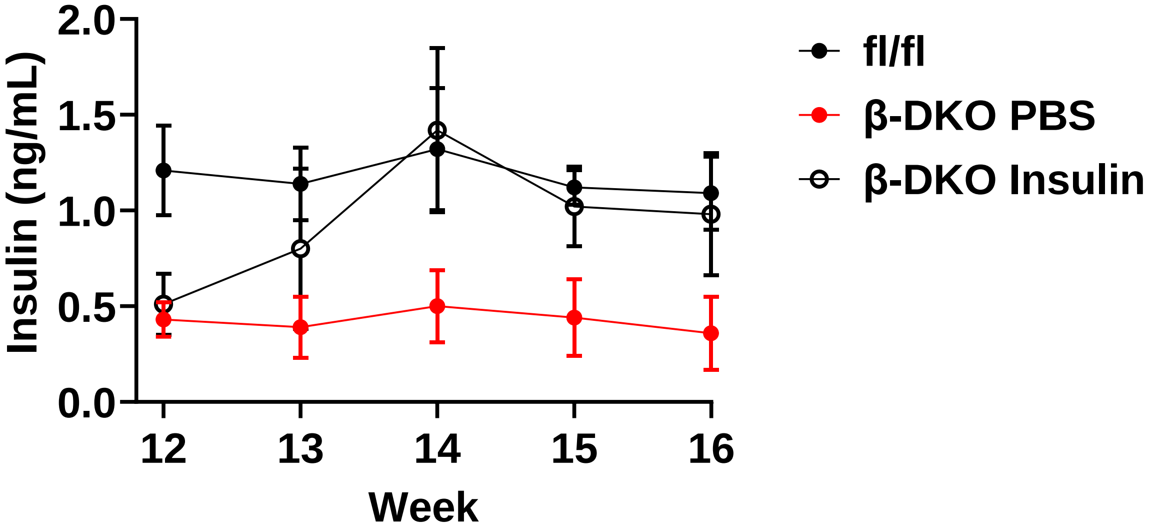
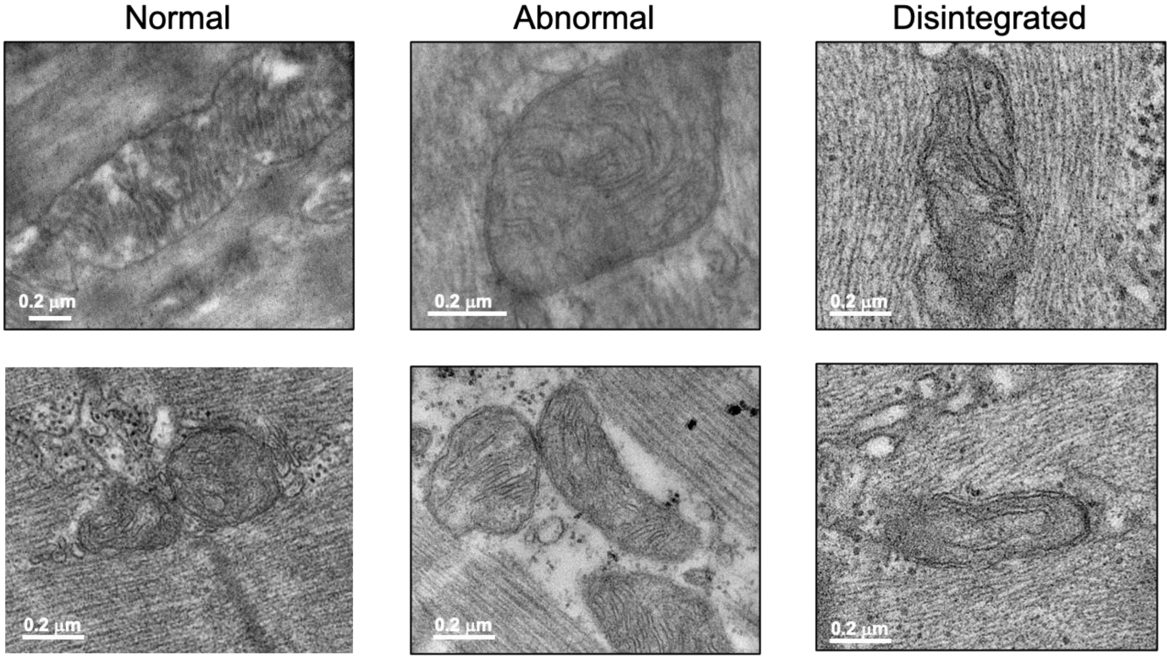


Supplementary Figure 1: Fed plasma insulin levels in control fl/fl mice and PBS- and insulin-supplemented β-DKO mice.



Supplementary Figure 2: Examples of mitochondria categories used for quantitative analysis of mitochondrial quality in EDL muscle by TEM.

Supplementary Table 1: Transcripts differentially expressed in EDL muscle between control fl/fl mice and β-DKO mice.

	Fold change	False discovery rate
Expression increased in β-DKO vs fl/fl control		
cadherin 4|Cdh4	3.892833	1.97E-05
RPTOR independent companion of MTOR, complex 2|Rictor	3.771738	1.63E-06
mab-21-like 1 (C. elegans)|Mab21l1	3.333985	0.020934
potassium voltage-gated channel, subfamily G, member 4|Kcng4	2.663953	1.63E-06
upstream transcription factor family member 3|Usf3	2.35029	2.64E-06
potassium voltage-gated channel, subfamily F, member 1|Kcnf1	2.348649	0.048006
S-adenosylmethionine decarboxylase 1|Amd1	2.086871	0.079413
tectonin beta-propeller repeat containing 2|Tecpr2	2.083586	0.002116
high mobility group AT-hook 2|Hmga2	1.902717	0.000487
serine/threonine kinase 11|Stk11	1.83706	0.041278
myosin, heavy polypeptide 4, skeletal muscle|Myh4	1.582213	8.36E-06
actinin alpha 3|Actn3	1.539407	7.1E-05
tropomyosin 1, alpha|Tpm1	1.507017	1.14E-05
creatine kinase, muscle|Ckm	1.38831	0.000742
muscle glycogen phosphorylase|Pygm	1.349962	0.074726
aldolase A, fructose-bisphosphate|Aldoa	1.267484	0.058175
Expression decreased in β-DKO vs fl/fl control		
myosin, heavy polypeptide 1, skeletal muscle, adult|Myh1	1.559699	0.001992
glutathione synthetase|Gss	1.762453	0.02551
creatine kinase, mitochondrial 2|Ckmt2	1.776419	0.048006
myosin binding protein C, slow-type|Mybpc1	1.927011	1.63E-06
actinin alpha 2|Actn2	2.042271	0.006034
protein tyrosine phosphatase, receptor type, Q|Ptprq	2.124977	0.074726
myoglobin|Mb	2.171065	0.006388
EPS8-like 2|Eps8l2	2.766763	0.068619
E74-like factor 1|Elf1	2.816357	0.094722
myosin, heavy polypeptide 2, skeletal muscle, adult|Myh2	2.851151	5.18E-06
spectrin repeat containing, nuclear envelope 1|Syne1	3.512969	0.068619
predicted gene 11127|Gm11127	3.762789	0.000473
leukocyte receptor cluster (LRC) member 8|Leng8	4.360866	0.068619
lactate dehydrogenase B|Ldhb	4.362688	0.053787
ankyrin repeat and zinc finger domain containing 1|Ankzf1	5.299245	0.000905
Ras association (RalGDS/AF-6) domain family (N-terminal) member 8|Rassf8	5.336577	0.074726

Supplementary Table 2: Transcripts differentially expressed in soleus muscle between control fl/fl mice and β-DKO mice.

	Fold change	False discovery rate
Expression increased in β-DKO vs fl/fl control		
metallothionein 2|Mt2	315.887858	0.00014109
predicted gene 45799|Timm10b	303.402064	1.8111E-05
tissue inhibitor of metalloproteinase 1|Timp1	281.767758	2.6728E-05
nuclear receptor subfamily 4, group A, member 3|Nr4a3	244.241966	5.5621E-13
collagen, type VIII, alpha 2|Col8a2	195.402066	1.013E-06
fibromodulin|Fmod	186.041089	5.054E-08
tenascin C|Tnc	156.304396	1.2894E-09
collagen, type XI, alpha 1|Col11a1	112.130395	7.4789E-07
angiopoietin-like 7|Angptl7	105.005396	0.00031537
integrin alpha M|Itgam	95.5273219	0.00012207
thrombospondin 1|Thbs1	87.7744799	0.00017669
chondroadherin|Chad	64.5891843	6.8925E-05
collagen, type XII, alpha 1|Col12a1	64.5152457	4.822E-07
pentraxin 4|Ptx4	58.0948417	2.155E-09
chemokine (C-C motif) ligand 6|Ccl6	57.7502693	4.2002E-05
hedgehog interacting protein-like 1|Hhipl1	56.9293577	1.3043E-11
cellular communication network factor 2|Ccn2	51.1747797	7.6078E-07
erythroferrone|Erfe	47.8343156	2.6255E-11
FBJ osteosarcoma oncogene|Fos	45.0717692	0.00688853
tenomodulin|Tnmd	44.9298892	8.8498E-06
sodium channel, voltage-gated, type V, alpha|Scn5a	35.7383512	0.00012335
zinc finger protein 697|Zfp697	35.1236675	9.4497E-08
versican|Vcan	34.5544107	2.155E-09
cartilage intermediate layer protein 2|Cilp2	33.7605039	0.02442613
cartilage oligomeric matrix protein|Comp	28.3777672	0.01256866
lymphatic vessel endothelial hyaluronan receptor 1|Lyve1	27.2160277	2.7314E-09
matrix metallopeptidase 19|Mmp19	26.0262394	5.6856E-06
embigin|Emb	25.2770684	3.8547E-06
proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protein)|Prg4	24.84306	0.00013438
runt related transcription factor 1|Runx1	23.5937908	9.8254E-08
mitogen-activated protein kinase kinase kinase 6|Map3k6	22.7629257	2.0134E-13
serine (or cysteine) peptidase inhibitor, clade A, member 3N|Serpina3n	22.0876518	4.822E-07
CD68 antigen|Cd68	22.0040844	0.00510463
early growth response 1|Egr1	21.4435819	0.00873695
coagulation factor II (thrombin) receptor-like 1|F2rl1	20.9021068	0.00075681
thrombospondin 4|Thbs4	20.3645731	1.1223E-05

cartilage intermediate layer protein, nucleotide pyrophosphohydrolase|Cilp	20.2733309	5.6165E-10
integrin, beta-like 1|Itgbl1	20.267565	0.00039092
fibronectin 1|Fn1	20.262844	2.1655E-05
salt inducible kinase 1|Sik1	19.9031347	0.00013438
latent transforming growth factor beta binding protein 2|Ltbp2	18.7408172	2.5832E-08
insulin receptor substrate 2|Irs2	18.4489986	0.0431585
glutamine fructose-6-phosphate transaminase 2|Gfpt2	18.2581954	0.00027226
peroxisome proliferative activated receptor, gamma, coactivator 1 alpha|Ppargc1a	17.9666502	2.0132E-05
CCAAT/enhancer binding protein (C/EBP), delta|Cebpd	17.8678223	0.00337059
collagen, type I, alpha 2|Col1a2	17.7717894	0.00100731
adhesion G protein-coupled receptor D1|Adgrd1	17.6359685	5.2755E-05
epithelial membrane protein 1|Emp1	17.2024533	0.00012572
integrin beta 2|Itgb2	17.0479969	0.00425523
cation channel, sperm associated 4|Catsper4	16.9025847	1.4063E-07
zinc finger protein 469|Zfp469	16.5022511	3.4609E-05
folliculin interacting protein 2|Fnip2	15.1485024	0.00019605
protein phosphatase 1, regulatory subunit 10|Ppp1r10	14.8919847	5.5621E-13
fibrinogen-like protein 2|Fgl2	14.8377892	0.00361599
N-myc downstream regulated gene 4|Ndrg4	13.7856373	0.00037263
CD44 antigen|Cd44	13.6675049	0.00077693
C-type lectin domain family 11, member a|Clec11a	13.6543471	0.00230666
dihydropyrimidinase-like 3|Dpysl3	13.2537405	0.00651421
a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 9|Adamts9	13.2042952	7.4983E-06
periostin, osteoblast specific factor|Postn	13.0331531	5.7526E-06
solute carrier family 15 (H+/peptide transporter), member 2|Slc15a2	12.9428167	0.00178861
collagen, type I, alpha 1|Col1a1	12.9026108	0.00267751
metallothionein 1|Mt1	12.7005705	0.01083837
lysyl oxidase-like 2|Loxl2	12.4237081	0.00344522
prostaglandin I2 (prostacyclin) synthase|-	12.0811996	0.00072563
RAB30, member RAS oncogene family|Rab30	12.0121819	0.01248442
Rho GTPase activating protein 30|Arhgap30	11.9758937	0.00084773
adhesion G protein-coupled receptor E1|Adgre1	11.9512669	0.00055322
Iqcj and Schip1 fusion protein|Iqschfp	11.8948686	0.00044205
predicted gene, 49804|-	11.7480552	0.00204405
lysosomal-associated protein transmembrane 5|Laptm5	11.6359713	1.5222E-05
coagulation factor XIII, A1 subunit|F13a1	11.2919924	2.6657E-05
adenylate cyclase 7|Adcy7	11.2915835	8.93E-06
HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2|Hecw2	11.1516857	0.00221707
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)|Maff	11.0823997	0.00065029
ectodermal-neural cortex 1|Enc1	11.0569355	0.00120168
lysophosphatidic acid receptor 1|Lpar1	10.9459954	0.00039616
serine (or cysteine) peptidase inhibitor, clade B, member 8|Serpinb8	10.8024305	1.1223E-05

cathepsin S|Ctss	10.7273549	0.00524671
fibronectin type III domain containing 1|Fndc1	10.6129895	2.6955E-05
proline arginine-rich end leucine-rich repeat|Prelp	10.6054774	0.00274157
secreted phosphoprotein 1|Spp1	10.5271111	0.0002661
lysyl oxidase|Lox	10.4327288	0.00618155
Ras-related associated with diabetes|Rrad	10.218397	0.02559645
OTU domain containing 1|Otud1	10.1063917	0.00045752
solute carrier family 38, member 2|Slc38a2	10.0500152	0.00213847
period circadian clock 2|Per2	9.65615931	0.00817409
interferon activated gene 205|Ifi205	9.64754521	0.00024503
lectin, galactose binding, soluble 3|Lgals3	9.28103767	0.00274157
fibulin 1|Fbln1	9.23244477	0.02012522
NUAK family, SNF1-like kinase, 2|Nuak2	9.20759265	0.00222847
cyclin D1|Ccnd1	9.17645131	0.02798475
sortilin-related VPS10 domain containing receptor 2|Sorcs2	9.10927714	0.00834923
WEE 1 homolog 1 (S. pombe)|Wee1	9.08699837	0.00065029
peptidase domain containing associated with muscle regeneration 1|Pamr1	9.00126956	0.01345282
guanine nucleotide binding protein, alpha stimulating, olfactory type|Gnal	8.93123087	0.00014109
N-acetyltransferase domain containing 1|Natd1	8.760899	0.00010963
colony stimulating factor 1 receptor|Csf1r	8.76029693	0.00284005
scavenger receptor cysteine rich family, 5 domains|Ssc5d	8.72194282	0.0257702
lysyl oxidase-like 3|Loxl3	8.5914209	0.00055322
nuclear receptor subfamily 4, group A, member 1|Nr4a1	8.51090577	0.00027591
drebrin 1|Dbn1	8.45805515	0.00066092
mal, T cell differentiation protein-like|Mall	8.44506523	0.00200937
elastin microfibril interfacer 2|Emilin2	8.41190081	0.00030487
myelocytomatosis oncogene|Myc	8.40416371	0.01651234
SRY (sex determining region Y)-box 9|Sox9	8.40348936	0.04473441
mannose receptor, C type 2|Mrc2	8.33397958	0.00158168
reelin|Reln	8.3091645	0.00891459
naked cuticle 2|Nkd2	8.26469802	0.00102932
G protein-coupled receptor 153|Gpr153	8.20302939	0.00348355
zinc finger protein 185|Zfp185	8.18927737	0.0002661
collagen, type XIV, alpha 1|Col14a1	8.1175145	0.00139387
Fc receptor, IgG, low affinity III|Fcgr3	7.81441262	0.00912103
mesenteric estrogen dependent adipogenesis|Medag	7.77438536	8.009E-05
collagen, type XVI, alpha 1|Col16a1	7.76486037	0.01502998
zinc finger and BTB domain containing 16|Zbtb16	7.67545137	4.3981E-05
tubulin, beta 6 class V|Tubb6	7.64289183	0.00344522
pyridoxal (pyridoxine, vitamin B6) kinase|Pdxk	7.59887828	0.00995548
LPS-induced TN factor|Litaf	7.59058792	0.00657922
carboxypeptidase X 2 (M14 family)|Cpxm2	7.54651399	0.00884467
keratin 80|Krt80	7.54373805	0.00149876
macrophage galactose N-acetyl-galactosamine specific lectin 2|Mgl2	7.53519209	0.01985801

feline leukemia virus subgroup C cellular receptor 1|Flvcr1	7.5301775	0.02199621
podoplanin|Pdpn	7.48006556	0.00183658
sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1|Svep1	7.47219164	0.00550052
phosphodiesterase 10A|Pde10a	7.3361616	0.00018081
CCAAT/enhancer binding protein (C/EBP), beta|Cebpb	7.21129504	0.00274157
procollagen lysine, 2-oxoglutarate 5-dioxygenase 2|Plod2	7.07009335	0.0014675
matrix metallopeptidase 2|Mmp2	7.06573722	0.0037345
advillin|Avil	7.05866928	1.6508E-05
platelet factor 4|Pf4	7.02928514	0.03585484
protocadherin 7|Pcdh7	6.91046647	0.00074448
phosphoinositide-3-kinase regulatory subunit 5|Pik3r5	6.90491314	0.00607362
mitogen-activated protein kinase 4|Mapk4	6.81230376	0.01201429
AE binding protein 1|Aebp1	6.79609015	0.00039659
epidermal growth factor receptor|Egfr	6.76756021	0.00393043
mannoside acetylglucosaminyltransferase 4, isoenzyme A|Mgat4a	6.74957771	0.00066955
Ras and Rab interactor 3|Rin3	6.72265403	0.00326217
dermatan sulfate epimerase|Dse	6.70193524	0.00271757
LRRN4 C-terminal like|Lrrn4cl	6.68675287	0.01434866
discoidin domain receptor family, member 2|Ddr2	6.52784821	0.02069978
solute carrier family 20, member 1|Slc20a1	6.48819816	0.00031537
collagen, type XXVII, alpha 1|Col27a1	6.48620469	0.00166425
follistatin-like 1|Fstl1	6.46539975	0.00434387
mesenchyme homeobox 1|Meox1	6.45591563	0.00202072
fibrillin 1|Fbn1	6.42163214	4.4461E-05
integrin alpha 11|Itga11	6.41694295	0.00274157
Ras association and DIL domains|Radil	6.41093768	0.00102932
plexin A2|Plxna2	6.37656903	0.01014739
proacrosin binding protein|Acrbp	6.35586507	0.00107002
ATPase, class V, type 10A|Atp10a	6.16706082	0.006084
stearoyl-Coenzyme A desaturase 1|Scd1	6.14968502	0.01532011
calcium channel, voltage-dependent, beta subunit associated regulatory protein|Cbarp	6.13632974	0.01345282
serine (or cysteine) peptidase inhibitor, clade F, member 1|Serpinf1	6.04494677	0.02234566
regulatory factor X, 2 (influences HLA class II expression)|Rfx2	6.02231851	0.04582482
DENN/MADD domain containing 2A|Dennd2a	5.990666	0.00084706
predicted gene 11756|Gm11756	5.93200883	0.00805211
growth arrest specific 1|Gas1	5.93058597	0.00753885
elongation factor RNA polymerase II|Ell	5.91322391	0.00438061
interleukin 17D|Il17d	5.91250418	0.02559645
plexin A4|Plxna4	5.87885105	1.2001E-05
v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)|Mafk	5.86462621	0.02026195
collagen, type VI, alpha 2|Col6a2	5.85196462	0.00291368
low density lipoprotein receptor-related protein 1|Lrp1	5.84744648	0.00075191
tumor necrosis factor receptor superfamily, member 25|Tnfrsf25	5.82106598	0.02934215

scleraxis|Scx	5.79195978	0.00034609
complement component factor h|Cfh	5.77817173	0.02529444
TBC1 domain family, member 9|Tbc1d9	5.75724638	0.01224856
myeloid-associated differentiation marker|Myadm	5.74757747	0.01393496
cysteine-serine-rich nuclear protein 1|Csrnp1	5.71080554	0.00689744
ENSMUSG00000121578	5.70323026	0.01155858
stromal cell-derived factor 2-like 1|Sdf2l1	5.64213861	0.01372805
Kruppel-like factor 3 (basic)|Klf3	5.63196996	0.00510463
proprotein convertase subtilisin/kexin type 5|Pcsk5	5.62031347	0.00232909
E74-like factor 4 (ets domain transcription factor)|Elf4	5.57009864	0.00425721
tenascin XB|Tnxb	5.55854386	0.00011146
regulator of calcineurin 1|Rcan1	5.53858966	4.1168E-05
AXL receptor tyrosine kinase|Axl	5.53691521	0.00682128
H1.9 linker histone|H1f9	5.52571745	0.00773557
thrombospondin 3|Thbs3	5.50847072	0.00077693
carboxylesterase 5A|Ces5a	5.4748406	0.00750199
CD109 antigen|Cd109	5.43003574	0.00230666
Rho GTPase activating protein 26|Arhgap26	5.41330348	0.02245268
matrix Gla protein|Mgp	5.39936149	0.02225316
cerebellar degeneration-related 2|Cdr2	5.39077385	0.00193926
tubulin, beta 2B class IIB|Tubb2b	5.33587057	0.00533211
slit guidance ligand 3|Slit3	5.31656619	0.00346577
collagen, type V, alpha 2|Col5a2	5.27074042	0.00626291
pre B cell leukemia homeobox 3|Pbx3	5.25387109	0.01393496
complement component 1, q subcomponent, C chain|C1qc	5.25333539	0.02483316
strawberry notch 2|Sbno2	5.24913287	0.00258716
nuclear factor, interleukin 3, regulated|Nfil3	5.20506727	0.01759268
sorbin and SH3 domain containing 3|Sorbs3	5.20192731	0.00022721
unc-13 homolog D|Unc13d	5.16992642	0.00434387
olfactomedin-like 2B|Olfml2b	5.15691555	0.01393496
chloride intracellular channel 4 (mitochondrial)|Clic4	5.15489816	0.00072048
solute carrier family 7 (cationic amino acid transporter, y+ system), member 1|Slc7a1	5.12964325	0.00102932
von Willebrand factor A domain containing 1|Vwa1	5.12267261	0.00906574
SH3 domain protein D19|Sh3d19	5.1183914	0.00425523
interferon activated gene 204|Ifi204	5.08152601	0.00556062
paralemmin A kinase anchor protein|Pakap	5.08088233	0.04110072
alkaline phosphatase, liver/bone/kidney|Alpl	5.03502833	0.00337059
a disintegrin and metallopeptidase domain 19 (meltrin beta)|Adam19	5.02576571	0.0431585
toll-like receptor 4|Tlr4	5.01236395	0.00380425
UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6|B4galt6	5.01164896	0.00274157
tumor necrosis factor receptor superfamily, member 12a|Tnfrsf12a	4.9800393	0.01083044
tissue inhibitor of metalloproteinase 2|Timp2	4.85259315	0.00907549
transgelin 2|Tagln2	4.82472343	0.02934215

anthrax toxin receptor 1|Antxr1	4.80748239	0.01336038
sushi-repeat-containing protein, X-linked 2|Srpx2	4.80078628	0.03908268
acetoacetyl-CoA synthetase|Aacs	4.7839415	0.00310573
coactosin-like 1 (Dictyostelium)|Cotl1	4.74828626	0.01807052
vimentin|Vim	4.73968773	0.00254365
vitrin|Vit	4.71461086	0.0388031
tropomyosin 4|Tpm4	4.71160534	0.02049759
S100 calcium binding protein A10 (calpactin)|S100a10	4.70823788	0.00968023
poliovirus receptor|Pvr	4.70113839	0.01004436
platelet-derived growth factor receptor-like|Pdgfrl	4.683342	0.00626291
Fraser extracellular matrix complex subunit 1|Fras1	4.6754029	0.00141916
lecithin cholesterol acyltransferase|Lcat	4.62697522	0.03951736
AHNAK nucleoprotein 2|Ahnak2	4.59316187	0.00750199
ENSMUSG00000095041	4.58785789	0.00525878
CDP-diacylglycerol synthase 1|Cds1	4.58400127	0.04110072
annexin A1|Anxa1	4.57150044	0.00223869
cysteine and glycine-rich protein 3|Csrp3	4.55811356	0.0280054
protein phosphatase 1, regulatory subunit 13 like|Ppp1r13l	4.55148548	0.01079525
biglycan|Bgn	4.52591981	0.01393496
death associated protein kinase 1|Dapk1	4.49901288	0.00750019
laminin, gamma 2|Lamc2	4.48323987	0.00274157
zinc finger and BTB domain containing 26|Zbtb26	4.48093318	0.03756582
transforming growth factor, beta induced|Tgfbi	4.47854087	0.01336038
microtubule-associated protein 1B|Map1b	4.4709083	0.00393043
integrin, alpha 10|Itga10	4.46649125	0.03982991
Sec24 related gene family, member D (S. cerevisiae)|Sec24d	4.42938814	0.01345282
collagen, type VI, alpha 1|Col6a1	4.4147565	0.0099896
collagen, type XVIII, alpha 1|Col18a1	4.39078253	0.01174358
NLR family, CARD domain containing 5|Nlrc5	4.37491322	0.03588503
epidermal growth factor-containing fibulin-like extracellular matrix protein 1|Efemp1	4.35614105	0.00817409
phosphodiesterase 5A, cGMP-specific|Pde5a	4.35052855	0.00890655
WD repeat domain 81|Wdr81	4.34261868	0.03509434
microtubule associated monooxygenase, calponin and LIM domain containing -like 1|Micall1	4.33564834	0.00036909
ret proto-oncogene|Ret	4.3256681	0.03990217
receptor-interacting serine-threonine kinase 3|Ripk3	4.31490109	0.03677365
a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8|Adamts8	4.28204334	0.02341984
carboxylesterase 2C|Ces2c	4.2809602	0.03002208
Jun dimerization protein 2|Jdp2	4.26638065	0.01653921
fibroblast growth factor receptor 3|Fgfr3	4.26278108	0.00772354
collagen, type VI, alpha 3|Col6a3	4.25156346	0.01735642
ring finger protein 144B|Rnf144b	4.25147582	0.01079525
annexin A2|Anxa2	4.23569249	0.00434387
proprotein convertase subtilisin/kexin type 6|Pcsk6	4.21986739	0.01133451
microfibrillar associated protein 5|Mfap5	4.21593664	0.00706405

endothelin receptor type B|Ednrb	4.20462609	0.0431585
prostate transmembrane protein, androgen induced 1|Pmepa1	4.19813485	0.02012522
RNA binding motif protein 12 B1|Rbm12b1	4.1917968	0.02341984
FYVE, RhoGEF and PH domain containing 3|Fgd3	4.19105663	0.00825343
EYA transcriptional coactivator and phosphatase 1|Eya1	4.1765802	0.0162846
transferrin receptor|Tfrc	4.16271718	0.01014739
chemokine-like receptor 1|Cmklr1	4.15864414	0.01226934
RIKEN cDNA 1110065P20 gene|1110065P20Rik	4.12216788	0.03158457
RAB3A interacting protein (rabin3)-like 1|Rab3il1	4.10582684	0.02988793
zinc finger SWIM-type containing 6|Zswim6	4.09863205	0.01130906
ski sarcoma viral oncogene homolog (avian)|Ski	4.09195668	0.02679512
ADP-ribosylation factor-like 13B|Arl13b	4.09171313	0.00753885
collagen, type V, alpha 1|Col5a1	4.06489257	0.0079776
forkhead box O1|Foxo1	4.0504303	0.0306347
tumor necrosis factor receptor superfamily, member 23|Tnfrsf23	4.03722408	0.04764597
UDP-glucose dehydrogenase|Ugdh	4.0301866	0.00264925
TOG array regulator of axonemal microtubules 2|Togaram2	4.02596612	0.01224856
collagen, type III, alpha 1|Col3a1	4.01251179	0.01336038
pleckstrin homology domain containing, family F (with FYVE domain) member 1|Plekhf1	4.00483924	0.03998977
cellular communication network factor 3|Ccn3	3.99111868	0.03542224
inter-alpha (globulin) inhibitor H5|Itih5	3.95945166	0.01248442
transcriptional and immune response regulator|Tcim	3.95046319	0.00689843
tensin 3|Tns3	3.94656826	0.03310089
calcium channel, voltage-dependent, T type, alpha 1G subunit|Cacna1g	3.94483098	0.00682128
expressed sequence C77080|C77080	3.9437829	0.01079525
signal-regulatory protein alpha|Sirpa	3.92615826	0.03644731
heat shock protein 1A|Hspa1a	3.90723182	0.00639162
forkhead box K1|Foxk1	3.88326081	0.01182355
sperm associated antigen 5|Spag5	3.87246051	0.0435929
sulfatase 2|Sulf2	3.87036674	0.00441282
histone deacetylase 4|Hdac4	3.85937218	0.04062149
Sec61 beta subunit|Sec61b	3.85499167	0.01652323
glucosamine-6-phosphate deaminase 1|Gnpda1	3.85000202	0.00753885
coiled-coil domain containing 50|Ccdc50	3.82823458	0.0079776
RNA binding motif protein 12 B2|Rbm12b2	3.81735424	0.03665714
cell adhesion molecule 3|Cadm3	3.80023202	0.04794045
filamin, alpha|Flna	3.751354	0.01234048
vascular endothelial growth factor A|Vegfa	3.73947505	0.01719525
family with sequence similarity 241, member A|Fam241a	3.73026615	0.01020465
meningioma 1|Mn1	3.7277615	0.01393496
tubulin, alpha 1A|Tuba1a	3.70429969	0.0420074
RIKEN cDNA 2610028H24 gene|2610028H24Rik	3.68899641	0.03994594
SMAD family member 7|Smad7	3.66441526	0.04618995
cytoskeleton-associated protein 4|Ckap4	3.63374454	0.00881584

pleckstrin homology like domain, family A, member 1|Phlda1	3.63367727	0.04467012
fibronectin type III domain containing 3B|Fndc3b	3.61351086	0.01906245
frizzled class receptor 7|Fzd7	3.59894267	0.02046178
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide|P4ha1	3.59691588	0.01435015
DENN/MADD domain containing 4A|Dennd4a	3.58085196	0.01636425
cysteine-rich with EGF-like domains 2|Creld2	3.58035091	0.00770529
WW domain binding protein 1 like|Wbp1l	3.55513209	0.00533211
low density lipoprotein receptor|Ldlr	3.54787694	0.04062149
xin actin-binding repeat containing 1|Xirp1	3.5392545	0.01083837
myelin basic protein expression factor 2, repressor|Myef2	3.53094085	0.03995983
folliculin|Flcn	3.48247031	0.01210247
myocilin|Myoc	3.45219983	0.01107458
DENN/MADD domain containing 5B|Dennd5b	3.44874778	0.04029732
ubiquitination factor E4B|Ube4b	3.4112675	0.01336038
ankyrin repeat domain 2 (stretch responsive muscle)|Ankrd2	3.38367226	0.01312
PWWP domain containing 2B|Pwwp2b	3.38161163	0.02232246
actin-binding LIM protein 1|Ablim1	3.36105424	0.00524217
PCF11 cleavage and polyadenylation factor subunit|Pcf11	3.35323871	0.02288639
growth arrest-specific 2 like 1|Gas2l1	3.33348816	0.01393496
alanyl (membrane) aminopeptidase|Anpep	3.32499391	0.03937018
ring finger protein 150|Rnf150	3.29262801	0.02199621
paralemmin A kinase anchor protein|Pakap	3.26504545	0.03982991
ATPase, class I, type 8B, member 2|Atp8b2	3.26459174	0.01831478
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1|Raph1	3.26324435	0.01188289
sulfatase 1|Sulf1	3.24460692	0.03908268
cystinosis, nephropathic|Ctns	3.22788074	0.04104955
solute carrier family 22 (organic cation transporter), member 4|Slc22a4	3.20973651	0.04144853
dishevelled segment polarity protein 2|Dvl2	3.19815221	0.02476066
ER degradation enhancer, mannosidase alpha-like 1|Edem1	3.1872383	0.04305617
cytokine receptor-like factor 1|Crlf1	3.18292805	0.04259879
solute carrier family 22, member 23|Slc22a23	3.06904838	0.02289676
tubulin, beta 5 class I|Tubb5	3.05815577	0.03816213
HECT domain E3 ubiquitin protein ligase 2|Hectd2	3.05098326	0.03809017
serine carboxypeptidase 1|Scpep1	3.03478636	0.0420074
mesencephalic astrocyte-derived neurotrophic factor|-	3.01255313	0.03858238
RUN and SH3 domain containing 2|Rusc2	2.96292475	0.02123101
dual specificity phosphatase 1|Dusp1	2.95055223	0.01411056
RIKEN cDNA 6430548M08 gene|6430548M08Rik	2.94433773	0.03373278
mannosidase 2, alpha B2|Man2b2	2.93409024	0.0484129
Expression decreased in β-DKO vs fl/fl control		
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2|B3galt2	11.4338965	2.7188E-06
zinc finger protein 750|Zfp750	9.13970537	0.00012572
aldehyde dehydrogenase 1 family, member L1|Aldh1l1	8.41543806	0.00128174

leucine rich repeat containing 38|Lrrc38	8.17258487	1.8005E-05
MEF2 activating motif and SAP domain containing transcriptional regulator|Mamstr	7.75273912	2.4859E-07
glycine N-methyltransferase|Gnmt	7.51519006	0.00534687
glutathione S-transferase, theta 2|Gstt2	7.25014622	0.03736185
perilipin 5|Plin5	6.15304681	0.00274157
zinc finger protein 879|Zfp879	6.13355465	0.00362567
predicted gene 4841|Gm4841	6.01736804	0.01680409
polo like kinase 2|Plk2	5.78643543	0.00657922
parathyroid hormone 1 receptor|Pth1r	5.6312026	0.00506048
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4|Cited4	5.59094959	0.01287261
ring finger protein 122|Rnf122	5.32658923	0.01983834
CECR2, histone acetyl-lysine reader|Cecr2	5.22087551	0.03469879
apolipoprotein L 10B|Apol10b	5.03866065	0.01812929
G0/G1 switch gene 2|G0s2	5.03002457	0.02808871
interferon-induced protein with tetratricopeptide repeats 3B|Ifit3b	5.00253492	0.01469158
solute carrier family 40 (iron-regulated transporter), member 1|Slc40a1	4.94374336	0.00614409
WSC domain containing 1|Wscd1	4.92391602	0.00425523
RIKEN cDNA 6430571L13 gene|6430571L13Rik	4.91955229	0.03038222
Rho GTPase activating protein 18|Arhgap18	4.8287183	0.00131644
4-hydroxyphenylpyruvate dioxygenase-like|Hpdl	4.82478487	0.00204405
synuclein, alpha interacting protein (synphilin)|Sncaip	4.73964006	0.0006381
myosin regulatory light chain interacting protein|Mylip	4.5218652	0.00066092
radical S-adenosyl methionine domain containing 2|Rsad2	4.49226092	0.03042766
tubulin, gamma 2|Tubg2	4.46478956	0.029444
HAUS augmin-like complex, subunit 4|Haus4	4.43162011	0.01133451
ectonucleotide pyrophosphatase/phosphodiesterase 3|Enpp3	4.4313483	0.00890655
NIM1 serine/threonine protein kinase|Nim1k	4.39256762	0.04029732
acyl-CoA thioesterase 2|Acot2	4.38582924	0.02864561
NAD(P)H dehydrogenase, quinone 1|Nqo1	4.38159969	0.01192778
armadillo-like helical domain containing 4|Armh4	4.3404354	0.00437052
DNA-damage-inducible transcript 4-like|Ddit4l	4.31098581	0.03593761
dihydrodiol dehydrogenase (dimeric)|Dhdh	4.28364601	0.00607362
zinc finger protein 52|Zfp52	4.25352579	0.03756582
cortexin 3|Ctxn3	4.21324324	0.01652323
indolethylamine N-methyltransferase|Inmt	4.20640946	0.0072803
myogenic differentiation 1|Myod1	4.20079844	0.01985801
Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2|Cited2	4.13755896	0.00232909
adhesion molecule with Ig like domain 3|Amigo3	4.09394199	0.04104955
dual specificity phosphatase 10|Dusp10	4.00580129	0.00066092
nuclear receptor subfamily 1, group D, member 1|Nr1d1	3.95636641	0.02012522
thyroid hormone responsive|Thrsp	3.84782958	0.01079525
carbonic anhydrase 14|Car14	3.84019653	0.0044909
6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1|Pfkfb1	3.76002189	0.0079776

solute carrier family 26, member 6|Slc26a6	3.75318929	0.00753885
kelch-like 33|Klhl33	3.72979227	0.00216916
secretin receptor|Sctr	3.72906345	0.02466707
MDS1 and EVI1 complex locus|Mecom	3.64528803	0.03756582
carbonic anhydrase 4|Car4	3.61749523	0.03181727
nuclear receptor subfamily 1, group H, member 3|Nr1h3	3.58793363	0.01335667
microsomal glutathione S-transferase 1|Mgst1	3.58431569	0.00200937
plexin domain containing 1|Plxdc1	3.57848845	0.02704906
target of EGR1, member 1 (nuclear)|Toe1	3.55096244	0.03038222
fibroblast growth factor receptor 4|Fgfr4	3.38389371	0.02507614
septin 4|Septin4	3.36587627	0.00998991
transmembrane and coiled-coil domains 4|Tmco4	3.3215674	0.01204016
signal transducer and activator of transcription 5A|Stat5a	3.28305043	0.02320622
pyruvate dehydrogenase phosphatase catalytic subunit 1|Pdp1	3.21620341	0.01345282
phospholipase C, delta 4|Plcd4	3.19970345	0.02442613
glutathione S-transferase, mu 2|Gstm2	3.11890944	0.01723242
isocitrate dehydrogenase 1 (NADP+), soluble|Idh1	3.10151072	0.02392418
polyamine oxidase (exo-N4-amino)|Paox	3.04228349	0.04501694
argininosuccinate lyase|Asl	3.01638018	0.04314435
pleckstrin homology domain containing, family H (with MyTH4 domain) member 3|Plekhh3	2.99715921	0.01572652
sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C|Sema6c	2.96476672	0.03276821
ankyrin repeat domain 9|Ankrd9	2.89643711	0.03042766
potassium inwardly-rectifying channel, subfamily J, member 8|Kcnj8	2.81555144	0.03756582
kyphoscoliosis peptidase|Ky	2.78095136	0.04446621
ral guanine nucleotide dissociation stimulator|Ralgds	2.73816817	0.04191859
CDC42 effector protein (Rho GTPase binding) 3|Cdc42ep3	2.69824731	0.04218048
FAST kinase domains 1|Fastkd1	2.65244329	0.04144358
caseinolytic mitochondrial matrix peptidase chaperone subunit|Clpx	2.64991331	0.02898906

Supplementary Table 3: Transcripts differentially expressed in EDL muscle between β-DKO mice treated with PBS and insulin.

	Fold change	False discovery rate
Expression increased in β-DKO Ins vs β-DKO PBS		
lactate dehydrogenase B|Ldhb	4.353275	0.080173
microtubule-associated protein 1 A|Map1a	4.070883	0.055235
EPS8-like 2|Eps8l2	3.439704	0.003969
myoglobin|Mb	2.250541	0.000735
creatine kinase, mitochondrial 2|Ckmt2	1.961628	0.011665
myosin binding protein C, slow-type|Mybpc1	1.599328	0.084026
myosin, heavy polypeptide 1, skeletal muscle, adult|Myh1	1.594162	0.009398
mitochondrially encoded NADH dehydrogenase 2|ND2	1.396794	0.017172
mitochondrially encoded cytochrome c oxidase III|COX3	1.197349	0.09742
Expression decreased in β-DKO Ins vs β-DKO PBS		
aldolase A, fructose-bisphosphate|Aldoa	1.209698	0.09742
ryanodine receptor 1, skeletal muscle|Ryr1	1.287901	0.055235
myosin binding protein C, fast-type|Mybpc2	1.417734	0.008806
dual specificity phosphatase 1|Dusp1	1.439174	0.080173
tropomyosin 1, alpha|Tpm1	1.511536	9.97E-07
myosin, heavy polypeptide 4, skeletal muscle|Myh4	1.697096	4.00E-21
frizzled class receptor 7|Fzd7	1.983316	0.000208
tectonin beta-propeller repeat containing 2|Tecpr2	2.165953	0.007169
potassium voltage-gated channel, subfamily G, member 4|Kcng4	2.625393	0.010772
potassium voltage-gated channel, subfamily F, member 1|Kcnf1	2.877588	0.015407
upstream transcription factor family member 3|Usf3	2.961892	5.16E-09
RPTOR independent companion of MTOR, complex 2|Rictor	3.522655	1.16E-05
cadherin 4|Cdh4	4.737905	3.12E-05
Myosin regulatory light chain 12B|-	13.11259	0.056071
aldolase A, fructose-bisphosphate|Aldoa	1.209698	0.09742
ryanodine receptor 1, skeletal muscle|Ryr1	1.287901	0.055235
myosin binding protein C, fast-type|Mybpc2	1.417734	0.008806
dual specificity phosphatase 1|Dusp1	1.439174	0.080173
tropomyosin 1, alpha|Tpm1	1.511536	9.97E-07
myosin, heavy polypeptide 4, skeletal muscle|Myh4	1.697096	4.00E-21
frizzled class receptor 7|Fzd7	1.983316	0.000208
tectonin beta-propeller repeat containing 2|Tecpr2	2.165953	0.007169
potassium voltage-gated channel, subfamily G, member 4|Kcng4	2.625393	0.010772
potassium voltage-gated channel, subfamily F, member 1|Kcnf1	2.877588	0.015407
upstream transcription factor family member 3|Usf3	2.961892	5.16E-09
RPTOR independent companion of MTOR, complex 2|Rictor	3.522655	1.16E-05
cadherin 4|Cdh4	4.737905	3.12E-05

Supplementary Table 4: Transcripts differentially expressed in soleus muscle between β-DKO mice treated with PBS and insulin.

	Fold change	False discovery rate
Expression increased in β-DKO Ins vs β-DKO PBS		
B cell leukemia/lymphoma 3|Bcl3	0.08841787	0.02524168
ankyrin repeat domain 1 (cardiac muscle)|-	0.09930934	0.00164911
predicted gene 13889|Gm13889	0.11185993	2.6666E-10
hemoglobin alpha, adult chain 1|Hba-a1	0.12352729	0.02045674
hemoglobin, beta adult t chain|Hbb-bt	0.17792673	0.03952168
ankyrin repeat domain 35|Ankrd35	0.17805746	0.00783436
leucine rich repeat containing 38|Lrrc38	0.18410922	0.00013545
CD68 antigen|Cd68	0.18857368	0.03952168
heat shock protein 1B|Hspa1b	0.18861857	0.00036588
potassium voltage-gated channel, subfamily G, member 2|Kcng2	0.23013122	0.04990613
cytochrome P450, family 39, subfamily a, polypeptide 1|Cyp39a1	0.24787265	0.01905892
phosphodiesterase 4B, cAMP specific|Pde4b	0.26250656	0.01421318
heat shock protein 1|Hspb1	0.26311706	0.00732982
H4 clustered histone 9|H4c9	0.2717768	0.01890276
dual specificity phosphatase 10|Dusp10	0.27977918	0.01619584
predicted gene 3893|-	0.28164255	0.03952168
heat shock protein 1A|Hspa1a	0.31126719	0.00192608
Expression increased in β-DKO Ins vs β-DKO PBS		
phosphoenolpyruvate carboxykinase 1, cytosolic|Pck1	27.9690394	0.03538523
dachshund family transcription factor 1|Dach1	14.9714951	1.7965E-11
predicted gene 20547|-	8.9544479	0.00141646
pentraxin 4|Ptx4	8.48018996	2.8531E-06
adenomatosis polyposis coli down-regulated 1|-	8.32195377	0.00471186
phosphodiesterase 3B, cGMP-inhibited|Pde3b	8.107231	0.00642456
solute carrier family 4 (anion exchanger), member 4|Slc4a4	8.09514442	0.01391817
NCK-associated protein 5|Nckap5	7.91214405	0.01378667
ADAMTS-like 1|Adamtsl1	7.88757225	0.00642456
HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2|Hecw2	6.66513645	0.00471186
phospholipase C, beta 1|Plcb1	6.40426037	0.000363
acyl-CoA thioesterase 1|Acot1	6.23687792	0.01064114
family with sequence similarity 117, member B|Fam117b	5.43000925	0.01504768
flavin containing monooxygenase 2|Fmo2	5.24272618	0.000363
RIKEN cDNA 9930111J21 gene 1|9930111J21Rik1	5.12557903	0.01382766
fibronectin 1|Fn1	4.99108511	0.00037872
butyrophilin-like 9|Btnl9	4.83043807	0.00642456
C1q and tumor necrosis factor related protein 1|C1qtnf1	4.77202699	0.04353263
reelin|Reln	4.74882176	0.00192608
ajuba LIM protein|Ajuba	4.46017912	0.00960412

predicted gene, 26566|-	4.424546	0.01582583
myelin basic protein expression factor 2, repressor|Myef2	4.29026669	0.00642456
DEPP1 autophagy regulator|Depp1	4.18411514	0.00192608
Kruppel-like factor 13|Klf13	4.18039964	0.01150915
guanine deaminase|Gda	4.14941667	0.00564087
Rap guanine nucleotide exchange factor (GEF) 5|Rapgef5	3.99789603	0.03043476
ATPase, Ca++ transporting, plasma membrane 4|Atp2b4	3.89576952	0.00471186
guanylate binding protein 7|Gbp7	3.81208348	0.02371283
angiomotin-like 2|Amotl2	3.72335557	0.00783436
papilin, proteoglycan-like sulfated glycoprotein|Papln	3.62550159	0.00643268
protein tyrosine phosphatase, receptor type, B|Ptprb	3.61551009	0.00036588
MAM domain containing 2|Mamdc2	3.61063068	0.01796555
cellular communication network factor 3|Ccn3	3.60055621	0.04016193
ATP-binding cassette, sub-family B (MDR/TAP), member 1A|Abcb1a	3.593384	0.00164911
bone morphogenetic protein 6|-	3.55786969	0.017957
junctional cadherin 5 associated|Jcad	3.55134259	0.00037872
slit guidance ligand 3|Slit3	3.46589552	0.00643268
tissue inhibitor of metalloproteinase 3|Timp3	3.44971659	0.01382766
golgi associated kinase 1B|Gask1b	3.44087829	0.00564087
phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2|Prex2	3.43321303	0.01796555
LIF receptor alpha|Lifr	3.42774368	0.04353263
forkhead box K1|Foxk1	3.4257517	0.03952168
shroom family member 4|Shroom4	3.27099122	0.02606346
ATP-binding cassette, sub-family A (ABC1), member 5|Abca5	3.24054358	0.00564087
mcf.2 transforming sequence-like|Mcf2l	3.17635601	0.00642456
folliculin interacting protein 2|Fnip2	3.17305993	0.03043476
zinc finger and BTB domain containing 10|Zbtb10	3.08119871	0.03952168
adhesion G protein-coupled receptor F5|Adgrf5	3.05350087	0.03538523
jagged 1|Jag1	3.02933175	0.03952168
SMAD family member 7|Smad7	3.00268082	0.03952168
early B cell factor 1|Ebf1	2.99380555	0.03952168
integrin alpha 6|Itga6	2.94607614	0.017957
plexin A2|Plxna2	2.93543586	0.0437692
caveolae associated 2|Cavin2	2.85356232	0.00732982
Von Willebrand factor|Vwf	2.58427128	0.04105607
proline rich 13|Prr13	0.36175919	0.04505914
rhomboid like 1|Rhbdl1	0.32862046	0.00642456
tenascin C|Tnc	0.32746827	0.02732075

Supplementary Table 5: Gene Ontology biological process results based on transcripts differentially expressed in EDL muscle between control fl/fl mice and β-DKO mice obtained from the Mouse Portal of the Rate Genome Database.

biological process	p value
muscle contraction	7.31E-12
muscle system process	3.20E-11
voluntary skeletal muscle contraction	4.53E-09
twitch skeletal muscle contraction	4.53E-09
striated muscle contraction	5.01E-08
slow-twitch skeletal muscle fiber contraction	9.39E-08
skeletal muscle contraction	3.36E-07
multicellular organismal movement	1.46E-06
musculoskeletal movement	1.46E-06
transition between fast and slow fiber	2.77E-06
regulation of the force of skeletal muscle contraction	8.34E-06
regulation of skeletal muscle contraction by chemo-mechanical energy conversion	8.34E-06
regulation of skeletal muscle adaptation	1.27E-05

Supplementary Table 6: Gene Ontology biological process results based on transcripts differentially expressed in soleus muscle between control fl/fl mice and β-DKO mice obtained from the Mouse Portal of the Rate Genome Database.

biological process	p value
tissue development	4.21E-23
anatomical structure development	1.39E-21
multicellular organism development	1.14E-20
extracellular matrix organization	1.82E-20
developmental process	1.85E-20
external encapsulating structure organization	2.26E-20
extracellular structure organization	2.26E-20
system development	2.31E-20
animal organ development	4.92E-19
collagen fibril organization	5.35E-18
positive regulation of cellular process	5.00E-16
positive regulation of biological process	5.26E-16
anatomical structure morphogenesis	3.56E-15
circulatory system development	4.78E-15
regulation of locomotion	5.21E-15
regulation of cell migration	5.24E-15
regulation of cell motility	1.32E-14
cell differentiation	2.06E-14
cellular developmental process	2.82E-14
regulation of multicellular organismal process	3.40E-14
regulation of programmed cell death	1.18E-13
negative regulation of cellular process	1.56E-13
regulation of developmental process	2.43E-13
cell adhesion	5.88E-13
regulation of apoptotic process	7.30E-13
negative regulation of biological process	8.39E-13
cellular response to chemical stimulus	8.51E-13
regulation of cell differentiation	1.35E-12
skeletal system development	3.71E-12
response to organic substance	4.60E-12
regulation of cell population proliferation	6.69E-12
vasculature development	2.03E-11
tube development	5.58E-11
response to external stimulus	8.56E-11
blood vessel development	8.59E-11
supramolecular fiber organization	1.03E-10
regulation of response to stimulus	1.29E-10
regulation of cell adhesion	1.40E-10
cellular response to oxygen-containing compound	2.33E-10
cell development	2.85E-10

biological regulation	3.26E-10
regulation of cellular process	7.32E-10
response to chemical	7.38E-10
tube morphogenesis	7.72E-10
homeostatic process	7.76E-10
positive regulation of cell migration	8.40E-10
cellular response to organic substance	1.02E-09
regulation of biological process	1.18E-09
response to acid chemical	1.28E-09
negative regulation of programmed cell death	1.98E-09
positive regulation of cell motility	2.46E-09
multicellular organismal-level homeostasis	2.67E-09
multicellular organismal process	2.78E-09
negative regulation of developmental process	2.82E-09
response to cytokine	2.96E-09
connective tissue development	3.00E-09
positive regulation of locomotion	4.52E-09
regulation of metabolic process	5.94E-09
ossification	6.55E-09
negative regulation of apoptotic process	7.14E-09
cell population proliferation	9.51E-09
cell surface receptor signaling pathway	1.11E-08
heart development	1.20E-08
positive regulation of metabolic process	1.26E-08
response to oxygen-containing compound	1.43E-08
anatomical structure formation involved in morphogenesis	1.77E-08
epithelium development	1.98E-08
response to endogenous stimulus	2.34E-08
cell migration	2.60E-08
sensory perception of chemical stimulus	2.63E-08
positive regulation of programmed cell death	2.99E-08
regulation of multicellular organismal development	3.38E-08
response to organonitrogen compound	3.68E-08
cartilage development	3.70E-08
cellular response to acid chemical	4.84E-08
nervous system development	5.80E-08
response to lipid	5.87E-08
regulation of response to external stimulus	6.24E-08
regulation of signaling	6.40E-08
negative regulation of multicellular organismal process	6.99E-08
enzyme-linked receptor protein signaling pathway	7.67E-08
regulation of signal transduction	8.23E-08
cellular response to cytokine stimulus	8.85E-08
blood vessel morphogenesis	1.03E-07
animal organ morphogenesis	1.22E-07
regulation of primary metabolic process	1.24E-07

sensory perception of smell	1.29E-07
positive regulation of apoptotic process	1.36E-07
positive regulation of nitrogen compound metabolic process	1.54E-07
muscle tissue development	1.58E-07
cellular process	1.76E-07
regulation of cellular component organization	1.82E-07
positive regulation of cell adhesion	2.16E-07
regulation of cellular metabolic process	2.27E-07
negative regulation of cell differentiation	2.35E-07
positive regulation of cellular metabolic process	2.53E-07
bone development	2.72E-07
response to inorganic substance	2.73E-07
positive regulation of cell differentiation	2.74E-07
regulation of cell communication	3.16E-07
regulation of epithelial cell proliferation	3.25E-07
cellular component organization	3.66E-07
response to nitrogen compound	4.08E-07
cell motility	4.11E-07
response to amino acid	4.81E-07
cellular response to stimulus	5.37E-07
skeletal system morphogenesis	5.73E-07
regulation of cell-substrate adhesion	5.86E-07
negative regulation of immune system process	5.93E-07
positive regulation of macromolecule metabolic process	7.22E-07
positive regulation of cell population proliferation	8.29E-07
positive regulation of cellular component organization	8.35E-07
chondrocyte differentiation	8.85E-07
embryo development	8.91E-07
regulation of cell development	9.34E-07
positive regulation of multicellular organismal process	1.00E-06
cell-substrate adhesion	1.04E-06
renal system development	1.22E-06
positive regulation of biosynthetic process	1.35E-06
positive regulation of cell-substrate adhesion	1.38E-06
regulation of macromolecule metabolic process	1.48E-06
apoptotic process	1.51E-06
regulation of substrate adhesion-dependent cell spreading	1.63E-06
positive regulation of developmental process	1.63E-06
regulation of cell activation	1.74E-06
regulation of immune system process	2.05E-06
regulation of fat cell differentiation	2.12E-06
positive regulation of cellular biosynthetic process	2.14E-06
regulation of phosphate metabolic process	2.18E-06
regulation of phosphorus metabolic process	2.20E-06
regulation of nitrogen compound metabolic process	2.25E-06
negative regulation of cell adhesion	2.31E-06

kidney development	2.31E-06
regulation of myotube differentiation	2.33E-06
regulation of biosynthetic process	2.56E-06
positive regulation of signal transduction	2.61E-06
regulation of smooth muscle cell migration	2.66E-06
negative regulation of cell population proliferation	2.85E-06
cellular component organization or biogenesis	3.34E-06
biomineral tissue development	3.42E-06
skeletal muscle cell differentiation	3.71E-06
positive regulation of smooth muscle cell migration	3.71E-06
positive regulation of signaling	3.82E-06
response to stress	3.85E-06
response to stimulus	3.96E-06
regulation of gene expression	4.34E-06
epithelial cell proliferation	4.94E-06
response to hormone	5.07E-06
cellular response to amino acid stimulus	5.14E-06
regulation of cellular biosynthetic process	5.28E-06
transmembrane receptor protein tyrosine kinase signaling pathway	5.65E-06
programmed cell death	5.77E-06
cell death	5.91E-06
sensory perception	6.22E-06
positive regulation of cell communication	6.23E-06
regulation of phosphorylation	6.56E-06
positive regulation of response to stimulus	6.59E-06
negative regulation of response to stimulus	8.72E-06
regulation of small molecule metabolic process	8.79E-06
positive regulation of DNA-templated transcription	9.51E-06
regulation of intracellular signal transduction	9.84E-06
positive regulation of RNA biosynthetic process	1.00E-05
endothelium development	1.01E-05
bone trabecula morphogenesis	1.03E-05
positive regulation of transcription by RNA polymerase II	1.16E-05
collagen metabolic process	1.22E-05
negative regulation of locomotion	1.27E-05
regulation of catalytic activity	1.27E-05
tendon development	1.30E-05
regulation of cold-induced thermogenesis	1.34E-05
tissue morphogenesis	1.36E-05
muscle structure development	1.40E-05
positive regulation of epithelial cell proliferation	1.49E-05
response to molecule of bacterial origin	1.51E-05
regulation of extracellular matrix organization	1.69E-05
regulation of molecular function	1.76E-05
bone mineralization	1.88E-05
endothelial cell differentiation	1.97E-05

chondrocyte development	2.20E-05
cellular response to lipid	2.26E-05
homeostasis of number of cells	2.37E-05
response to lipopolysaccharide	2.42E-05
intracellular signal transduction	2.42E-05
angiogenesis	2.55E-05
positive regulation of protein metabolic process	2.75E-05
endochondral bone morphogenesis	3.10E-05
regeneration	3.17E-05
response to abiotic stimulus	3.28E-05
response to wounding	3.41E-05
positive regulation of cell projection organization	3.42E-05
regulation of biological quality	3.56E-05
positive regulation of smooth muscle cell proliferation	3.64E-05
locomotion	3.77E-05
regulation of neuron projection development	4.06E-05
wound healing	4.15E-05
regulation of body fluid levels	4.27E-05
negative regulation of cell motility	4.43E-05
cellular response to endogenous stimulus	4.44E-05
endothelial cell development	4.48E-05
regulation of anatomical structure size	4.88E-05
trabecula morphogenesis	5.00E-05
chemotaxis	5.12E-05
positive regulation of RNA metabolic process	5.21E-05
taxis	5.41E-05
response to extracellular stimulus	5.69E-05
negative regulation of leukocyte activation	5.86E-05
artery morphogenesis	5.88E-05
bone trabecula formation	5.89E-05
positive regulation of cell development	5.98E-05
negative regulation of metabolic process	6.02E-05
cellular response to oxidative stress	6.43E-05
regulation of inflammatory response	6.75E-05
positive regulation of macromolecule biosynthetic process	7.09E-05
regulation of anatomical structure morphogenesis	7.17E-05
muscle organ development	7.41E-05
regulation of leukocyte activation	7.46E-05
tissue remodeling	7.47E-05
positive regulation of catalytic activity	8.24E-05
regulation of DNA-templated transcription	9.03E-05
negative regulation of cell migration	9.20E-05
neutrophil homeostasis	9.21E-05
response to oxidative stress	9.23E-05
neurogenesis	9.34E-05
regulation of RNA metabolic process	9.42E-05

regulation of RNA biosynthetic process	9.54E-05