

1 Muscle-derived ERK1/2 MAP kinases are required for the maintenance of adult
2 myofibers and their neuromuscular junctions

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13 Running Head: ERK1/2 in NMJ and myofiber maintenance *in vivo*

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25 **ABSTRACT**

26 The Ras-ERK1/2 pathway appears important for the development, maintenance,
27 aging and pathology of mammalian skeletal muscle. Yet no gene targeting of *Erk1/2* in
28 muscle fibers *in vivo* has been reported to date. We combined a germline mutant *Erk1*
29 with Cre-loxP *Erk2* inactivation in skeletal muscle to produce, for the first time, mice
30 lacking ERK1/2 selectively in skeletal myofibers. Animals lacking muscle ERK1/2
31 displayed stunted postnatal growth, muscle weakness and shorter lifespan. Their
32 examined muscles here, sternomastoid and tibialis anterior, displayed fragmented
33 neuromuscular synapses and a mixture of modest fiber atrophy and loss, but failed to
34 show major changes in fiber type composition or absence of cell surface dystrophin.
35 Whereas lack of only ERK1 had no effects on the phenotypes studied, lack of myofiber
36 ERK2 explained synaptic fragmentation in the sternomastoid, but not the tibialis anterior,
37 and a decrease in the expression of the acetylcholine receptor (AChR) epsilon subunit
38 gene mRNA in both muscles. A reduction in AChR protein was documented in line with
39 the above mRNA results. Evidence of partial denervation was found in the sternomastoid
40 but not the tibialis anterior. Thus, myofiber ERK1/2 are differentially required for the
41 maintenance of myofibers and neuromuscular synapses in adult mice.

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46 **INTRODUCTION**

47 Mitogen-activated protein kinases (MAPKs) are components of intracellular
48 signaling modules that control a myriad of cellular processes. MAPK modules consist of
49 3 core protein kinase components. The most downstream is the actual MAPK, a S/T
50 kinase that phosphorylates the transcription factors, cytoskeletal elements or other
51 kinases, that are the targets of regulation by signaling cascades started at the cell surface.
52 A MAPK is activated by an upstream MAPK kinase (MAP2K), which in turn is activated
53 by a MAP2K kinase (MAP3K). MAP3Ks are usually at the receiving end of signals
54 derived from small, monomeric GTPases such as the Ras family or by other more
55 intricate mechanisms (1). In mammalian cells, the prototypical MAPK module is
56 composed of the MAPKs extracellular-signal regulated kinases 1 and 2 (ERK1/2), the
57 MAP2Ks MEK1/2 and the MAP3K Raf. ERK1/2 regulate normal cellular responses to
58 multiple growth factors and cytokines in proliferation, differentiation and apoptosis (2,
59 3).

60 Multiple studies suggest an important role for the Ras-ERK1/2 pathway in the
61 development, normal maintenance, aging and pathology of mammalian skeletal muscle.
62 Thus ERK1/2 activity has both stimulatory and inhibitory roles in the differentiation of
63 cultured skeletal myotubes that vary with the stage of this protracted process (4–8).
64 ERK1/2 have been implicated in the maintenance of adult skeletal muscle mass (9), and,
65 seemingly paradoxically, in the control of both the fast-twitch (10), and the slow-twitch
66 (11) fiber type phenotypes. Alterations in levels of ERK1/2 activity in aging rodent
67 muscle correlate with sarcopenia (12), the loss of muscle mass and strength that occurs
68 with aging (13). Ras-ERK1/2 pathway activity dysregulation underlies the pathology of

69 neuromuscular diseases such as autosomal Emery-Dreifuss muscular dystrophy (14) and
70 of the RASopathies, a group of rare genetic diseases with accompanying skeletal muscle
71 abnormalities (15–17). Our own work in cultured myotubes (18) suggests a modulatory
72 role for ERK1/2 on the activity of agrin (19), a key synaptogenic factor in the formation
73 and maintenance of the neuromuscular junction (NMJ), the synapse between a
74 motoneuron and a skeletal muscle fiber (20). In vitro and in vivo studies implicated
75 ERK1/2 in the control of synapse-specific expression of acetylcholine receptor (AChR)
76 subunit genes at the NMJ, particularly of *Chrne*, the gene coding the adult AChR
77 subunit (21–23).

78 Most of the experiments that have been carried out to characterize the role of
79 ERK1/2 in skeletal muscle biology have been done in cultured cells, using either
80 pharmacological tools, in particular MEK inhibitors, siRNA, constitutively active or
81 dominant-negative constructs for the different components of the Ras-ERK1/2 pathway.
82 However, no gene targeting investigations on the role of ERK1/2 in developing muscle
83 fibers *in vivo* have been reported to date. We combined a germline *Erk1* mutant with Cre-
84 loxP inactivation of *Erk2* in skeletal muscle to produce, for the first time, mice lacking
85 ERK1/2 selectively in skeletal myofibers. We report that ERK1/2 are required for the
86 maintenance of myofibers and NMJs in adult animals.

87 **MATERIALS AND METHODS**

88 **Ethics statement.** Care and treatments of all animals followed the National Institutes of
89 Health Guide for the Care and Use of Laboratory Animals and were approved by the
90 Institutional Animal Care and Use Committee of Texas A&M University under animal
91 use protocol 2012-168.

92 **Mice and genotyping.** The Cre-driver mice in which Cre is under control of the human
93 α -skeletal muscle actin promoter are represented as *Hsa-Cre*^{+/-}. The *Erk2* floxed allele is
94 represented as *Erk2*^f. Local colonies were established from breeders obtained initially as
95 follows: *Hsa-Cre*^{+/-} mice from Jackson labs (JAX stock# 006149); *Erk1*^{+/-}; *Erk2*^{f/+} and
96 *Erk2*^{f/f} mice from the Landreth lab, Case Western Reserve University. These crosses were
97 used to generate experimental animals: *Erk1*^{-/-} mice came from *Erk1*^{+/-} X *Erk1*^{-/-}. Mice
98 deficient in muscle ERK2 (referred in the text as *mErk2*^{CKO}) came from *Hsa-Cre*^{+/-};
99 *Erk2*^{f/+} X *Hsa-Cre*^{-/-}; *Erk2*^{f/f}. Mice deficient in germline ERK1 and muscle ERK2
100 (referred in the text as DKO) came from *Hsa-Cre*^{+/-}; *Erk1*^{+/-}; *Erk2*^{f/f} X *Hsa-Cre*^{-/-}; *Erk1*^{-/-};
101 *Erk2*^{f/f}. Genotyping was done by PCR with the following primers: *Cre*: 5'-
102 GCGGTCTGGCAGTAAAACTATC-3'; 5'-GTGAAACAGCATTGCTGTCACCTT-3'.
103 *Erk1*: wild type and null allele were detected with these primers: 5'-
104 GTATCTTGGGTTCCCCATCC-3'; 5'-GGGGAACCTCCTGACTAGGG-3'; 5'-
105 GCTCCATGTCTGAAGGTGAAT-3'. *Erk2*: wild type and floxed allele were detected
106 with these primers: 5'-AGCCAACAATCCCAAACCTG-3'; 5'-
107 GGCTGCAACCATCTCACAAT-3'. Mice were housed at 25°C with a 12h light/dark
108 cycle, fed *ad libitum* and monitored daily.

109 **Western blotting.** Muscles were dissected, snapped frozen in liquid N₂ and stored at -
110 80°C until use. Most tissue homogenates were prepared in the following buffer: 25mM
111 Tris pH 7.4, 95mM NaCl, 1mM EDTA, 1mM EGTA, 1% SDS, 10% Protease Inhibitor
112 Cocktail (P8340, Sigma), 5mM NaF, 2mM Na₃VO₄, 2.5mM Na₄P₂O₇. Lysates used to
113 analyze p38 were made in 1% Triton X-100, 30 mM triethanolamine pH 7.5, 50 mM
114 NaCl, 5 mM EGTA, 5 mM EDTA, with the same phosphatase and protein inhibitors as

115 above. Total protein was measured using Biorad Protein Assay, and 50 μ g per sample
116 were run on 10% acrylamide denaturing gels. Proteins were transferred to polyvinylidene
117 difluoride (PVDF) membranes using a semi-dry blotter (Biorad). Suppliers of primary
118 antibodies and dilutions were: Epitomics: Anti-ERK1 (1171-1, 1:1000); anti-ERK2
119 (1586-1, 1:1000). Cell Signaling: Anti-tERK1/2 (9102, 1:1000); anti-p38 (9212, 1:1000);
120 anti-pp38 (4511, 1:1000); anti-JNK (9252, 1:500). Santa Cruz Biotechnology: Anti-
121 pERK1/2 (SC7383, 1:200); anti-pJNK (SC6254, 1:200). Sigma: Anti- α -Tub (T6199,
122 1:4000). Horseradish peroxidase-secondary antibodies (SC2020 and SC2031, Santa Cruz
123 Biotechnology; 111-035-003 and 315-035-003, Jackson ImmunoResearch) were used at
124 1:1000-1:3000. Blots were visualized by chemiluminescence following manufacturer's
125 instructions (PerkinElmer). Images were acquired and analyzed with an AlphaImager gel
126 imaging system (Protein Simple).

127 **AChR affinity isolation and probing.** AChRs were isolated and detected as previously
128 described with minor modifications (24). Briefly, muscles were lysed in 1% Triton X-
129 100, 30 mM triethanolamine pH 7.5, 50 mM NaCl, 5 mM EGTA, 5 mM EDTA, 10%
130 Protease Inhibitor Cocktail (P8340, Sigma), 5mM NaF, 2mM Na₃VO₄, 2.5mM Na₄P₂O₇.
131 One mg of total protein per muscle lysate was incubated for 30 min with 200 nM biotin-
132 α -bungarotoxin (BBTX; B-1196, Life Technologies) at 4°C. Streptavidin-agarose
133 (SA100-04, Life Technologies) was used to precipitate the BBTX-AChR complexes.
134 After washing with lysis buffer, complexes were separated by SDS-PAGE, transferred to
135 PVDF membranes, and probed with a goat-polyclonal to AChR ϵ at 1:250 (ab166931,
136 Abcam). Bands were visualized by chemiluminescence and quantified as above.

137 **Grip strength assay.** Forelimb grip strength was assessed with a grip strength meter with
138 single sensor and a standard pull bar and software (Columbus Instruments) as previously
139 described (25). Briefly, mouse was directed to grip the bar with forelimbs then pulled off
140 the bar by the tail, and peak force (in g) was recorded for 3 consecutive trials. Trial
141 averages were normalized to body weight (g).

142 **Rotarod.** A Rotarod Series 8 (IITC Life Science Inc.) was used for rotarod analysis.
143 From 7-19 weeks of age, mice were subjected to two rotarod modes every other week.
144 First, constant speed of 4 rpm for 5 min, immediately followed by 0.1 rpm/sec
145 acceleration to a maximum speed of 30 rpm, ending the trial at 5 min (25). Time-to-fall
146 (sec) was recorded for both modes. Mice were allowed to rest for 10 min and the above
147 procedure was repeated twice more for a total of 3 trials. Time-to-fall per mode was
148 averaged for the 3 trials. Data for week 7 were considered as adaptation and are not
149 presented in the results.

150 **Whole mount staining, confocal microscopy and NMJ morphological**
151 **characterization.** Whole mount staining of sternomastoid (STN) and tibialis anterior
152 (TA) was essentially done as previously described (26). Anti-synaptophysin (SYN)
153 (180130, Life Technologies) was used at 1:200, fluorescein-BTX (F-1176, Life
154 Technologies) was used at 1:1000. Rhodamine-rabbit secondary antibody (111-025-144,
155 Jackson ImmunoResearch) was used at 1:400. At the dilution of anti-SYN used, both
156 nerve terminal and pre-terminal axon were visible in many cases. Vectashield (Vector
157 Laboratories)-mounted muscle bundles from these preparations were imaged on an A1
158 confocal microscope (Nikon), with 40X (NA 1.30) and 60X (NA 1.40) oil immersion
159 objectives. Images were acquired and maximal intensity projections were generated with

160 NIS Elements software (Nikon). On the maximal projections, NMJ morphology was
161 studied by counting: (i) number of AChR domains per endplate; (ii) faint or weakly-BTX
162 stained NMJs, defined as those endplates with noticeably weaker or dimmer BTX stain
163 relative to others on the same field; (iii) terminal sprouts, defined as extensions of any
164 length and direction of nerve terminal staining beyond AChR stain at a synaptic site.

165 **Central myonuclei quantification.** One slide with several 12-14 μm -thick frozen cross
166 sections from the belly of a STN was stained for H&E by a standard procedure. Images
167 from 5, 20X fields per slide were acquired with an EC3 camera and software (Leica),
168 mounted on an Eclipse E1000 microscope (Nikon). Total number of fibers and fibers
169 with central nuclei were counted. Replicates within a genotype were averaged for final
170 quantification.

171 **Real-time quantitative PCR.** Total RNA extraction, reverse transcription, and real-time
172 PCR were done essentially as previously reported (26). 200 ng of total RNA per sample
173 were used to generate cDNA. All Taqman primer sets and probes were from ABI/Life
174 Technologies as follows: *Chrna*, Mm00431629_m1; *Chrn b*, Mm00680412_m1; *Chrnd*,
175 Mm00445545_m1; *Chrne*, Mm00437411_m1; *Chrng*, Mm00437419_m1; *Runx1*,
176 Mm01213404_m1; *Myh3*, Mm01332463_m1; 18S rRNA, 4333760F.

177 **Myofiber morphological analysis.** Dystrophin staining of transverse frozen sections was
178 performed essentially as previously described (26), except that sections were not fixed
179 and individual primary antibodies to myosin heavy chains (MyHCs) were co-incubated
180 with the anti-dystrophin antibody (15277, Abcam). All MyHC antibodies were from the
181 Developmental Studies Hybridoma Bank as follows: type 1, A4.840; type 2A, SC-71;
182 type 2B, 10F5; type 2X, 6H1. All but SC-71, which was sometimes used at 1:600, were

183 used undiluted. Fluorophore-conjugated secondary antibodies that matched the primary
184 isotype (Jackson Immunoresearch and Sigma) were used at 1:400 and 1:128,
185 respectively. Fiber area analysis was carried out as previously described (26) on
186 overlapping 10X images that covered an entire muscle cross section. Care was taken not
187 to measure the same fibers more than once. For fiber typing, 10X overlapping images of
188 individual MyHC type and dystrophin staining were assembled in Photoshop (Adobe) to
189 reconstruct an entire muscle cross section. Total fibers were counted from the dystrophin
190 staining, and MyHC type fibers were counted from the respective antibody staining.
191 Replicates per muscle/genotype were averaged for final quantification.

192 **Statistical analysis.** Quantitative data are expressed as mean \pm SEM. Kaplan-Meier
193 survival curves were generated and tested for statistical significance using the log-rank
194 test with Prism5 (GraphPad Software). Analysis of the Variance (ANOVA) was
195 performed at <http://vassarstats.net/>. One- and two-sample Student's t-tests were computed
196 with Prism5 (GraphPad Software) and Microsoft Excel (Microsoft Corporation),
197 respectively. Wilcoxon Rank Sum test probabilities were computed at
198 <http://socr.stat.ucla.edu>. Significance was set at $p < 0.05$.

199 **RESULTS**

200 **Generation of skeletal muscle-selective *Erk2* conditional mice and of mice lacking** 201 **ERK1/2 in skeletal muscle fibers.**

202 While germline *Erk1*^{-/-} mice are viable and fertile but display defective thymocyte
203 maturation (27, 28), *Erk2*^{-/-} mice are early embryonic lethal due to failure to form the
204 ectoplacental cone and extra-embryonic ectoderm (29, 30). *Erk2*^{-/-} embryos do not form
205 mesoderm (31). A conditional *Erk2* allele (*Erk2*^{fl/fl}) was generated by Landreth and

206 colleagues (32). To delete *Erk2* selectively in developing and adult skeletal muscle fibers,
207 *Erk2^{ff}* mice were crossed to mice that express Cre under control of the human α -skeletal
208 muscle actin promoter (*Hsa-Cre^{+/-}*) (33, 34). Expression of Cre under this promoter was
209 detected beginning at embryonic day (E) 9.5 onwards (33) and in skeletal muscle is
210 restricted to myofibers. Neither myoblasts nor satellite cells express Cre in these mice
211 (35). *Hsa-Cre^{+/-}; Erk2^{ff}* mice (hereafter referred to as *mErk2^{CKO}*) were viable and fertile.
212 Western blots of muscle extracts showed a ~90% reduction in ERK2 levels in *mErk2^{CKO}*
213 mice (Fig 1A). Full removal of ERK2 from whole muscle tissue was not expected as
214 myofiber nuclei only represent ~41% of the total nuclei in muscle tissue (36). ERK1
215 levels in *mErk2^{CKO}* mutants were ~20% lower than in controls (Fig 1B). As expected,
216 ERK1 was completely absent in muscle homogenates from germline *Erk1^{-/-}* mice (Fig
217 1C, top panel). Mice lacking both ERK1 and ERK2 in skeletal muscle fibers were
218 generated by crossing *Erk1^{-/-}* and *mErk2^{CKO}* animals (for details see methods). Skeletal
219 muscle from *Hsa-Cre^{+/-}; Erk1^{-/-}; Erk2^{ff}* mice (hereafter referred to as DKO) lacked
220 ERK1 and had a great reduction of ERK2 as expected (Fig 1C, top panel).
221 Phosphorylated ERK2 (pERK2) was diminished to similar extent in both *mErk2^{CKO}* and
222 DKO mutants, in direct correspondence to the decrease in total ERK2 (Fig 1C, bottom
223 panel). The reduction in ERK2 was specific to skeletal muscle as it was not observed in
224 heart, spinal cord or liver (Fig 1D). However, a ~50% reduction in kidney ERK2 levels
225 was detected in DKO animals relative to control (Fig 1D).

226 **Mice lacking ERK1/2 in skeletal muscle fibers are viable but display stunted**
227 **postnatal growth, muscle weakness and shorter lifespan.**

228 DKO animals were born at the expected Mendelian ratios predicted from the
229 crosses. Thus, from the cross *Hsa-Cre^{-/-}; Erk1^{-/-}; Erk2^{ff}* x *Hsa-Cre^{+/-}; Erk1^{+/-}; Erk2^{ff}*,
230 78/317 pups (i.e. the expected 1/4) showed the *Hsa-Cre^{+/-}; Erk1^{-/-}; Erk2^{ff}* genotype when
231 assayed post-weaning. We followed their weight starting at week 4 after birth. Starting at
232 week 7, we also assayed muscle strength and overall motor coordination and fatigue
233 resistance by measuring forelimb grip strength and by subjecting mice to a rotarod
234 protocol, respectively. Muscle ERK2-deficient, and germline ERK1-deficient mice
235 showed no difference in weight progression and forelimb grip strength relative to control
236 animals (*Hsa-Cre^{-/-}; Erk1^{+/+}; Erk2^{ff}*), whereas DKO mutants failed to gain weight and
237 showed a progressive loss of grip strength as young adults (Fig 2A and B). Interestingly,
238 double mutants could be divided into two groups according to how fast they lost weight
239 (Fig 2A). “Severe” animals lost weight rapidly starting at about 7 weeks of age, while
240 “mild” double mutants were able to keep their weight at that age but clearly failed to keep
241 up with controls or single mutants (Fig 2A). We currently do not understand the basis of
242 this differential effect on weight. When normalized to body weight, both types of DKO
243 mutants showed very similar reduction of grip strength (Fig 2B). “Severe” mice were not
244 tested with the rotarod due to their overall frailty. However, “mild” DKO mice displayed
245 a clear tendency to fall earlier from an accelerating rotarod (Fig 2C). DKO mutants do
246 not survive as long as controls or single mutants. Their deaths were either sudden and
247 unexplained or followed weight loss of such severity that demanded humane euthanasia
248 according to protocol guidelines. Their median lifespans were: 71 days, n=23 (severe);
249 121 days, n=7 (mild). (Fig 2D). Interestingly, all 5 registered deaths among the “mild”
250 DKO animals were males, while the 2 females remained alive. Kyphosis, a sign of

251 muscle weakness, was clearly evident in the long-surviving animals (Fig 2E) and in at
252 least one of the males that lived for 120 days. Thus, these results suggest that muscle
253 depletion of either ERK1 or ERK2 has no overt phenotypic effects on the mice and that
254 ERK1 and ERK2 together are required for myofiber postnatal maintenance or growth.

255 **Extensive fragmentation of the mature NMJ in ERK1/2-deficient muscle.**

256 These studies were prompted by our previous results with cultured myotubes. We
257 found that agrin stimulated the transient activation of ERK1/2 in an LDL receptor related
258 protein 4 (Lrp4)/muscle-specific kinase (MuSK)-dependent fashion. Pharmacological
259 blockade of this activation failed to inhibit agrin-induced acetylcholine receptor (AChR)
260 clustering. Instead, it potentiated it by ~60%. These, and other observations, led us to
261 propose that agrin-induced ERK1/2 activation is part of a feedback loop that keeps
262 agrin's clustering activity in check, at least *in vitro* (18). The fact that the DKO mice are
263 viable and appear normal well after NMJs have formed and matured suggests that this
264 ERK-dependent feedback mechanism is dispensable for the formation of the NMJ in
265 vivo. However, it was still possible that ERK signaling had some role in NMJ
266 maintenance, especially in light of the overall postnatal muscle weakness of the DKO
267 mice (Fig 2). We stained whole mounts of the neck sternomastoid (STN) muscle in
268 control and DKO young adults for pre- and postsynaptic markers and examined the
269 samples under confocal microscopy. The STN has been used by others to study the
270 effects of aging and amyotrophic lateral sclerosis (ALS) on the structure of the mature
271 NMJ (37–39). In control muscle, the NMJs exhibited their characteristic “pretzel” shape
272 with long, continuous domains of postsynaptic AChRs labeled by α -bungarotoxin (BTX)
273 tightly apposed by nerve terminals labeled by synaptophysin (SYN) (Fig 3A). In STN

274 DKO muscles, many NMJs looked very fragmented with small, mostly round AChR
275 domains variably apposed to nerve terminal staining (Fig 3B,C). This synaptic
276 fragmentation, reminiscent of NMJs in aged normal animals (37, 38, 40), mdx and
277 utrophin/dystrophin knockout mice (41, 42), was observed in males and females from
278 both “severe” and “mild” DKO muscle (Fig 3B,C).

279 **Lack of myofiber ERK2 is sufficient to observe extensive synaptic fragmentation in**
280 **the sternomastoid muscle.**

281 Next we sought to explore whether synaptic fragmentation required the deficiency
282 of both muscle ERK1 and ERK2, or whether the lack of only one of these two kinases
283 was sufficient for this phenotype. STNs from control (*Hsa-Cre*^{-/-}; *Erk1*^{+/+}; *Erk2*^{fl/fl}), *Erk1*^{-/-}
284 , *mERK2*^{CKO} and “mild” DKO young adults were dissected, stained and imaged by
285 confocal microscopy as above. We chose to work with the “mild” DKO animals because
286 they survive longer and displayed an overall better health than the “severe” DKO mice.
287 The number of AChR domains per endplate was quantified on NMJs viewed “en face”.
288 For animals between 3 to 6 months of age, the average number of AChR domains per
289 endplate was 7.26 ± 0.38 for control (n=85 NMJs, 5 mice), 12.15 ± 1.69 for DKO (n=52
290 NMJs, 3 mice), 8.38 ± 0.94 for *Erk1*^{-/-} (n=80 NMJs, 4 mice) and 12.93 ± 0.91 for
291 *mErk2*^{CKO} (n=90 NMJs, 6 mice). Thus, endplates from DKO and *mErk2*^{CKO}, but not *Erk1*^{-/-}
292 STN had significantly more AChR fragments on average than control. We plotted the
293 percentage of NMJs vs. the number of AChR domains (in bins of 5) for each genotype
294 (Fig 4A). While a shift to NMJs with larger number of AChR fragments could be
295 appreciated for all 3 mutants, the most striking observation was that NMJs with more
296 than 20 AChR domains were only found in DKO and *mErk2*^{CKO} STN, not in control or

297 *Erk1^{-/-}* muscle (Fig 4A). These highly fragmented endplates constituted up to 20% of
298 total NMJs in the *mErk2^{CKO}* STN (Fig 4A). Statistical comparison of the mutant
299 distributions relative to control using the Wilcoxon Rank Sum test showed that only the
300 DKO and *mErk2^{CKO}* distributions were significantly different than control (DKO vs.
301 control: $p=0.000003$; *mErk2^{CKO}* vs. control: $p=0.000002$; *Erk1^{-/-}* vs. control: $p=0.05$).
302 Furthermore, statistical comparison using the same test of the DKO vs. the *mErk2^{CKO}*
303 distributions showed no difference between them ($p=0.88$). Lastly, as an additional
304 control we quantified AChR domains/NMJ in STN from *Hsa-Cre^{+/-}* driver mice. We
305 found an average of 5.96 ± 0.57 ($n=77$ NMJs, 2 mice), slightly lower than our control. An
306 example of a highly fragmented synapse in *mERK2^{CKO}* STN is shown in Fig 5A.
307 Therefore, lack of muscle ERK2 is sufficient to yield extensive synaptic fragmentation in
308 the STN.

309 **Differential sensitivity to the lack of ERK2 between different muscles.**

310 Next we studied synapse morphology in the hind limb tibialis anterior (TA)
311 muscle, which was also used recently to study effects of aging on the NMJ (40, 43). The
312 TA showed a different response than the STN (Fig 4B). First, control NMJs were much
313 less fragmented in the TA than the STN to begin with. Average AChR domains per
314 endplate in control TA were 3.85 ± 0.25 ($n=65$, 4 mice). Second, NMJs in *mErk2^{CKO}* and
315 *Erk1^{-/-}* TA muscles appeared on average as fragmented as control. The former had a mean
316 of 4.30 ± 0.25 AChR domains/endplate ($n=112$ NMJs, 5 mice), and the latter had $4.91 \pm$
317 0.52 ($n=32$ NMJs, 2 mice). Third, only DKO endplates displayed statistically significant
318 fragmentation as their average number of AChR domains/endplate rose to 6.46 ± 0.75
319 ($n=37$ NMJs, 3 mice; $p=0.003$, Wilcoxon Sum Rank test). Fourth, NMJs with more than

320 15 AChR domains were never seen in control or *Erk1^{-/-}* muscle, were extremely rare in
321 *mERK2^{CKO}* TA and reached less than 10% of the junctions in DKO muscle. Fifth, NMJs
322 with more than 20 AChR fragments, which were easily detected in *mErk2^{CKO}* and DKO
323 STN, were absent from the sampled TA junctions, at these ages or even at 9-months of
324 age (data not shown). An example of a control and a highly fragmented NMJ in DKO TA
325 are shown in Figure 5B & C, respectively. Thus at the ages studied, the NMJs of STN
326 and TA displayed differential intrinsic fragmentation and a differential sensitivity to the
327 lack of myofiber ERK1/2.

328 In order to account for the inherent differences in fragmentation of control NMJs
329 between STN and TA that our data reveal (Fig 4), we propose that a fragmented NMJ
330 could be defined as one having more AChR domains than the control median. The
331 median number of AChR domains were 7 and 3, for control NMJs in STN and TA,
332 respectively. Using this criterion, synaptic fragmentation becomes a predominant feature
333 in the majority of NMJs from DKO muscle as ~70% of the sampled NMJs had more
334 AChR domains than their respective control medians. Thus, 71.15% (37/52) and 67.57%
335 (25/37) NMJs in DKO STN and TA showed more than 7 and 3 AChR domains,
336 respectively. This high-level of fragmentation above control median was also reached in
337 the *mErk2^{CKO}* STN (66.67%; 60/90).

338 **Absence of central myonuclei in muscle ERK2-deficient sternomastoid**

339 Others have suggested that synaptic fragmentation in aging and dystrophic muscle
340 is due to degeneration/regeneration cycles in the synaptic portion of the muscle fiber (38,
341 41). We sought to determine if the same was happening in *mErk2^{CKO}* and DKO muscle.
342 Nuclei within normal muscle fibers localize towards the periphery of the cell, adjacent to

343 the sarcolemma. Muscle fiber damage induces degeneration of the old fibers and
344 regeneration of new ones, which are derived from satellite cells, muscle stem cells
345 present in the tissue (44). A hallmark of this process is the accumulation of myonuclei
346 towards the center of the cell. We counted fibers with central nuclei in transverse sections
347 of STN stained for hematoxylin & eosin (H&E). Numbers of myofibers with central
348 nuclei in control, *Erk1^{-/-}* and *mErk2^{CKO}* STN did not differ from each other, hovering
349 around 2% (Fig 6). DKO STN had more fibers with central nuclei than control, but they
350 only reached about 4% of the total (Fig 6). Experiments with Evans blue dye confirmed
351 sarcolemma integrity in *mErk2^{CKO}* muscle (data not shown). Thus NMJ fragmentation
352 was prominent in the *mErk2^{CKO}* STN despite it having the same percentage of fibers with
353 central nuclei as control. Moreover, a doubling in the number of fibers with central nuclei
354 in the DKO STN did not enhance NMJ fragmentation quantitatively (Fig 4A).

355 **ERK1/2 regulate AChR levels at the NMJ.**

356 In addition to the synaptic fragmentation studied above, we observed that about a
357 third of NMJs in DKO muscles had relatively weak or sometimes faint BTX staining
358 even in the presence of strong nerve terminal staining (Fig 7A). Quantification showed
359 that only ~6% of control NMJs, but ~29% and ~38% of endplates in DKO STN and TA
360 respectively, showed dim AChR stain (Fig 7B). While the fraction of endplates from
361 *Erk1^{-/-}* muscle with dim AChR staining was similar to control, it tended to be higher in
362 *mErk2^{CKO}* muscles, but only reached statistical significance in DKO samples (Fig 7B;
363 $p=0.03$ STN; $p=0.006$ TA). To check if this apparent reduction in surface AChR protein
364 levels was accompanied by a decrease in mRNA levels of its encoding subunit genes, we
365 used real-time PCR to measure steady state levels for the four genes that encode the adult

366 AChR (45). Cycle threshold (Ct) values obtained for 18S rRNA were used to equalize
367 differences in total RNA per sample (26). Transcript level fold-change was determined
368 by the $2^{-\Delta\Delta Ct}$ method (46) and values were normalized to the Ct values obtained for
369 control muscle for each gene (Fig 7C). We found that *Chrne* mRNA was consistently
370 reduced almost 2-fold in both *mErk2^{CKO}* and DKO muscle. The reduction was
371 statistically significant in DKO TA and *mErk2^{CKO}* STN and TA, but was borderline
372 ($p=0.05$) in the DKO STN (Fig 7C). *Chrnd* mRNA levels were essentially similar to
373 control regardless of genotype or muscle examined (Fig 7C). *Chrna* and *Chrn b* mRNAs
374 tended to be slightly lower than control in *mErk2^{CKO}* and DKO TA, while they tended to
375 increase particularly in the DKO STN (Fig 7C). Lack of only ERK1 did not affect the
376 mRNA levels for the subunits of the adult receptor (Fig 7C), nor was *Chrne* mRNA
377 different between control and *Hsa-Cre^{+/-}* driver muscle (data not shown). Thus, a
378 somewhat selective, muscle-ERK2-dependent reduction in mRNA *Chrne* expression was
379 observed. We next checked if the expression of AChR ϵ protein was also affected in DKO
380 mice. We affinity-purified AChRs from lysates of control and DKO TA muscle using
381 biotinylated BTX and streptavidin-agarose and probed for AChR ϵ subunit by Western
382 blotting. In the DKO TA there was as highly-statistically significant decrease in *Chrne*
383 mRNA (Fig 7C). AChR ϵ protein in DKO TA was ~2-3-fold lower than in control
384 ($p=0.03$, Fig 8). *Chrne*, the gene encoding the AChR ϵ subunit indicative of the adult
385 receptor \square is transcribed almost exclusively at the synaptic site (47), so its transcription
386 reflects the production of the synaptic AChR protein. Taken together, the weaker AChR
387 staining at about a third of DKO NMJs, the decrease in AChR ϵ protein demonstrated in

388 the DKO TA, and the reduction in *Chrne* mRNA levels in *mErk2^{CKO}* and DKO muscle
389 suggest that ERK1/2 regulate expression of the synaptic AChR.

390 Most prominently in DKO STN, we observed NMJs with AChR patches without
391 overlying SYN staining (i.e. aneural AChR patches, Fig 3) and evidence of nerve
392 terminal sprouting (as illustrated in Fig 7A, top panel). Thus, 45% NMJs (18/40, 3 mice)
393 in the DKO STN, while 16% in control STN (6/38, 4 mice) had terminal sprouts. Because
394 these morphological features are hallmarks of partial denervation (48), we next used real-
395 time PCR to check for mRNA levels for *Chrng*, the gene encoding the distinctive AChR γ
396 subunit of the fetal AChR (45), which is strongly induced by functional denervation in
397 the adult (49). *Chrng* mRNA levels were similar to control in TA muscle from all three
398 mutant genotypes. However, *Chrng* mRNA was moderately increased in *mErk2^{CKO}* STN
399 (2-fold) and reached 40-fold induction in the DKO STN (Fig 7D). mRNA for *Runx1* and
400 the embryonic myosin heavy chain *Myh3*, two other genes strongly induced by
401 denervation (50), were also selectively increased in DKO STN (Fig 7E). The sharp
402 increases in these denervation markers in the DKO STN, but not the DKO TA, were
403 consistent with the trend towards elevated mRNA levels for *Chrna*, *Chrnb* and *Chrnd* in
404 the DKO STN, but not in the DKO TA (Fig 7C), as these AChR genes are also induced
405 by denervation (51). Thus, together these results suggest that loss of myofiber ERK1/2 led
406 to significant partial denervation selectively in the STN.

407 **Myofiber number, size and type effects.**

408 Lastly, we studied myofiber number, size and type in STN and TA muscles to
409 determine whether there was a correlation between potential changes in these parameters
410 and the synapse maintenance phenotypes described above. Cross sections from the belly

411 of the muscles were co-stained for dystrophin, to mark the boundaries of individual
412 myofibers, and for the 4 canonical myosin heavy chain (MyHC) isoforms that define
413 adult fiber types (1, 2A, 2B, 2X) (52). Dystrophin was present on the surface of muscle
414 fibers of these DKO muscles just as it was in controls and single *Erk* mutants (Fig 9
415 A,B). Total number of fibers per TA cross section were similar across all four genotypes,
416 while there was a statistically significant 21% reduction in fiber numbers limited to the
417 DKO STN ($p=0.02$, Fig 9C). DKO STN and TA showed modest average fiber atrophy
418 ($\sim 14\%$ and $\sim 11\%$, respectively) that was statistically significant for the DKO TA
419 ($p=0.008$, Fig 9D). The *Erk1^{-/-}* and *mErk2^{CKO}* muscles tended to have slightly
420 hypertrophied fibers on average compared to controls (Fig 9D). Thus, the modest fiber
421 atrophy in both TA and STN together with the fiber loss in the STN, are consistent with
422 the lower weight of DKO animals relative to controls (Fig 2A). We sought to determine
423 the fiber type composition of the STN and TA in our *Erk1/2* mutant mice. In the adult
424 mouse, STN and TA are predominantly fast-fiber muscles (53–55). Our experiments
425 confirmed these published observations as our control and 3 mutant STN and TA muscles
426 had a maximum of 0.2% type 1 fibers (data not shown). Analysis of MyHC staining in
427 STN showed ERK1-lacking mice were similar to controls in the distribution of fast fibers
428 (2A, 2B, 2X) (Fig 9E). There was a tendency towards fewer 2B and more 2A fibers than
429 control in DKO STN that did not reach statistical significance (Fig 9E). *mErk2^{CKO}* and
430 DKO STN displayed a statistically significant $\sim 7\%$ increase in 2X fibers ($p=0.004$ and
431 $p=0.03$, respectively, Fig 9E). Although the variability in the data prevents a clear-cut
432 conclusion, this slight increase in 2X fibers seems to be at the expense of 2B fibers.
433 Mutant TA was no different to control regarding fast fibers (Fig 9F). Thus the analysis of

434 the predominantly fast-twitch muscles STN and TA showed only modest changes in fiber
435 type composition due to lack of muscle ERK1/2. Consistent with this conclusion, and
436 with its proposed role in regulating fiber type composition (56), levels of active p38
437 MAPK were unaltered in DKO muscle relative to control (Fig 10). Active c-jun NH₂-
438 terminal kinase (JNK) levels in DKO were also statistically similar to control. Fold
439 change vs. control: STN p46JNK: 0.99±0.10; STN p54JNK: 0.52±0.05; TA p46JNK:
440 1.79±0.76; TA p54JNK: 0.55±0.19.

441 **DISCUSSION**

442 We have for the first time selectively abrogated ERK1/2 in skeletal muscle fibers.

443 We found that ERK1/2 are needed for the maintenance of myofibers and NMJs. DKO
444 animals displayed stunted postnatal growth, muscle weakness and shorter lifespan. The
445 muscles examined here, STN and TA, displayed a combination of modest fiber atrophy
446 and loss without major changes in fiber type composition or absence of cell surface
447 dystrophin. Loss of myofiber ERK1/2 yielded both overlapping and distinct changes in
448 synaptic morphology and AChR gene expression that depended on the muscle studied.
449 Whereas lack of only ERK1 had no apparent effects on the phenotypes studied, lack of
450 myofiber ERK2 explained synaptic fragmentation in the STN, but not the TA, and a
451 decrease in the expression of *Chnre* mRNA in both muscles. A corresponding reduction
452 in AChR protein was documented in the TA. Evidence of partial denervation was also
453 found in the STN but not the TA. Thus, myofiber ERK1/2 are differentially required for
454 the maintenance of myofibers and neuromuscular synapses in adult mice.

455 The cause/effect relationship between muscle weakness and stunted growth in the
456 DKO mice is unclear. One possibility is that muscles involved in mastication and

457 swallowing become weak leading to reduced food intake and weight loss. Although the
458 weight loss of the DKO mice correlated with the combined muscle fiber loss and atrophy
459 observed in their STN and TA muscles, it is possible minor renal problems might have
460 also contributed to this phenotype. Kidneys from DKO mice had about half ERK2 levels
461 than control (Fig 1D). However, only a few isolated single cells in adult kidney tissue
462 express a LacZ reporter that is driven by the same Hsa-Cre mice used here
463 ([http://www.informatics.jax.org/recombinase/specificity?id=MGI:2447635&systemKey=](http://www.informatics.jax.org/recombinase/specificity?id=MGI:2447635&systemKey=4856358)
464 [4856358](http://www.informatics.jax.org/recombinase/specificity?id=MGI:2447635&systemKey=4856358)). It is unlikely that this low level of expression accounts for the 50% reduction
465 in kidney ERK2 in DKO mice. This reduction, and perhaps any ensuing renal
466 complications, may be secondary effects stemming from the overall muscle weakness.
467 We do not know why the DKO mice die. All of the DKO mild animals that die were
468 males while the surviving ones were females. One of the male DKO mild animals that
469 died at 16 weeks of age displayed kyphosis and showed compromised respiration before
470 humane euthanasia. However, other animals died younger and failed to exhibit
471 respiratory distress or kyphosis that was evident to the naked eye. Moreover, the
472 surviving DKO mild females show clear kyphosis (Fig 2E). Future experiments will be
473 needed to clarify these issues.

474 There was an intrinsic difference in fragmented NMJs between control STN and
475 TA muscles. The average NMJ in control STN had about twice the number of AChR
476 domains than the average NMJ in control TA. This correlated with the sensitivity to NMJ
477 fragmentation in these muscles following the reduction in ERK1/2. Even after abrogation
478 of myofiber ERK1/2, this difference was maintained as the most fragmented synapses
479 occurred in the STN and not the TA. It remains possible that these differences disappear

480 in older animals. Wild type TA and STN muscles showed no difference in NMJ
481 fragmentation when examined at 2 years of age (39). However, synaptic fragmentation in
482 that study was defined differently than here. To account for the intrinsic differences in
483 fragmentation of control NMJs in various muscles, we propose that a fragmented NMJ
484 could be defined as one having more AChR domains than the control median. In control
485 muscle, the frequency of fragmented synapses using this criterion will always be by
486 definition 50% at most. Two other groups previously used a threshold of AChR
487 fragments to define a fragmented NMJ. Valdez and colleagues (39, 40), defined a
488 fragmented NMJ as one having 5 or more AChR islands or a segment of the postsynaptic
489 apparatus with severe abnormalities such as a small or irregularly shaped AChR cluster.
490 Li and co-workers (38) defined a fragmented NMJ as one having 10 or more AChR
491 domains. When applied to our data, the Valdez criterion suggests the puzzling conclusion
492 that most of the NMJs in control STN are fragmented. In this regard, our control
493 genotype was not wild type for *Erk2*; it was *Erk2^{fl}*. Because the average AChR
494 patches/NMJ in the STN from the Cre driver mice (genotype *Erk1^{+/+}; Erk2^{+/+}*) was a bit
495 lower than in our control STN, it is possible that the *Erk2^f* allele might have a small effect
496 on fragmentation. Li and colleagues studied the STN and their more stringent criterion
497 perhaps resulted from studying this muscle, whose synapses appear particularly prone to
498 fragmentation. This criterion was rather uninformative for our experiments in the TA
499 because it sets the threshold for fragmentation (≥ 10 fragments) even above the average
500 AChR domains per NMJ obtained in the DKO TA (~ 6.46). Thus we believe our control-
501 median-based criterion, in combination with the statistical analysis in Figure 4, is more

502 fitting to define a fragmented NMJ and to account for the intrinsic differences in
503 fragmentation that may occur among synapses in various muscles.

504 Unlike in the TA, loss of myofiber ERK2 in the STN was sufficient to yield the
505 same levels of synaptic fragmentation as in the DKO (Fig 4). These results were
506 unexplained by higher HSA-Cre-driven ERK2 reduction, or higher ERK1 decrease as a
507 consequence of *Erk2^{fl}* recombination in STN than TA (Fig 1). Nor were endogenous
508 levels of ERK2 higher in control TA than in control STN by Western blotting (data not
509 shown). Although ERK1 and ERK2 are generally viewed as functionally redundant, the
510 differential embryonic lethality between their germline mutants and other evidence (57–
511 59), suggest specific roles for these two kinases in some physiological contexts.

512 Alternatively, the more dramatic phenotypes we find in *mErk2^{CKO}* animals may simply
513 reflect the higher levels of expression of ERK2 relative to ERK1 in skeletal muscle fibers
514 in general.

515 The extensive synaptic fragmentation in the *mErk2^{CKO}* STN failed to correlate to
516 changes in animal weight, forelimb grip strength, survival, fiber number or fiber size,
517 because none of these parameters were different to control. We measured a small increase
518 (~7%) in 2X fibers in the *mErk2^{CKO}* STN relative to control. However, it is unlikely that
519 this accounts for the synaptic fragmentation in this muscle because 67% of the NMJs in
520 the *mErk2^{CKO}* STN were fragmented according to our control-median-based criterion.

521 Although other general changes in the fibers might be linked to synaptic fragmentation,
522 notably changes in metabolic capacity and generation of reactive oxygen species (ROS)
523 (60), our results suggest that ERK2 regulates mechanisms that locally control synapse
524 maintenance. In this context, NMJ fragmentation by excess ROS needs them produced in

525 motoneurons and not in muscle fibers (61, 62). Hence mechanisms underlying NMJ
526 fragmentation by excess ROS and by muscle ERK1/2 deficiency may be fundamentally
527 distinct. There was no correlation between the accumulation of central myonuclei (Fig 6)
528 and the synaptic fragmentation phenotype in *mErk2^{CKO}* and DKO STN (Fig 4A).
529 Postsynaptic mechanisms other than local fiber degeneration/regeneration may account
530 for NMJ fragmentation (63). This does not exclude that some of the fragmented NMJs in
531 our mutant muscles result from degeneration/regeneration in the subsynaptic area. Our
532 measurements of central nuclei were from extrasynaptic regions of the fibers. The
533 relatively small subsynaptic portion of the muscle fiber in mutant muscle could be more
534 prone to damage than the rest of the fiber and/or central nuclei could be transient and
535 migrate quickly to the periphery of the fiber so that we would miss them in our
536 experiments (38).

537 NMJs with dimly BTX-stained AChRs were present both in DKO STN and TA,
538 although they were more easily detected in the latter (Fig 7). Fewer AChRs at the
539 synaptic site could be due to one or a combination of the following processes: Lower rate
540 of synthesis and/or multimeric assembly, higher rate of degradation, lower insertion rate
541 of the receptors in the synaptic sarcolemma or higher retrieval from it. Synthesis depends
542 highly on the rate of local transcription. We found a consistent reduction of the AChR ϵ
543 subunit gene mRNA, which was myofiber ERK2-dependent (Fig 7C). We also
544 documented a corresponding reduction in AChR ϵ protein in the DKO TA (Fig 8).
545 Transcription of all AChR subunit genes is highly enriched at the subsynaptic myonuclei
546 (64–66); however, *Chrne*'s is perhaps the most synaptic of them all (47). Thus, a
547 reduction in *Chrne* mRNA is expected to affect the synaptic AChR selectively. This

548 reduction was not due to general fiber atrophy as it was detected in *mErk2^{CKO}* muscle,
549 which was no different to control regarding fiber morphology (Fig 9). The ~2-fold
550 reduction in whole *mErk2^{CKO}* and DKO muscle *Chrne* mRNA may underestimate the
551 reduction at those NMJs with faint AChR staining (Fig 7B). Dominant-negative mutants
552 for Ras, Raf and MEK1 selectively inhibited synapse-specific expression of *Chrne*-
553 luciferase reporters that were expressed in adult TA muscle following DNA injection
554 (23). These experiments suggested that ERK signaling regulates *Chrne* expression at the
555 transcriptional level. Our data showing parallel reductions in both AChR ϵ protein and
556 mRNA are consistent with this mechanism for the role of ERK in controlling *Chrne*
557 expression.

558 The presence of terminal sprouts and of AChR patches lacking apposing nerve
559 terminal staining in some NMJs from DKO STN is consistent with the significant
560 increase in *Chrng* mRNA and suggests that a relevant proportion of NMJs in this muscle
561 are at least functionally denervated. This effect explains the tendency towards increased
562 levels of *Chrna*, *Chrnb* and *Chrnd* mRNA in the DKO STN (Fig 7C), as denervation is
563 well known to induce expression of these AChR subunit genes along the entire muscle
564 fiber (51). It might also explain why *Chrne* mRNA levels in the DKO STN were just
565 borderline different than control ($p=0.05$), while those in *mErk2^{CKO}* STN were
566 significantly lower ($p<0.05$, Fig 8C). This was not observed in the DKO TA, which
567 highlights another important distinction in the response to the lack of myofiber ERK1/2
568 between these two muscles. Unlike synaptic fragmentation in the STN, full expression of
569 this partial denervation-like effect required removal of both ERK1 and ERK2. This
570 suggests that synaptic fragmentation and the apparent denervation are not tightly

571 correlated. The fiber loss and the increased proportion of regenerating fibers detected in
572 the DKO STN (Figs 9 & 6) could account, at least in part, for the upregulation of *Chrn*
573 in this muscle, as increased AChR expression was observed in regenerating muscle (67).
574 In this context, complete denervation is rare in NMJs from aged normal STN, however,
575 partial denervation, terminal sprouts and aneural AChRs were detected (38, 39). Changes
576 in *Chrn* in aged normal STN have not been studied, however, increases in expression of
577 *Chrn* and other denervation markers were reported in aged normal quadriceps (68), and
578 seemed unaccompanied by motoneuron loss (69).

579 The significant fiber loss that we observed in the DKO STN, together with the
580 mild fiber atrophy in DKO STN and TA, are consistent with a role for ERK1/2 in
581 maintaining skeletal muscle mass, and with prior studies that suggested so in C2C12 cells
582 and rats (9). On the other hand, our analysis of fiber type composition in the STN and TA
583 disagrees with the notion that ERK1/2 are essential to preserve the fast-twitch fiber
584 phenotype as previously proposed (10). To inactivate ERK1/2 signaling in vivo, the latter
585 study used overexpression of MAPK phosphatase -1 (MKP-1) by electroporation of adult
586 mouse muscle. However, MKP-1 not only inactivates ERK1/2 but actually shows
587 substrate preference for other MAPKs such as JNK and p38 (56). Thus, the in vivo
588 effects on fast fiber expression reported in this study could have been unspecific to the
589 inactivation of pERK1/2. Others have posited that ERK1/2 are critical to promote slow-
590 fiber differentiation (11). Because the STN and TA muscles studied here bear such a low
591 fraction of type 1 fibers, compelling conclusions about the role of ERK1/2 on the slow
592 fiber phenotype from our animals will have to wait until we examine muscles with
593 significant content of type 1 fibers such as the soleus.

594 Intrinsic distinctions in the normal development and maintenance of NMJs among
595 different muscles were described (70), and might underlie the differences in the response
596 of the NMJs in STN and TA to the lack of myofiber ERK1/2. Thus, the STN is a delay
597 synapsing muscle while the TA is a fast synapsing one (70). Muscles display differential
598 susceptibility to sarcopenia and to neuromuscular diseases. Some are highly affected
599 while others appear resistant. In many cases, these muscle-selective effects include how
600 their NMJs react to these conditions (39, 71, 72). The mechanisms underlying these
601 unique sensitivities remain elusive and are likely to be complex and condition-specific.
602 Reduction in active ERK1/2 levels with aging were reported in specific muscles of the rat
603 (13). Significant skeletal muscle abnormalities (16, 17) were found in patients suffering
604 from a group of genetic conditions collectively known as RASopathies, in which
605 different components of the Ras/MAPK pathway are anomalously activated (15).
606 Recently, patients with deletions encompassing *MEK2* were shown to have overlapping
607 features with RASopathies, which suggests that haploinsufficiency of Ras-Erk1/2
608 pathway components is a potential novel mechanism underlying these disorders (73). Our
609 results showing that myofiber-derived ERK1/2 are necessary for the maintenance/growth
610 of adult muscle fibers and for the stability of their NMJs in a muscle-specific fashion
611 further support an important role for this signaling pathway in muscle-selective
612 sarcopenia and are informative as to relevant neuromuscular phenotypes that may be
613 affected by the dysregulation of Ras-ERK signaling in RASopathies.

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855 **LEGENDS TO FIGURES**

856

857 **Figure 1. Mice generation and characterization of their ERK1/2 expression. (A)**

858 Sternomastoid (STN) and tibialis anterior (TA) extracts from 14-week-old mice were

859 probed simultaneously with antibodies to ERK2 and α -tubulin (α -Tub). Genotypes were:860 Control: *Hsa-Cre*^{-/-}; *Erk2*^{fl/fl}. Het: *Hsa-Cre*^{+/-}; *Erk2*^{fl/+}. *mErk2*^{CKO}: *Hsa-Cre*^{+/-}; *Erk2*^{fl/fl}.

861 Histograms show normalized quantification relative to control. A 90%-reduction in

862 ERK2 levels in both muscles in *mErk2*^{CKO} animals (n=3) relative to control (n=2) was863 observed (**, p<0.01). **(B)** Same extracts in (A) were probed simultaneously with864 antibodies to ERK1 and α -Tub. Histograms show normalized quantification relative to865 control. A 20% reduction in ERK1 in *mErk2*^{CKO} muscle was observed (*, p<0.05). **(C)**866 TA extracts from 14-week-old control, *Erk1*^{-/-}, *mErk2*^{CKO} and DKO mice were first

867 probed with antibodies to phosphorylated ERK1/2 (pERK1/2) (bottom panel). The blot

868 was stripped and reprobed simultaneously with antibodies to total ERK1/2 (tERK1/2) and

869 α -Tub (Top panel). ERK1 is totally absent in *Erk1*^{-/-} and DKO muscle, and reduced870 pERK2 in *mErk2*^{CKO} and DKO is in line with reduced tERK2 levels. Same results were871 obtained with STN extracts (not shown). **(D)** Spinal cord (SPC), heart, kidney and liver

872 extracts from 9-week-old control and DKO mice probed with antibodies to tERK1/2 and

873 α -Tub. ERK2/ α -Tub ratios are shown at the bottom of the blots. Except for kidney, no

874 reduction in ERK2 levels was observed in these tissues.

875 **Figure 2. DKO animals displayed stunted postnatal growth, muscle weakness and**876 **shorter lifespan. (A)** Male weight progression was similar to control for *Erk1*^{-/-} and877 *mErk2*^{CKO} mice, whereas mild DKO animals failed to gain weight from around week 9

878 and severe DKO began losing weight around week 7. Similar weight progression was

879 seen in females (not shown). Per time-point: Control (n \geq 5); *Erk1*^{-/-} (n \geq 6); *mErk2*^{CKO}
880 (n \geq 7); mild DKO (n \geq 3, weeks 4-16; n=2, week 18); severe DKO (n \geq 4, weeks 4-10; n=2,
881 week 11). DKO mild, p<0.01 vs. matching time-point control, t-test, starting at week 6
882 onwards. DKO severe, p<0.01 starting at week 5 onwards. **(B)** Forelimb grip strength
883 was measured every other week starting at week 7 in males and females. Peak tension (g)
884 was normalized to body weight (g). DKO mild and severe animals showed comparable
885 decline in muscle strength, while *Erk1*^{-/-} and *mErk2*^{CKO} mice were similar to control. Per
886 time-point: Control (n \geq 4); *Erk1*^{-/-} (n \geq 4); *mErk2*^{CKO} (n \geq 5); DKO mild (n \geq 4, weeks 7-13;
887 n=2, week 15; n=1, week 17); DKO severe (n \geq 3, weeks 7-9; n=1, week 11). DKO mild
888 and severe, p<0.01, ANOVA, week 9 onwards. **(C)** Mice were subjected to an
889 accelerating rotarod protocol, and the time-to-fall (s) was recorded. No significant
890 differences between controls and *Erk1*^{-/-} or *mErk2*^{CKO} were resolved. DKO mild animals
891 fell off the rotating drum consistently earlier than controls (p<0.01 vs. control, ANOVA).
892 Per time-point: Control (n \geq 5); *Erk1*^{-/-} (n \geq 3, week 9-17; n=2, week 19); *mErk2*^{CKO} (n \geq 5);
893 DKO mild (n \geq 3, weeks 9-13; n=2, week 15; n=1, week 17). **(D)** Kaplan-Meier survival
894 curves for DKO mild and severe mice. Median lifespan were: 71 days, n=23 (severe);
895 121 days, n=7 (mild); p<0.0001, Log-rank test. **(E)** A surviving female mild DKO mouse
896 that developed kyphosis (arrowhead), absent in a matched control.

897 **Figure 3. Fragmented NMJs in STN from young adult DKO mice.** **(A)** An example of
898 a control NMJ labeled with fluorescein-BTX to mark AChRs (A') and with antibodies to
899 synaptophysin (SYN), followed by rhodamine-conjugated secondary antibodies, to label
900 nerve terminals (A''). Long, continuous domains of postsynaptic AChRs are tightly
901 apposed by nerve terminals. **(B)** and **(C)** Examples of fragmented NMJs in severe and

902 mild DKO STN, respectively. Small, mostly round AChR domains variably apposed by
903 nerve terminal staining. Scale bars: 10 μ m.

904 **Figure 4. Quantification of synaptic fragmentation in STN and TA.** Number of
905 AChR domains per endplate was counted from confocal maximal projections of NMJs in
906 STN (**A**) and TA (**B**) from all 4 genotypes. Data were grouped in bins of 5 as represented
907 in the X-axis, and the percent of NMJs in those bins were plotted in the Y-axis. STN:
908 Control (n= 85 NMJs, 5 mice); *Erk1*^{-/-} (80, 4); *mErk2*^{CKO} (90, 6); DKO (52, 3). TA:
909 Control (n= 65, 4); *Erk1*^{-/-} (32, 2); *mErk2*^{CKO} (112, 5); DKO (37,3). The results section
910 describes the statistical analysis of the data.

911 **Figure 5. Fragmented NMJs in *mErk2*^{CKO} STN and DKO TA.** An example of a
912 highly fragmented NMJ from *mErk2*^{CKO} STN (**A**), a normal NMJ from control TA (**B**)
913 and a fragmented NMJ from DKO TA muscle (**C**). Overexposure in the rhodamine
914 channel explains the strong intensity of the SYN staining in C''. Scale bars: 10 μ m.

915 **Figure 6. Quantification of central myonuclei in the STN.** STN cross sections from
916 14-week-old mice were stained for H&E. 20X fields were selected, and total number of
917 fibers and fibers with centrally located nuclei (arrows) were counted. Representative 20X
918 field from control (**A**) and from mild DKO muscle (**B**). Scale bar: 50 μ m. (**C**)
919 Quantification. Control, *Erk1*^{-/-} and *mErk2*^{CKO} muscle had a similar proportion of fibers
920 with central nuclei, while DKO had about twice as many. **, p<0.01 vs. control. N=3
921 muscles for all genotypes except *Erk1*^{-/-} (n=2). Total fibers scored: Control, 1928; *Erk1*^{-/-},
922 1234; *mErk2*^{CKO}, 1405; DKO, 1767.

923 **Figure 7. Regulation of AChR expression by ERK1/2.** (**A**) Examples of fields with
924 DKO NMJs showing weaker (top panel) or faint (bottom panel) AChR staining (big

925 single arrowheads) relative to those in the same field that show more normal levels of
926 AChR staining (small double arrowheads). Two examples of nerve terminal sprouts
927 (arrows) in the DKO STN, labeled for SYN, are shown in the top panel. The short sprout
928 in the bottom right appears to induce/connect with two small AChR clusters in the next
929 myofiber. Scale bars: 10 μm . **(B)** Quantification of weak/faint BTX-stained NMJs. N= 2-
930 6 muscles/genotype. **(C)** Real-time PCR for the adult AChR subunit mRNAs in 9-week-
931 old STN and TA muscle. Values were normalized to control. A consistent decrease in
932 *Chrne* mRNA was observed in *mErk2^{CKO}* and DKO muscle. **(D)** Real-time PCR for the
933 fetal AChR γ subunit gene (*Chrng*) mRNA in 9-week-old STN and TA muscle. Values
934 were normalized to control. A 40-fold increase in *Chrng* mRNA was detected selectively
935 in DKO STN. **(E)** Real-time PCR for two additional denervation markers, *Runx-1* and
936 *Myh3*. Values were normalized to control. Significant induction for these markers was
937 restricted to DKO STN. For all real-time PCR assays, n=6 for both muscles and all
938 genotypes except n=5 for *Erk1^{-/-}* muscles. Muscles from both male and female animals
939 were combined because no significant gender differences were found in the Ct values. *,
940 p<0.05; **, p<0.01.

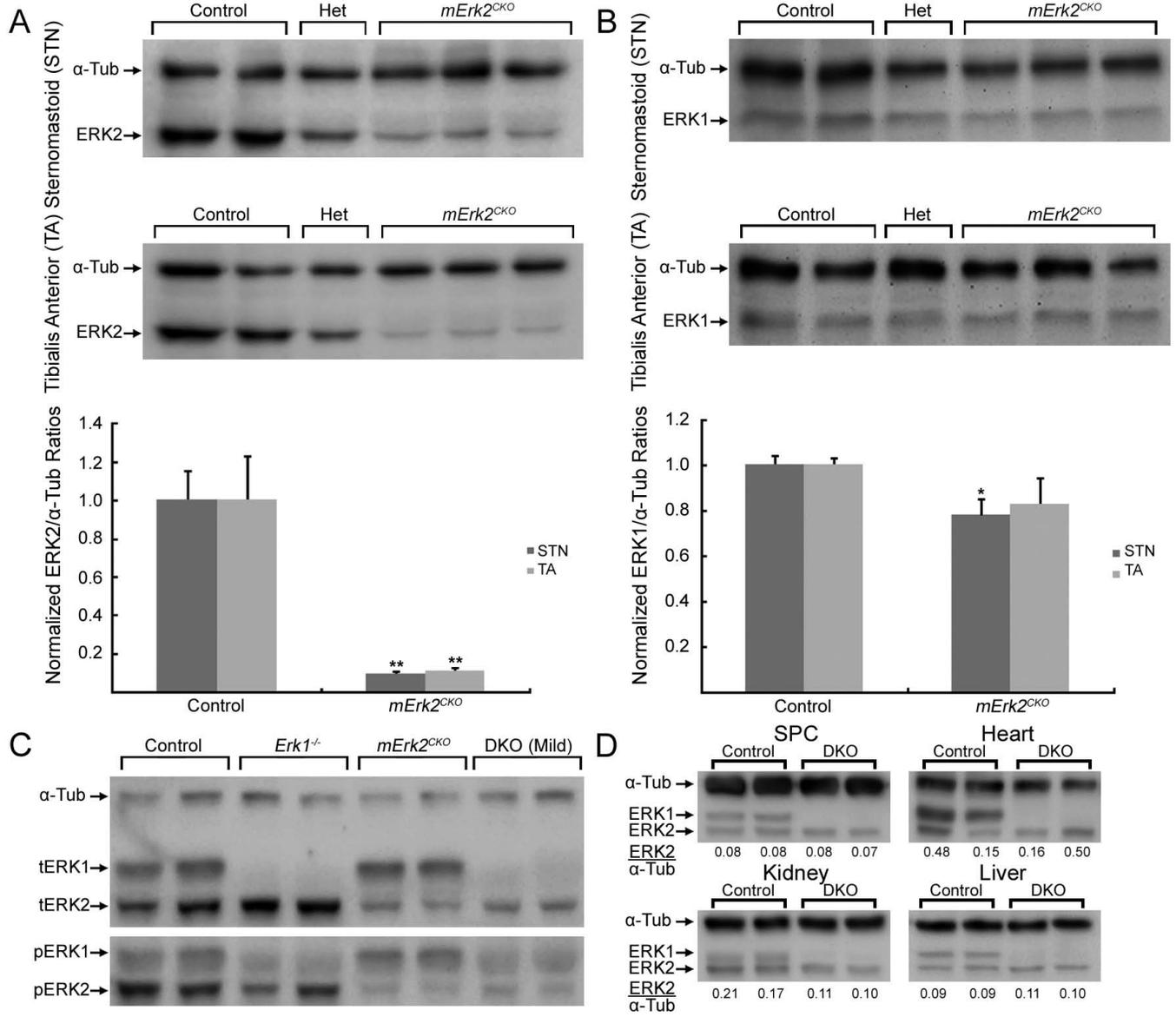
941 **Figure 8. Reduced AChR ϵ protein in DKO TA.** AChRs were affinity purified from 1
942 mg-lysates from 3 control and 3 DKO TA muscles using biotin-BTX (BBTX) and
943 streptavidin-agarose. Precipitates were subjected to SDS-PAGE, transferred to a PVDF
944 membrane and probed for AChR ϵ (arrow). Histogram shows average \pm SEM of band
945 intensities in arbitrary units. *, p<0.05.

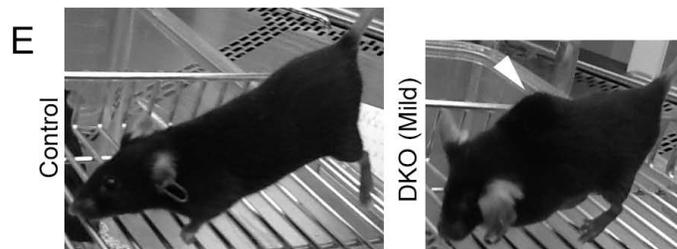
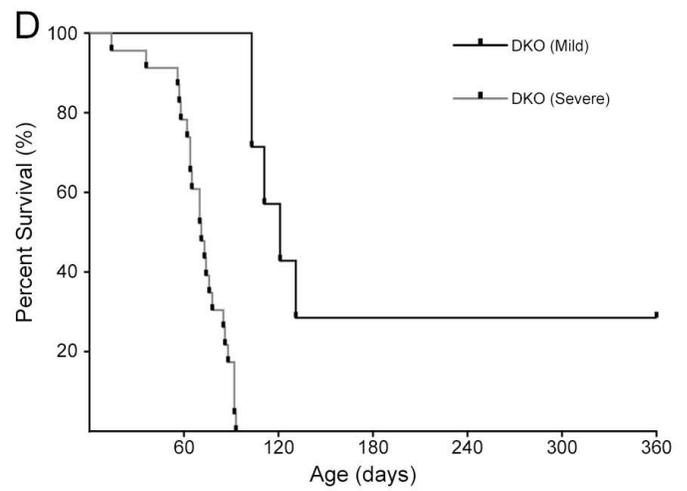
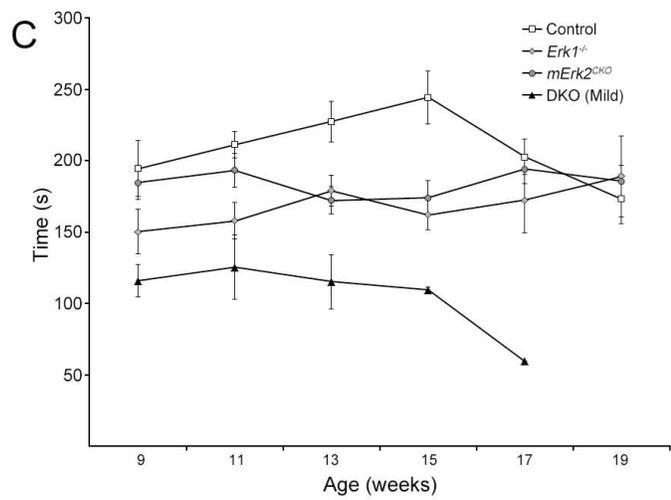
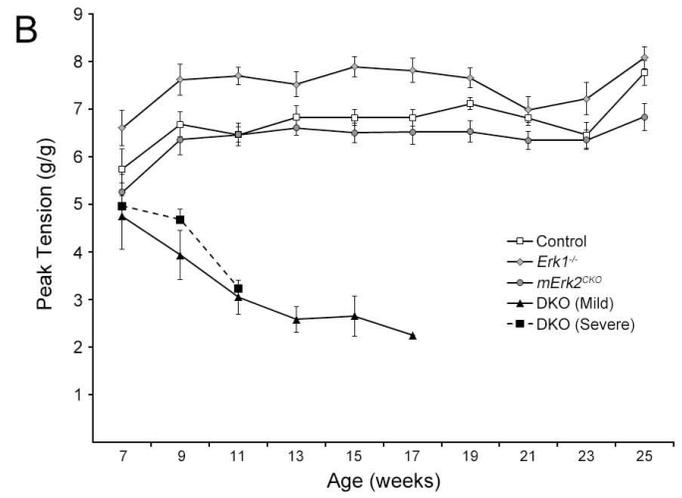
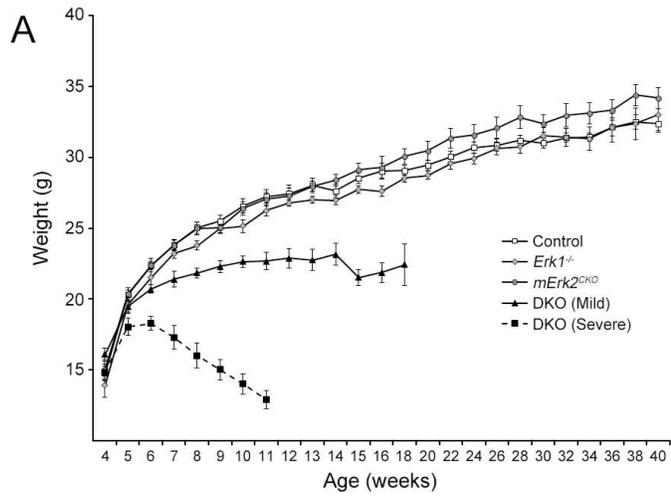
946 **Figure 9. Effects on fiber number, size and type.** **(A)** Representative cross sections of
947 STN muscles from 14-week-old female mice stained for dystrophin. Scale bar: 200 μm .

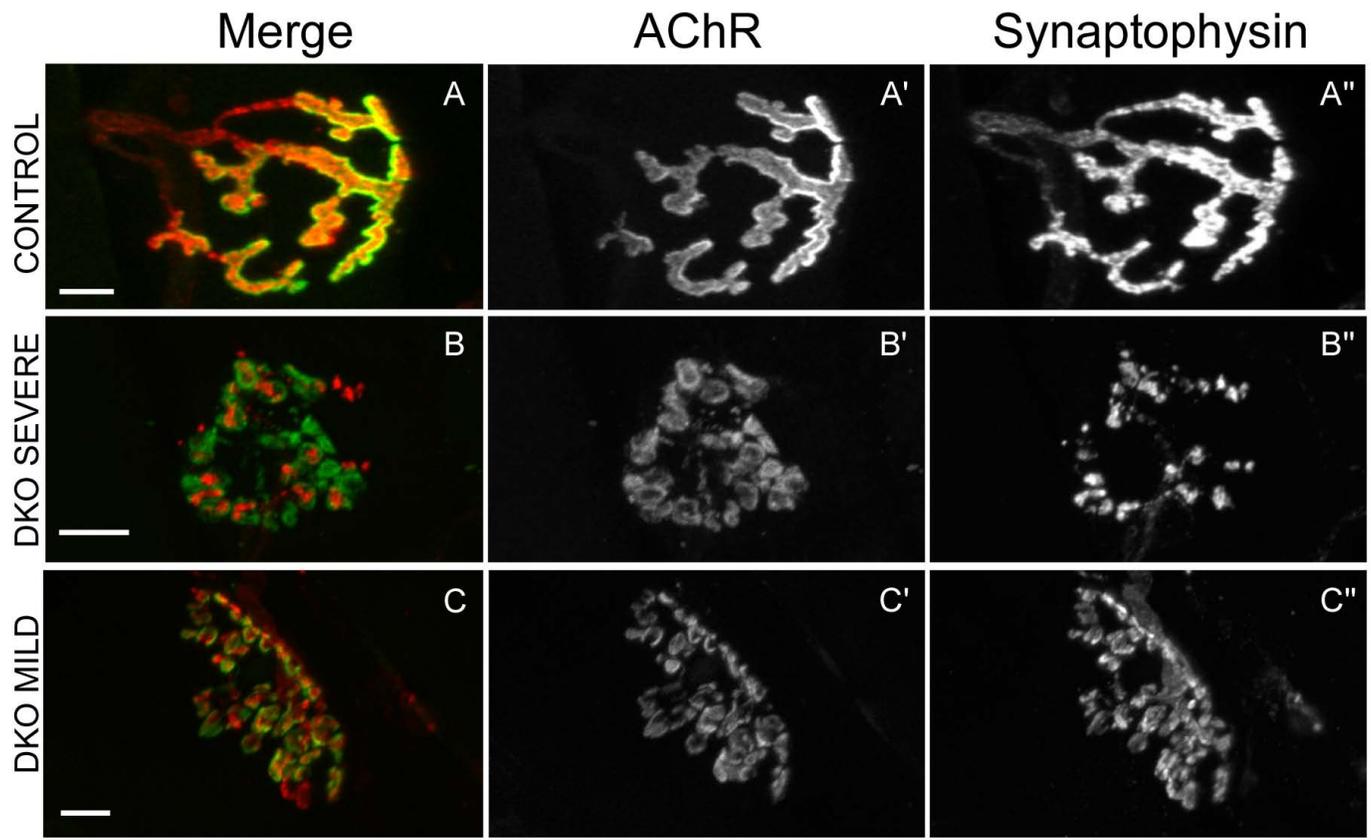
948 **(B)** Representative cross sections of TA muscles from 14-week-old female mice stained
949 for dystrophin. Scale bar: 400 μm . **(C)** Quantification of fiber numbers. A significant
950 reduction in total fibers per cross section was detected in the DKO STN. N=5 for controls
951 and n=3 for all other genotypes. We combined data for males and females per genotype
952 because no significant gender differences were found for this parameter. **(D)**
953 Quantification of average fiber area. Because of gender differences in fiber area, raw data
954 was normalized relative to control of the same sex. Controls were set at 100% and a one-
955 sample t-test was used to statistically compare the results relative to control. N=3 for both
956 muscles and all genotypes. DKO muscle had a smaller average fiber area that was
957 statistically significant for the TA. **(E)** Distribution of fast fiber types in STN. Small but
958 significant increases in 2X fibers were observed in muscles from *mErk2^{CKO}* and DKO
959 mice. **(F)** Distribution of fast fiber types in TA. No changes in fiber type distribution due
960 to genotype were observed in this muscle. We combined data within each muscle for
961 males and females per genotype because no significant gender differences were found for
962 this parameter. N=3 for both muscles and all genotypes. *, $p < 0.05$; **, $p < 0.01$.

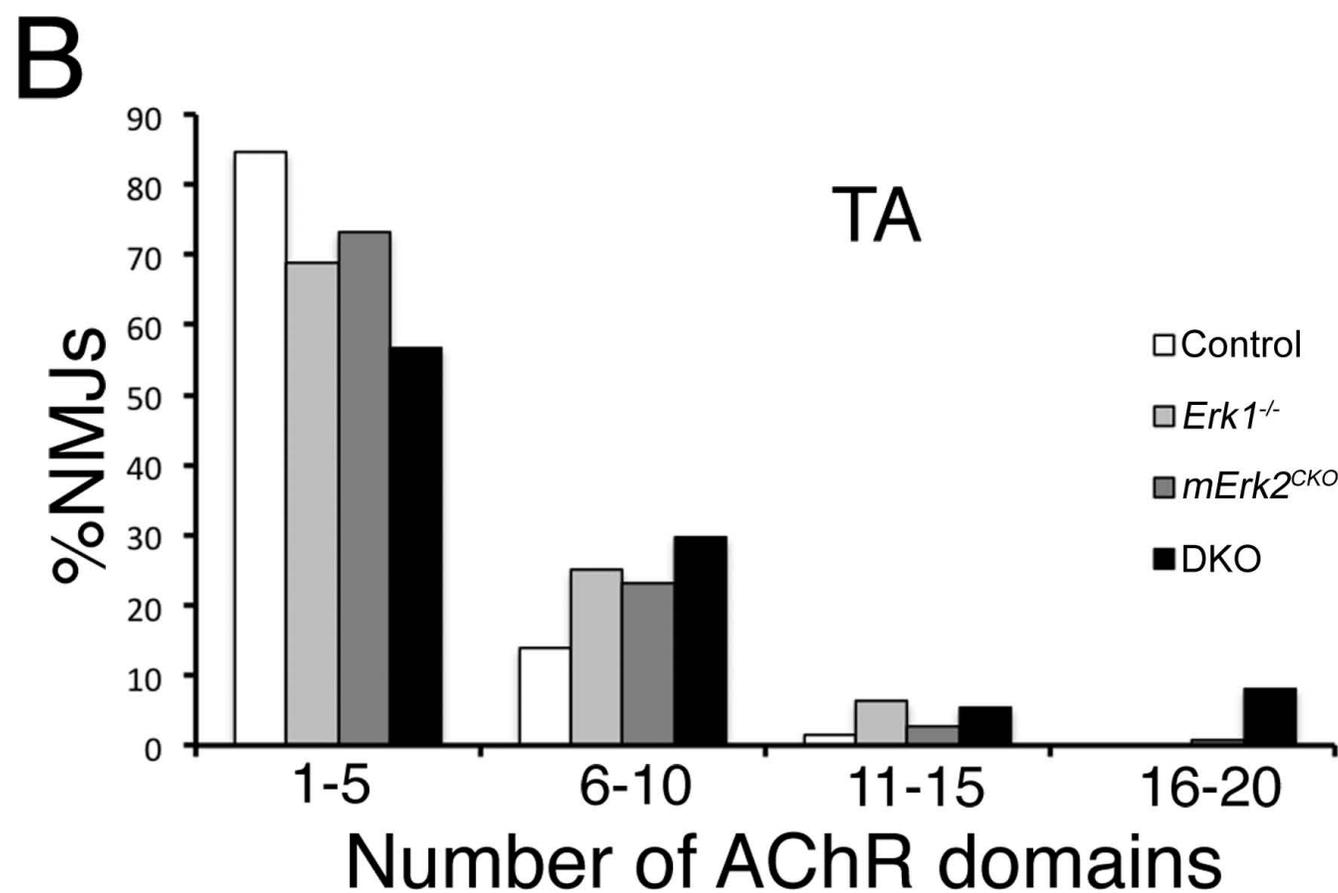
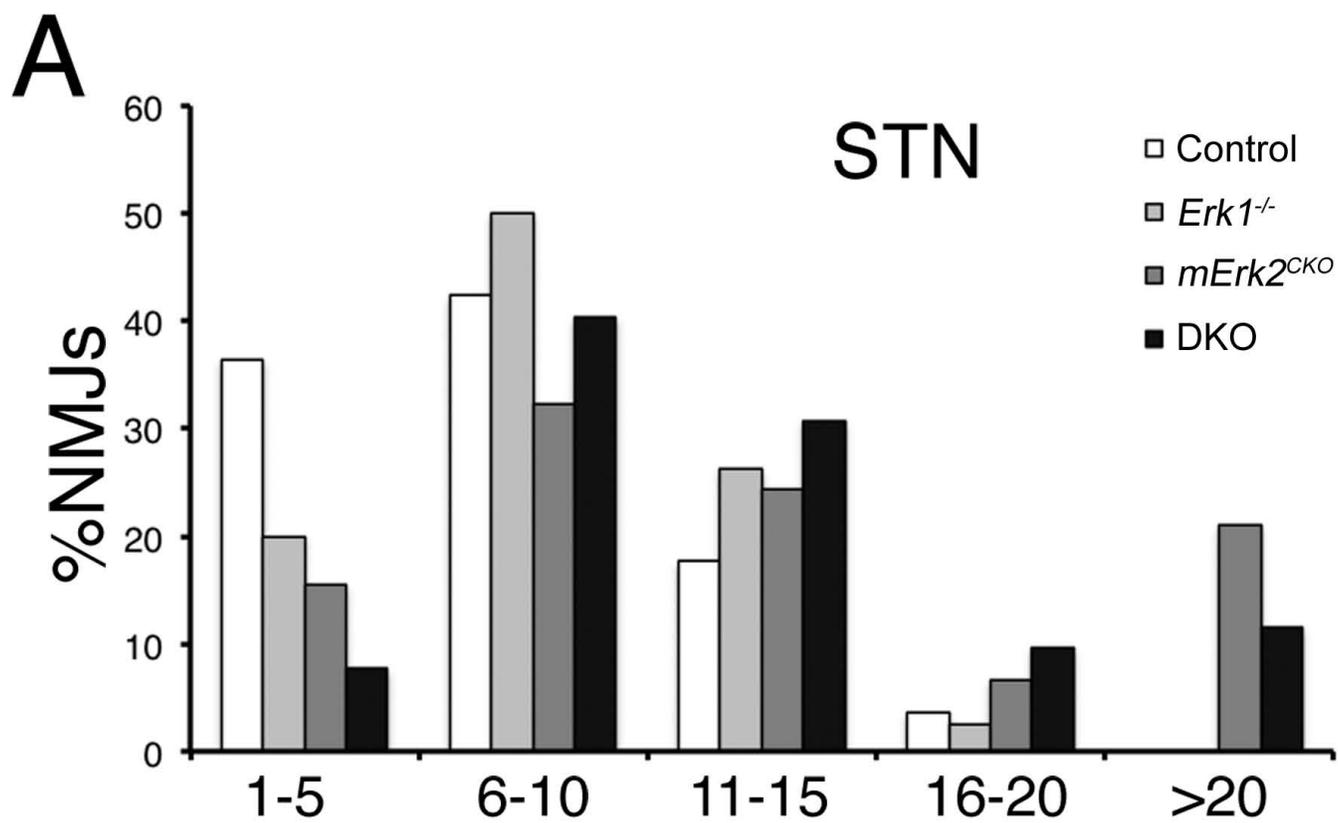
963 **Figure 10. Activated p38 in DKO muscle.** **(A)** Control and DKO STN and TA extracts,
964 n=3 per muscle/genotype, were probed with antibodies to phosphorylated p38 (pp38),
965 total p38 (p38). Variations in loading were checked by stripping membranes and probing
966 for α -Tub. **(B)** Normalized phosphorylated/total protein ratios for p38 showed no
967 statistically significant changes in the activation of this kinase in DKO muscle relative to
968 control.

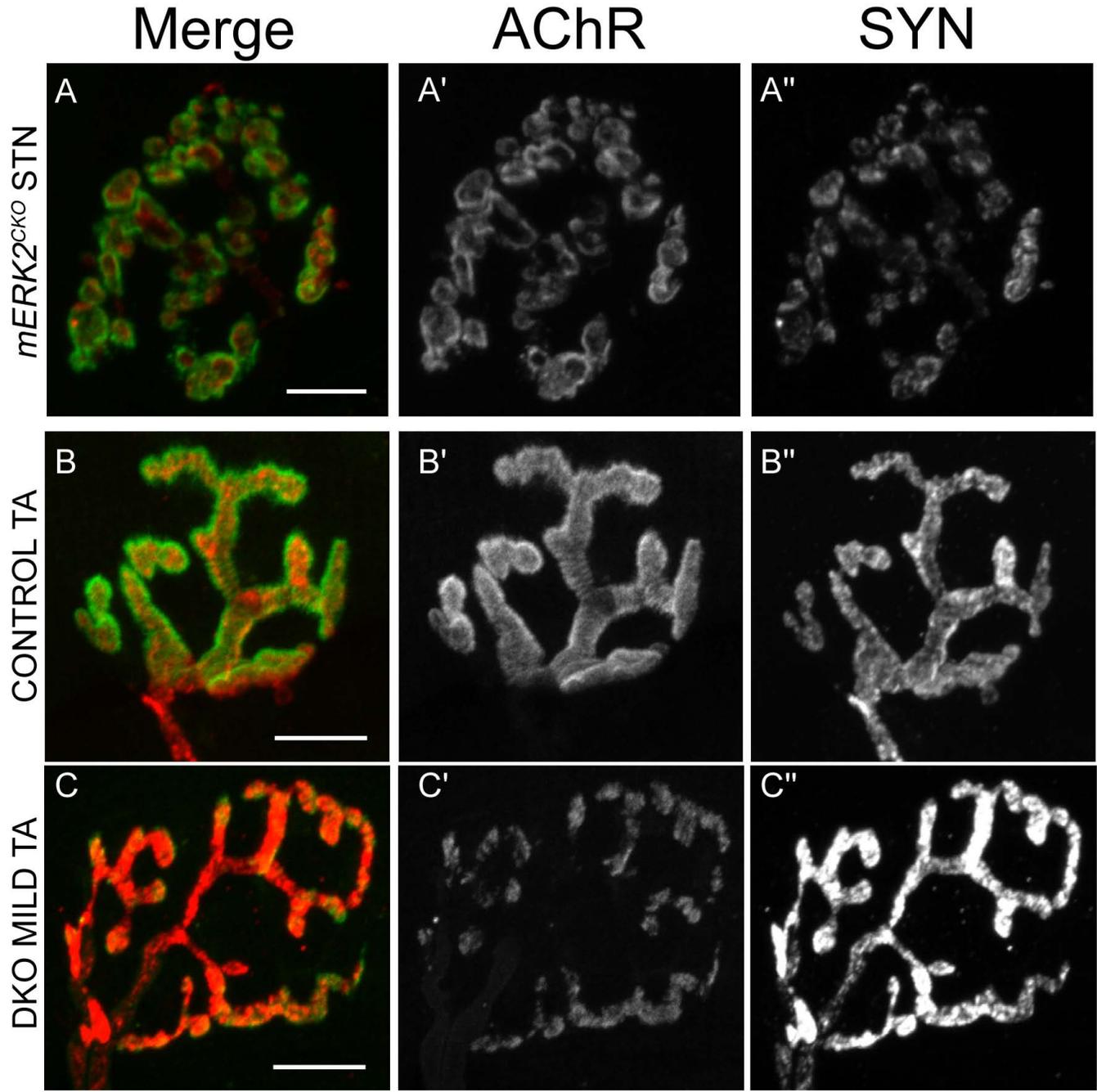
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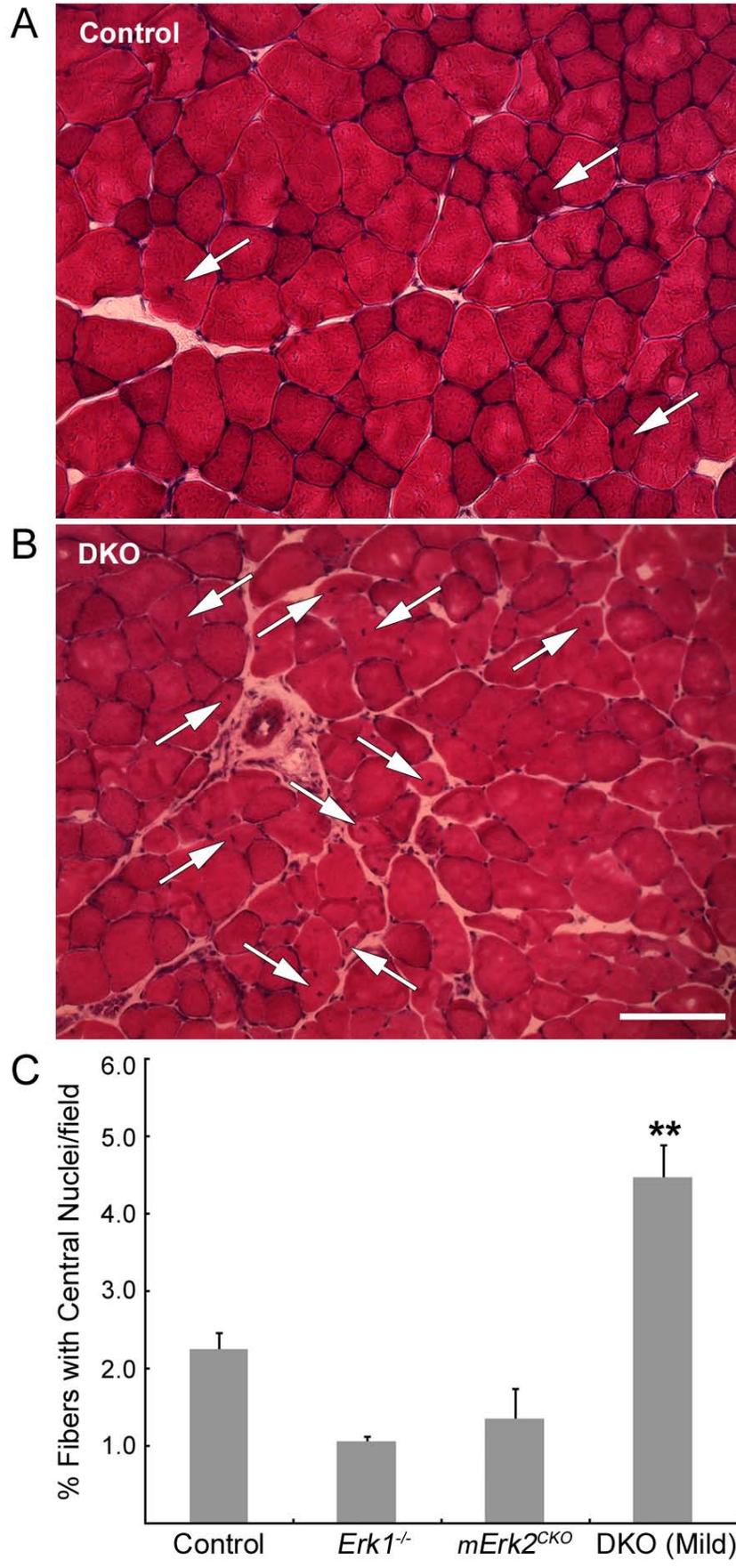


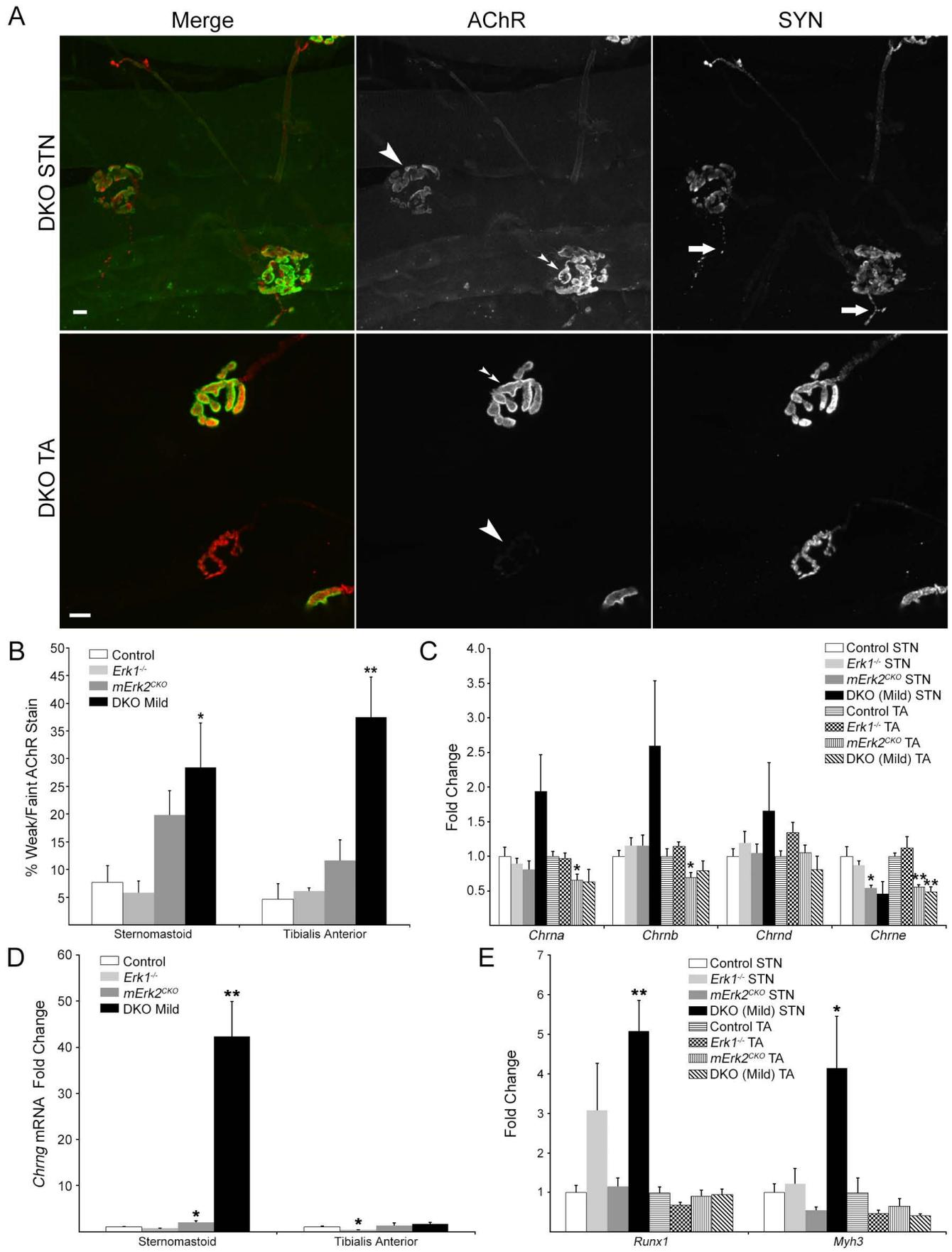


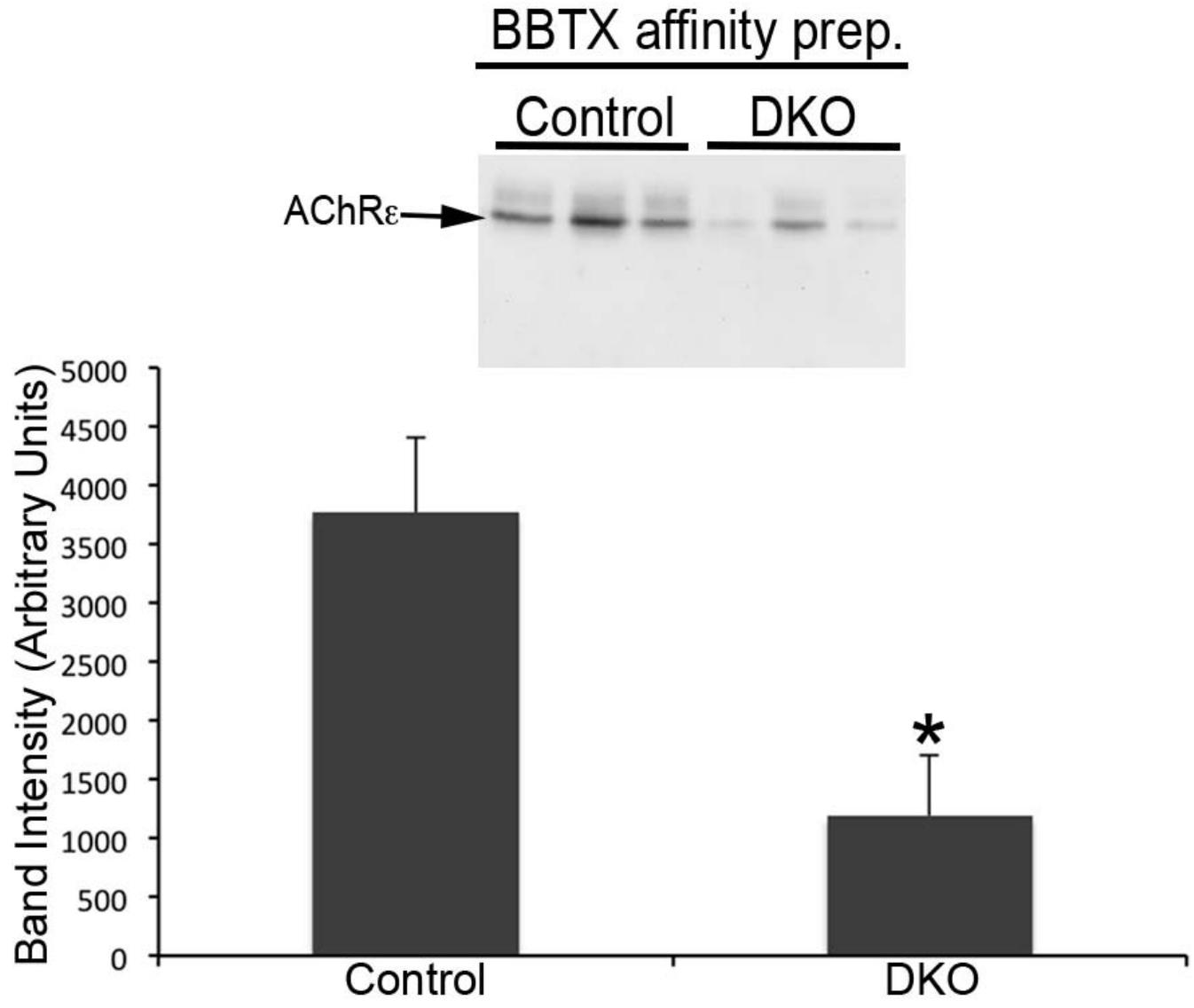


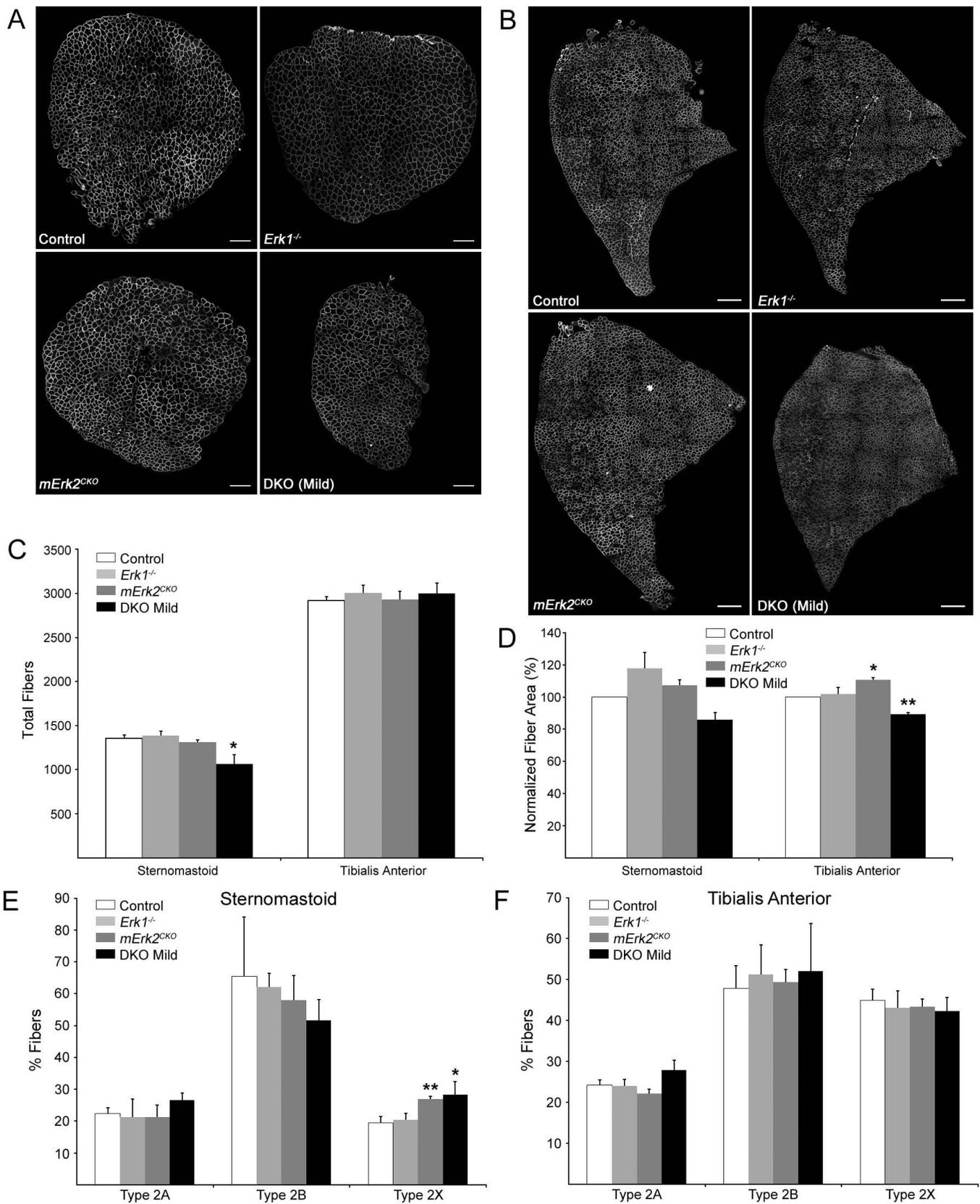


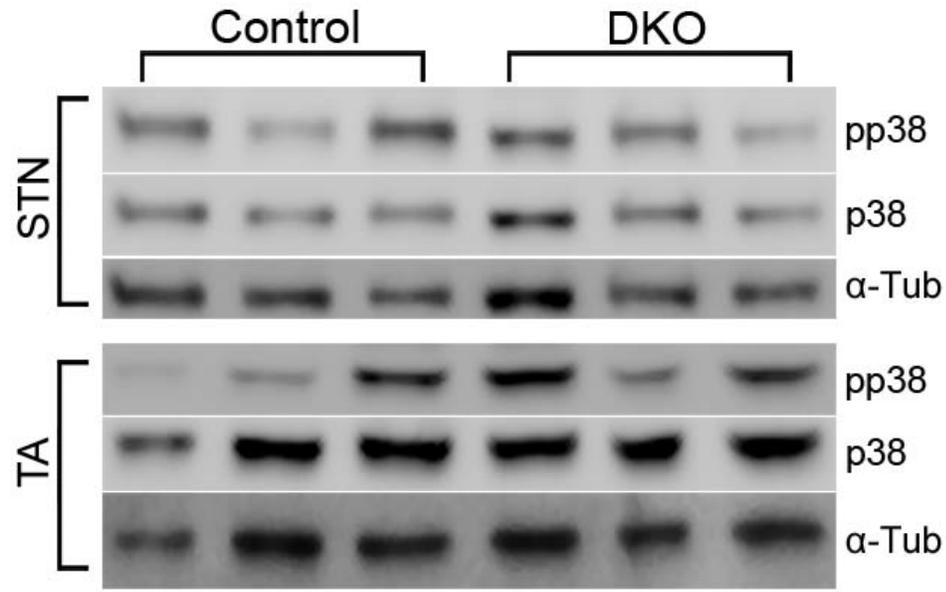










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