Supporting Information File: DEPDC5 muscle specific inducible knockout

Skeletal Muscle Specific Knockout of DEPDC5 Increases mTORC1 Signaling,

Muscle Cell Hypertrophy, and Mitochondrial Respiratory Capacity

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Running Title: DEPDC5 muscle specific inducible knockout

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Supporting Information File

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	Sex:		Male	-			Female			
Data Type	МНС Туре	WT (n=5)	KO (n=6)	%dif	Р	WT (n=5)	KO (n=8)	%dif	Р	
SOL CSA µm ²	MHC 1	1322.4 ± 43.5	1458.5 ± 52.6	13.2	0.034	1252.2 ± 48.2	1168.0 ± 59.1	-6.7	0.341	
	MHC 2a	1132.7 ± 42.9	1320.5 ± 71.8	19.2	0.036	1069.9 ± 80.9	998.2 ± 50.6	6.7	0.443	
	MHC 2x	1304.8 ± 56.9	1588.2 ± 63.8	21.7	0.010	1196.9 ± 150.6	1055.1 ± 51.2	-11.8	0.310	
	MHC 2b	1418.3 ± 197.6	1391.6 ± 8.8	-1.9	0.933	N/A	2068.3a	N/A	N/A	
	combined	1227.6 ± 34.5	1424.0 ± 61.4	16.0	0.027	1161.1 ± 63.2	1089.1 ± 54.8	-6.2	0.418	
SOL Fiber Type Distribution %	MHC 1	37.0±2.0	34.0 ± 1.1	-8.2	0.206	45.2 ± 2.4	45.4 ± 2.1	0.6	0.937	
	MHC 2a	51.1 ± 1.6	$54.2\ \pm 1.2$	6.1	0.153	48.2 ± 2.4	$45.6\ \pm 2.0$	-5.5	0.420	
	MHC 2x	10.1 ± 0.76	9.9 ± 1.00	-2.4	0.859	6.6 ± 1.3	8.1 ± 1.2	23.8	0.396	
	MHC 2b	1.66 ± 0.72	1.85 ± 1.33	11.4	0.908	0.0	0.82 ± 0.77	N/A	0.452	
		Male								
	Sex:		Male				Female			
Data Type	Sex: MHC Type	WT (n=8)	Male KO (n=5)	%dif	Р	WT (n=5)	Female KO (n=8)	%dif	Р	
Data Type	Sex: MHC Type MHC 1	WT (n=8) 501.8 ± 88.5	Male KO (n=5) 424.7 a	%dif N/A	P N/A	WT (n=5) N/A	Female KO (n=8)	%dif N/A	P N/A	
Data Type	Sex: MHC Type MHC 1 MHC 2a	WT (n=8) 501.8 ± 88.5 865.4 ± 64.1	Male KO (n=5) 424.7 a 1012.3 ± 42.8	%dif N/A 17.0	P N/A 0.089	WT (n=5) N/A 841.0 ± 89.1	Female KO (n=8) 757.6 ± 64.4	%dif N/A -9.9	P N/A 0.454	
Data Type TA CSA	Sex: MHC Type MHC 1 MHC 2a MHC 2x	WT (n=8) 501.8 ± 88.5 865.4 ± 64.1 1557.6 ± 128.5	Male KO (n=5) 424.7 a 1012.3 ± 42.8 1546.4 ± 49.8	%dif N/A 17.0 -0.7	P N/A 0.089 0.634	WT (n=5) N/A 841.0 ± 89.1 1435.1 ± 163.4	Female KO (n=8) 757.6 ± 64.4 1152.5 ± 91.1	%dif N/A -9.9 -19.7	P N/A 0.454 0.128	
Data Type TA CSA µm ²	Sex: MHC Type MHC 1 MHC 2a MHC 2x MHC 2b	WT (n=8) 501.8 ± 88.5 865.4 ± 64.1 1557.6 ± 128.5 2614.4 ± 144.6	Male KO (n=5) 424.7 a 1012.3 ± 42.8 1546.4 ± 49.8 2689.7 ± 47.7	%odif N/A 17.0 -0.7 2.9	P N/A 0.089 0.634 0.937	WT (n=5) N/A 841.0 ± 89.1 1435.1 ± 163.4 2451.8 ± 185.3	Female KO (n=8) 757.6 ± 64.4 1152.5 ± 91.1 2082.6 ± 181.1	%dif N/A -9.9 -19.7 -15.1	P N/A 0.454 0.128 0.204	
Data Type TA CS A µm ²	Sex: MHC Type MHC 1 MHC 2a MHC 2x MHC 2b combined	WT (n=8) 501.8 ± 88.5 865.4 ± 64.1 1557.6 ± 128.5 2614.4 ± 144.6 1812.7 ± 125.9	MaleKO (n=5) $424.7 a$ 1012.3 ± 42.8 1546.4 ± 49.8 2689.7 ± 47.7 2081.6 ± 127.5	%dif N/A 17.0 -0.7 2.9 14.8	P N/A 0.089 0.634 0.937 0.164	WT (n=5) N/A 841.0 ± 89.1 1435.1 ± 163.4 2451.8 ± 185.3 1868.8 ± 133.5	Female KO (n=8) 757.6 ± 64.4 1152.5 ± 91.1 2082.6 ± 181.1 1633.0 ± 143.2	%dif N/A -9.9 -19.7 -15.1 -12.6	P N/A 0.454 0.128 0.204 0.287	
Data Type TA CSA μm ²	Sex: MHC Type MHC 1 MHC 2a MHC 2x MHC 2b combined MHC 1	WT (n=8) 501.8 ± 88.5 865.4 ± 64.1 1557.6 ± 128.5 2614.4 ± 144.6 1812.7 ± 125.9 1.0 ± 0.34	MaleKO (n=5) $424.7 a$ 1012.3 ± 42.8 1546.4 ± 49.8 2689.7 ± 47.7 2081.6 ± 127.5 0.2 ± 0.2	%dif N/A 17.0 -0.7 2.9 14.8 -79.3	P N/A 0.089 0.634 0.937 0.164 0.051	WT (n=5) N/A 841.0 ± 89.1 1435.1 ± 163.4 2451.8 ± 185.3 1868.8 ± 133.5 0.0	FemaleKO (n=8) 757.6 ± 64.4 1152.5 ± 91.1 2082.6 ± 181.1 1633.0 ± 143.2 0.1 ± 0.06	%dif N/A -9.9 -19.7 -15.1 -12.6 N/A	P N/A 0.454 0.128 0.204 0.287 0.453	
Data Type TA CSA µm ² TA Fiber Type	Sex: MHC Type MHC 1 MHC 2a MHC 2x MHC 2b combined MHC 1 MHC 2a	WT (n=8) 501.8 ± 88.5 865.4 ± 64.1 1557.6 ± 128.5 2614.4 ± 144.6 1812.7 ± 125.9 1.0 ± 0.34 17.3 ± 4.9	MaleKO (n=5) $424.7 a$ 1012.3 ± 42.8 1546.4 ± 49.8 2689.7 ± 47.7 2081.6 ± 127.5 0.2 ± 0.2 5.9 ± 2.4	%dif N/A 17.0 -0.7 2.9 14.8 -79.3 -65.8	P N/A 0.089 0.634 0.937 0.164 0.051 0.064	WT (n=5) N/A 841.0 ± 89.1 1435.1 ± 163.4 2451.8 ± 185.3 1868.8 ± 133.5 0.0 16.0 ± 6.0	FemaleKO (n=8) 757.6 ± 64.4 1152.5 ± 91.1 2082.6 ± 181.1 1633.0 ± 143.2 0.1 ± 0.06 10.4 ± 3.2	%dif N/A -9.9 -19.7 -15.1 -12.6 N/A -34.6	P N/A 0.454 0.128 0.204 0.287 0.453 0.391	
Data Type TA CS A μm ² TA Fiber Type Distribution	Sex: MHC Type MHC 1 MHC 2a MHC 2x MHC 2b combined MHC 1 MHC 2a MHC 2a	WT (n=8) 501.8 ± 88.5 865.4 ± 64.1 1557.6 ± 128.5 2614.4 ± 144.6 1812.7 ± 125.9 1.0 ± 0.34 17.3 ± 4.9 43.4 ± 3.4	MaleKO (n=5) $424.7 a$ 1012.3 ± 42.8 1546.4 ± 49.8 2689.7 ± 47.7 2081.6 ± 127.5 0.2 ± 0.2 5.9 ± 2.4 43.8 ± 5.7	%dif N/A 17.0 -0.7 2.9 14.8 -79.3 -65.8 1.0	P N/A 0.089 0.634 0.937 0.164 0.051 0.064 0.952	WT (n=5) N/A 841.0 ± 89.1 1435.1 ± 163.4 2451.8 ± 185.3 1868.8 ± 133.5 0.0 16.0 ± 6.0 31.3 ± 2.8	FemaleKO (n=8) 757.6 ± 64.4 1152.5 ± 91.1 2082.6 ± 181.1 1633.0 ± 143.2 0.1 ± 0.06 10.4 ± 3.2 31.8 ± 4.2	%dif N/A -9.9 -19.7 -15.1 -12.6 N/A -34.6 1.7	P N/A 0.454 0.128 0.204 0.287 0.453 0.391 0.927	

Table SI1. Muscle Fiber CSA and Fiber Typing. MHC = myosin heavy chain, SOL = soleus, TA = tibialis anterior, CSA = cross sectional area, WT = non-tamoxifen treated control mice, KO = tamoxifen treated experimental mice, % dif = percentage difference between WT and KO, P = P-value from 2-tailed Student's t-test, N/A = not applicable (due to division by zero, no data points in group, or other error). Data is expressed as mean of group \pm the standard error. Numbers in italics indicates a trend (P<0.010) or significant difference (P<.050). ^a Only one mouse in the group expressed this MHC.

		Sex:	Male Female				•			
Muscle	Data Type	Unit	WT (n=7)	KO (n=11)	%dif	Р	WT (n=9)	KO (n=13)	%dif	Р
EDL	Pt	mN	78.6 ± 6.2	69.9 ± 4.5	-11.1	0.211	63.3 ± 4.5	61.8 ± 4.4	-2.4	0.825
	P ₀	mN	384.7 ± 19.2	378.1 ± 23.4	-1.7	0.211	309.7 ± 17.0	297.3 ± 10.1	-4.0	0.511
	P _{0,} Hz.	Hz	150.0 ± 9.3	152.7 ± 2.7	1.8	0.720	143.0 ± 4.4	156.9 ± 3.6	9.7	0.028
	Sp. F.	mN/mm ²	41.7 ± 2.5	42.1 ± 2.5	1.0	0.902	41.1 ± 2.3	42.6 ± 2.0	3.6	0.628
	PCSA	mm²	9.60 ± 0.31	9.29 ± 0.46	-3.2	0.629	7.55 ± 0.19	7.04 ±0.16	-6.8	0.055
	Lo	mm	12.1 ± 0.3	12.3 ± 0.3	1.7	0.615	11.7 ± 0.2	12.2 ± 0.2	4.3	0.169
		Sex:		Male				Female		
Muscle	Data Type	Unit	WT (n=10)	KO (n=14)	%dif	Ρ	WT (n=11)	KO (n=14)	%dif	Р
SOL	Pt	mN	49.4 ± 4.2	42.7 ± 3.4	-13.6	0.221	40.8 ± 4.2	39.1 ± 1.6	-4.2	0.695
	P ₀	mN	294.8 ± 16.4	277.3 ± 13.1	-5.9	0.409	234.1 ± 19.0	232.4 ± 9.7	-0.7	0.931
	P _{0,} Hz.	Hz	112.0 ± 3.3	111.4 ± 4.9	-0.5	0.930	120.9 ± 6.2	117.9 ± 5.3	-2.5	0.710
	Sp. F.	mN/mm²	27.2 ± 1.3	26.6 ± 1.4	-2.2	0.764	27.3 ± 2.8	26.1 ± 1.3	-4.4	0.697
	PCSA	mm²	10.95 ± 0.66	10.53 ± 0.34	-3.8	0.541	8.98 ± 0.51	9.05 ± 0.31	0.8	0.987
	Lo	mm	11.8 ± 0.4	12.5 ± 0.2	5.9	0.059	10.8 ± 0.4	10.9 ± 0.2	0.9	0.948
		Sex:	Male					Female		
Muscle	Data Type	Unit	WT (n=10)	KO (n=15)	%dif	Р	WT (n=11)	KO (n=14)	%dif	Р
GAST	Mass	mg	155.7 ± 3.34	169.57 ± 5.3	8.9	0.061	118.5 ± 11.7	117.6 ± 9.4	-0.8	0.951
PLANT	Mass	mg	20.7 ± 1.0	22.4 ± 0.9	8.2	0.234	16.3 ± 0.8	16.1 ± 0.5	-1.2	0.788
ТА	Mass	mg	53.00 ± 1.8	50.0 ± 1.6	-5.7	0.234	42.5 ± 1.2	39.2 ± 0.9	-7.8	0.040
SOL	Mass	mg	13.5 ± 1.1	14.1 ± 0.5	4.4	0.615	10.3 ± 0.7	10.4 ± 0.4	1.0	0.871
EDL	Mass	mg	12.1 ± 0.28	12.9±0.4	6.6	0.108	9.9 ± 0.5	9.1 ± 0.2	-8.1	0.123
Bodymass	%change	%	1.50 ± 1.49	3.74 ± 1.02	149.3	0.211	6.3 ± 1.7	2.7 ± 1.4	-57.1	0.102

Table SI2: Contractile and Muscle Properties. EDL = extensor digitorum longus; SOL = soleus; WT = wild type; KO = knockout; P_t = peak twitch force; P_0 = peak isometric tetanic force; P_0 , Hz = frequency of stimulation in Hertz at P_0 ; SP. F. = specific force; PCSA = physiological cross-sectional area, determined by formula; L_0 = muscle length at P_t ; % dif = percent difference between WT and KO; P = P-value from independent t-test; data presented as mean of group ± standard error; italics = P<0.100.



Figure SI1: A. Map of lox sites on the Depc5 gene and primer locations. The lox sites are on either side of exon 5. Exon 5 is expressed in all isoforms, thus transgenic ablation of exon 5 using cre-recombinase represses Depdc5 gene expression. LoxP1, LoxP2 and LoxP3 on the figure show the location of primers. **B. Amplicons produced from PCR with LoxP1, P2 and P3.** The PCR product of LoxP1 and LoxP2 has amplicons at 431 bp if the lox site is present and at 368 bp if the allele is wild type. The PCR product of LoxP3 and LoxP2 has amplicons at 1349 bp for the floxed allele, 1069 bp if the allele is wild type, and at 749 bp in a recombinant allele (exon 5 not expressed). The amplicon at 1349 is not replicated when all 3 primers are used in one PCR Reaction. See Figure 1 for amplicons formed with only LoxP2 and LoxP3. Bp = base pairs; - or + signs = presence of allele in Cre^{+/+ or +/-} (homo- or heterozygous Tg^(ACTA1-cre/Esr1*)2Kesr) and Depdc5^{fl/fl} (homozygous Depdc5^{tm1c(EUCOMM)Hmgu)} rows and whether or not tamoxifen was given; Depdc5^{fl/-} (heterozygous for Depdc5^{tm1c(EUCOMM)Hmgu}), recomb. = recombination product, F = female, M = male, L = liver, E = skin (from ear punch), H = heart, P = plantaris, G = gastrocnemius, TA = tibialis anterior, S = soleus.



Treadmill

Figure SI2. Endurance Not Improved in Knockout Mice. Function did not change significantly within any group from pre- to post- testing. WT = wild type mice, KO = transgenic knock-out mice, each symbol (circle for WT and diamond for KO) represents an individual mouse. To the right of each group the rectangle= the mean \pm standard error. M = male, F = female. Pre = before tamoxifen induced recombination, Post = 6 weeks after tamoxifen. A 2x2x2 ANCOVA (2 treatment groups, WT and KO; 2 sexes; 2 timepoints, before and 6-weeks after tamoxifen treatment in the EXP group, and 6 weeks after the pre-testing for the WT group) adjusted for body mass was used to determine differences with the least significant difference posthoc test (paired t-test) set at significance of P<0.05.



Rotarod

Figure SI3. Overall Motor Function Not Improved in Knockout Mice. Function did not change significantly within any group from pre- to posttesting. WT = wild type mice, KO = transgenic knock-out mice, each symbol represents an individual mouse. To the right of each group the rectangle = the mean \pm standard error. M = male, F = female. Pre = before tamoxifen-induced recombination, Post = 6 weeks after tamoxifen-induced recombination. A 2x2x2 ANCOVA (2 treatment groups, WT and KO; 2 sexes; 2 timepoints, before and 6-weeks after tamoxifen treatment in the EXP group, and 6 weeks after the pre-testing for the WT group) adjusted for body mass was used to determine differences with the least significant difference posthoc test (paired t-test) set at significance of P<0.05.



Figure SI4. Forelimb Grip Strength Not Improved in Knockout Mice. Other than the male KO who lost function, grip strength did not change significantly within any group from pre- to post- testing. WT = wild type mice, KO = transgenic knock-out mice, each symbol represents an individual mouse. To the right of each group the rectangle = the mean \pm standard error. M = male, F = female. Pre = before recombination, Post = 6 weeks after recombination. A 2x2x2 ANCOVA (2 treatment groups, WT and KO; 2 sexes; 2 timepoints, before and 6-weeks after tamoxifen treatment in the EXP group, and 6 weeks after the pre-testing for the WT group) adjusted for body mass was used to determine differences with the least significant difference posthoc test (paired t-test) set at significance of P<0.05.



Figure SI5. Activity Rate Not Improved in Knockout Mice. Function did not change significantly within any group from pre- to posttesting. WT = wild type mice, KO = transgenic knock-out mice. The error bar is \pm standard error. M = male, F = female. Pre = before tamoxifen-induced recombination, Post = 6 weeks after tamoxifen-induced recombination. A 2x2x2 ANCOVA (2 treatment groups, WT and KO; 2 sexes; 2 timepoints, before and 6-weeks after tamoxifen treatment in the EXP group, and 6 weeks after the pre-testing for the WT group) adjusted for body mass was used to determine differences with the least significant difference posthoc test (paired t-test) set at significance of P<0.05. Different letter indicates significant difference.



Figure SI6 Mitochondrial Respiration in TA muscle. **A. Respiration.** Respiration in stages I-IV is higher in KO per unit of muscle. **B. Ratios.** The ratios demonstrate no difference in mitochondrial efficiency. KO = knockout mice; WT = wild type control

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200x, Soleus, M KO, 58% SDH+, mean CSA 1648 µm²



200x, Soleus, M WT, 47% SDH+, mean CSA 1189 µm²

Figure SI7 SOL SDH Enzymatic Activity. Cells were counted as either positive (dark stain) or negative (light stain). Degree of staining indicates higher SDH activity. **A**) M KO cells had significantly more (P<0.05) positive cells than the combined WT (M + F) or the F KO. Different letter indicates significance. **B**) There is a moderate positive correlation of cell size with SDH positive percentage. **C**) When the one outlier (>2 sd above mean for SDH+) is removed, the association becomes moderately strong. **D**) and **E**) are representative images. Each symbol represents the aggregate percentage of positive cells in one mouse. SD = standard deviation. SDH = succinate dehydrogenase, + = highly active cells, - = less active cells, SOL = soleus, Mean CSA is in microns squared, M = male, F = female, WT = wild type, KO = knockout, equations are simple linear regressions.