

Supplemental Material (Scharf et al.)

Supplementary Table S1

DESCRIPTION	LOCUS	MK2/3 ^{-/-}
ANGIOGENESIS		
angiopoietin 1	Angpt1	2.324
angiopoietin-like 7	Angptl7	5.202
CD55 antigen	Cd55	-1.622
CARBOHYDRATE METABOLISM		
<i>aldolase A, fructose-bisphosphate</i>	Aldoa	-1.649
<i>enolase 3, beta muscle</i>	Eno3	-1.711
fructose bisphosphatase 2	Fbp2	1.504
glycogen synthase 1, muscle	Gys1	2.632
lactate dehydrogenase B	Ldhb	1.444
phosphoenolpyruvate carboxykinase 1, cytosolic	Pck1	1.486
phosphoglycerate kinase 1 (Pgk1)	Pgk1	-1.935
CELL GROWTH		
insulin-like growth factor binding protein 6	Igfbp6	1.555
myostatin	Mstn	-2.542
myogenin	Myog	1.344
CONTRACTILE APPARATUS		
actin, alpha 1, skeletal muscle	Acta1	1.005
myosin binding protein C, slow-type	Mybpc1	2.363
myosin binding protein C, fast-type	Mybpc2	-3.788
myosin binding protein H	Mybph	2.251
myosin, heavy polypeptide 1 (d/x), skeletal muscle, adult	Myh1	-2.289
myosin, heavy polypeptide 2 (IIa), skeletal muscle, adult	Myh2	1.581
myosin, heavy polypeptide 3, skeletal muscle, embryonic	Myh3	3,208
myosin, heavy polypeptide 4 (IIb), skeletal muscle	Myh4	-2.227
myosin, heavy polypeptide 6, cardiac muscle, alpha	Myh6	1,594
myosin, heavy polypeptide 7 (I/β), cardiac muscle, beta	Myh7	1.718
myosin, light polypeptide 1, MLC1F/MLC3F	Myll	-2.478
myosin, light polypeptide 3, MLC1v/MLC1s	Myl3	1.370
myosin light chain, phosphorylatable, fast skeletal muscle	Mylpf	-1.784
PDZ and LIM domain 3	Pdlim3	1.159
troponin I, skeletal, slow 1	Tnni1	1.329
troponin I, skeletal, fast 2	Tnni2	-1.469
troponin T1, skeletal, slow	Tnnt1	1.457
FAT METABOLISM		
ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1a	1.350
ATP-binding cassette, sub-family D (ALD), member 2	Abcd2	2.065
acyl-Coenzyme A dehydrogenase, short chain	Acads	1.495
catalase	Cat	1.810
CD36 antigen	Cd36	1.751
carnitine palmitoyltransferase 1b, muscle	Cpt1b	2.000
fatty acid binding protein 3, muscle and heart	Fabp3	1.760
fatty acid binding protein 5, epidermal	Fabp5	-1.371
fatty acid synthase	Fasn	2.032
Lipase, hormone sensitive	Lipe	1.576
lipoprotein lipase	Lpl	1.670
pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	1.362
resistin	Retn	2.046
stearoyl-Coenzyme A desaturase 1	Scd1	1.662
solute carrier family 27	Slc27a1	1.893
uncoupling protein 3	Ucp3	1.388
UEV and lactate/malate dehydrogenase domains	Uevld	2.355
HEAT SHOCK RESPONSE		
crystallin, alpha B	Cryab	2.163
heat shock protein 1	Hspb1	1.712

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<p>INTERSTITIAL TISSUE COMPONENT / EXTRACELLULAR MATRIX collagen, type XVI, alpha 1 collagen, type I, alpha 1 matrix metalloproteinase 2 tissue inhibitor of metalloproteinase 2 tenascin C Tenomodulin</p>	<p>Coll16a1 Coll1a1 Mmp2 Timp2 Tnc Tnmd</p>	<p>1.652 1.597 1.658 1.855 4.979 5.219</p>
<p>MITOCHONDRIAL PROTEINS ATP synthase, H⁺ transporting, mitochondrial F1 complex, alpha subunit 1 ATP synthase, H⁺ transporting, mitochondrial F1 complex, beta subunit mitochondrially encoded cytochrome c oxidase I mitochondrially encoded cytochrome c oxidase II mitochondrially encoded cytochrome c oxidase III <i>microsomal glutathione S-transferase 1</i> microsomal glutathione S-transferase 2 NADH dehydrogenase (ubiquinone) flavoprotein 1 NADH dehydrogenase (ubiquinone) flavoprotein 2 NADH dehydrogenase (ubiquinone) flavoprotein 3 pyruvate dehydrogenase complex, component X solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), member 20 solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25 superoxide dismutase 2, mitochondrial</p>	<p>Atp5a1 Atp5b COX1 COX2 COX3 <i>Mgst1</i> Ndufv1 Ndufv2 Ndufv3 Mgst2 Pdhx Slc25a20 Slc25a25 Sod2</p>	<p>1.725 1.844 2.153 1.610 1.368 -1.575 1.761 1.592 1.975 1.753 1.627 1.602 2.876 2.060</p>
<p>OXYGEN CARRIERS hemoglobin, beta adult major chain myoglobin <i>solute carrier family 38, member 4</i></p>	<p>Hbb-b2 Mb <i>Slc38a4</i></p>	<p>1.819 1.479 -1.824</p>
<p>TRANSCRIPTION ankyrin repeat domain 2 <i>calcium channel, voltage-dependent, L type, skeletal muscle, Cav1.1</i> CCAAT/enhancer binding protein (C/EBP), delta cAMP responsive element binding protein 1 <i>E2F transcription factor 2</i> <i>early growth response 1</i> HOP homeobox Jun oncogene myocyte enhancer factor 2C nuclear factor of activated T-cells, cytoplasmic nuclear receptor subfamily 4, group A, member 2 nuclear respiratory factor 1 paired box gene 7 Plexin A1 peroxisome proliferative activated receptor, gamma, coactivator 1 alpha, PGC-1α <i>retinol binding protein 1, cellular</i> <i>serum response factor</i></p>	<p>Ankrd2 <i>Cacna1s</i> Cebpd Creb1 <i>E2f2</i> <i>Egr1</i> Hopx Jun Mef2c Nfatc1 Nr4a2 Nrf1 Pax7 Plxna1 Ppargc1a <i>Rbp1</i> <i>Srf</i></p>	<p>3.631 -1.030 2.010 1.830 -1.096 -1.926 1.026 1.568 1.702 2.712 3.079 2.040 2.627 1.130 2.456 -2.282 -1.025</p>
<p>TRANSPORT ATPase, Ca²⁺ transporting (<i>SERCA1</i>), fast twitch 1 ATPase, Ca²⁺ transporting (<i>SERCA2</i>), slow twitch 2 Phospholamban ryanodine receptor 1, skeletal muscle (Ryr1) ryanodine receptor 2, cardiac (Ryr2) sodium channel, voltage-gated, type V, alpha solute carrier family 2 (facilitated glucose transporter), member 1 solute carrier family 1 (neutral amino acid transporter), member 5 sodium/calcium exchanger, member 1, NCX1 <i>sodium/calcium exchanger, member 2, NCX2</i> <i>sodium/calcium exchanger, member 3, NCX3</i> <i>transporter 1, ATP-binding cassette</i> Transferrin</p>	<p><i>Atp2a1</i> Atp2a2 Pln/Plb RyR1 RyR2 Scn5a Slc2a1 Slc1a5 Slc8a1 <i>Slc8a2</i> <i>Slc8a3</i> <i>Tap1</i> Trf</p>	<p>-1.570 3.148 1.204 1.110 1.106 1.556 1.002 4.620 1.300 -1.062 -1.352 -2.736 1.539</p>

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OTHERS		
adrenergic receptor, beta 3	Adrb3	2.435
annexin A6	Anxa6	2.105
aldehyde dehydrogenase family 3, subfamily A1	Aldh3a1	1.977
arrestin domain containing 2	Arrdc2	3.173
cDNA sequence BC053393	BC053393	-5.625
calsequestrin 1, fast type skeletal muscle isoform	Casq1	-1.362
calsequestrin 2, cardiac muscle isoform	Casq2	1.812
calcium/calmodulin-dependent protein kinase II, alpha	Camk2a	1.158
calcium/calmodulin-dependent protein kinase II, beta	Camk2b	1.047
calcium/calmodulin-dependent protein kinase II, gamma	Camk2d	1.250
carbonic anhydrase 3	Car3	1.295
carbonic anhydrase 4	Car4	1.231
cartilage intermediate layer protein 2	Cilp2	3.021
cadherin 15	Cdh15	2.090
creatine kinase, muscle	Ckm	-1.572
cartilage oligomeric matrix protein	Comp	4.296
cytochrome P450, family 2, subfamily e, polypeptide 1	Cyp2e1	1.274
gelsolin	Gsn	2.610
metallothionein 2	Mt2	4.452
myomesin family, member 3	Myom3	1.810
Ngfi-A binding protein 1	Nab1	-1.033
Ngfi-A binding protein 2	Nab2	1.047
protein tyrosine phosphatase-like, member b	Ptpfb	1.415
parvalbumin	Pvalb	-3.504
suprabasin	Sbsn	2.139
sarcophilin	Sln	-1.185
tropomodulin 3	Tmod3	-2.081
xin actin-binding repeat containing 1	Xirp1	2.169

Table S1 Effects of MK2/3-deficiency on the expression of functional groups of fiber type-specific genes identified by DNA microarray analysis. Shown is a set of transcripts filtered for genes characteristic of fast and slow muscle fiber types in addition to other classified genes. Changes in mRNA expression in MK2/3^{-/-} compared with WT soleus, as revealed by DNA microarray analysis, with down-regulated genes shown in bold. Each sample was pooled from soleus of three mice. Data are the average of n=3 samples in each group.

Beside the altered expression of genes implicated in fiber type-specific gene expression, some of the genes found to be up-regulated in MK2/3-deficient soleus encode for proteins involved in regeneration/repair processes, such as embryonic MyHC (Myh3; see also Fig. 3B) and α -cardiac MyHC (Myh6), both markers of newly forming myofibers in regenerating muscle (1). Further up-regulated genes are involved in satellite cells activation (11), such as cadherin 15 (Cdh15) and paired box gene 7 (Pax7; see also Fig. 3B). Regeneration requires proliferation of myogenic and non-myogenic cells, often accompanied by increased amounts of connective tissue formation (1). Together with increased expression of components of the extracellular matrix as found in the endo- and epimysium of muscle fibers, like tenomodulin (Tnmd) and collagen type I (Coll1a1), and of a marker of collagen processing, matrix

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matrix metalloproteinase 2 (Mmp2), the data imply a regeneration/repair process in soleus muscle from MK2/3^{-/-} mice.

This process might be caused by down-regulation of myostatin (Mstn), a negative regulator of satellite activation (9), together with increased p38 γ signaling which positively regulates the expansion of amplifying satellite cells (7). Since regeneration and repair can result from intense, but also from continuous contractile activity (10), slow fiber-rich muscles contain more satellite cells than fast muscles (6), and are suggested to have a higher turnover rate during normal physiological maintenance of the muscle. Therefore, data indicating a regeneration/repair process are in line with the increased content of slow and decreased number of fast fibers in MK2/3-deficient soleus. Alternatively, given that p38 and MK2/3 are involved in the cellular response to a variety of stress stimuli including oxidative stress (5), the cellular response to oxidative or even mechanical stress stimuli might be somewhat hampered by MK2/3 ablation thus inducing the regeneration processes. Accordingly, the mRNA for matrix metalloproteinase 2, important for elevated collagen processing and biosynthesis following mechanical stress (8), and tenascin C of the endomysium, essential for full-scale muscle damage repair (2, 4), are elevated in MK2/3-deficient soleus. In addition, heat shock proteins as markers for fiber transformation resulting from enhanced neuromuscular activity are enhanced (3).

Supplementary Table S2

DESCRIPTION	LOCUS	MK2/3 ^{-/-}
TRANSCRIPTION <i>early growth response 1</i> myocyte enhancer factor 2C peroxisome proliferative activated receptor, gamma, coactivator 1 alpha, PGC-1 α <i>serum response factor</i>	<i>Egr1</i> Mef2c Ppargc1a <i>Srf</i>	-2.034 1.172 2.156 -1.015
TRANSPORT ATPase, Ca ²⁺ transporting (SERCA2), slow twitch 2 <i>calcium channel, voltage-dependent, L type, cardiac, Cav1.2a</i> Phospholamban ryanodine receptor 2, cardiac (Ryr2) sodium/calcium exchanger, member 1, NCX1 sodium/calcium exchanger, member 3, NCX3	Atp2a2 <i>Cacna1c</i> Pln/Plb RyR2 Slc8a1 Slc8a3	3.148 -1.015 1.014 1.106 1.150 1.103
OTHERS actin, alpha 1, skeletal muscle calsequestrin 2, cardiac muscle isoform calcium/calmodulin-dependent protein kinase II, alpha calcium/calmodulin-dependent protein kinase II, beta calcium/calmodulin-dependent protein kinase II, gamma myosin, heavy polypeptide 7 (I/ β), cardiac muscle, beta natriuretic peptide precursor typeA, atrial natriuretic factor (ANF) natriuretic peptide precursor typeB, brain natriuretic peptide (BNP)	Acta1 Casq2 Camk2a Camk2b Camk2d Myh7 Nppa Nppb	1.032 1.012 1.880 1.971 1.750 1.103 1.057 1.098

Table S2 Effects of MK2/3-deficiency on the expression of selected genes in the heart determined by DNA microarray analysis. Changes in transcript levels are shown for a filtered set of genes encoding for transcription factors, transporters, Ca²⁺-handling proteins, and markers for hypertrophy in MK2/3^{-/-} vs. WT heart. Down-regulated genes are indicated in bold. Each sample was pooled from the heart of three mice.

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