008706
Tm2d3	TM2 domain containing 3	24	9	33	-2.66	0.0008706
Lrp5	Low density lipoprotein receptor-related protein 5	24	9	33	-2.66	0.0014572
Rela	V-rel reticuloendotheliosis viral oncogene homolog A (avian)	24	9	33	-2.66	0.0014638
Wdr13	WD repeat domain 13	69	26	95	-2.65	0.0000001
Fxc1	Fractured callus expressed transcript 1	79	30	109	-2.63	0.0000000
1110051M20Rik	RIKEN cDNA 1110051M20 gene	29	11	40	-2.63	0.0003244
Chrna2	Cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	29	11	40	-2.63	0.0003244
Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	71	27	98	-2.62	0.0000000
Per3	Period homolog 3 (Drosophila)	34	13	47	-2.61	0.0001235
Ampd3	AMP deaminase 3	26	10	36	-2.6	0.0008891
Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	36	14	50	-2.57	0.0000763
Usp20	Ubiquitin specific peptidase 20	43	17	60	-2.52	0.0000293
Nrxn2	Neurexin II	70	28	98	-2.5	0.0000002
2310043N10Rik	RIKEN cDNA 2310043N10 gene	483	194	677	-2.48	0.0000000
Ubqln4	Ubiquilin 4	67	27	94	-2.48	0.0000004
Hrbl	HIV-1 Rev binding protein-like	52	21	73	-2.47	0.0000043
Hsd17b11	Hydroxysteroid (17-beta) dehydrogenase 11	170	70	240	-2.42	0.0000000
Hdac7a	Histone deacetylase 7A	41	17	58	-2.41	0.0001195
Ociad1	OCIA domain containing 1	172	72	244	-2.38	0.0000000
Ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	43	18	61	-2.38	0.0000744
Scd4	Stearoyl-coenzyme A desaturase 4	38	16	54	-2.37	0.0001976
Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	26	11	37	-2.36	0.0014561
Clec2d	C-type lectin domain family 2, member d	125	53	178	-2.35	0.0000000
Tpd52l1	Tumor protein D52-like 1	35	15	50	-2.33	0.0005020
Cacna1a	cDNA sequence BY080835	51	22	73	-2.31	0.0000264
Tnpo3	Transportin 3	44	19	63	-2.31	0.0001133
Gpc1	Glypican 1	120	52	172	-2.3	0.0000000
Lima1	LIM domain and actin binding 1	30	13	43	-2.3	0.0008668
Yipf1	Yip1 domain family, member 1	55	24	79	-2.29	0.0000160
Mm.417366	Transcribed locus	39	17	56	-2.29	0.0003008
Mm.413858	Transcribed locus	32	14	46	-2.28	0.0012878
Txndc5	Thioredoxin domain containing 5	63	28	91	-2.25	0.0000056
Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	27	12	39	-2.25	0.0022733
Slc1a5	Solute carrier family 1 (neutral amino acid transporter), member 5	27	12	39	-2.25	0.0022733
Hmox1	Heme oxygenase (decycling) 1	65	29	94	-2.24	0.0000053
4732415M23Rik	RIKEN cDNA 4732415M23 gene	56	25	81	-2.24	0.0000237
BC021381	CDNA sequence BC021381	67	30	97	-2.23	0.0000051
Ehhadh	Enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	38	17	55	-2.23	0.0007021
Arvcf	Armadillo repeat gene deleted in velo-cardio-facial syndrome	69	31	100	-2.22	0.0000031
Usp8	Ubiquitin specific peptidase 8	40	18	58	-2.22	0.0002871
Rasgef1b	RasGEF domain family, member 1B	40	18	58	-2.22	0.0004310
Gmpr	Guanosine monophosphate reductase	157	71	228	-2.21	0.0000000
Blmh	Bleomycin hydrolase	42	19	61	-2.21	0.0002725
Pcx	Pyruvate carboxylase	31	14	45	-2.21	0.0013204
Ehd2	EH-domain containing 2	55	25	80	-2.2	0.0000363
Gas6	Growth arrest specific 6	123	56	179	-2.19	0.0000000
Ctsz	Cathepsin Z	48	22	70	-2.18	0.0001005
Ap2a1	Adaptor protein complex AP-2, alpha 1 subunit	35	16	51	-2.18	0.0007656
2510039O18Rik	RIKEN cDNA 2510039O18 gene	39	18	57	-2.16	0.0009981
Fbln1	Fibulin 1	75	35	110	-2.14	0.0000037
A230106M15Rik	RIKEN cDNA A230106M15 gene	30	14	44	-2.14	0.0020582
Cldn5	Claudin 5	30	14	44	-2.14	0.0020582
Bcat2	Branched chain aminotransferase 2, mitochondrial	156	73	229	-2.13	0.0000000
Mgll	Monoglyceride lipase	404	190	594	-2.12	0.0000000
Jund	Jun proto-oncogene related gene d	51	24	75	-2.12	0.0001308
Gcat	Glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	36	17	53	-2.11	0.0011089
Ppp1r9b	Protein phosphatase 1, regulatory subunit 9B	36	17	53	-2.11	0.0016224
A230097K15Rik	RIKEN cDNA A230097K15 gene	42	20	62	-2.1	0.0005931

Mark2	MAP/microtubule affinity-regulating kinase 2	40	19	59	-2.1	0.0006365
Ivd	Isovaleryl coenzyme A dehydrogenase	497	238	735	-2.08	0.0000000
Ppargc1b	Peroxisome proliferative activated receptor, gamma, coactivator 1 beta	48	23	71	-2.08	0.0002186
Plec1	Plectin 1	83	40	123	-2.07	0.0000027
Trim44	Tripartite motif-containing 44	58	28	86	-2.07	0.0000971
A630033E08Rik	RIKEN cDNA A630033E08 gene	56	27	83	-2.07	0.0001050
Hdac3	Histone deacetylase 3	39	19	58	-2.05	0.0014415
Dcxr	Dicarbonyl L-xylulose reductase	35	17	52	-2.05	0.0016846
Tmem16k	Transmembrane protein 16K	94	46	140	-2.04	0.0000006
Brap	BRCA1 associated protein	49	24	73	-2.04	0.0003043
Sppl3	Signal peptide peptidase 3	43	21	64	-2.04	0.0008223
Gstk1	Glutathione S-transferase kappa 1	79	39	118	-2.02	0.0000063
1810037I17Rik	RIKEN cDNA 1810037I17 gene	412	206	618	-2	0.0000000
Ppm1a	Protein phosphatase 1A, magnesium dependent, alpha isoform	234	117	351	-2	0.0000000
Synpo2l	Synaptopodin 2-like	138	69	207	-2	0.0000000
Bola1	BolA-like 1 (E. coli)	62	31	93	-2	0.0000561
Rnf126	Ring finger protein 126	46	23	69	-2	0.0010210
Clock	Circadian locomoter output cycles kaput	40	20	60	-2	0.0019618
Rpl35	Ribosomal protein L35	381	192	573	-1.98	0.0000000
Lonp2	Lon peptidase 2, peroxisomal	101	51	152	-1.98	0.0000008
Txnip	Thioredoxin interacting protein	978	494	1472	-1.97	0.0000000
Pfn1	Profilin 1	173	88	261	-1.96	0.0000000
Cdc2l1	Cell division cycle 2-like 1	55	28	83	-1.96	0.0003201
Pkd2	Polycystic kidney disease 2	53	27	80	-1.96	0.0004866
Setx	Senataxin	47	24	71	-1.95	0.0009320
Mrpl46	Mitochondrial ribosomal protein L46	43	22	65	-1.95	0.0011668
Rars	Arginyl-tRNA synthetase	72	37	109	-1.94	0.0000490
Bckdhb	Branched chain ketoacid dehydrogenase E1, beta polypeptide	68	35	103	-1.94	0.0000810
Mm.397227	Transcribed locus	118	61	179	-1.93	0.0000002
Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	62	32	94	-1.93	0.0001609
Ckb	Creatine kinase, brain	58	30	88	-1.93	0.0001924
Tmem182	Transmembrane protein 182	237	123	360	-1.92	0.0000000
Tacc1	Transforming, acidic coiled-coil containing protein 1	79	41	120	-1.92	0.0000237
Phf21a	PHD finger protein 21A	54	28	82	-1.92	0.0006385
C030002C11Rik	RIKEN cDNA C030002C11 gene	88	46	134	-1.91	0.0000076
C330023M02Rik	RIKEN cDNA C330023M02 gene	67	35	102	-1.91	0.0000848
Dennd4b	DENN/MADD domain containing 4B	65	34	99	-1.91	0.0001339
Stk24	Serine/threonine kinase 24 (STE20 homolog, yeast)	46	24	70	-1.91	0.0019482
Myot	Myotilin	217	114	331	-1.9	0.0000000
Arhgap26	Rho GTPase activating protein 26	84	44	128	-1.9	0.0000179
Sh2d3c	SH2 domain containing 3C	78	41	119	-1.9	0.0000484
Metapl1	Methionine aminopeptidase-like 1	59	31	90	-1.9	0.0002549
Txnrd2	Thioredoxin reductase 2	72	38	110	-1.89	0.0000875
Spnb1	Spectrin beta 1	105	56	161	-1.87	0.0000022
Slc25a34	Solute carrier family 25, member 34	244	131	375	-1.86	0.0000000
Cyyr1	cysteine/tyrosine-rich 1	56	30	86	-1.86	0.0004036
Sp1	Trans-acting transcription factor 1	43	23	66	-1.86	0.0022599
Ank3	Ankyrin 3, epithelial	91	49	140	-1.85	0.0000123
Tmem34	Transmembrane protein 34	78	42	120	-1.85	0.0000654
Zrsr1	Zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1	65	35	100	-1.85	0.0003351
Rnh1	Ribonuclease/angiogenin inhibitor 1	63	34	97	-1.85	0.0003707
0610010K14Rik	RIKEN cDNA 0610010K14 gene	52	28	80	-1.85	0.0012989
Snrpf	Small nuclear ribonucleoprotein polypeptide F	52	28	80	-1.85	0.0012989
Dctn1	Dynactin 1	92	50	142	-1.84	0.0000157
Acad9	Acyl-Coenzyme A dehydrogenase family, member 9	81	44	125	-1.84	0.0000718
Clcn7	Chloride channel 7	61	33	94	-1.84	0.0004308
Acaa1a	Acetyl-Coenzyme A acyltransferase 1A	61	33	94	-1.84	0.0005793
H13	Histocompatibility 13	48	26	74	-1.84	0.0016758
Nrip1	Nuclear receptor interacting protein 1	48	26	74	-1.84	0.0022630
Setd7	SET domain containing (lysine methyltransferase) 7	66	36	102	-1.83	0.0004252

Atp11c	Atpase, class VI, type 11C	57	31	88	-1.83	0.0007103
2810410M20Rik	RIKEN cDNA 2810410M20 gene	53	29	82	-1.82	0.0012337
Ddx28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	53	29	82	-1.82	0.0012337
Fbxo6	F-box protein 6	51	28	79	-1.82	0.0018344
Glud1	Glutamate dehydrogenase 1	169	93	262	-1.81	0.0000000
Atp1b3	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	78	43	121	-1.81	0.0001113
Mm.429877	Transcribed locus	58	32	90	-1.81	0.0009039
Aldh6a1	Aldehyde dehydrogenase family 6, subfamily A1	374	207	581	-1.8	0.0000000
Mboat5	Membrane bound O-acyltransferase domain containing 5	74	41	115	-1.8	0.0001435
Ehbp1l1	EH domain binding protein 1-like 1	72	40	112	-1.8	0.0001588
Ppp5c	Protein phosphatase 5, catalytic subunit	63	35	98	-1.8	0.0006599
Tns1	Tensin 1	958	534	1492	-1.79	0.0000000
Acox1	Acyl-Coenzyme A oxidase 1, palmitoyl	846	471	1317	-1.79	0.0000000
Oat	Ornithine aminotransferase	167	93	260	-1.79	0.0000000
Tmem111	Transmembrane protein 111	61	34	95	-1.79	0.0007726
Cuta	CutA divalent cation tolerance homolog (E. coli)	61	34	95	-1.79	0.0010222
Rcan1	Regulator of calcineurin 1	73	41	114	-1.78	0.0002010
Acss1	Acyl-CoA synthetase short-chain family member 1	763	430	1193	-1.77	0.0000000
Tbcel	Tubulin folding cofactor E-like	96	54	150	-1.77	0.0000286
A930001N09Rik	RIKEN cDNA A930001N09 gene	62	35	97	-1.77	0.0009690
Ppp2r5d	Protein phosphatase 2, regulatory subunit B (B56), delta isoform	62	35	97	-1.77	0.0012709
Sbf2	SET binding factor 2	55	31	86	-1.77	0.0019634
Fbxo31	F-box protein 31	300	170	470	-1.76	0.0000000
Slc27a1	Solute carrier family 27 (fatty acid transporter), member 1	249	141	390	-1.76	0.0000000
Vamp2	Vesicle-associated membrane protein 2	92	52	144	-1.76	0.0000487
Myo18a	Myosin XVIIIa	76	43	119	-1.76	0.0002272
Mpnd	MPN domain containing	60	34	94	-1.76	0.0014171
Rps29	Ribosomal protein L29	1151	654	1805	-1.75	0.0000000
Acot2	Acyl-CoA thioesterase 2	1059	602	1661	-1.75	0.0000000
Adprhl1	ADP-ribosylhydrolase like 1	259	148	407	-1.75	0.0000000
Lgals1	Lectin, galactose binding, soluble 1	181	103	284	-1.75	0.0000000
Hibadh	3-hydroxyisobutyrate dehydrogenase	177	101	278	-1.75	0.0000000
Psmd2	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	126	72	198	-1.75	0.0000036
Ablim3	Actin binding LIM protein family, member 3	65	37	102	-1.75	0.0010220
Smtn	Smoothelin	110	63	173	-1.74	0.0000162
C130006E23	Hypothetical protein C130006E23	87	50	137	-1.74	0.0001486
Ppp2r5b	Protein phosphatase 2, regulatory subunit B (B56), beta isoform	75	43	118	-1.74	0.0004096
Gys1	Glycogen synthase 1, muscle	137	79	216	-1.73	0.0000023
Tbc1d22a	TBC1 domain family, member 22a	99	57	156	-1.73	0.0000515
Plcb1	Phospholipase C, beta 1	80	46	126	-1.73	0.0002962
Aga	Aspartylglucosaminidase	59	34	93	-1.73	0.0019529
Atp1a2	ATPase, Na+/K+ transporting, beta 3 polypeptide	833	483	1316	-1.72	0.0000000
Coq10a	Coenzyme Q10 homolog A (yeast)	635	368	1003	-1.72	0.0000000
Ash1l	Ash1 (absent, small, or homeotic)-like (Drosophila)	62	36	98	-1.72	0.0015655
Bsdc1	BSD domain containing 1	57	33	90	-1.72	0.0016683
Pnpla2	Patatin-like phospholipase domain containing 2	1275	744	2019	-1.71	0.0000000
9130213B05Rik	RIKEN cDNA 9130213B05 gene	75	44	119	-1.7	0.0005308
Als2cr2	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 (human)	68	40	108	-1.7	0.0010634
Glul	Glutamate-ammonia ligase (glutamine synthetase)	1144	676	1820	-1.69	0.0000000
Rbl2	Retinoblastoma-like 2	95	56	151	-1.69	0.0001432
Dapk1	Death associated protein kinase 1	78	46	124	-1.69	0.0007410
Fabp4	Fatty acid binding protein 4, adipocyte	2366	1401	3767	-1.68	0.0000000
Cpeb3	Cytoplasmic polyadenylation element binding protein 3	222	132	354	-1.68	0.0000000
Pank1	Pantothenate kinase 1	150	89	239	-1.68	0.0000021
Pcyt1a	Phosphate cytidylyltransferase 1, choline, alpha isoform	69	41	110	-1.68	0.0010062
Dbt	Dihydrolipoamide branched chain transacylase E2	287	171	458	-1.67	0.0000000
Mm.468129	Transcribed locus, moderately similar to NP_112605.1 acyl-CoA thioesterase 1 [Rattus norvegicus]	251	150	401	-1.67	0.0000000
Psmd4	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	104	62	166	-1.67	0.0000616
C230096C10Rik	RIKEN cDNA C230096C10 gene	92	55	147	-1.67	0.0002273
Adra1b	Adrenergic receptor, alpha 1b	67	40	107	-1.67	0.0014458

Gcdh	Glutaryl-Coenzyme A dehydrogenase	67	40	107	-1.67	0.0015288
Psap	Prosaposin	153	92	245	-1.66	0.0000036
Gmnn	Geminin	88	53	141	-1.66	0.0003604
Myh6	Myosin, heavy polypeptide 6, cardiac muscle, alpha	11098	6701	17799	-1.65	0.0000000
Ankrd23	Ankyrin repeat domain 23	579	350	929	-1.65	0.0000000
8430408G22Rik	RIKEN cDNA 8430408G22 gene	448	271	719	-1.65	0.0000000
Msrb3	Methionine sulfoxide reductase B3	248	151	399	-1.64	0.0000000
Eif3s10	Eukaryotic translation initiation factor 3, subunit 10 (theta)	155	94	249	-1.64	0.0000030
Slc35e1	Solute carrier family 35, member E1	84	51	135	-1.64	0.0006028
Klf15	Kruppel-like factor 15	82	50	132	-1.64	0.0007126
Wipi2	WD repeat domain, phosphoinositide interacting 2	74	45	119	-1.64	0.0011789
Nnt	Nicotinamide nucleotide transhydrogenase	822	503	1325	-1.63	0.0000000
Cdh5	Cadherin 5	380	233	613	-1.63	0.0000000
Aldh4a1	Aldehyde dehydrogenase 4 family, member A1	180	110	290	-1.63	0.0000008
Popdc2	Popeye domain containing 2	180	110	290	-1.63	0.0000008
Ece1	Endothelin converting enzyme 1	163	100	263	-1.63	0.0000037
Chd4	Chromodomain helicase DNA binding protein 4	124	76	200	-1.63	0.0000562
Zfp771	Zinc finger protein 771	93	57	150	-1.63	0.0004350
Gsk3b	Glycogen synthase kinase-3 beta	75	46	121	-1.63	0.0017763
Dynll2	Dynein light chain LC8-type 2	306	188	494	-1.62	0.0000000
Scamp2	Secretory carrier membrane protein 2	117	72	189	-1.62	0.0000697
Elf2	E74-like factor 2	88	54	142	-1.62	0.0007626
Higd1a	HIG1 domain family, member 1A	321	200	521	-1.6	0.0000000
Zbtb16	Zinc finger and BTB domain containing 16	133	83	216	-1.6	0.0000475
Hspa1b	Heat shock 70kDa protein 1B	119	74	193	-1.6	0.0000975
Abhd1	Abhydrolase domain containing 1	114	71	185	-1.6	0.0001688
Smcr7	Smith-Magenis syndrome chromosome region, candidate 7 homolog (human)	96	60	156	-1.6	0.0004358
Grb10	Growth factor receptor bound protein 10	88	55	143	-1.6	0.0009000
Ogdh	Oxoglutarate dehydrogenase (lipoamide)	643	402	1045	-1.59	0.0000000
Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	495	310	805	-1.59	0.0000000
Tenc1	Tensin like C1 domain-containing phosphatase	430	270	700	-1.59	0.0000000
Lrrc2	Leucine rich repeat containing 2	323	202	525	-1.59	0.0000000
Bicd2	Bicaudal D homolog 2 (Drosophila)	166	104	270	-1.59	0.0000056
Rxra	Retinoid X receptor alpha	163	102	265	-1.59	0.0000086
Calcoco1	Calcium binding and coiled coil domain 1	147	92	239	-1.59	0.0000244
Hagh	Hydroxyacyl glutathione hydrolase	121	76	197	-1.59	0.0001343
Ddx17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	94	59	153	-1.59	0.0004873
4931406P16Rik	RIKEN cDNA 4931406P16 gene	97	61	158	-1.59	0.0005138
Alkbh7	AlkB, alkylation repair homolog 7 (E. coli)	83	52	135	-1.59	0.0013353
Ntn1	Netrin 1	352	222	574	-1.58	0.0000000
Mrpl33	Mitochondrial ribosomal protein L33	257	162	419	-1.58	0.0000000
Nckap1	NCK-associated protein 1	79	50	129	-1.58	0.0020834
Aebp2	AE binding protein 2	104	66	170	-1.57	0.0006201
Arhgap21	Rho GTPase activating protein 21	96	61	157	-1.57	0.0006745
Pex16	Peroxisome biogenesis factor 16	85	54	139	-1.57	0.0014015
Oxct1	3-oxoacid CoA transferase 1	2083	1332	3415	-1.56	0.0000000
2310016E02Rik	RIKEN cDNA 2310016E02 gene	214	137	351	-1.56	0.0000009
Ltbp4	Latent transforming growth factor beta binding protein 4	135	86	221	-1.56	0.0000798
Lamb2	Laminin, beta 2	100	64	164	-1.56	0.0006301
Xpr1	Xenotropic and polytropic retrovirus receptor 1	83	53	136	-1.56	0.0020553
Tnnc1	Troponin C, cardiac/slow skeletal	3209	2068	5277	-1.55	0.0000000
Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3	115	74	189	-1.55	0.0003487
Myh14	Myosin, heavy polypeptide 14	95	61	156	-1.55	0.0008819
H2-Ke6	H2-K region expressed gene 6	95	61	156	-1.55	0.0010857
S3-12	Plasma membrane associated protein, S3-12	404	261	665	-1.54	0.0000000
Rabac1	Rab acceptor 1 (prenylated)	335	217	552	-1.54	0.0000000
Atp6v1f	ATPase, H+ transporting, lysosomal V1 subunit F	105	68	173	-1.54	0.0006800
Mm.403851	Transcribed locus	99	64	163	-1.54	0.0010057
Dyrk1a	Dynein light chain Tctex-type 1	94	61	155	-1.54	0.0014896
Cnksr3	Cnksr family member 3	85	55	140	-1.54	0.0021358

Tsc2	Tuberous sclerosis 2	143	93	236	-1.53	0.0000842
Rbpms	RNA binding protein with multiple splicing	358	235	593	-1.52	0.0000000
Hsp110	Heat shock protein 110	140	92	232	-1.52	0.0001870
Ppm1k	Protein phosphatase 1K (PP2C domain containing)	104	68	172	-1.52	0.0011305
Psme3	Proteaseome (prosome, macropain) 28 subunit, 3	99	65	164	-1.52	0.0014946
Pmpcb	Peptidase (mitochondrial processing) beta	102	67	169	-1.52	0.0015326
Mafk	V-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	90	59	149	-1.52	0.0022781
Lpl	Lipoprotein lipase	12696	8379	21075	-1.51	0.0000000
Hist1h1c	Histone cluster 1, H1c	212	140	352	-1.51	0.0000038
Trak1	Trafficking protein, kinesin binding 1	174	115	289	-1.51	0.0000447
Speg	SPEG complex locus	91	60	151	-1.51	0.0021534
Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	94	62	156	-1.51	0.0022123
OTTMUSG00000008561	Predicted gene, OTTMUSG00000008561	184	122	306	-1.5	0.0000234
Obscn	Obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	955	640	1595	-1.49	0.0000000
Nploc4	Nuclear protein localization 4 homolog (S. cerevisiae)	109	73	182	-1.49	0.0014307
Nrap	Nebulin-related anchoring protein	666	447	1113	-1.48	0.0000000
Eif2s2	Eukaryotic translation initiation factor 2, subunit 2 (beta)	287	193	480	-1.48	0.0000003
Ankrd17	Ankyrin repeat domain 17	221	149	370	-1.48	0.0000078
Pccb	Propionyl Coenzyme A carboxylase, beta polypeptide	212	143	355	-1.48	0.0000111
Adhfe1	Alcohol dehydrogenase, iron containing, 1	183	123	306	-1.48	0.0000507
Cpt1a	Carnitine palmitoyltransferase 1a, liver	174	117	291	-1.48	0.0000508
Ola1	Obg-like ATPase 1	153	103	256	-1.48	0.0001636
Flnc	Filamin C, gamma (actin binding protein 280)	154	104	258	-1.48	0.0001854
Tfdp2	Transcription factor Dp 2	131	88	219	-1.48	0.0004682
Tom1l2	Target of myb1-like 2 (chicken)	135	91	226	-1.48	0.0005393
Ubr5	Ubiquitin protein ligase E3 component n-recognin 5	104	70	174	-1.48	0.0015671
Hes1	Hairy and enhancer of split 1 (Drosophila)	107	72	179	-1.48	0.0015982
Itga7	Integrin alpha 7	111	75	186	-1.48	0.0017439
Hadha	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	1667	1127	2794	-1.47	0.0000000
Malat1	Metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	710	481	1191	-1.47	0.0000000
Bckdha	Branched chain ketoacid dehydrogenase E1, alpha polypeptide	701	475	1176	-1.47	0.0000000
Lmo7	LIM domain only 7	378	256	634	-1.47	0.0000000
Canx	Calnexin	355	241	596	-1.47	0.0000000
Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1	305	207	512	-1.47	0.0000002
AI314180	Expressed sequence AI314180	284	192	476	-1.47	0.0000006
Hhatl	Hedgehog acyltransferase-like	228	155	383	-1.47	0.0000102
Enah	Enabled homolog (Drosophila)	201	136	337	-1.47	0.0000222
Ttc7b	Tetratricopeptide repeat domain 7B	176	119	295	-1.47	0.0000652
Smad4	MAD homolog 4 (Drosophila)	159	108	267	-1.47	0.0001601
Mgea5	Meningioma expressed antigen 5 (hyaluronidase)	159	108	267	-1.47	0.0001908
Tnrc6a	Trinucleotide repeat containing 6A	147	100	247	-1.47	0.0003593
Slc6a6	Solute carrier family 6 (neurotransmitter transporter, taurine), member 6	140	95	235	-1.47	0.0004647
AI467657	Expressed sequence AI467657	139	94	233	-1.47	0.0004906
Lypla2	Lysophospholipase 2	106	72	178	-1.47	0.0020277
Ankrd1	Ankyrin repeat domain 1 (cardiac muscle)	4962	3379	8341	-1.46	0.0000000
Acadvl	Acyl-Coenzyme A dehydrogenase, very long chain	867	593	1460	-1.46	0.0000000
Ablim1	Actin-binding LIM protein 1	411	281	692	-1.46	0.0000000
Slc43a3	Solute carrier family 4 (anion exchanger), member 3	211	144	355	-1.46	0.0000246
Timp4	Tissue inhibitor of metalloproteinase 4	182	124	306	-1.46	0.0000756
Lyrm5	LYR motif containing 5	126	86	212	-1.46	0.0011674
Pnpla7	Patatin-like phospholipase domain containing 7	119	81	200	-1.46	0.0015163
Hrc	Histidine rich calcium binding protein	463	318	781	-1.45	0.0000000
Luc7l2	LUC7-like 2 (S. cerevisiae)	248	170	418	-1.45	0.0000056
Sar1a	SAR1 gene homolog A (S. cerevisiae)	188	129	317	-1.45	0.0000732
1700081L11Rik	RIKEN cDNA 1700081L11 gene	156	107	263	-1.45	0.0003331
Timm17a	Translocase of inner mitochondrial membrane 17a	153	105	258	-1.45	0.0003910
Pitrm1	Pitrilysin metallepetidase 1	148	102	250	-1.45	0.0004551
Zfp664	Zinc finger protein 664	119	82	201	-1.45	0.0021353
Ech1	Enoyl coenzyme A hydratase 1, peroxisomal	2289	1583	3872	-1.44	0.0000000

Clint1	Clathrin interactor 1	239	165	404	-1.44	0.0000095
Limch1	LIM and calponin homology domains 1	197	136	333	-1.44	0.0000675
Snw1	SNW domain containing 1	139	96	235	-1.44	0.0008208
Tra2a	Transformer 2 alpha homolog (Drosophila)	130	90	220	-1.44	0.0012528
Ube3b	Ubiquitin protein ligase E3B	123	85	208	-1.44	0.0019273
S100a1	S100 calcium binding protein A1	1268	885	2153	-1.43	0.0000000
Son	Son cell proliferation protein	378	264	642	-1.43	0.0000001
2310061I04Rik	RIKEN cDNA 2310061I04 gene	308	215	523	-1.43	0.0000013
Tcea3	Transcription elongation factor A (SII), 3	256	178	434	-1.43	0.0000076
Nrp1	Neuropilin 1	206	144	350	-1.43	0.0001048
Sparcl1	SPARC-like 1 (mast9, hevin)	634	445	1079	-1.42	0.0000000
Vegfb	Vascular endothelial growth factor B	497	348	845	-1.42	0.0000000
Vldlr	Very low density lipoprotein receptor	451	317	768	-1.42	0.0000000
Atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C	308	216	524	-1.42	0.0000018
Rpl11	Ribosomal protein L11	231	162	393	-1.42	0.0000416
Zmynd11	Zinc finger, MYND domain containing 11	168	118	286	-1.42	0.0004964
Slc2a4	Solute carrier family 2 (facilitated glucose transporter), member 4	147	103	250	-1.42	0.0007902
Emp2	Epithelial membrane protein 2	140	98	238	-1.42	0.0012733
Pgcp	Plasma glutamate carboxypeptidase	131	92	223	-1.42	0.0018436
Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	4078	2887	6965	-1.41	0.0000000
Ctsd	Cathepsin D	1797	1269	3066	-1.41	0.0000000
Mybpc3	Myosin binding protein C, cardiac	1161	823	1984	-1.41	0.0000000
D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	425	300	725	-1.41	0.0000000
Flii	Flightless I homolog (Drosophila)	139	98	237	-1.41	0.0013426
Saps1	SAPS domain family, member 1	132	93	225	-1.41	0.0020509
Sesn1	Sestrin 1	388	276	664	-1.4	0.0000003
Acacb	Acetyl-Coenzyme A carboxylase beta	287	205	492	-1.4	0.0000098
Phb2	Prohibitin 2	236	168	404	-1.4	0.0000562
Mrps12	Mitochondrial ribosomal protein S12	220	157	377	-1.4	0.0001271
Ewsr1	Ewing sarcoma breakpoint region 1	194	138	332	-1.4	0.0002515
9430029L20Rik	RIKEN cDNA A630084N20 gene	185	132	317	-1.4	0.0004420
Mm.415917	Transcribed locus	175	125	300	-1.4	0.0005757
2310003F16Rik	RIKEN cDNA 2310003F16 gene	160	114	274	-1.4	0.0009254
Herpud1	Homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	1069	764	1833	-1.39	0.0000000
Cyb5	Cytochrome b-5	1010	725	1735	-1.39	0.0000000
Igfbp7	Insulin-like growth factor binding protein 7	581	416	997	-1.39	0.0000000
Hnrnpl	Heterogeneous nuclear ribonucleoprotein L	295	211	506	-1.39	0.0000097
Sult1a1	Sulfotransferase family 1A, phenol-preferring, member 1	279	200	479	-1.39	0.0000188
Mrpl44	Mitochondrial ribosomal protein L44	235	168	403	-1.39	0.0000796
Ube2s	Ubiquitin-conjugating enzyme E2S	192	138	330	-1.39	0.0003758
Msn	Moesin	177	127	304	-1.39	0.0007001
Ndg2	Nur77 downstream gene 2	2959	2143	5102	-1.38	0.0000000
Golga4	Golgi autoantigen, golgin subfamily a, 4	581	419	1000	-1.38	0.0000000
Selenbp1	Selenium binding protein 1	276	200	476	-1.38	0.0000335
Cugbp2	CUG triplet repeat, RNA binding protein 2	265	191	456	-1.38	0.0000362
Taok1	TAO kinase 1	191	138	329	-1.38	0.0005294
Tmtc1	Transmembrane and tetratricopeptide repeat containing 1	143	103	246	-1.38	0.0022426
Art1	ADP-ribosyltransferase 1	332	241	573	-1.37	0.0000070
Glg1	Golgi apparatus protein 1	283	206	489	-1.37	0.0000344
Smpd1	Sphingomyelin phosphodiesterase 1, acid lysosomal	222	161	383	-1.37	0.0001952
Plaa	Phospholipase A2, activating protein	233	170	403	-1.37	0.0002065
Rdx	Radixin	196	143	339	-1.37	0.0008328
Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	183	133	316	-1.37	0.0008759
Serpine1	Serine (or cysteine) peptidase inhibitor, clade E, member 1	169	123	292	-1.37	0.0012792
C130038G02Rik	RIKEN cDNA C130038G02 gene	171	124	295	-1.37	0.0013337
Fus	Fusion, derived from t(12;16) malignant liposarcoma (human)	155	113	268	-1.37	0.0022733
Rps9	Ribosomal protein S9	1101	806	1907	-1.36	0.0000000
Echs1	Enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	282	206	488	-1.36	0.0000414
Arpc2	Actin related protein 2/3 complex, subunit 2	260	190	450	-1.36	0.0001177
Maea	Macrophage erythroblast attacher	237	173	410	-1.36	0.0002231

D830007F02Rik	RIKEN cDNA D830007F02 gene	236	173	409	-1.36	0.0002343
Fxr2	Fragile X mental retardation, autosomal homolog 2	177	130	307	-1.36	0.0014300
Nfia	Nuclear factor I/A	172	126	298	-1.36	0.0016792
Nfic	Nuclear factor I/C (CCAAT-binding transcription factor)	169	124	293	-1.36	0.0019501
Vim	Vimentin	165	121	286	-1.36	0.0021799
Sorbs1	Sorbin and SH3 domain containing 1	2384	1760	4144	-1.35	0.0000000
Idh3b	Isocitrate dehydrogenase 3 (NAD+) beta	1143	846	1989	-1.35	0.0000000
Nfib	Nuclear factor I/B	501	370	871	-1.35	0.0000002
Tmem38a	Transmembrane protein 38A	373	276	649	-1.35	0.0000073
Hint1	Histidine triad nucleotide binding protein 1	316	233	549	-1.35	0.0000300
Eif4h	Eukaryotic translation initiation factor 4H	311	230	541	-1.35	0.0000454
Capzb	Capping protein (actin filament) muscle Z-line, beta	247	182	429	-1.35	0.0002131
Pdk4	Pyruvate dehydrogenase kinase, isoenzyme 4	5085	3791	8876	-1.34	0.0000000
Gsto1	Glutathione S-transferase omega 1	736	549	1285	-1.34	0.0000000
Dag1	Dystroglycan 1	420	313	733	-1.34	0.0000037
D930001I22Rik	RIKEN cDNA D930001I22 gene	303	226	529	-1.34	0.0000695
Kcnk3	Potassium channel, subfamily K, member 3	302	225	527	-1.34	0.0000764
Snx3	Sorting nexin 3	272	202	474	-1.34	0.0001440
Phyhd1	Phytanoyl-CoA dioxygenase domain containing 1	235	175	410	-1.34	0.0004187
Psmd7	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	221	164	385	-1.34	0.0006415
Slc4a3	Solute carrier family 4, anion exchanger, member 3	224	167	391	-1.34	0.0006860
Zcrb1	Zinc finger CCHC-type and RNA binding motif 1	179	133	312	-1.34	0.0018543
Cpt1b	Carnitine palmitoyltransferase 1b, muscle	762	569	1331	-1.33	0.0000000
Egln1	EGL nine homolog 1 (C. elegans)	593	443	1036	-1.33	0.0000000
Xirp2	Xin actin-binding repeat containing 2	361	271	632	-1.33	0.0000244
Acads	Acyl-Coenzyme A dehydrogenase, short chain	190	142	332	-1.33	0.0019003
Ahnak	AHNAK nucleoprotein (desmoyokin)	786	592	1378	-1.32	0.0000000
Mm.401817	Transcribed locus	549	414	963	-1.32	0.0000003
Me1	Malic enzyme 1, NADP(+)-dependent, cytosolic	497	376	873	-1.32	0.0000015
Sgcg	Sarcoglycan, gamma (dystrophin-associated glycoprotein)	463	350	813	-1.32	0.0000031
Pnpla8	Patatin-like phospholipase domain containing 8	247	187	434	-1.32	0.0007579
Bloc1s1	Biogenesis of lysosome-related organelles complex-1, subunit 1	211	159	370	-1.32	0.0016625
Crry	Complement receptor related protein	204	154	358	-1.32	0.0018923
Wnk1	WNK lysine deficient protein kinase 1	200	151	351	-1.32	0.0021167
Tnnt2	Troponin T2, cardiac	5751	4381	10132	-1.31	0.0000000
Cpt2	Carnitine palmitoyltransferase 2	434	331	765	-1.31	0.0000117
Clip4	CAP-GLY domain containing linker protein family, member 4	385	293	678	-1.31	0.0000308
Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	270	205	475	-1.31	0.0004488
Ttn	Tubulin tyrosine ligase-like 1	3876	2967	6843	-1.3	0.0000000
Peci	Peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	711	545	1256	-1.3	0.0000000
Txlnb	Taxilin beta	714	548	1262	-1.3	0.0000001
Mm.415233	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530001O10 product:unclassifiable, full insert sequence	319	244	563	-1.3	0.0001796
Tcf4	Transcription factor 4	309	236	545	-1.3	0.0002177
Aadacl1	Arylacetamide deacetylase-like 1	246	188	434	-1.3	0.0010075
Ubr2	Ubiquitin protein ligase E3 component n-recognin 2	241	184	425	-1.3	0.0010467
Psmd3	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	238	182	420	-1.3	0.0012014
Cd36	CD36 antigen	2910	2242	5152	-1.29	0.0000000
Spnb2	spectrin beta 2	625	482	1107	-1.29	0.0000005
Serpinb6b	Serine (or cysteine) peptidase inhibitor, clade B, member 6b	417	321	738	-1.29	0.0000316
Sfrs2	Splicing factor, arginine/serine-rich 2 (SC-35)	391	301	692	-1.29	0.0000563
Mtus1	Mitochondrial tumor suppressor 1	360	279	639	-1.29	0.0002026
Klf9	Kruppel-like factor 9	271	209	480	-1.29	0.0010800
Rnaset2a	Ribonuclease T2A	248	191	439	-1.29	0.0016379
Clu	Clusterin	713	555	1268	-1.28	0.0000002
Trim54	Tripartite motif-containing 54	582	453	1035	-1.28	0.0000027
Rab14	RAB14, member RAS oncogene family	404	315	719	-1.28	0.0001037
Ppif	Peptidylprolyl isomerase F (cyclophilin F)	335	261	596	-1.28	0.0004311
D10Wsu52e	DNA segment, Chr 10, Wayne State University 52, expressed	313	243	556	-1.28	0.0004318
Fkbp4	FK506 binding protein 4	258	201	459	-1.28	0.0020852

Tacc2	Transforming, acidic coiled-coil containing protein 2	1975	1549	3524	-1.27	0.0000000
Ehd4	EH-domain containing 4	1030	806	1836	-1.27	0.0000000
Myom1	Myomesin 1	1013	794	1807	-1.27	0.0000000
Hdlbp	High density lipoprotein (HDL) binding protein	668	522	1190	-1.27	0.0000007
BC005537	CDNA sequence BC005537	435	342	777	-1.27	0.0000973
Plekhc1	Pleckstrin homology domain containing, family C (with FERM domain) member 1	394	309	703	-1.27	0.0001721
Slc25a39	Solute carrier family 25, member 39	324	257	581	-1.26	0.0010810
Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	1062	847	1909	-1.25	0.0000000
Ces3	Carboxylesterase 3	354	281	635	-1.25	0.0007619
Des	Desmin	3843	3093	6936	-1.24	0.0000000
Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	787	632	1419	-1.24	0.0000017
Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	633	509	1142	-1.24	0.0000229
Nhsl1	NHS-like 1	1720	1395	3115	-1.23	0.0000000
Eef1a2	Eukaryotic translation elongation factor 1 alpha 2	1659	1343	3002	-1.23	0.0000000
Myl7	Myosin, light polypeptide 7, regulatory	816	659	1475	-1.23	0.0000022
Bag3	Bcl2-associated athanogene 3	682	554	1236	-1.23	0.0000274
Pfkm	Phosphofructokinase, muscle	407	329	736	-1.23	0.0008667
Mm.412722	Transcribed locus	398	323	721	-1.23	0.0013215
Ldhb	Lactate dehydrogenase B	5358	4361	9719	-1.22	0.0000000
Pcbp2	Poly(rC) binding protein 2	1164	949	2113	-1.22	0.0000001
Etfdh	Electron transferring flavoprotein, dehydrogenase	3369	2767	6136	-1.21	0.0000000
Hexb	hexosaminidase B (beta polypeptide)	3116	2561	5677	-1.21	0.0000000
Ndrg2	N-myc downstream regulated gene 2	1428	1177	2605	-1.21	0.0000000
Actn2	Actinin alpha 2	1264	1041	2305	-1.21	0.0000001
Nppa	Natriuretic peptide precursor type A	978	804	1782	-1.21	0.0000020
Lbh	Limb-bud and heart	738	607	1345	-1.21	0.0000373
App	Amyloid beta (A4) precursor protein	677	556	1233	-1.21	0.0000720
Trdn	Triadin	568	468	1036	-1.21	0.0003321
Pdk2	Pyruvate dehydrogenase kinase, isoenzyme 2	544	449	993	-1.21	0.0005750
Prei4	Preimplantation protein 4	422	346	768	-1.21	0.0014866
Sucla2	Succinate-Coenzyme A ligase, ADP-forming, beta subunit	422	346	768	-1.21	0.0014866
Pja2	Praja 2, RING-H2 motif containing	404	332	736	-1.21	0.0021989
Fth1	Ferritin heavy chain 1	9825	8148	17973	-1.2	0.0000000
Nola3	Nucleolar protein family A, member 3	635	529	1164	-1.2	0.0003666
Mm.445729	Transcribed locus, moderately similar to XP_001082071.1 similar to NADH-ubiquinone oxidoreductase chain 1 (NADH dehydrogenase subunit 1) [Macaca mulatta]	8032	6743	14775	-1.19	0.0000000
Kif5b	Kinesin family member 5B	715	598	1313	-1.19	0.0002260
Sorbs2	Sorbin and SH3 domain containing 2	671	560	1231	-1.19	0.0002727
Slc25a20	Solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20	501	418	919	-1.19	0.0018187
Pde4dip	Phosphodiesterase 4D interacting protein (myomegalin)	1952	1656	3608	-1.17	0.0000000
C1qbp	Complement component 1, q subcomponent binding protein	661	562	1223	-1.17	0.0013356
Sdha	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	2001	1712	3713	-1.16	0.0000001
1500032D16Rik	RIKEN cDNA 1500032D16 gene	1711	1487	3198	-1.15	0.0000080
Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	1475	1273	2748	-1.15	0.0000138
Uqcrc1	Ubiquinol-cytochrome c reductase core protein 1	3024	2648	5672	-1.14	0.0000000
Got1	Glutamate oxaloacetate transaminase 1, soluble	2770	2417	5187	-1.14	0.0000000
Uqcrc2	Ubiquinol cytochrome c reductase core protein 2	2036	1776	3812	-1.14	0.0000023
Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	1847	1615	3462	-1.14	0.0000099
Serinc1	Serine incorporator 1	1246	1084	2330	-1.14	0.0001578
Cabc1	Chaperone, ABC1 activity of bc1 complex like (S. pombe)	855	746	1601	-1.14	0.0020589
Idh2	Isocitrate dehydrogenase 2 (NADP+), mitochondrial	7034	6193	13227	-1.13	0.0000000
Uba52	Ubiquitin A-52 residue ribosomal protein fusion product 1	5043	4473	9516	-1.12	0.0000000
Ndufa11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	1188	1056	2244	-1.12	0.0020218
Mm.450207	Transcribed locus, strongly similar to XP_001083687.1 similar to guanine nucleotide binding protein, alpha stimulating activity polypeptide 1 isoform c isoform 5 [Macaca mulatta]	60328	53892	114220	-1.11	0.0000000
Mm.458391	CDNA clone IMAGE:3582855	61476	55335	116811	-1.11	0.0000000
Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	1428	1277	2705	-1.11	0.0012964
Cox5a	Cytochrome c oxidase, subunit Va	10008	9112	19120	-1.09	0.0000000
Mdh1	Malate dehydrogenase 1, NAD (soluble)	8665	7896	16561	-1.09	0.0000000
Ldb3	LIM domain binding 3	2579	2345	4924	-1.09	0.0003162
Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	7015	6539	13554	-1.07	0.0000221

Mm.384744	Transcribed locus, weakly similar to NP_149931.1 dehydrogenase subunit 1 [Trichosurus vulpecula]	30097	28966	59063	-1.03	0.0000352
Hist1h1e	Histone cluster 1, H1e	8	0	8	0	0.0001520
4633401B06Rik	RIKEN cDNA 2810453I06 gene	7	0	7	0	0.0003924
Rfc5	Replication factor C (activator 1) 5	6	0	6	0	0.0010131
Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	22324	22712	45036	1.01	0.0004510
Mm.455357	Osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420007J21 product:unclassifiable, full insert sequence	22977	24255	47232	1.05	0.0000000
2900073G15Rik	RIKEN cDNA 2900073G15 gene	4281	4501	8782	1.05	0.0006374
Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	4596	4898	9494	1.06	0.0000144
Uqcr	Ubiquinol-cytochrome c reductase (6.4kD) subunit	4888	5287	10175	1.08	0.0000001
Aco2	Aconitase 2, mitochondrial	3320	3596	6916	1.08	0.0000063
Laptm4a	Lysosomal-associated protein transmembrane 4A	1641	1780	3421	1.08	0.0012611
Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	4556	4991	9547	1.09	0.0000000
Slc25a4	Solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	16696	18493	35189	1.1	0.0000000
Ivns1abp	Influenza virus NS1A binding protein	1688	1863	3551	1.1	0.0000927
Dcn	Decorin	1430	1575	3005	1.1	0.0004214
Mm.441437	CDNA clone IMAGE:40049146	414361	460800	875161	1.11	0.0000000
Ckmt2	Creatine kinase, mitochondrial 2	6978	7832	14810	1.12	0.0000000
Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	1609	1818	3427	1.12	0.0000031
Sdhb	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	1697	1902	3599	1.12	0.0000077
Pdlim5	Enigma-like PDZ and LIM domains protein	983	1109	2092	1.12	0.0003352
Atp5b	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	9401	10694	20095	1.13	0.0000000
Sepp1	Selenoprotein P, plasma, 1	1263	1429	2692	1.13	0.0000305
Rac1	RAS-related C3 botulinum substrate 1	906	1029	1935	1.13	0.0002777
Rps5	Ribosomal protein S5	830	944	1774	1.13	0.0004424
Tmsb4x	Thymosin, beta 4, X chromosome	724	823	1547	1.13	0.0010391
Rps10	Ribosomal protein S10	715	813	1528	1.13	0.0011205
Slmap	Sarcolemma associated protein	781	898	1679	1.14	0.0002291
D10Jhu81e	DNA segment, Chr 10, Johns Hopkins University 81 expressed	646	738	1384	1.14	0.0013710
Tmem109	Transmembrane protein 109	569	653	1222	1.14	0.0017870
Uqcrq	Ubiquinol-cytochrome c reductase, complex III subunit VII	5061	5850	10911	1.15	0.0000000
Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	1118	1290	2408	1.15	0.0000060
Prnp	Prion protein	606	698	1304	1.15	0.0010408
Cox5b	Cytochrome c oxidase, subunit Vb	1401	1633	3034	1.16	0.0000001
Paip2	Polyadenylate-binding protein-interacting protein 2	581	677	1258	1.16	0.0005148
Mm.458030	Transcribed locus, weakly similar to XP_001098128.1 corticosteroid binding globulin isoform 2 [Macaca mulatta]	84387	98925	183312	1.17	0.0000000
Timp3	Tissue inhibitor of metalloproteinase 3	960	1132	2092	1.17	0.0000016
Pgk1	Phosphoglycerate kinase 1	803	944	1747	1.17	0.0000161
Eef1g	Eukaryotic translation elongation factor 1 gamma	694	812	1506	1.17	0.0001011
Deb1	Differentially expressed in B16F10 1	553	649	1202	1.17	0.0004039
Chpt1	Choline phosphotransferase 1	540	635	1175	1.17	0.0004086
Sln	Sarcolipin	455	535	990	1.17	0.0012078
Srp14	Signal recognition particle 14	604	713	1317	1.18	0.0001210
Ly6c1	Lymphocyte antigen 6 complex, locus C1	505	597	1102	1.18	0.0003692
Prdx6	Peroxiredoxin 6	404	478	882	1.18	0.0013616
Fabp3	Fatty acid binding protein 3, muscle and heart	12502	14978	27480	1.19	0.0000000
Rpl32	Ribosomal protein L32	1385	1650	3035	1.19	0.0000000
Psma2	Proteasome (prosome, macropain) subunit, alpha type 2	587	702	1289	1.19	0.0000438
Lamp2	Lysosomal-associated membrane protein 2	539	644	1183	1.19	0.0001103
Sord	Sorbitol dehydrogenase	463	551	1014	1.19	0.0004975
Ugp2	UDP-glucose pyrophosphorylase 2	403	481	884	1.19	0.0008363
Pln	Phospholamban	13426	16119	29545	1.2	0.0000000
Cox7b	cytochrome c oxidase subunit 7B, mitochondrial	6247	7539	13786	1.2	0.0000000
2010107E04Rik	RIKEN cDNA 2010107E04 gene	4411	5297	9708	1.2	0.0000000
Grinl1a	Glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	543	653	1196	1.2	0.0000489
Mm.455364	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230350D20 product:unclassifiable, full insert sequence	8806	10698	19504	1.21	0.0000000
Tpm1	Tropomyosin 1, alpha	5885	7178	13063	1.21	0.0000000
Shfm1	Split hand/foot malformation (ectrodactyly) type 1	1009	1222	2231	1.21	0.0000000
Mm.458422	Transcribed locus, weakly similar to NP_042565.1 dehydrogenase subunit 4 [Chlamydomonas reinhardtii]	876	1062	1938	1.21	0.0000001
Drr1	Developmentally regulated repeat element-containing transcript 1	570	691	1261	1.21	0.0000154

Apobec2	Apolipoprotein B editing complex 2	367	446	813	1.21	0.0004820
Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	349	423	772	1.21	0.0006887
Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	3196	3914	7110	1.22	0.0000000
Cpe	Carboxypeptidase E	380	464	844	1.22	0.0002817
Txnl1	Thioredoxin-like 1	271	333	604	1.22	0.0015049
Kpna4	Karyopherin (importin) alpha 4	249	306	555	1.22	0.0021976
Prkar1a	Protein kinase, cAMP dependent regulatory, type I, alpha	456	561	1017	1.23	0.0000317
Uqcrfs1	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	1753	2178	3931	1.24	0.0000000
Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	1461	1814	3275	1.24	0.0000000
Art3	ADP-ribosyltransferase 3	842	1052	1894	1.24	0.0000000
Smyd1	SET and MYND domain containing 1	414	514	928	1.24	0.0000336
Cops4	COP9 constitutive photomorphogenic homolog subunit 4	254	316	570	1.24	0.0010555
Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	691	868	1559	1.25	0.0000000
0610008C08Rik	RIKEN cDNA 0610008C08 gene	495	621	1116	1.25	0.0000023
B2m	Beta-2 microglobulin	362	453	815	1.25	0.0000665
Lypla1	Lysophospholipase 1	330	414	744	1.25	0.0001083
Cdc42	Cell division cycle 42 homolog (S. cerevisiae)	282	354	636	1.25	0.0003708
Mm.429298	Transcribed locus	264	332	596	1.25	0.0004811
Chchd7	Coiled-coil-helix-coiled-coil-helix domain containing 7	264	331	595	1.25	0.0005273
Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	251	316	567	1.25	0.0005935
H2-K1	Histocompatibility 2, K1, K region	519	659	1178	1.26	0.0000003
Mm.395009	Transcribed locus, moderately similar to XP_001086547.1 mitochondrial trifunctional protein, beta subunit [Macaca mulatta]	461	583	1044	1.26	0.0000023
Ccng1	Cyclin G1	1058	1350	2408	1.27	0.0000000
Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	704	896	1600	1.27	0.0000000
Car14	Carbonic anhydrase 14	299	381	680	1.27	0.0000815
Mcfd2	Multiple coagulation factor deficiency 2	253	323	576	1.27	0.0002672
Gm561	Gene model 561, (NCBI)	255	324	579	1.27	0.0003690
Rpl14	Ribosomal protein L14	526	678	1204	1.28	0.0000000
Serpinb6a	Serine (or cysteine) peptidase inhibitor, clade B, member 6a	235	302	537	1.28	0.0003025
Eif3k	Eukaryotic translation initiation factor 3, subunit K	207	265	472	1.28	0.0008681
Bag2	Bcl2-associated athanogene 2	176	227	403	1.28	0.0014949
Usmg5	Upregulated during skeletal muscle growth 5	9100	11754	20854	1.29	0.0000000
Ghitm	Growth hormone inducible transmembrane protein	1098	1422	2520	1.29	0.0000000
Ensa	Endosulfine alpha	624	808	1432	1.29	0.0000000
Mrpl12	Mitochondrial ribosomal protein L12	199	257	456	1.29	0.0006420
Phyh	Phytanoyl-CoA hydroxylase	1704	2223	3927	1.3	0.0000000
Them2	Thioesterase superfamily member 2	746	975	1721	1.3	0.0000000
Rab18	RAB18, member RAS oncogene family	415	542	957	1.3	0.0000003
Sf3b1	Splicing factor 3b, subunit 1	337	440	777	1.3	0.0000038
Fech	Ferrochelatase	299	389	688	1.3	0.0000206
Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	147	192	339	1.3	0.0019728
Prdx5	Peroxiredoxin 5	672	883	1555	1.31	0.0000000
Vdac3	Voltage-dependent anion channel 3	620	817	1437	1.31	0.0000000
Mrpl54	Mitochondrial ribosomal protein L54	260	341	601	1.31	0.0000449
Mm.380875	Transcribed locus	241	316	557	1.31	0.0000775
Stx4a	Syntaxin 4A (placental)	171	225	396	1.31	0.0007260
2310003L22Rik	RIKEN cDNA 2310003L22 gene	171	225	396	1.31	0.0008087
Pcbd2	Pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	151	200	351	1.32	0.0010326
Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	838	1117	1955	1.33	0.0000000
Rabgap1l	RAB GTPase activating protein 1-like	207	277	484	1.33	0.0000771
Dpt	Dermatopontin	212	283	495	1.33	0.0000771
Acta2	Actin, alpha 2, smooth muscle, aorta	148	198	346	1.33	0.0009772
Mrpl13	Mitochondrial ribosomal protein L13	568	764	1332	1.34	0.0000000
Arl6ip5	ADP-ribosylation factor-like 6 interacting protein 5	198	267	465	1.34	0.0000751
Fuca2	Fucosidase, alpha-L- 2, plasma	196	264	460	1.34	0.0000793
Nit2	Nitrilase family, member 2	128	172	300	1.34	0.0015341
Ndufab1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	1784	2424	4208	1.35	0.0000000
Dohh	Deoxyhypusine hydroxylase/monooxygenase	243	329	572	1.35	0.0000074
Lsmd1	LSM domain containing 1	210	285	495	1.35	0.0000261

Smyd2	SET and MYND domain containing 2	204	276	480	1.35	0.0000419
2310056P07Rik	RIKEN cDNA 2310056P07 gene	624	849	1473	1.36	0.0000000
Cryab	Crystallin, alpha B	542	741	1283	1.36	0.0000000
Hccs	Holocytochrome c synthetase	325	444	769	1.36	0.0000001
0610012G03Rik	RIKEN cDNA 0610012G03 gene	183	250	433	1.36	0.0000575
Gata6	GATA binding protein 6	179	244	423	1.36	0.0000796
Atp5g3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 3	13417	18434	31851	1.37	0.0000000
2310028O11Rik	RIKEN cDNA 2310028O11 gene	1347	1857	3204	1.37	0.0000000
Dstn	Destrin	426	587	1013	1.37	0.0000000
Rnf128	Ring finger protein 128	125	172	297	1.37	0.0007105
Rxrg	Retinoid X receptor gamma	108	149	257	1.37	0.0016458
Atpif1	ATPase inhibitory factor 1	1024	1421	2445	1.38	0.0000000
Hspb8	Heat shock protein 8	470	650	1120	1.38	0.0000000
Hmgn1	High mobility group nucleosomal binding domain 1	212	293	505	1.38	0.0000096
Ipo7	Importin 7	309	431	740	1.39	0.0000000
Bcl2l13	BCL2-like 13 (apoptosis facilitator)	271	378	649	1.39	0.0000002
Calm2	Calmodulin 2	197	275	472	1.39	0.0000101
Thbd	Thrombomodulin	166	232	398	1.39	0.0000491
Usp14	Ubiquitin specific peptidase 14	152	212	364	1.39	0.0000937
2410006H16Rik	RIKEN cDNA 2410006H16 gene	115	160	275	1.39	0.0008553
Coq10b	Coenzyme Q10 homolog B (S. cerevisiae)	294	413	707	1.4	0.0000000
Smpx	Small muscle protein, X-linked	202	284	486	1.4	0.0000049
Vps26a	Vacuolar protein sorting 26 homolog A (yeast)	149	210	359	1.4	0.0000761
Ccng2	Cyclin G2	113	159	272	1.4	0.0006113
Tnni3	Troponin I, cardiac	8417	11937	20354	1.41	0.0000000
Slc25a5	Solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	930	1313	2243	1.41	0.0000000
Tspo	Translocator protein	294	415	709	1.41	0.0000000
Mrpl23	Mitochondrial ribosomal protein L23	154	218	372	1.41	0.0000415
5730437N04Rik	RIKEN cDNA 2310061I04 gene	134	189	323	1.41	0.0001473
Glrx	Glutaredoxin	105	151	256	1.43	0.0004096
Lum	Lumican	249	359	608	1.44	0.0000000
Myl2	Myosin, light polypeptide 2, regulatory, cardiac, slow	4674	6793	11467	1.45	0.0000000
Fhl2	Four and a half LIM domains 2	3404	4944	8348	1.45	0.0000000
Tmem50b	Transmembrane protein 50B	106	154	260	1.45	0.0002674
Txnrd1	Thioredoxin reductase 1	196	287	483	1.46	0.0000003
5730536A07Rik	RIKEN cDNA 2310056P07 gene	128	187	315	1.46	0.0000419
Capns1	Calpain, small subunit 1	96	141	237	1.46	0.0003565
Asph	Aspartate-beta-hydroxylase	244	361	605	1.47	0.0000000
Tmbim4	Transmembrane BAX inhibitor motif containing 4	191	282	473	1.47	0.0000003
Spcs1	Signal peptidase complex subunit 1 homolog (S. cerevisiae)	132	195	327	1.47	0.0000196
Atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	109	161	270	1.47	0.0000957
Psmb5	Proteasome (prosome, macropain) subunit, beta type 5	806	1196	2002	1.48	0.0000000
Ndufc2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	639	950	1589	1.48	0.0000000
Kremen1	Kringle containing transmembrane protein 1	285	422	707	1.48	0.0000000
Ube2e1	Ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog (yeast)	152	226	378	1.48	0.0000024
0610009B22Rik	RIKEN cDNA 0610009B22 gene	110	163	273	1.48	0.0000612
Psmb6	Proteasome (prosome, macropain) subunit, beta type 6	105	156	261	1.48	0.0001153
2610001J05Rik	RIKEN cDNA 2610001J05 gene	95	141	236	1.48	0.0002337
Ppp1ca	Protein phosphatase 1, catalytic subunit, alpha isoform	417	622	1039	1.49	0.0000000
Map2k1ip1	Mitogen-activated protein kinase kinase 1 interacting protein 1	259	387	646	1.49	0.0000000
Itga6	Integrin alpha 6	67	100	167	1.49	0.0014445
Snx2	Sorting nexin 2	71	107	178	1.5	0.0010183
1100001H23Rik	RIKEN cDNA 1100001H23 gene	68	102	170	1.5	0.0014182
Tek	Endothelial-specific receptor tyrosine kinase	72	109	181	1.51	0.0008592
Grb14	Growth factor receptor bound protein 14	658	1006	1664	1.52	0.0000000
Mid1ip1	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	69	105	174	1.52	0.0007600
Hbxip	Hepatitis B virus x interacting protein	97	149	246	1.53	0.0000510
Ppp1r3c	Protein phosphatase 1, regulatory (inhibitor) subunit 3C	67	103	170	1.53	0.0006613
Cish	Cytokine inducible SH2-containing protein	62	95	157	1.53	0.0012864
A230075M04Rik	RIKEN cDNA 5730437N04 gene	128	198	326	1.54	0.0000022

Il1r1	Interleukin 1 receptor, type I	143	222	365	1.55	0.0000004
Ell2	Elongation factor RNA polymerase II 2	78	121	199	1.55	0.0001471
Tceal1	Transcription elongation factor A (SII)-like 1	56	87	143	1.55	0.0018490
Zcchc14	Zinc finger, CCHC domain containing 14	52	81	133	1.55	0.0022332
Josd2	Josephin domain containing 2	62	97	159	1.56	0.0009354
Mm.390478	Transcribed locus, moderately similar to XP_001097441.1 similar to Cytochrome c oxidase polypeptide VIc precursor [Macaca mulatta]	431	679	1110	1.57	0.0000000
Lhfp	Lipoma HMGIC fusion partner	175	276	451	1.57	0.0000000
Arl6ip2	ADP-ribosylation factor-like 6 interacting protein 2	83	131	214	1.57	0.0000462
Mm.392391	Transcribed locus	167	265	432	1.58	0.0000000
BC031181	CDNA sequence BC031181	55	87	142	1.58	0.0009643
Rorc	RAR-related orphan receptor gamma	236	377	613	1.59	0.0000000
Mm.465439	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230033O15 product:Warning: possibly chimeric clone, full insert sequence	107	172	279	1.6	0.0000017
Skiv2l2	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)	88	141	229	1.6	0.0000170
Cldn12	Claudin 12	55	88	143	1.6	0.0008140
Mm.447910	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230315J10 product:unclassifiable, full insert sequence	15006	24300	39306	1.61	0.0000000
Pkig	Protein kinase inhibitor, gamma	222	359	581	1.61	0.0000000
Med21	Mediator complex subunit 21	203	330	533	1.62	0.0000000
Rnf34	Ring finger protein 34	78	127	205	1.62	0.0000232
Eid1	EP300 interacting inhibitor of differentiation 1	160	263	423	1.64	0.0000000
Herc3	Hect domain and RLD 3	71	117	188	1.64	0.0000450
Blvrb	Biliverdin reductase B (flavin reductase (NADPH))	56	92	148	1.64	0.0004098
Setdb2	SET domain, bifurcated 2	43	71	114	1.65	0.0013331
Gadd45gip1	Growth arrest and DNA-damage-inducible, gamma interacting protein 1	129	215	344	1.66	0.0000000
Lix1l	Lix1-like	61	102	163	1.67	0.0000708
Hcfc1r1	Host cell factor C1 regulator 1 (XPO1-dependent)	92	155	247	1.68	0.0000011
Sdhd	Succinate dehydrogenase complex, subunit D, integral membrane protein	109	185	294	1.69	0.0000001
Aspn	Asporin	50	85	135	1.7	0.0001870
Cnbp	Cellular nucleic acid binding protein	307	531	838	1.72	0.0000000
Tbk1	TANK-binding kinase 1	55	95	150	1.72	0.0000652
Art4	ADP-ribosyltransferase 4	115	201	316	1.74	0.0000000
Mm.60041	15 days embryo embryonic body below diaphragm cDNA, RIKEN full-length enriched library, clone:8230401F05 product:unclassifiable, full insert sequence	201	355	556	1.76	0.0000000
Ccrl2	Chemokine (C-C motif) receptor-like 2	77	136	213	1.76	0.0000008
Mm.427661	Transcribed locus, moderately similar to XP_001090091.1 similar to 60S ribosomal protein L32 [Macaca mulatta]	67	118	185	1.76	0.0000046
Marveld1	MARVEL (membrane-associating) domain containing 1	34	60	94	1.76	0.0009613
Fmr1	Fragile X mental retardation syndrome 1 homolog	32	57	89	1.78	0.0013811
Bche	Butyrylcholinesterase	53	95	148	1.79	0.0000237
A930005H10Rik	RIKEN cDNA A930005H10 gene	40	72	112	1.8	0.0003402
Tusc2	Tubulin, beta 2c	35	63	98	1.8	0.0006699
4833439L19Rik	RIKEN cDNA 4833439L19 gene	58	105	163	1.81	0.0000067
Mm.455390	Transcribed locus, weakly similar to NP_039499.1 c oxidase 1 [Schizosaccharomyces pombe]	56	102	158	1.82	0.0000117
Rras	Harvey rat sarcoma oncogene, subgroup R	35	64	99	1.82	0.0004460
Igsf1	Immunoglobulin superfamily, member 1	29	53	82	1.82	0.0010167
Hfe	Hemochromatosis	29	54	83	1.86	0.0006617
Rgs2	Regulator of G-protein signaling 2	142	269	411	1.89	0.0000000
Tmod4	Tropomodulin 4	28	53	81	1.89	0.0007936
Tppp3	Tubulin polymerization-promoting protein family member 3	36	69	105	1.91	0.0001053
Mm.420899	Transcribed locus, moderately similar to XP_001084755.1 similar to mitochondrial ribosomal protein 63 [Macaca mulatta]	27	52	79	1.92	0.0007650
Megf9	Multiple EGF-like-domains 9	26	50	76	1.92	0.0011429
Ptdss1	Phosphatidylserine synthase 1	33	64	97	1.93	0.0001392
Fkbp7	FK506 binding protein 7	38	74	112	1.94	0.0000307
Fcgr3	Fc receptor, IgG, low affinity III	29	57	86	1.96	0.0002179
2310073E15Rik	RIKEN cDNA 2310073E15 gene	25	49	74	1.96	0.0008821
Mm.403476	Transcribed locus	41	81	122	1.97	0.0000121
Pxmp3	Peroxisomal membrane protein 3	83	166	249	2	0.0000000
H2-Ab1	Histocompatibility 2, class II antigen A, beta 1	20	40	60	2	0.0021065
Mm.237238	Malonyl-CoA decarboxylase	54	111	165	2.05	0.0000001
Tmem37	Transmembrane protein 37	21	44	65	2.09	0.0005392
Arrdc4	Arrestin domain containing 4	38	80	118	2.1	0.0000031
Ppp1r3b	Protein phosphatase 1, regulatory (inhibitor) subunit 3B	22	47	69	2.13	0.0002170

Gch1	GTP cyclohydrolase 1	35	75	110	2.14	0.0000023
Eef1b2	Eukaryotic translation elongation factor 1 beta 2	23	50	73	2.17	0.0001424
1110019K23Rik	RIKEN cDNA 1110019K23 gene	17	37	54	2.17	0.0007906
Mm.393589	CDNA, clone:Y0G0121O19, strand:minus, reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST00000047864, based on BLAT search	23	51	74	2.21	0.0000863
Nup62	Nucleoporin 62	22	49	71	2.22	0.0001022
Zfp704	Zinc finger protein 704	546	1253	1799	2.29	0.0000000
Rps26	Ribosomal protein L26	169	399	568	2.36	0.0000000
Gng11	Guanine nucleotide binding protein (G protein), gamma 11	56	134	190	2.39	0.0000000
Ap4s1	Adaptor-related protein complex AP-4, sigma 1	54	134	188	2.48	0.0000000
Sec23b	SEC23B (S. cerevisiae)	12	32	44	2.66	0.0003060
Egln2	EGL nine homolog 2 (C. elegans)	13	36	49	2.76	0.0000607
2210408F21Rik	RIKEN cDNA 2210408F21 gene	9	25	34	2.77	0.0011310
Gls2	glutaminase 2 (liver, mitochondrial)	8	24	32	3	0.0012970
Cd151	CD151 antigen	48	165	213	3.43	0.0000000
Ube1c	Ubiquitin-activating enzyme E1C	6	21	27	3.5	0.0004854
Dse	Dermatan sulfate epimerase	5	19	24	3.8	0.0007230
Hrasls	HRAS-like suppressor	3	14	17	4.66	0.0010096
Stbd1	Starch binding domain 1	3	15	18	5	0.0015510
AW060394	expressed sequence AW060394	3	21	24	7	0.0000050

Supplemental Table 2. Quantification of mRNA expression levels by RT-PCR array

At early phase (4 weeks) after deletion of Txnip in temporally-inducible cardiomyocyte-specific Txnip-KO mice

		2^-ΔC_t		Cardiac-KO /Control		
NCBI Unigen Symbol	Gene Name	Cardiac-KO (n=3)	Control (n=3)	Fold Up- or Down-Regulation	p-value	
Pcx	***Pyruvate carboxylase***	***0.014***	***0.026***	***-1.943***	***0.005***	p<0.01
Idh2	***Isocitrate dehydrogenase 2 (NADP+), mitochondrial***	***3.666***	***4.482***	***-1.223***	***0.047***	p<0.05
Pdk4	Pyruvate dehydrogenase kinase, isozyme 4	2.071	0.976	2.122	0.048	p<0.05
Phkg2	Phosphorylase kinase gamma 2	0.033	0.040	-1.218	0.019	p<0.05
Bpgm	2,3-Biphosphoglycerate mutase	0.038	0.030	1.246	0.020	p<0.05
Gbe1	Glucan (1,4-alpha-), branching enzyme 1	0.315	0.252	1.251	0.023	p<0.05
4833426J09Rik	Riken cDNA 4833426J09	0.015	0.025	-1.674	0.048	p<0.05

At late phase (15 weeks) after deletion of Txnip in temporally-inducible cardiomyocyte-specific Txnip-KO mice

		2^-ΔC_t		Cardiac-KO /Control		
NCBI Unigen Symbol	Gene Name	Cardiac-KO (n=3)	Control (n=3)	Fold Up- or Down-Regulation	p-value	
Pcx	***Pyruvate carboxylase***	***0.023***	***0.033***	***-1.443***	***0.035***	p<0.05
Idh2	***Isocitrate dehydrogenase 2 (NADP+), mitochondrial***	***4.222***	***5.225***	***-1.238***	***0.039***	p<0.05
Idh3a	Isocitrate dehydrogenase 3 (NAD+) alpha	2.783	2.464	1.129	0.031	p<0.05
Phkg1	Phosphorylase kinase gamma 1	0.067	0.051	1.334	0.035	p<0.05
Aldob	Aldolase B, fructose-bisphosphate	0.001	0.001	1.458	0.022	p<0.05
Gck	Glucokinase	0.027	0.041	-1.498	0.020	p<0.05
Hk3	Hexokinase 3	0.001	0.001	1.531	0.048	p<0.05
Suclg1	Succinate-CoA lgase, GDP-forming, alpha subunit	1.056	0.917	1.152	0.015	p<0.05

Wild type mice (Txnip$^{+/+}$) at 4 weeks after 4-hydroxy-tamoxifen (4OHT) treatment

		2^-ΔC_t		4OHT /Vehicle		-
NCBI Unigen Symbol	Gene Name	4OHT (n=3)	Vehicle (n=3)	Fold Up- or Down-Regulation	p-value	
Pcx	Pyruvate carboxylase	0.025	0.027	-1.092	0.304	p=NS
Idh2	Isocitrate dehydrogenase 2 (NADP+), mitochondrial	6.044	6.436	-1.065	0.489	p=NS
Pdk4	Pyruvate dehydrogenase kinase, isozyme 4	0.834	0.690	1.209	0.582	p=NS
Phkg2	Phosphorylase kinase gamma 2	0.036	0.034	1.065	0.756	p=NS
Bpgm	2,3-Biphosphoglycerate mutase	0.050	0.053	-1.063	0.700	p=NS
Gbe1	Glucan (1,4-alpha-), branching enzyme 1	0.193	0.154	1.251	0.556	p=NS
4833426J09Rik	Riken cDNA 4833426J09	0.027	0.027	1.015	0.961	p=NS
Idh3a	Isocitrate dehydrogenase 3 (NAD+) alpha	2.202	1.678	1.313	0.332	p=NS
Phkg1	Phosphorylase kinase gamma 1	0.031	0.033	-1.041	0.794	p=NS
Aldob	Aldolase B, fructose-bisphosphate	0.001	0.000	1.226	0.117	p=NS
Gck	Glucokinase	0.062	0.055	1.130	0.264	p=NS
Hk3	Hexokinase 3	0.002	0.003	-1.358	0.043	p<0.05
Suclg1	Succinate-CoA lgase, GDP-forming, alpha subunit	1.317	0.889	1.482	0.158	p=NS

Supplemental Table 3: Proteomic analysis for novel binding partners of Txnip in human cells

Protein Name	Accession number	MW (Da)	Txnip	GST
Carbonyl reductase [NADPH] 1	IPI00295386	30362	290	263
Isoform 1 of Alpha-1-antitrypsin	IPI00553177	46725	57	
Apolipoprotein A-I	IPI00021841	30766	47	
Alpha-2-macroglobulin	IPI00478003	163287	34	
Isoform 1 of Tuftelin-interacting protein 11	IPI00015924	96819	32	12
Isoform A of GC-rich sequence DNA-binding factor homolog	IPI00001364	104802	31	21
Haptoglobin	IPI00902590	45193	28	
Probable ATP-dependent RNA helicase DDX41	IPI00007208	69830	27	14
IGKC protein	IPI00909649	25632	24	
Isoform 1 of Protein disulfide-isomerase A6	IPI00644989	48109	23	
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	IPI00396435	90929	18	8
Complement component 4B	IPI00887154	192765	17	
Isoform 1 of Alpha-1-antichymotrypsin	IPI00847635	47639	16	
Complement C3 (Fragment)	IPI00783987	187163	15	
IGHV3OR16-13 IGHA1 protein	IPI00061977	54144	13	
Tubulin alpha-1B chain	IPI00387144	19360	11	8
IGL protein	IPI00154742	24778	10	
Splicing factor 3B subunit 4	IPI00017339	44373	10	8
Inter-alpha (globulin) inhibitor H4	IPI00896419	103360	9	
IGHG1 protein	IPI00448925	60092	8	
Splicing factor 45	IPI00176706	44950	8	7
Ceruloplasmin	IPI00017601	122201	7	
Splicing factor 3 subunit 1	IPI00017451	88887	7	5
Apolipoprotein A-IV precursor	IPI00847179	45368	6	
Hemopexin	IPI00022488	51664	6	
Isoform 1 of Serine/arginine repetitive matrix protein 1	IPI00647720	102331	5	4
cDNA FLJ55673, highly similar to Complement factor B	IPI00019591	140947	4	
alpha 1B-glycoprotein precursor	IPI00745089	54242	3	
Isoform 1 of Gelsolin	IPI00026314	85694	3	
Hemoglobin subunit beta	IPI00654755	15982	3	
Plastin 3	IPI00216694	70802	3	
Thioredoxin domain containing 5 isoform 2	IPI00395646	43658	3	
Vitronectin	IPI00298971	54296	3	
cDNA FLJ60715, highly similar to Pyruvate carboxylase, mitochondrial	IPI00909014	57916	2	
Alpha-fetoprotein	IPI00022443	68673	2	
Isoform 1 of Complement factor H	IPI00029739	139095	2	
Isoform 2 of Eukaryotic translation initiation factor 3 subunit B	IPI00719752	99036	2	
Inter-alpha (Globulin) inhibitor H2	IPI00645038	105216	2	
Cleavage and polyadenylation specificity factor subunit 5	IPI00646917	26213	2	
cDNA FLJ58826, highly similar to Plasma protease C1 inhibitor	IPI00879931	59484	2	
Serotransferrin	IPI00022463	77039	2	

Values are numbers of hits by mass spectrometry