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10 Agrin/Lrp4 signal constrains MuSK activity during neuromuscular synapse development in
11 appendicular muscle
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25 SUMMARY STATEMENT

26 In addition to their conserved roles in neuromuscular development of axial muscle, we uncover a
27 second role for Agrin and Lrp4 to constrain MuSK activity in appendicular muscle

29 ABSTRACT

30 The receptor tyrosine kinase MuSK, its co-receptor Lrp4 and the Agrin ligand constitute a signaling
31 pathway critical in axial muscle for neuromuscular synapse development, yet whether this pathway
32 functions similarly in appendicular muscle is unclear. Here, using the larval zebrafish pectoral fin,
33 equivalent to tetrapod forelimbs, we show that like axial muscle, developing appendicular muscles
34 develop aneural acetylcholine receptor (AChR) clusters prior to innervation. As motor axons arrive,
35 neural AChR clusters form, eventually leading to functional synapses in a MuSK-dependent manner.
36 Surprisingly, we find that loss of Agrin or Lrp4 function, which abolishes synaptic AChR clusters in axial
37 muscle, results in enlarged presynaptic nerve endings and progressively expanding appendicular
38 AChR clusters, mimicking the consequences of motoneuron ablation. Moreover, *muskl* depletion in *lrp4*
39 mutants partially restores synaptic AChR patterning. Combined, our results provide compelling
40 evidence that, in contrast to axial muscle in which Agrin/Lrp4 stimulates MuSK activity, Agrin/Lrp4
41 signaling in appendicular muscle constrains MuSK activity to organize neuromuscular synapses. Thus,
42 we reveal a previously unappreciated role for Agrin/Lrp4 signaling, thereby highlighting distinct
43 differences between axial and appendicular synapse development.

45 INTRODUCTION

46 Movement depends on coordinating development of functional synapses called neuromuscular
47 junctions (NMJs) between motor axons and skeletal muscle. Prior to axon arrival, the central region of
48 muscles exhibit a 'prepattern' of clustered acetylcholine receptors (AChR), which requires the receptor
49 tyrosine kinase MuSK. Prepatterning is important for axon guidance, as axons navigate towards
50 aneural AChR clusters on muscles and incorporate them into newly formed NMJs (Panzer et al., 2006).
51 Disruption of prepatterning, such as in *muskl* mutants, leads to exuberant motor axon outgrowth (Jing
52 et al., 2009; Kim and Burden, 2008). Subsequently, as motor axons contact the muscle and transform
53 into nerve endings, they release the glycoprotein Agrin which binds to the low-density lipoprotein
54 receptor-related protein 4 (Lrp4) on the muscle membrane to stimulate phosphorylation of MuSK. Upon
55 activation, MuSK initiates a downstream signaling cascade to cluster AChRs in apposition to axons,
56 thereby forming neural synapses. While there are many additional proteins that modulate NMJ
57 development, mutants of *lrp4*, *agrin*, and *muskl* all fail to form NMJs in the mouse and zebrafish trunk,

58 demonstrating their critical and conserved role in this process (Kim and Burden, 2008; Kim et al., 2008;
59 Zhang et al., 2008; Jing et al., 2010; Remédo et al., 2016; Gribble et al., 2018). The muscular system
60 is comprised of two divisions: axial and appendicular muscles. Axial muscles, such as the diaphragm,
61 attach to the bones of the trunk whereas appendicular muscles move appendages, such as limbs.
62 Extensive work on neuromuscular synapse development that identified the Agrin/Lrp4/MuSK pathway
63 has focused predominantly on axial muscles. In contrast, significantly less is known about the cellular
64 and molecular mechanisms critical for NMJ development in appendicular muscles.

65 Here, we employ the larval zebrafish pectoral fin, which is evolutionarily analogous to tetrapod
66 forelimbs (Mercader, 2007), to study the process of neuromuscular synapse development in a paired
67 appendage. In development, fin buds arise from mesenchymal protrusions oriented vertically just dorsal
68 to the yolk and lateral to the second and third myotome (Grandel and Schulte-Merker, 1998). As the fin
69 bud forms into the pectoral fin, it rotates approximately 90 degrees so the tip points caudally.
70 Additionally, the fin migrates anteriorly, such that it is positioned posterior to the otic vesicle and anterior
71 to the yolk by 60 hours post fertilization (hpf). At 120 hpf (5 days post fertilization (dpf)), pectoral fins
72 are comprised of two antagonistic muscles, the abductor and adductor, separated by an endoskeletal
73 disk (Fig. 1A,B). Each muscle consists of ~50-55 fast-twitch muscle fibers that extend longitudinally
74 from the proximal fin base, where it attaches to the trunk, out to the distal tip of the fin. At the fin base
75 the abductor and adductor muscles are each 2-3 muscle fibers thick, but muscles then thin out to be a
76 single fiber layer throughout most of the fin (Thorsen et al., 2004). The abductor and adductor muscles
77 are innervated by 4 distinct motor nerves, which we refer to here as nerves 1-4, with cell bodies in
78 anterior spinal cord segments 3 through 6 (Myers, 1985; Thorsen and Hale, 2007). Motor axons enter
79 the fin at a dorsal (nerves 1-3) or ventral (nerve 4) plexus to sort between the abductor or adductor
80 muscles (Thorsen and Hale, 2007). Axons then progressively defasciculate as they grow towards the
81 distal tip of the fin such that each muscle fiber is polyinnervated and motor axons create a patchwork
82 pattern across the fin muscles. This innervation pattern remains unchanged until juvenile stages at
83 three weeks (5.4-5.8 mm) when the muscles divide, nerves increase in arborization, and bone forms
84 (Grandel and Schulte-Merker, 1998; Thorsen and Hale, 2007). The genetic-tractability, transgenic tools
85 to label specific cell types, optical transparency suitable for live imaging, and behavioral readout of fin
86 movement make the larval zebrafish pectoral fin an ideal vertebrate system to interrogate mechanisms
87 of neuromuscular synapse development within appendicular muscles.

88 The axial trunk and the pectoral fin neuromuscular systems differ in several key ways. First, axon
89 innervation of the axial muscles begins between 16-24 hours post fertilization (hpf) (Eisen et al., 1986)
90 whereas in appendicular/fin muscles it is delayed by approximately 24 hours. Secondly, the trunk and

91 the fin differ broadly in their muscle fiber anatomy. The trunk is comprised of several medial layers of
92 fast-twitch (fast) muscle fibers and a single lateral slow-twitch (slow) muscle fiber layer that are
93 arranged in repeating segments. In contrast, the fin muscles are only 1 fiber thick, comprised solely of
94 fast fibers, and are approximately 2.5 times longer than trunk muscle fibers (Thorsen and Hale, 2007).
95 Additionally, after exiting the spinal cord, axons in the trunk grow perpendicular to and along the center
96 of muscle fibers. In contrast, the motor axons that innervate the pectoral fin grow through the body wall,
97 sort at a plexus and then branch to create elaborate innervation patterns that can be perpendicular to
98 and also parallel to muscle fibers in the fin. Axonal innervation of the fin is topographic, with axons from
99 anterior spinal segments innervating the dorsal fin and axons from posterior segments innervating the
100 ventral fin (Thorsen and Hale, 2007). Finally, in the trunk, aneural AChRs are present on slow muscle
101 fibers, which are absent in the pectoral fin (Flanagan-Steet et al., 2005). Whether AChRs are
102 prepatterned and how axon outgrowth occurs in the pectoral fin has not yet been described.

103 While many of the signals that mediate NMJ development have been well-characterized in axial
104 muscles, whether the same cellular and molecular mechanisms underlie NMJ development within the
105 complicated muscle arrangement of paired appendages has remained unclear. Here, we reveal that
106 while some aspects of neuromuscular synapse development, such as pre patterning with aneural AChR
107 clusters and the requirement for MuSK to form neural AChR clusters, are shared between the trunk
108 and the pectoral fin, there are key muscle-specific differences in the fin. We show that both axonally
109 released Agrin and Lrp4 on muscle cells are required to form the distributed patterning of AChR clusters
110 in the fin. While *agrin* and *lrp4* mutants fail to form synapses in the trunk, in the pectoral fin they instead
111 lead to the formation of giant AChR clusters and axonal innervation abnormalities. A developmental
112 timecourse in *agrin* mutant fins reveals that these clusters likely arise from prepatterned AChR clusters
113 that continue to grow over time. These giant clusters sequester navigating growth cones, thereby
114 disrupting the innervation patterning. Partial depletion of *muskl* moderately suppresses the formation of
115 these clusters in *agrin* and *lrp4* mutants. Based on our results, we propose a model for NMJ formation
116 in the appendicular fin muscle in which Agrin/Lrp4 signaling transitions MuSK from a pre patterning state
117 to an axon-dependent, focal AChR clustering state. Without Agrin or Lrp4, MuSK remains active within
118 prepatterned islands and AChR clusters grow. Importantly, this work exposes key differences in
119 neuromuscular synapse development between axial muscles of the trunk and appendicular muscles of
120 the pectoral fin.

123 RESULTS

124 Development of pectoral fin innervation is a tightly coordinated and dynamic process

125 At 120 hpf zebrafish pectoral fins have established a complex neuromuscular organization with
126 motor axons forming an elaborate pattern across the abductor and adductor muscles. To visualize the
127 organization between nerve and muscle within the fin we used transgenic *mnx1:GFP* or *Xla.tubb:dsRed*
128 to label the majority if not all motor axons that innervate the pectoral fin and *α -actin:GFP* to label
129 pectoral fin muscle fibers (Fig. 1A-C). Although the fin is comprised of both abductor and adductor
130 muscles with independent innervation fields (Fig. 1D, H), for simplicity we include only the abductor
131 innervation unless otherwise noted (Fig. 1E-G). Labeling of nicotinic AChRs with α -bungarotoxin (α -
132 Btx) revealed hundreds of small, evenly spaced *en passant* neuromuscular synapses juxtaposed to
133 motor axons (Fig. 1F-G). The largest postsynaptic AChR clusters are associated with the major nerve
134 branch localized closest to the proximal fin base, while AChR clusters are smaller as the finer nerve
135 branches defasciculate towards the distal tip of the fin musculature.

136 The developing pectoral fin is a dynamic structure. Previous work has described the development
137 of the structure of the fin, from fin bud to adult (Yano et al., 2012; Siomava et al., 2018), as well as the
138 innervation and musculature of the fin after 120 hpf (Thorsen and Hale, 2007), a timepoint at which the
139 larval innervation pattern is relatively stable. Yet, to our knowledge the development of the zebrafish
140 pectoral fin musculature and its complex innervation pattern prior to 120 hpf have not been described.
141 To observe the process of muscle development and axonal innervation of the pectoral fin, we used
142 long-term timelapse imaging of transgenic embryos to observe muscles (*Tg(α -actin:GFP)*) and axons
143 (*Tg(Xla.tubb:dsRed)*) in developing zebrafish. By approximately prim-25 (36 hpf), motor axons from
144 nerves 1-3 coalesce at what will form the dorsal plexus and nascent muscle fibers in the pectoral fin
145 bud, located laterally to the axons, have just started expressing *α -actin:GFP* (Fig. 2A-B, Movie S1).
146 Muscle fibers continue to divide and reorganize through the long-pec stage as the fin moves further
147 medial, closer to the plane of the dorsal plexus, and motor axons begin to grow into the abductor and
148 then adductor muscles beginning around the long-pec stage at 46 hpf. Concurrently, axons in nerve 4
149 make a sharp turn dorsally to innervate the fin via the ventral plexus. Thick axon bundles first grow
150 perpendicular to muscle fibers near the proximal fin base, but subsequently axons turn posteriorly to
151 grow mostly parallel to muscle fibers and towards the fin tip. As muscle fibers elongate, branching motor
152 axons follow close behind to form a diffuse innervation network. By ~68 hpf, a simplified innervation
153 pattern is established (Fig. 2B,G) that will become more complex through 120 hpf. Thus, the
154 development of the innervation and musculature of the pectoral fin is a highly dynamic yet tightly
155 coordinated process.

156 Pectoral fins start moving rhythmically as early as 3 dpf (Uemura et al., 2020), prompting us to
157 examine when during development neuromuscular synapses in the pectoral fin form, and to what
158 degree this process mirrors synapse development in axial muscle. To observe neuromuscular synapse
159 development in pectoral fins we fixed transgenic *mnx1:GFP* larvae (to label presynaptic motor axons)
160 at various timepoints and labeled AChRs with fluorescently-conjugated α -Btx. In vertebrates,
161 'prepatterned' AChR clusters form on muscle fibers prior to motor neuron innervation (Lin et al., 2001;
162 Yang et al., 2001), but whether or when this occurs in developing appendicular muscle of pectoral fins
163 has not been investigated. At the high-pec stage (~42 hpf), when the pectoral fin bud is located lateral
164 to the nascent dorsal plexus and axons have not yet entered the fin, AChR clusters are undetectable
165 (Fig. 2C). By 46 hpf, as axons have just started to grow past the plexus onto the fin musculature, we
166 observe small AChR clusters near the base of the fin that are not yet associated with labeled axons
167 (Fig. 2D). At 51 hpf, axons growing from the dorsal and ventral plexi extend towards each other along
168 the fin base and innervate nearby AChR clusters, while remaining axon free or aneural AChR clusters
169 at the not yet innervated medial region of the fin increase in size (Fig. 2E). By 60 hpf all AChR clusters
170 at the proximal fin base are associated with axons (Fig. 2F).

171 The entry of axons into the fin initiates a second phase of neuromuscular synapse formation. As
172 axons grow beyond the fin base and branch to extend along muscle fibers, new AChR clusters are
173 formed. These new AChR clusters are always associated with axons (Fig. 2F-G). The number of AChR
174 clusters increases as the innervation pattern becomes more complex, such that by 120 hpf axons are
175 dotted with hundreds of regularly spaced AChR clusters that remain relatively small ($<5 \mu\text{m}^2$) (Fig. 2G).
176 In contrast, the clusters at the fin base that preceded axon outgrowth continue to increase in size,
177 perhaps as they are innervated by additional axons, such that by 120 hpf the biggest AChR clusters in
178 the fin ($>20 \mu\text{m}^2$) are in this proximal region. Thus, neuromuscular synapse development in
179 appendicular muscle of the pectoral fin mirrors that in axial muscle of the trunk, with a prepatterned
180 phase and an axon-associated phase of synapse formation.

181 **MuSK signaling is required for neuromuscular synapse development in pectoral fin muscle**

182 Given the similarities in AChR pre patterning and axon-associated AChR clustering between the
183 trunk and the pectoral fin, we wondered if the well-established genetic pathway that regulates
184 neuromuscular synapse development in axial muscle is also critical for this process in pectoral fin
185 muscle. In vertebrate axial muscles, AChR pre patterning and the formation of neuromuscular synapses
186 requires the receptor tyrosine kinase MuSK (DeChiara et al., 1996; Lefebvre et al., 2007). We first
187 asked if *musk* is also required for AChR pre patterning within larval zebrafish appendicular muscle by
188 staining sibling and *musk* mutant pectoral fins with α -Btx to label AChR clusters during the time of axon

189 navigation into the fin. At the long-pec stage (46 hpf), when wildtype sibling animals have developed
190 robust prepatterned aneural AChR clusters, staining of *musk* mutant pectoral fins failed to reveal any
191 evidence of prepatterned AChR clusters (Fig. S1). To account for a possible delay in pectoral fin
192 development or aneural cluster formation we also examined *musk* mutants at later timepoints. At 51
193 hpf and 60 hpf, the extent of axon growth in the fin is comparable between siblings and *musk* mutants.
194 At these timepoints wild type axons have innervated prepatterned AChR clusters and new clusters
195 have formed, while in *musk* mutant fins α -Btx staining remains diffuse and muscles lack discernible
196 AChR clusters. Thus, as in trunk axial muscle, *musk* is required for AChR pre patterning in appendicular
197 fin muscle.

198 Next, we examined the role of MuSK in the formation of neural AChR clusters characteristic of
199 neuromuscular synapses. In the zebrafish trunk, motor axons branch and form synapses distributed
200 along myofibers throughout the myotome. Consistent with previous work (Lefebvre et al., 2007; Jing et
201 al., 2010), we find that at 120 hpf, trunk axial muscle fibers in *musk* mutants exhibit diffuse bungarotoxin
202 staining with fewer and smaller AChR clusters, compared to sibling controls (Fig. 3 A-B, D). Similar to
203 what we observe in trunk axial muscle fibers, appendicular muscle fibers in *musk* mutants display
204 mostly diffuse bungarotoxin staining and lack wild type-like AChR clusters (Fig. 3C). While *musk*
205 mutants exhibit some AChR clusters that form in apposition to axons, compared to sibling controls they
206 are fewer and smaller in size. These circular clusters resemble the dystroglycan-dependent clusters
207 that form on zebrafish axial muscle fibers in the absence of *musk* (Lefebvre et al., 2007). Moreover,
208 compared to wild type controls, motor axons in *musk* mutant pectoral fins are less fasciculated, similar
209 to what has been reported previously for axial muscle fibers in zebrafish and mouse lacking MuSK
210 (Kim and Burden, 2008; Jing et al., 2009).

211 Finally, we asked whether MuSK acts through its well-established downstream effector Rapsyn
212 during appendicular neuromuscular development. Like *musk*, *rapsyn* is required for AChR clustering in
213 mouse and zebrafish axial muscle (Gillespie et al., 1996; Ono et al., 2002). Similar to its role in axial
214 muscle, *rapsyn* is required for AChR clustering in the pectoral fin, as *rapsyn* mutants display diffuse α -
215 Btx signal throughout pectoral fin muscles (Fig. S2). Yet interestingly, in contrast to *musk* mutants,
216 which have a defasciculated and overgrown pectoral fin axon patterning (Fig. 3C, 7B), we find that
217 motor neuron innervation in the pectoral fin of *rapsyn* mutants is indistinguishable from wildtype (Fig.
218 S2), similar to what has been observed in *rapsyn* mutant trunk innervation (Zhang et al., 2004; Gribble
219 et al., 2018). Thus, *musk* and *rapsyn* are required for NMJ development in the pectoral fin, suggesting
220 that postsynaptic mechanisms critical for synapse formation are shared between trunk and
221 appendicular muscle.

Axonal derived signals are critical for appendicular AChR patterning

Neuromuscular junction development requires precise, bidirectional coordination between axons and muscles. To determine the overall role of motor axon derived signals on the postsynaptic innervation pattern, we laser-ablated the motor neurons that innervate the dorsal portion of the pectoral fin muscle. Specifically, we ablated the cell bodies of motor neurons in spinal segments 3-6 at 42 hpf, prior to the growth of motor axons into the pectoral fin bud, and then re-ablated any newly formed motor neurons 24 hours later. Importantly, we left intact all motor neurons in spinal segment 4, which innervate the ventral muscle region of the fin, to serve as an internal control when comparing the innervation patterns of innervated and nerve-deprived muscle fibers. As expected, at 120 hpf AChR patterning in the innervated ventral region of the fin was indistinguishable compared to non-ablated controls, with small, evenly spaced AChR clusters in apposition to axons (Fig. 4A-C). Surprisingly, in the dorsal region of the motor neuron-ablated fin, which had never been innervated, fewer but much larger AChR clusters formed (Fig. 4C). These clusters were globular and evenly dispersed throughout the non-innervated musculature and differ vastly in size and distribution from those observed in the absence of MuSK or Rapsyn (Fig. 3; Fig. S2). Thus, while lack of the MuSK-dependent postsynaptic signal transduction machinery blocks the formation of AChR clusters almost completely, absence of axonal-derived signals results in unpatterned yet exuberantly sized AChR clusters, which going forward we refer to as giant AChR clusters. We conclude that axonal-derived signals are critical for AChR patterning and for limiting AChR cluster size.

Agrin and Lrp4 are required for appendicular neuromuscular development

The opposing consequences of blocking MuSK-dependent postsynaptic signaling versus eliminating all presynaptic signaling prompted us to examine the role of signaling components that activate MuSK. The heparan sulfate proteoglycan Agrin is an axon-derived signal that coordinates MuSK-dependent AChR clustering between nerve terminals and muscle fibers (Kim et al., 2008; Zhang et al., 2008), and zebrafish mutants lacking the motoneuron-derived Agrin isoforms lack synaptic AChR clusters along axial trunk muscle fibers (Fig. 5A) (Gribble et al., 2018). We therefore hypothesized that Agrin might play a similar critical role in inducing neural AChRs in pectoral fin muscle fibers. Throughout the fin of wild type siblings, hundreds of $<5 \mu\text{m}^2$ AChR clusters are evenly distributed along appendicular muscles fibers. In contrast, AChR clusters in *agrin* mutants were reduced in numbers yet increased in size ($>20 \mu\text{m}^2$) (Fig. 5B, E), indistinguishable from the giant AChR clusters we observed in nerve-deprived fins (Fig. 4C). To quantify the number of neural AChR clusters and their size distribution across genotypes, we focused on AChR clusters present on abductor muscle fibers, although quantification of adductor muscles across all genotypes revealed similar results (Fig. S3). Wildtype abductor muscle

255 fibers exhibit 294.4 ± 21.5 α -Btx-positive AChR clusters per fin with a median cluster size of 3.9 ± 0.6
256 μm^2 (Fig. 5C-E). In contrast, *agrin* mutant abductor muscle fibers have significantly fewer clusters per
257 fin (51.6 ± 5.9 , unpaired t-test $p < 0.0001$) yet exhibit a vastly increased median cluster size of 18.4 ± 4.7
258 (t-test $p < 0.0001$). Thus, in striking contrast to *agrin* mutant trunk muscle fibers that exhibit only small
259 AChR clusters (median cluster size, siblings: $3.5 \pm 0.7 \mu\text{m}^2$ ($n=17$), *agrin*^{-/-}: $1.7 \pm 0.7 \mu\text{m}^2$ ($n=9$), t-test
260 $p < 0.0001$), *agrin* mutant appendicular muscle fibers exhibit greatly enlarged AChR clusters.

261 The strikingly divergent appendicular NMJ phenotypes observed in *muskl* mutants that display an
262 almost complete loss of AChR clusters versus the giant AChR clusters present in *agrin* mutants
263 prompted us to examine the role of the Agrin receptor Lrp4. Upon binding Agrin, Lrp4 induces MuSK
264 phosphorylation to initiate synaptic differentiation (Kim et al., 2008; Zong et al., 2012). To determine
265 whether *Lrp4* mutants display the phenotype exhibited by its canonical ligand Agrin or by its co-receptor
266 MuSK, we examined the role of Lrp4 in appendicular neuromuscular development. Like *muskl* and *agrin*,
267 *Lrp4* is required for neuromuscular junction development in axial muscles of the zebrafish trunk, as
268 mutants form fewer and smaller synapses (Remédios et al., 2016). Identical to the *agrin* mutant fin
269 muscle phenotype, and in contrast to the *Lrp4* mutant phenotype in axial trunk muscles (Remédios et al.,
270 2016), at 120 hpf *Lrp4* mutant pectoral fin muscles displayed large AChR clusters (Fig. 6A-B, D-F).
271 Moreover, in fins of *Lrp4* mutants lacking the intracellular domain (Saint-Amant et al., 2008) we also
272 observe giant AChR clusters (Fig. S4), providing compelling evidence that Lrp4 acts through a ligand-
273 dependent mechanism to regulate appendicular NMJ development. Despite the abnormal AChR
274 clusters in *Lrp4* mutants, we failed to detect differences in the morphology of muscles or muscle fibers
275 in pectoral fin muscles labeled with *Tg(α -actin:GFP)* indicating that in these mutants appendicular
276 muscle development is unaffected (Fig. S4). Interestingly, co-labeling of AChR clusters and muscle
277 fibers reveals that the enlarged clusters in *Lrp4* mutants often nestle between adjacent muscle fibers
278 but can also span across multiple fibers, similar to the enlarged clusters near the proximal fin base in
279 wild type pectoral fins, suggesting extrinsic coordination between muscle fibers to form or stabilize
280 these giant AChR clusters. Finally, expressing Lrp4 using a muscle specific promoter *Tg(α -actin:*Lrp4*-
281 *GFP*)* (Gribble et al., 2018) in otherwise *Lrp4* mutant animals fully restored neuromuscular synapse
282 development in appendicular muscle fibers (Fig. 6C-F), indicating that Lrp4 functions in muscle. Thus,
283 loss of Agrin or Lrp4, while associated with a significant reduction in neural AChR cluster numbers in
284 both axial and appendicular muscle, also leads to an increase in AChR cluster size on appendicular
285 muscle, distinct from their mutant phenotypes in axial muscle.

287 **Agrin/Lrp4 regulates the size and patterning of appendicular neuromuscular synapses**

288 The giant AChR clusters we observe on appendicular muscle fibers of nerve-deprived pectoral fins
289 as well as in *agrin* and *Lrp4* mutants resemble what has previously been described in *Xenopus* and
290 chick muscle cells grown in the absence of axons as AChR ‘hot spots’, which disperse upon innervation
291 (Bekoff and Betz, 1976; Moody-Corbett and Cohen, 1982; Peng, 1986). We therefore asked whether
292 these giant AChR clusters we observe in *agrin* or *Lrp4* mutant pectoral fins are caused by the lack of
293 axonal innervation. Analysis of the axonal innervation pattern in wildtype and mutant animals at 120
294 hpf revealed that in both *agrin* and *Lrp4* mutants the overall innervation pattern and extent of axon
295 growth in pectoral fins is comparable to that of wild type, indicating that overall axon guidance
296 mechanisms are largely intact. However, unlike in wild type siblings, in both *agrin* and *Lrp4* mutant fins
297 we observe large axonal ‘swellings’ (Fig. 5B; 6B). These axonal swellings co-localize with the enlarged
298 postsynaptic AChR clusters, supporting the notion that, rather than being aneural AChR hot spots,
299 these giant AChR clusters are indeed innervated and do not disperse upon axon contact. Moreover,
300 expressing *Lrp4* using a muscle specific promoter *Tg(α -actin:*Lrp4*-GFP)* (Gribble et al., 2018) in
301 otherwise *Lrp4* mutant animals fully suppressed formation of presynaptic axonal swellings (Fig. 6C-F),
302 indicating that muscle-derived *Lrp4* signaling plays a role in establishing both presynaptic and
303 postsynaptic neuromuscular synapse patterning.

304 To further investigate the nature of these axonal swellings, we used the Znp-1 antibody against the
305 presynaptic marker Synaptotagmin 2. In sibling control pectoral fins, the Znp-1 signal concentrates at
306 α -Btx-positive postsynaptic areas, demarcating presumptive presynaptic sites. Similarly, in *agrin*
307 mutant pectoral fins, the Znp-1 signal colocalizes with the giant AChR clusters (Fig. S5). Likewise, we
308 assessed the localization of the postsynaptic protein Dystrophin (*Dmd*) by analyzing a gene trap line
309 (*dmd-citrine*) that labels endogenous *Dmd* (Ruf-Zamojski et al., 2015). The *Dmd*-citrine signal in sibling
310 control pectoral fins is diffuse, with concentrations between muscle fibers and at synaptic regions, which
311 we confirmed by co-labeling with fluorescent α -Btx. Similarly, in *Lrp4* mutant pectoral fins, the *Dmd*-
312 citrine signal is concentrated at regions marked by presynaptic axonal swellings and enlarged
313 postsynaptic AChR clusters (Fig. S6). Thus, while in *agrin* and *Lrp4* mutants AChR cluster size and
314 distribution is altered, both presynaptic and postsynaptic proteins are recruited to these giant clusters
315 suggesting that they are *bona fide* synapses.

316 We next examined the prominent presynaptic ‘swellings’ in *Lrp4* and *agrin* mutants that form in
317 opposition to enlarged AChR clusters. The *mnx1:GFP* or *Xla.tubb:dsRed* transgenic lines both label
318 the entire population of motor axons in the pectoral fin, precluding us from visualizing the nature of
319 these presynaptic swellings at the single axon level. These innervation swellings could be formed by

1) local distension or an increase in diameter of individual axons, 2) many individual axons forming synapses in a single spot on a muscle fiber, 3) abnormally enlarged axonal endings in a single spot on a muscle fiber, or 4) individual axons looping continuously in a single spot on a muscle fiber. To determine how individual axons contribute to the innervation swellings, we employed a sparse labeling strategy using *mnx1:mKate* to visualize individual axons in the context of the entire population of motor axons (*mnx1:GFP*). We screened for larvae that expressed *mnx1:mKate* in only a few of the motor neurons that innervate the pectoral fin. In wild type siblings, we find that single axons branch and fasciculate with other axons to form complex patterns. Axons terminate abruptly, with endings that are approximately the same diameter as the rest of the labeled axon (Fig. 6G-H). In *lrp4* mutants, most individually labeled axons exhibit similarly complex trajectories, are similar in diameter to sibling controls, and occasionally form simplified endings. However, we also observed individual *mnx1:Kate*-positive axons that form bulbous and swollen structures. These globular endings of *mnx1:mKate* axons were part of larger *mnx1:GFP* swellings, indicating that many independent axons contribute to these swellings. As these swellings co-localize with α -Btx (Fig. 6B), we conclude that despite their abnormal morphology, they represent presynaptic terminals. This result strongly suggests that during appendicular neuromuscular development Agrin/Lrp4-dependent signaling not only promotes the formation postsynaptic AChR clusters but also limits their size, possibly by dispersing nascent AChR clusters or limiting cluster growth. In addition, Agrin/Lrp4 signaling also influences presynaptic patterning. Independent of the precise mechanisms by which Agrin and Lrp4 regulate pre and postsynaptic development, our data reveal that the role of Agrin and Lrp4 in zebrafish appendicular fin is distinctly different from its well-characterized function in trunk axial muscle.

***musk* depletion partially suppresses the *lrp4* giant AChR cluster phenotype**

Our results reveal that, unlike in axial trunk muscle of mice and zebrafish in which *musk*, *lrp4*, and *agrin* mutants all phenocopy each other, in appendicular muscle of the zebrafish pectoral fin loss of *agrin* or *lrp4* results in a phenotype that is distinct from *musk* mutants. Specifically, in *musk* mutants, appendicular muscle displays an almost complete loss of AChR clusters, while in *agrin* and *lrp4* mutant appendicular muscle, albeit exhibiting reduced numbers of AChRs, display a prominent, strikingly divergent phenotype characterized by enlarged AChR clusters. Combined, this led us to first ask whether, in the context of appendicular NMJ development, Agrin and Lrp4 act through MuSK, similar to what is observed in axial trunk muscle. Indeed, we find that *musk;lrp4* double mutants recapitulate the *musk* mutant phenotype as they fail to cluster AChRs and display axon overgrowth, confirming that Lrp4 acts through MuSK in NMJ development in both axial and appendicular muscle (Fig. 7A-B).

352 As MuSK is necessary for both aneural and neural AChR clustering in the pectoral fin in both wild
353 type and *lrp4* mutants and MuSK expression is sufficient to induce AChR clusters (Kim and Burden,
354 2008), we hypothesized that MuSK drives the formation of the enlarged AChR clusters in the absence
355 of *agrin* or *lrp4* mutants. This would suggest, unexpectedly, that in appendicular muscle Agrin/Lrp4 may
356 restrict MuSK function. If so, we would predict that dampening MuSK activity in *lrp4* mutants would
357 suppress the giant AChR cluster phenotype. To this end, we examined *lrp4* mutants that lack one copy
358 of *musk* (*lrp4^{-/-};musk^{+/-}*). Indeed, *lrp4* mutant animals that are also heterozygous for *musk* exhibit a less
359 severe phenotype than *lrp4* homozygous mutants. While fins in *lrp4^{-/-};musk^{+/-}* larvae still contained
360 some giant AChR clusters, portions of the fins in these animals also contained smaller, evenly-
361 dispersed neural clusters that resemble the sibling patterning. Additionally, the portions of the fin with
362 smaller AChR clusters also lacked presynaptic axonal swellings. When compared to *lrp4^{-/-}* mutants,
363 *lrp4^{-/-};musk^{+/-}* mutants displayed an increase in the number of α -Btx-positive AChR clusters per fin (Fig.
364 7E), a rescue of the median cluster size (Fig. 7F), and a rescue of the overall distribution of cluster
365 sizes in the fin (Fig. 7G). In *lrp4^{-/-};musk^{+/-}* pectoral fins, the giant clusters that formed often were closer
366 to the proximal fin base, similar to the earlier-formed prepatterned clusters (Fig. 7D). In contrast, smaller
367 clusters were often found in the distal fin, where AChR clusters formed later. This further supports the
368 idea that Agrin/Lrp4 signaling restrains MuSK activity within appendicular muscle.

369 **Agrin/Lrp4 signaling restrains MuSK activity during appendicular NMJ development**

370 To further explore the idea that, unlike in axial muscle, in appendicular NMJ development Agrin
371 plays a critical role in restraining MuSK activity, we examined the progression of appendicular NMJ
372 development in siblings and *agrin* mutants. We hypothesized that prior to the arrival of motor axons,
373 the Agrin-independent formation of aneural prepatterned AChR clusters should be indistinguishable
374 between wild type and *agrin* mutants. Indeed, we find that at 46 hpf (the long-pec stage), while axons
375 are sorting at the dorsal plexus prior to growing into the fin, *agrin* mutant fins are prepatterned with
376 AChR clusters and are indistinguishable from siblings (Fig. 8A). Moreover, like sibling controls,
377 navigating axons in *agrin* mutants tend to occupy the prepatterned region near the proximal fin prior to
378 extending towards the distal fin (Fig. 8B). Subsequently, in wild type, the arrival of motor axons and the
379 release of Agrin induces the formation of small neural clusters, akin to the process previously described
380 in axial muscle (Panzer et al 2006).

381 If nerve derived Agrin indeed restrains MuSK activity, we predicted that in *agrin* mutants these
382 initially aneural clusters would retain their size (or even grow), despite the arrival of motor axons. We
383 also predicted that lack of Agrin-mediated local MuSK activation would result in the failure to form new
384 small neural clusters that normally emerge along growing axons. Indeed, at 60hpf (pec fin stage) the

385 difference in cluster size, number, and distribution between genotypes is prominent. In wild type
386 siblings, the AChR cluster field mirrors the innervation pattern. As motor axons continue to grow further
387 towards the distal fin, even the furthest-reaching navigating axons are associated with small AChR
388 clusters, suggesting that as axons grow, new clusters are rapidly formed. In contrast, in *agrin* mutants,
389 AChR clusters have increased in size and remain globular (Fig. 8C). Unlike in wild type siblings, in *agrin*
390 mutants presynaptic swellings apposed to AChR clusters become apparent by 72 hpf, with stretches
391 of axon deprived of any discernible AChR clusters (Fig. 8D). This observation supports the idea that
392 navigating growth cones are inappropriately attracted to and sequestered by these prepatterned
393 'islands'. Between 72 and 120 hpf, both sibling and mutant axons continue to grow to occupy the entire
394 muscle territory. In wild type siblings, the majority of the AChR clusters remain small (below 5 μm^2) and
395 evenly-dispersed throughout the appendicular muscle. In contrast, in *agrin* mutants both presynaptic
396 axonal swellings and neural AChR clusters continued to grow throughout the entire appendicular
397 muscle (Fig. 8D-F). Thus, lack of *agrin* leads to a progressive size increase of synaptic AChR clusters,
398 consistent with the idea that in wild type appendicular muscle Agrin functions to counteract or to restrain
399 MuSK activity. Together, our results suggest a model for appendicular NMJ development in which
400 Agrin/Lrp4 signaling, different from its sole role in axial muscle to activate MuSK and promote NMJ
401 development, also restrains MuSK activity to properly size and pattern neuromuscular synapses.

403 DISCUSSION

404 Axial muscles of the mouse diaphragm or the larval zebrafish trunk have been major *in vivo* models
405 to study neuromuscular synapse development. Genetic studies using these models have converged
406 on an evolutionarily conserved, canonical pathway in which the axonally released glycoprotein Agrin
407 binds its receptor Lrp4 on the muscle membrane to locally activate the receptor tyrosine kinase MuSK
408 and cluster AChRs. Here, we employ the larval zebrafish pectoral fin as a genetically-tractable model
409 system in which to study the development of the neuromuscular system within appendicular muscle.
410 We use static and live-imaging to describe the coordinated growth of nascent muscle fibers, motor axon
411 patterning, and postsynaptic AChR clustering in the fin. Using this framework, we provide compelling
412 *in vivo* evidence that Agrin and Lrp4 play an additional, previously unappreciated role to regulate
413 neuromuscular synapse development in appendicular muscle. We report that Agrin, Lrp4, and MuSK
414 are required for the formation of neural AChR clusters in appendicular muscle, similar to their roles in
415 axial muscle. In addition, we find that Agrin and Lrp4 play a second role to suppress the growth of
416 aneural AChR clusters selectively in appendicular muscle. Consequently, only *lrp4* and *agrin* but not
417 *musk* mutants form abnormally large postsynaptic AChR clusters in the pectoral fin. In addition,

418 Agrin/Lrp4 signaling influences presynaptic axonal patterning, as in *lrp4* and *agrin* mutants multiple
419 axons inappropriately innervate these giant AChR clusters. The formation of these abnormal synapses
420 can be partially suppressed by depleting *musk*, providing compelling genetic evidence that Agrin and
421 Lrp4 constrain MuSK activity to establish appropriate neural synapse formation in appendicular muscle.
422 Thus, our work reveals a key difference in the regulation of neuromuscular synapse development
423 between two major divisions of the muscular system, i.e. axial and appendicular muscles.

424 **Key differences between axial versus and appendicular NMJ development**

425 In contrast to the neuromuscular system in axial muscle, little is known about the steps by which the
426 complicated innervation pattern of appendicular muscle found in paired appendices including the
427 pectoral fin arises, the genetic pathways that control it, nor how it might compare to NMJ development
428 in axial muscles. Our work reveals key differences in neuromuscular synapse development between
429 axial muscle in the zebrafish trunk and appendicular muscle in the pectoral fin. First, innervation of the
430 trunk myotome occurs much earlier than the pectoral fin; trunk motor axon outgrowth begins at 16hpf
431 (Panzer et al., 2006), whereas we first observe axons sorting at the fin plexus around 46 hpf. Secondly,
432 both the trunk and the pectoral fin musculature are prepatterned with MuSK-dependent aneural AChR
433 clusters. Somewhat surprisingly, prepatterned AChR clusters only form on adaxial, slow muscle fibers
434 in the trunk (Flanagan-Steet et al., 2005; Panzer et al., 2006) and have not been detected in fast muscle
435 fibers of the trunk, while in the pectoral fin, which lacks slow muscle fibers, prepatterned AChR clusters
436 form exclusively on fast muscle fibers. This demonstrates that both slow and fast muscle fibers have
437 the capacity to develop AChR pre patterning, thus it will be interesting to determine the mechanisms
438 that selectively promote AChR pre patterning in trunk slow muscle and/or suppress it in adjacent fast
439 muscle fibers. Third, in both zebrafish trunk and mouse diaphragm muscle, prepatterned AChRs are
440 restricted to the central region of muscle fibers. We find that AChR pre patterning in pectoral fins is also
441 restricted, but to the proximal region of individual muscle fibers. In the absence of live cell imaging, we
442 cannot exclude the possibility that prepatterned AChR clusters initially arise in the 'center' of nascent
443 pectoral fin muscle fibers, and, as these fibers elongate, clusters rapidly become off-center and shift
444 towards the proximal region of muscle fibers. Independent of this possibility, our analysis of
445 appendicular NMJ development reveals that AChR pre patterning is not strictly restricted to the center
446 but instead can localize to other muscle fiber areas.

447 Finally, like AChR pre patterning, early axial motor axon outgrowth is confined to the center of the
448 myotome and navigating growth cones contact prepatterned AChR clusters that form in this region.
449 Similar to the trunk (Panzer et al., 2006), our developmental timepoints suggest that early extending
450 axons selectively grow towards prepatterned muscle regions. Yet beyond the prepatterned region,

451 axons in the pectoral fin form intricate patterns across muscle fibers. This growth pattern is more similar
452 to later axon outgrowth in the trunk in which motor axons branch to innervate fast muscle fibers deep
453 in the myotome (Beattie, 2000). These differences in prepatterning and axon outgrowth may be a
454 consequence of the anatomy of the pectoral fin, in which axons converge at a dorsal or ventral plexus
455 prior to topographically innervating longitudinal muscle fibers. Indeed, pectoral fin neuroanatomy is
456 similar to that of the muscles of tetrapod forelimbs, in which axons sort at the brachial plexus to
457 innervate distinct muscles. While we identify a conserved requirement for MuSK to establish
458 prepatterning across muscles, these key anatomical and developmental differences between
459 appendicular and axial muscles indicate that the signals that determine the location of AChR
460 prepatterning and direct axon pathfinding are differentially regulated in appendicular muscle, leading to
461 open questions regarding additional molecular mechanisms and pathway components that orchestrate
462 NMJ development selectively in appendicular muscle.

463 **A dual role for Agrin/Lrp4 signaling in appendicular neuromuscular synapse development**

464 Consistent with previous work, we find that loss of Agrin and Lrp4 leads to a significant reduction of
465 neural AChR clusters on appendicular muscle fibers, demonstrating a critical and conserved role for
466 both genes in promoting the formation these synaptic AChR clusters (Fig. 5C, Fig. 6D). Examining
467 *agrin/lrp4* mutants as well as nerve-deprived pectoral fins revealed evidence for a previously
468 unappreciated role for Agrin/Lrp4 signaling. While fins lacking Agrin or Lrp4 display reduced number of
469 neural AChR clusters, the clusters that form are significantly enlarged in their median size, over 4-fold
470 in *agrin* mutants (Fig. 5D). Strikingly, without Agrin or Lrp4, the giant AChR giant clusters can be
471 partially suppressed by depleting *musk*. A developmental timecourse suggests these giant clusters are
472 derived from MuSK-dependent prepatterned AChR clusters that expand over time. Combined our
473 findings strongly support the idea that Agrin and Lrp4 play a dual role to both promote the formation of
474 axon-induced AChR clusters and unexpectedly, to constrain Agrin-independent MuSK activity thereby
475 restricting the growth and development of initial aneural clusters into synapse-associated AChR
476 clusters. Future studies will be necessary to identify the downstream signaling events that allow
477 Agrin/Lrp4 signaling to simultaneously potentiate and attenuate MuSK signaling in appendicular muscle
478 at different regions on the same muscle fiber.

479 **Presynaptic axon patterning in appendicular muscle**

480 Navigating growth cones respond to local extrinsic cues to determine where to form a synapse. This
481 'stop signal' requires MuSK signaling, as *musk* mutants in mouse and fish have an overgrown,
482 defasciculated axon pattern (DeChiara et al., 1996; Zhang et al., 2004; Kim and Burden, 2008). In the

zebrafish, this axon patterning role for MuSK is independent of AChR clustering, as *rapsyn* mutants that lack clustered AChRs have normal axon patterning (Zhang et al., 2004; Gribble et al., 2018) (Fig. S2). Thus, MuSK independently clusters AChRs postsynaptically and regulates axon patterning presynaptically, although the mechanism is poorly understood. Unexpectedly, we find that in the pectoral fin the presynaptic consequence of *agrln* or *lrp4* loss is for multiple axons to form mature synapses in apposition to postsynaptic AChR giant clusters, suggesting an overactive ‘stop signal’ in these regions. These giant cluster regions likely represent ‘islands’ of enhanced MuSK activity, as depletion of *musk* suppresses the formation of presynaptic swellings. Taken together, these results suggest that Lrp4 signaling, induced by the arrival of axonally released Agrin, may inhibit the MuSK-dependent ‘stop signal’ in the appendicular muscle of the pectoral fin. Such a mechanism could be a way to signal to new waves of navigating growth cones that this synaptic region is occupied.

Our data demonstrate that MuSK plays distinct roles to establish both the presynaptic axonal pattern and postsynaptic AChR clusters, but that both processes are constrained by Agrin/Lrp4 signaling within appendicular muscle. One attractive candidate for how MuSK might influence neuromuscular synapse development in an Agrin/Lrp4-dependent manner is through Wnt signaling. MuSK can bind Wnts through its extracellular cysteine-rich domain (CRD) (Jing et al., 2009; Strochlic et al., 2012; Zhang et al., 2012b). Indeed, in the zebrafish trunk, Wnt4a and Wnt11r binding through the MuSK CRD are required for AChR prepatterning and axon guidance (Jing et al., 2009; Gordon et al., 2012). While a functional role for Wnt:MuSK signaling to establish prepatterning in mouse is more controversial (Messéant et al., 2015; Remédio et al., 2016), in mammals Wnt proteins do regulate both AChR clustering (Strochlic et al., 2012; Zhang et al., 2012a) and axon guidance (reviewed in Zou, 2004). Interestingly, as the MuSK CRD domain can adopt two distinct conformations with differential abilities to bind Wnts (Stiegler et al., 2006), Guarino *et al.* speculate that Agrin/Lrp4 binding to MuSK can promote a conformational change to make MuSK unable to bind Wnts thereby shifting downstream MuSK signaling (Guarino et al., 2020). Therefore, it is tempting to speculate that in the pectoral fin prior to axon innervation, MuSK:Wnt signaling promotes both prepatterning of AChRs and local ECM cues to ‘catch’ navigating growth cones at future synaptic sites, perhaps through noncanonical Wnt signaling (Jing et al., 2009). Once the axon arrives, it releases Agrin, which binds Lrp4 on the muscle membrane and induces a conformational change in MuSK such that it can no longer bind Wnts. Thus, via competition through binding, Agrin/Lrp4 could locally constrain MuSK signaling. An outstanding question is why Agrin/Lrp4 regulate MuSK signaling differently between axial and appendicular muscle. As there are 23 Wnts in the zebrafish genome (Lu et al., 2011) with dynamic and differential expression throughout larval development, perhaps the relevant Wnt ligand is expressed in the pectoral fin but not in the trunk. Of course, there are many additional proteins that interact directly or indirectly with Agrin,

Lrp4, or MuSK to influence synaptic development. Independently of the underlying mechanism, our results uncover a novel role for Agrin/Lrp4 signaling to constrain MuSK activity in appendicular muscle. The noncanonical nature of our findings reveal that there is diversity in the molecular pathways that mediate neuromuscular synapse development and validate the application of the larval zebrafish pectoral fin to study these processes beyond axial muscle.

METHODS

Zebrafish strains and animal care

Protocols and procedures involving zebrafish (*Danio rerio*) are in compliance with the University of Pennsylvania Institutional Animal Care and Use Committee regulations. All transgenic lines were maintained in the Tübingen or Tupfel long fin genetic background and raised as previously described (Mullins et al., 1994). The following transgenic lines were used: *Tg(mnx1:GFP)^{ml2}* (Flanagan-Steet et al., 2005), *Tg(α -actin:Lrp4-GFP)^{p159Tg}* (Gribble et al., 2018), *Tg(Xla.Tubb:DsRed)^{zf148}* (Peri and Nüsslein-Volhard, 2008), *Gt(dmd-citrine)^{ct90a}* (a kind gift from Dr. Sharon Amacher) (Ruf-Zamojski et al., 2015), and *Tg(α -actin:GFP)* (Higashijima et al., 1997). The following mutant strains were used: *agrin^{p168}* (Gribble et al., 2018), *lrp4^{p184}* (Remédio et al., 2016), *lrp4^{mi36}* (Saint-Amant et al., 2008), *muskl^{tb72}* (Granato et al., 1996; Zhang et al., 2004), and *rapsyn(two^{th26})* (Ono et al., 2002). Homozygous mutants for these genes can be phenotyped at ~36 hpf as they all display motor defects when prodded with a probe. The *lrp4^{p184}*, *two^{th26}*, and *agrin^{p168}* alleles were genotyped using Kompetitive Allele Specific PCR (KASP, LGC Biosearch Technologies). Animals were staged as previously published (Grandel and Schulte-Merker, 1998; Kimmel et al., 1995). As our experiments in larval zebrafish occur prior to sex determination, sex was not a biological variable (Kossack and Draper, 2019).

Whole-mount immunohistochemistry and imaging

Zebrafish embryos or larvae immobilized with tricaine (MS-222) and then were fixed for 1 hour at room temperature in sweet fix (4% paraformaldehyde with 125mM sucrose in PBS) plus 0.1% Triton X-100 (Fisher, BP151). Animals were washed in phosphate buffer and incubated overnight at 4°C in primary chicken anti-GFP antibody (1:2000, Aves labs, GFP-1010) or mouse anti-Znp-1 (1:200, Developmental Studies Hybridoma Bank) in incubation buffer (2 mg/mL BSA, 0.5% Triton X-100, 1% NGS). After washing in phosphate buffer, animals were incubated overnight at 4°C in Alexa Fluor 488 donkey anti-chicken secondary antibody (1:1000, Jackson ImmunoResearch, 703-545-155), Alexa Fluor 594 goat anti-mouse secondary antibody (1:1000, Invitrogen, A-21125) and/or alpha-bungarotoxin Alexa Fluor 594 (1:500, Molecular Probes, B-13423) in incubation buffer. Animals were mounted in agarose in a

549 glass-bottomed dish and imaged in 1.5 μm slices using a x40 or x63 water immersion lens on a Zeiss
550 LSM880 confocal microscope using Zen software (Fig. 2C and 8) or a x40 water immersion lens on an
551 ix81 Olympus spinning disk confocal microscope using Slidebook Software.

552 553 Sparse neuronal labeling

554 A DNA vector encoding *mnx1:mKate* was injected as previously described (Gribble et al., 2018;
555 Thermes et al., 2002) into one-cell-stage embryos. Embryos were screened at 1 dpf for larvae
556 expressing mKate sparsely in the anterior spinal cord. At 5dpf, animals were mounted in agarose and
557 imaged live at x40 on an Olympus spinning disk confocal if they had sparse mKate-expressing axons
558 innervating the pectoral fin.

559 560 Timelapse imaging

561 Embryos expressing both *α -actin:GFP* and *Xla.Tubb:DsRed* were anesthetized with tricaine and
562 mounted in agarose around 35hpf. Animals were timelapsed using a 40x lense on an ix81 Olympus
563 spinning disk confocal in a temperature chamber set to 28°C as previously described (Rosenberg et
564 al., 2012). Stacks through the developing fin bud were captured in 1.5 μm slices with 30 minute
565 intervals. Animals were imaged continuously for up to 3 days, with some adjustments to account for
566 drifting and the pectoral fin moving out of frame.

567 568 Motor neuron ablation

569 *mnx1:GFP* animals were mounted in agarose and motor neurons from spinal cord segments 3-5 were
570 ablated using an Ablate! 532 nm attenuable pulse laser (Intelligent Imaging Innovations (3I), Denver,
571 CO) beginning at 2 dpf, prior to axons innervating the pectoral fin bud. Neurons were considered
572 ablated when there were no GFP+ cell bodies present in the ablated spinal cord region and axons
573 showed signs of fragmentation. Neurons were re-ablated at 3 dpf to ensure any regenerated motor
574 neurons in the spinal cord did not innervate the fin. Fins were visually inspected to confirm absence of
575 GFP+ motor axon signal within the denervated region of the fin. Animals were fixed and stained with
576 alpha-bungarotoxin at 5 dpf.

577 578 Image processing and quantification

579 To simplify data visualization and quantification, signal from the abductor or adductor innervation of
580 was manually separated from stacks through pectoral fins. Individual channel image stacks were
581 opened in Fiji (Schindelin et al., 2012), background subtracted, channels were merged, and the image
582 was changed to RGB. Stacks were visualized using the 3D viewer plugin and rotated to a top-down

583 view so the separation between abductor and adductor innervation was distinct. Axon signal from the
584 opposite innervation field and other fluorescent signal from the larval body wall was selected and filled,
585 resulting in the corresponding region filled with black on the RGB stack. Any residual signal from the
586 opposing innervation field or trunk was removed directly on the RGB stack. This resulted in signal
587 specific to the abductor or adductor muscles, as specified. Stacks were converted to maximum
588 projections. For quantification of α -Btx puncta, a custom CellProfiler (Lamprecht et al., 2007) pipeline
589 was created to detect and measure the area of α -Btx punta per fin. Mutants that do not form distinct α -
590 Btx puncta (*musk* and *rapsyn*) could not be quantified using CellProfiler pipelines. Fin images were
591 excluded from analysis if the maximum projection did not include the whole fin, the fin was damaged
592 or abnormally small, or if measurements were clear outliers from other fins of the same genotype in the
593 dataset. All figures show only abductor innervation except for early developmental stages in figures 2
594 and 7, which are a maximum projection of the entire pectoral fin bud or where otherwise noted.

595 596 Statistical analysis

597 Data were imported into Graphpad Prism for statistical analysis. Groups were compared using an
598 unpaired t-test or one-way ANOVA with either Dunnett's or Sidak's multiple comparisons tests. For
599 histogram of cluster sizes, the area of all AChR clusters measured in each genotype were pooled and
600 binned into 5 μm^2 bins, with any cluster over 20 μm^2 included in the same bin. Distributions were
601 compared using a Kruskal-Wallis test with Dunn's multiple comparisons test. In figures where the
602 control group is labeled as "siblings" we pooled wild type and heterozygous animals together as there
603 was no statistical difference between these groups.

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610 611 **COMPETING INTERESTS**

612 No competing interests declared.

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748 **FIGURE LEGENDS**

749 **Figure 1: Pectoral fin anatomy.** A) Schematic of 120 hour post fertilization (hpf; 5 days post
750 fertilization) zebrafish larvae. Anterior (A) is to the left, dorsal (D) is up. B) Schematic of pectoral fin
751 motor neuron innervation. Motor neuron cell bodies are in the anterior four segments of the spinal
752 cord (SC). Nerves 1-3 enter the fin at the dorsal plexus (DP) while nerve 4 enters the fin at the ventral
753 plexus (VP). All nerves innervate both the abductor (Ab) and adductor (Ad) muscles. C) Abductor
754 innervation of 120 hpf *Tg(α-actin:GFP);Tg(Xla.Tubb:DsRed)* pectoral fin stained with α-bungarotoxin
755 to visualize muscle fibers, axons, and acetylcholine receptors (AChRs), respectively. n = 7. D)
756 Maximum projection of *Tg(mnx1:GFP)* axon innervation in pectoral fin. Abductor (green) and adductor
757 (magenta) innervation patterns are pseudo-colored. E) Abductor innervation alone F) Abductor
758 innervation with AChRs labeled with α-bungarotoxin G) AChR labeling alone. n > 77 wildtype pectoral
759 fins for D-G. H) Cross-section of pectoral fin at approximate region marked by arrow in D. Asterisk
760 marks endoskeletal disk that separates the two distinct muscles. Scale bars are 25 microns.

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Figure 2: Development of pectoral fin innervation. A) Schematic of zebrafish larvae at 42 hours post fertilization (hpf), high pec stage, and 68 hpf, pec fin stage. Inset highlights motor neurons from spinal cord (SC) segments 1-4 and their corresponding axons projecting to the dorsal plexus (P) to innervate the abductor (Ab) and adductor (Ad) muscles of the pectoral fin. B) Maximum projection stills from timelapse imaging of *Tg(α -actin:GFP);Tg(Xla.Tubb:DsRed)* larvae to label muscles and axons, respectively. Dotted line outlines pectoral fin musculature. Axons converge at a dorsal plexus prior to innervating nascent muscle fibers. As muscle fibers elongate the axonal innervation pattern elaborates. n = 7 wild type animals. Static timepoints of *Tg(mnx1:GFP)* larvae stained with α -bungarotoxin to label acetylcholine receptors (AChRs). Nerve 4 (4) is labeled. C) At 42 hpf the pectoral fin bud is still lateral to the plexus, so axons and muscles are not yet in the same plane. Asterisk notes developing vasculature that is also labeled by *mnx1:GFP*. D) Axons have just grown past the plexus (adductor axons labeled in double arrowhead). Arrowheads point to aneural AChR clusters. E-G) Abductor innervation only. Axons occupy prepatterned clusters and induce new AChR clusters as they grow throughout the fin. Filled arrowhead points to fin axon branch already associated with AChR clusters. n = 5-10 per timepoint for C-G. Scale bars are 25 microns.

Figure 3: MuSK is required for pectoral fin neuromuscular synapse development. A) Schematic of Agrin/Lrp4/MuSK pathway B) Schematic of 120 hpf larval zebrafish. Red boxes outline regions of fin and trunk that were imaged for C-D. Spinal cord (SC). C) Abductor muscle innervation in the pectoral fin from 120 hpf larvae expressing *Tg(mnx1:GFP)* to label motor neurons and stained with α -bungarotoxin to label acetylcholine receptors (AChRs). *musk* heterozygous sibling pectoral fins exhibit an innervation pattern with numerous small AChR clusters (n = 45/45) while *musk* mutants have an exuberant innervation pattern with diffuse AChR signal throughout muscle fibers in the fin and some focal AChR clusters (n= 25/25). D) Trunk innervation from the same animals shown in C. *musk* mutants form fewer and smaller neuromuscular synapses. All images are maximum intensity projections that include the same number of slices for both genotypes. Scale bars are 25 microns.

Figure 4: Pectoral fin muscles are predisposed to form large AChR clusters. A) Motor neuron cell bodies from spinal cord (SC) segments 1-3 were laser-ablated at 2 and 3 days post fertilization (dpf) to prevent motor axon innervation of the dorsal pectoral fin. A/P = anterior/posterior, D/V = dorsal/ventral B) Pectoral fins from control *Tg(mnx1:GFP)* larvae stained with α -bungarotoxin to label acetylcholine receptors (AChRs). C) Pectoral fin in *Tg(mnx1:GFP)* wild-type larvae after motor neuron ablation. The ventral fin was still innervated (outlined region) with input from unablated nerve 4. Non-innervated

dorsal region of the fin has enlarged AChR clusters. N= 3/3 unablated controls, 6/6 wildtype pectoral fins with full or partial ablations at 120 hours post fertilization (5 dpf). Scale bar is 25 microns.

Figure 5: Agrin is required for correct axon innervation and AChR patterning in the pectoral fin. A) Trunk innervation in 120 hpf larvae expressing *Tg(mnx1:GFP)* to label motor axons and stained with α -bungarotoxin to label acetylcholine receptors (AChRs). Trunks in *agrin* mutants form fewer and smaller neuromuscular synapses. B) Abductor muscle innervation in the pectoral fin from the same animals shown in A. *Agrin* sibling animals exhibit an innervation pattern with numerous small AChR clusters while *agrin* mutants have swellings in the innervation pattern directly opposed to enlarged AChR clusters throughout muscle fibers in the fin. Scale bar is 25 microns. Inset from boxed region shows even distribution of small magenta AChR clusters in siblings while mutants have large AChR clusters that colocalize with green axon swellings. Inset scale bar is 10 microns. All images are maximum intensity projections that include the same number of slices for both genotypes. Quantification of the number of AChR clusters per fin (C) and the median cluster size per fin (D). E) Histogram of the distribution of AChR cluster sizes across all fins quantified (5 square micron bins). ****; $P < 0.0001$, t-test. n = 23 (siblings), 21 (mutants).

Figure 6: Lrp4 is required for correct axon innervation and AChR patterning in the pectoral fin. Abductor muscle innervation in the pectoral fin in 120 hours post fertilization larvae expressing *Tg(mnx1:GFP)* to label motor neurons and stained with α -bungarotoxin to label acetylcholine receptors (AChRs). A) *Lrp4* sibling animals exhibit innervation patterns with numerous small AChR clusters. B) *Lrp4* mutants exhibit abnormal swellings in the innervation pattern directly opposed to large AChR clusters. C) Expression of *Lrp4-GFP* in muscles of *Lrp4* mutants is sufficient to rescue the mutant innervation pattern. Scale bar is 25 microns. Dotted boxes outline region shown in insets (scale bar of insets is 10 microns). Quantification of the number of AChR clusters per fin (D) and the median cluster size per fin (E). F) Histogram of the distribution of AChR cluster sizes across all animals quantified (5 square micron bins). n = 15 (siblings), 23 (*Lrp4* mutants), 16 (siblings plus *Tg(act:Lrp4-GFP)*), 20 (*Lrp4* mutants plus *Tg(act:Lrp4-GFP)*). G) Sparse labeling of axons injected with *mnx1:mKate*, with all motor axons labeled with *Tg(mnx1:GFP)*. Sparse labeling does not label entire 'swelling' but axon ends appear bulbous, indicating that multiple axons contribute to the abnormal innervation swellings in *Lrp4* mutants. Orange arrowheads point to axon endings. Dotted box outlines insets. n = 11/12 (siblings), 7/7 (mutants) Scale bar is 25 microns. H) Schematic summarizing axonal organization and AChR clusters. ns= not significant, * $p < 0.05$, **** $p < 0.0001$, one way ANOVA with Dunnett's multiple comparisons test.

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830 **Figure 7: Musk depletion partially suppresses *Irp4* mutant phenotype.** A) *Irp4*^{+/-};*musk*^{+/-} trans
831 heterozygotes have an innervation pattern indistinguishable from wild type while B) *Irp4*;*musk* double
832 mutants phenocopy *musk* mutants with defasciculated axonal patterning labeled with Tg(*mnx1:GFP*)
833 and diffuse acetylcholine receptor (AChR) staining as labeled by bungarotoxin. C) *Irp4* mutant motor
834 axons have swellings in their innervation pattern that are opposed to large AChR clusters. D) While
835 *Irp4* mutants that are heterozygous for *musk* (*Irp4*^{+/-};*musk*^{+/-}) still have some large AChR clusters similar
836 to *Irp4* mutants (orange arrows), they also have regions of the fin with smaller AChR clusters (orange
837 dotted region). Quantification of E) the number of AChR clusters per fin, F) the median cluster size per
838 fin (square microns), and G) the distribution of cluster sizes (5 square micron bins, ****p< 0.001, one-
839 way Anova with Sidak's (E) or Dunnett's (F) multiple comparisons test. n= 8 (wild type), 21 (*Irp4*^{+/-}
840 ;*musk*^{+/-}), 4 (*Irp4*^{-/-};*musk*^{-/-}), 33 (*Irp4*^{-/-}), 39 (*Irp4*^{+/-};*musk*^{+/-}).

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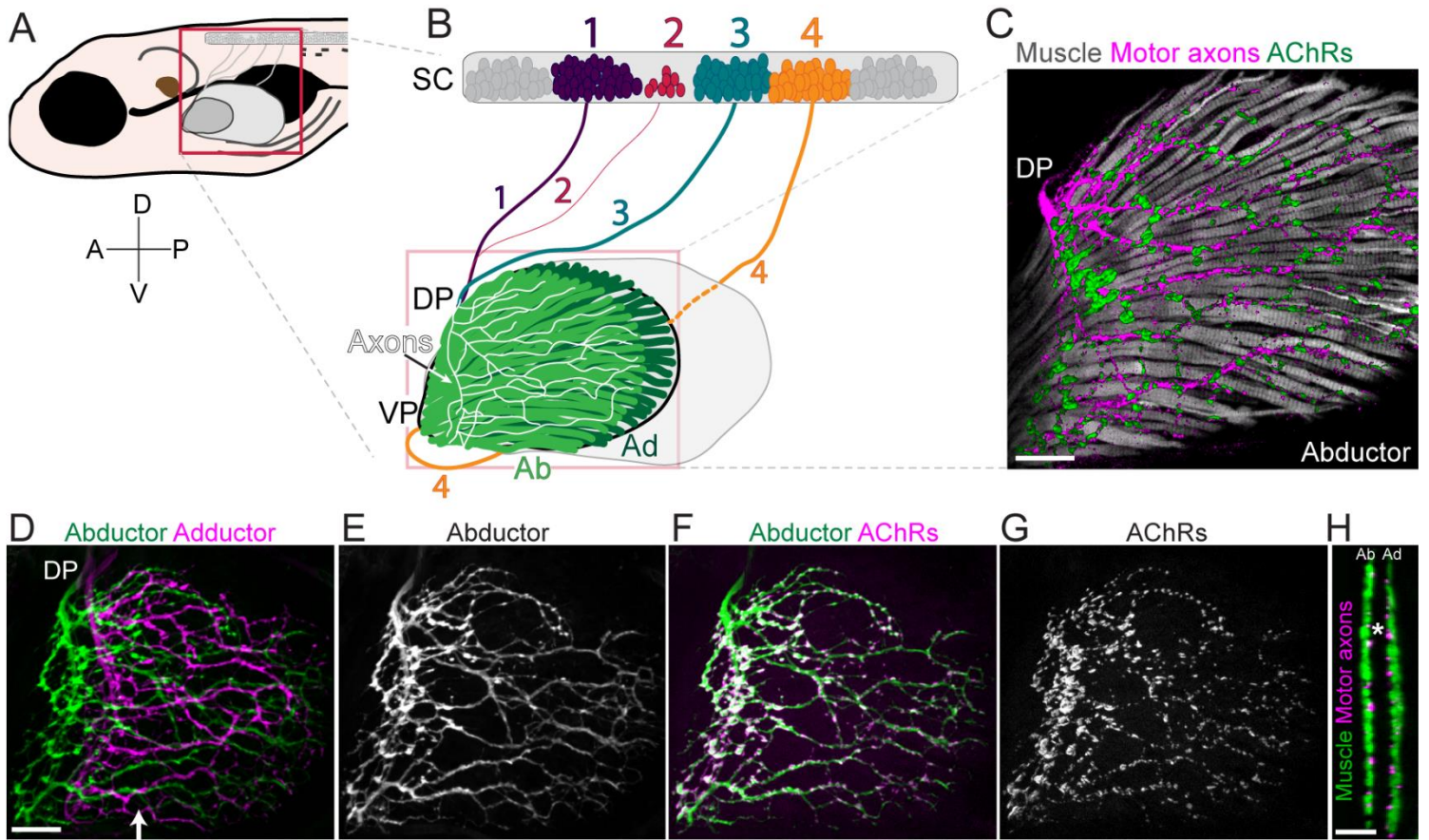
842 **Figure 8: Agrin restricts presynaptic terminal and neural AChR cluster size.** Developmental
843 timecourse from Tg(*mnx1:GFP*) larvae to label motor neurons stained with α-bungarotoxin to label
844 acetylcholine receptors (AChR). A-B). At 46 and 51 hpf, axons growing from the dorsal plexus (P) have
845 not yet innervated all prepatterned AChR clusters (arrowheads). Asterisks note endothelial or
846 endoskeletal cells labeled in the green channel. C-E) While small clusters are added as axons grow
847 into the pectoral fin in sibling animals, clusters mainly increase in size in *agrin* mutants. D) Double arrow
848 points to presynaptic swelling colocalized with an AChR cluster. Only abductor innervation is shown,
849 with fin area outlined in dotted white line. Scale bar is 25 microns. G) Schematic summarizing
850 developmental timecourse. Both siblings and *agrin* mutants look similar during pre patterning stage.
851 Incoming axons induce small AChR clusters in sibling animals while in *agrin* mutants AChR clusters
852 and axonal swellings increase in size over time. n= 4-10 animals per genotype per timepoint.

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855 **FIGURES**

856 **Figure 1**



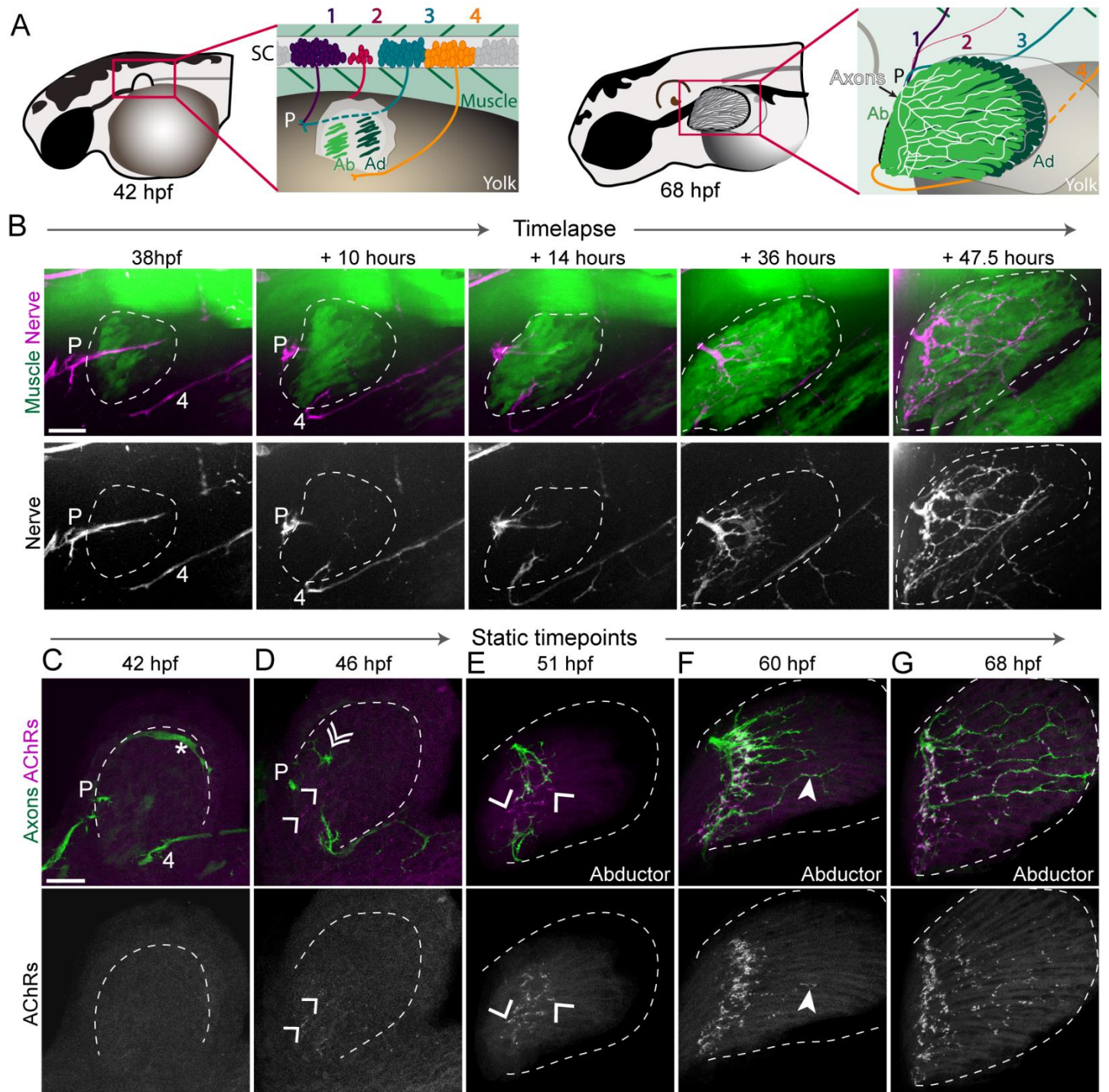
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Figure 2

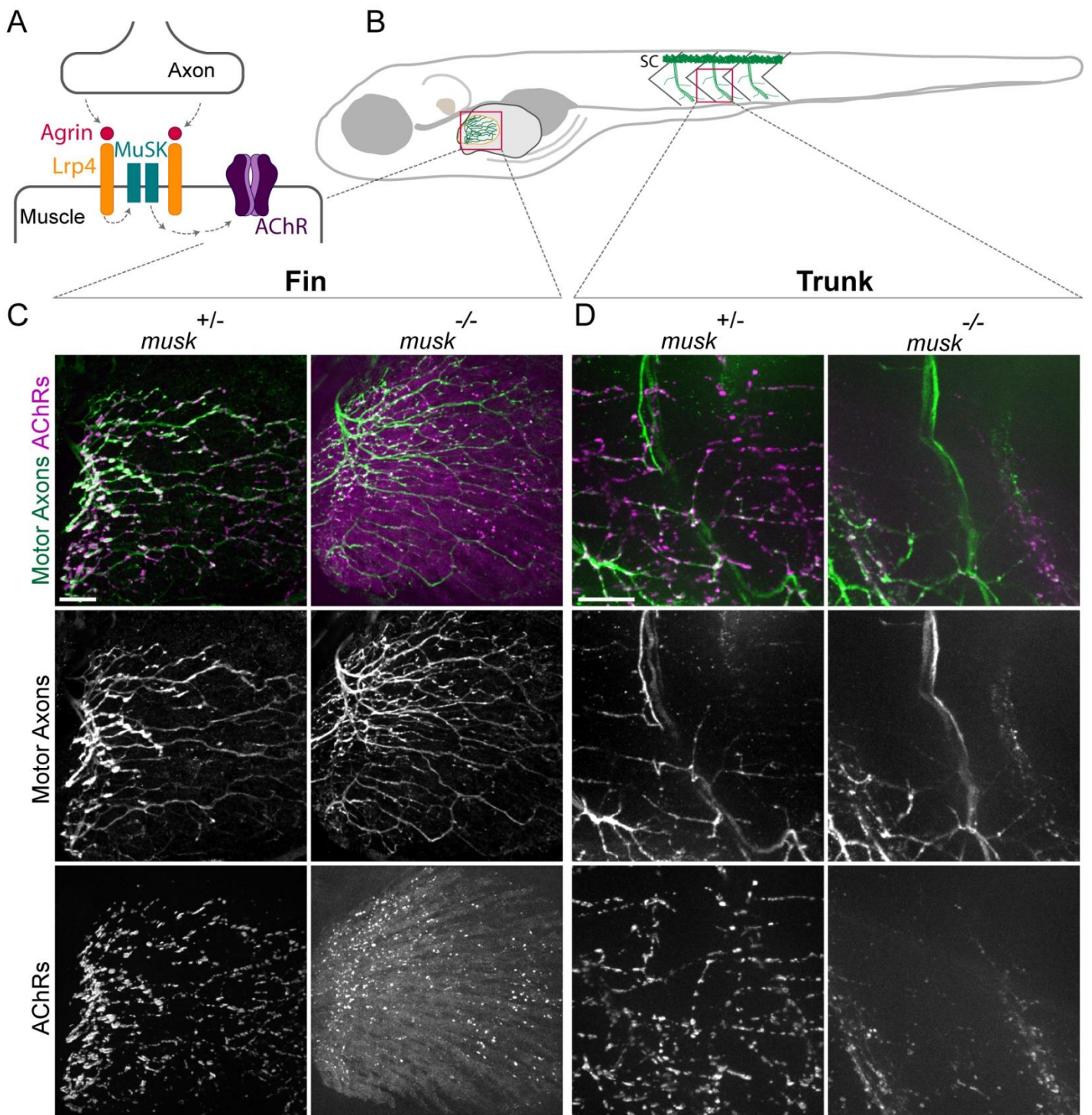


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Figure 3



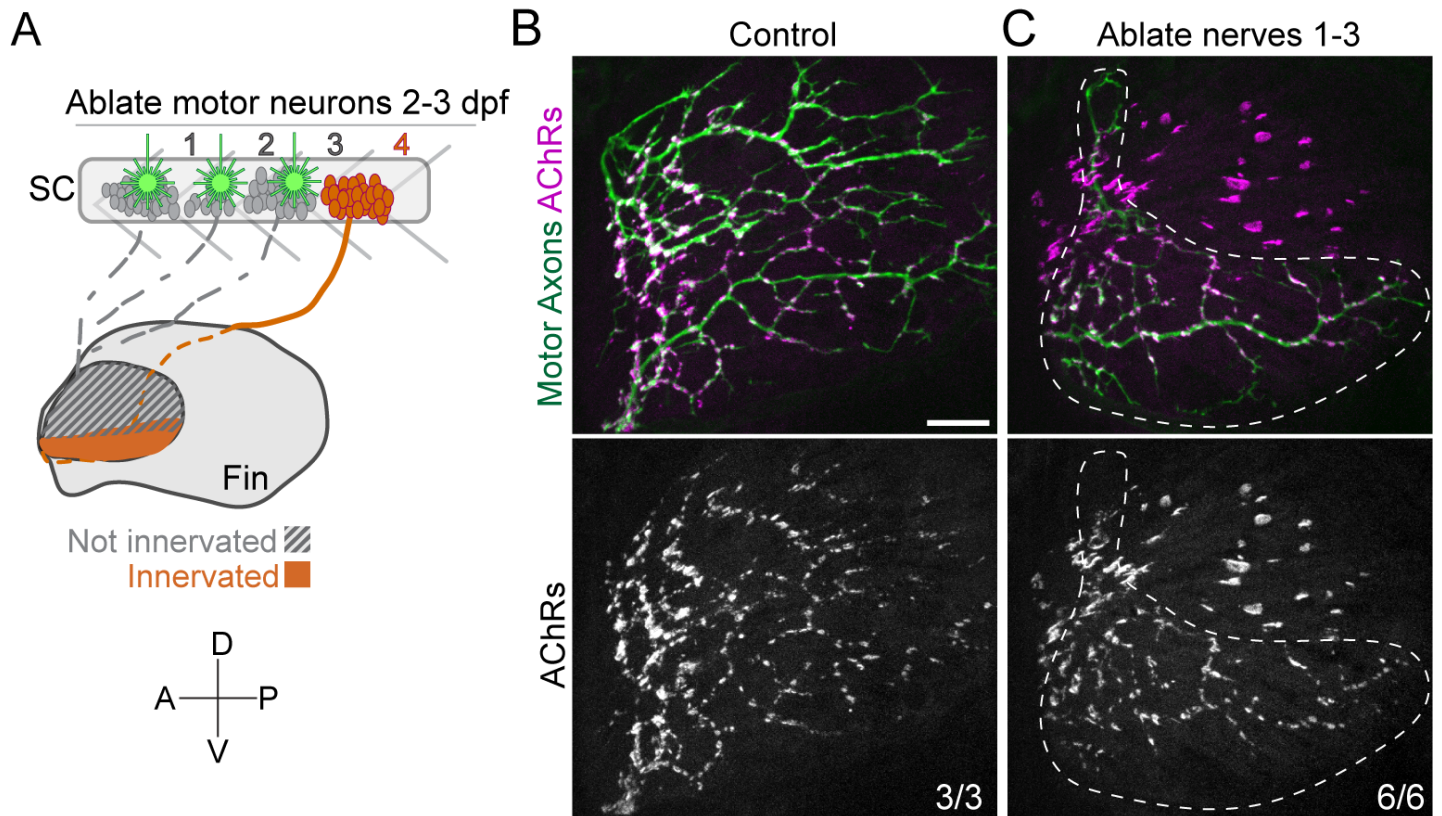
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Figure 4



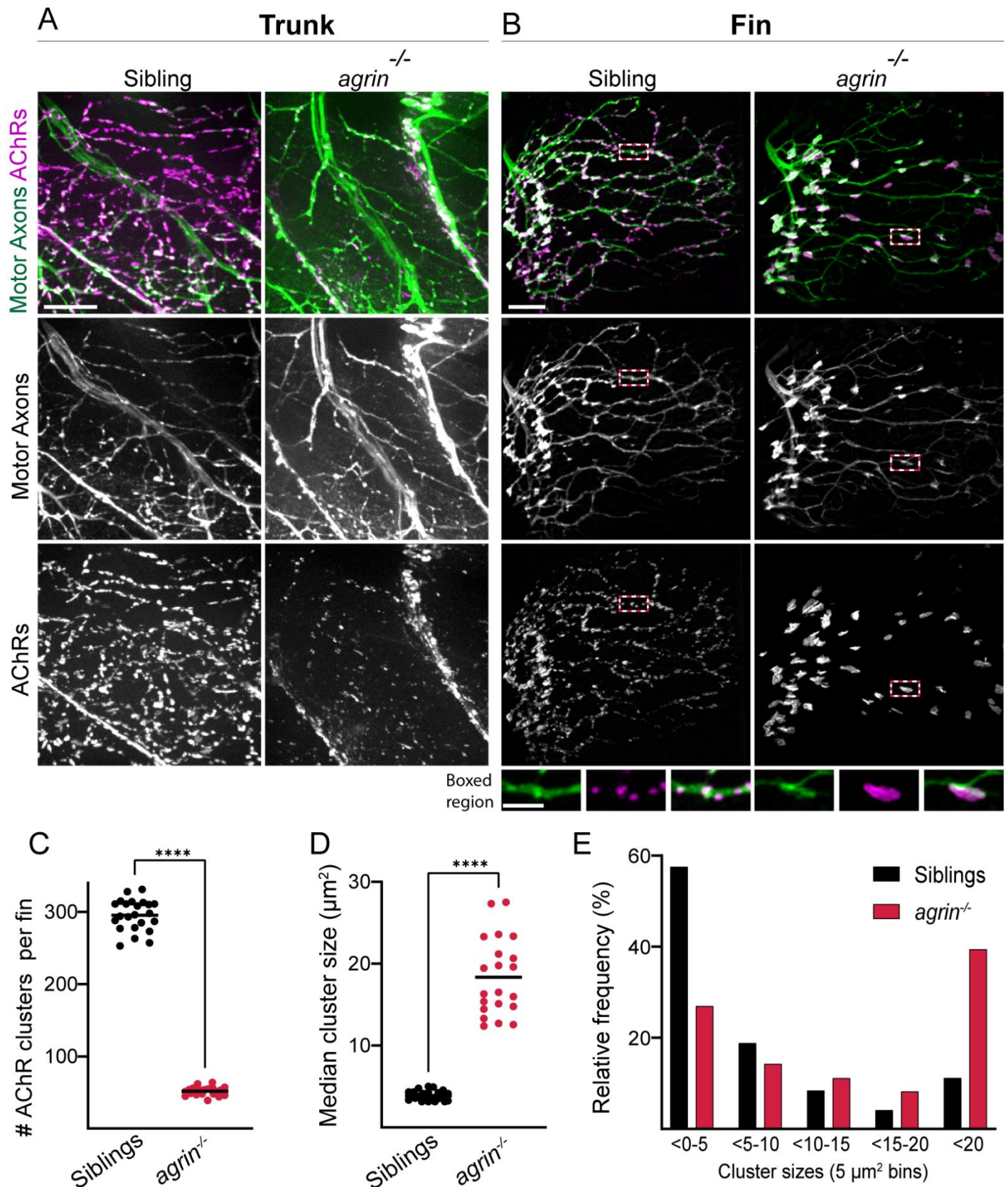
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Figure 5

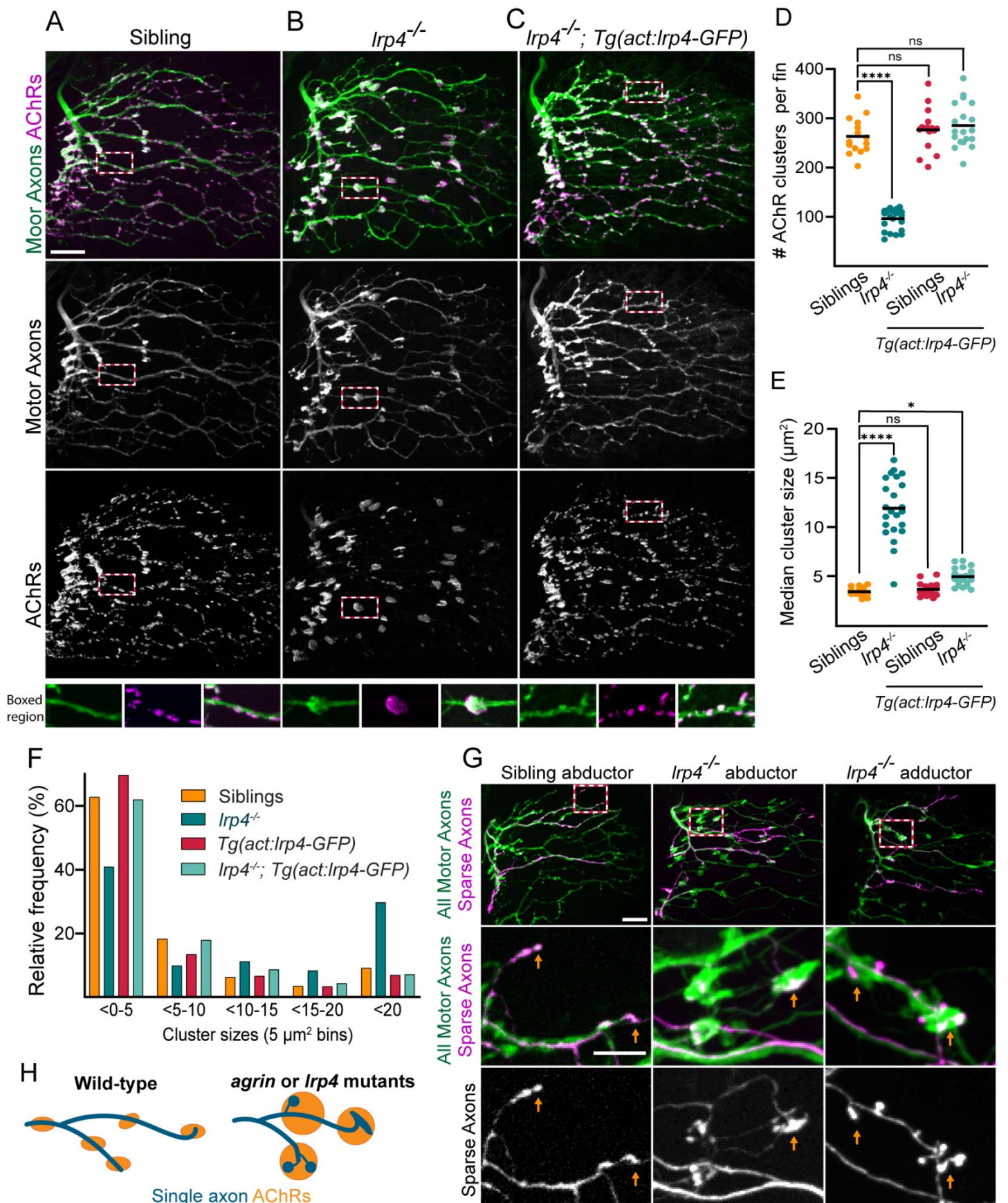


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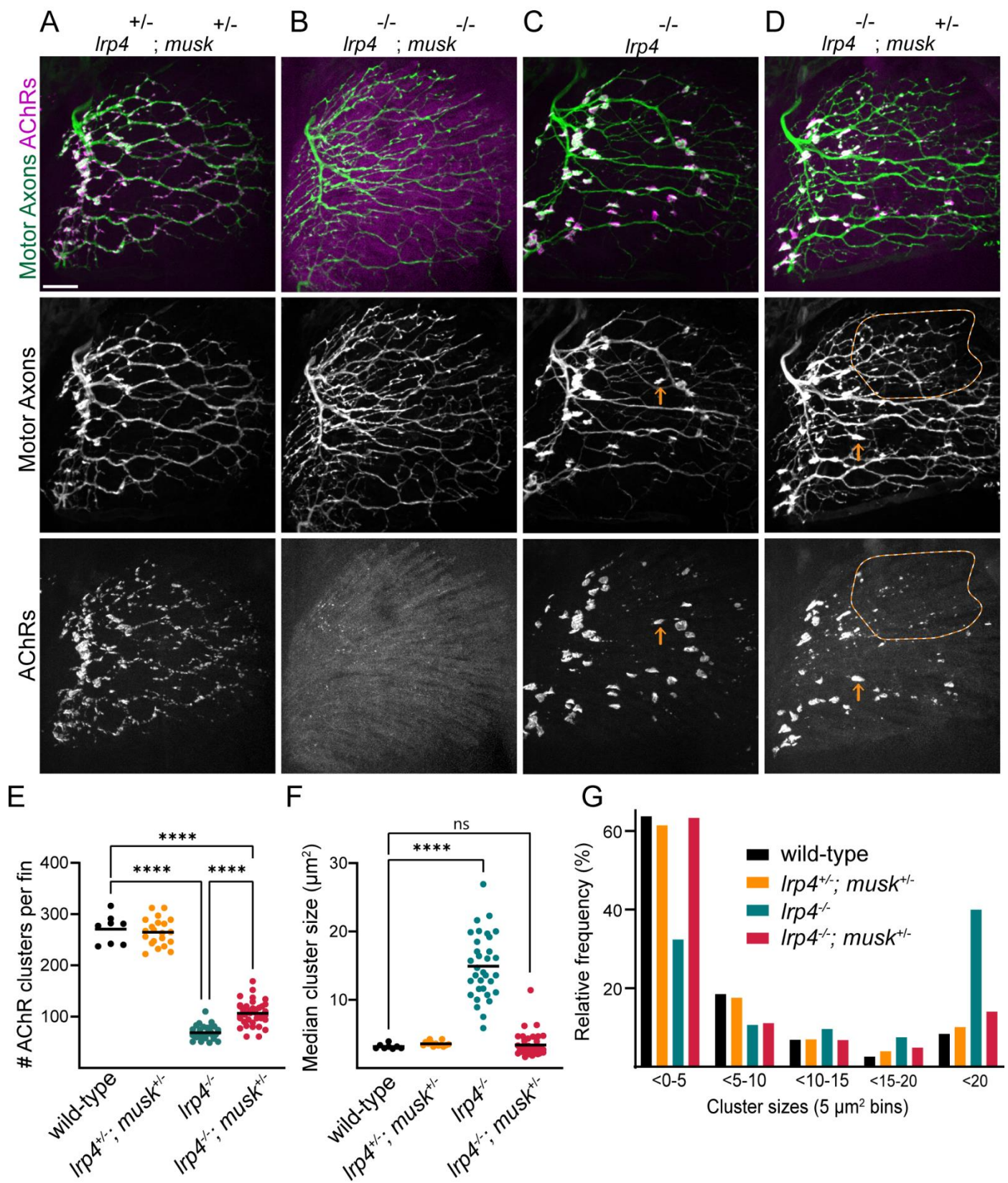
Figure 6



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Figure 7

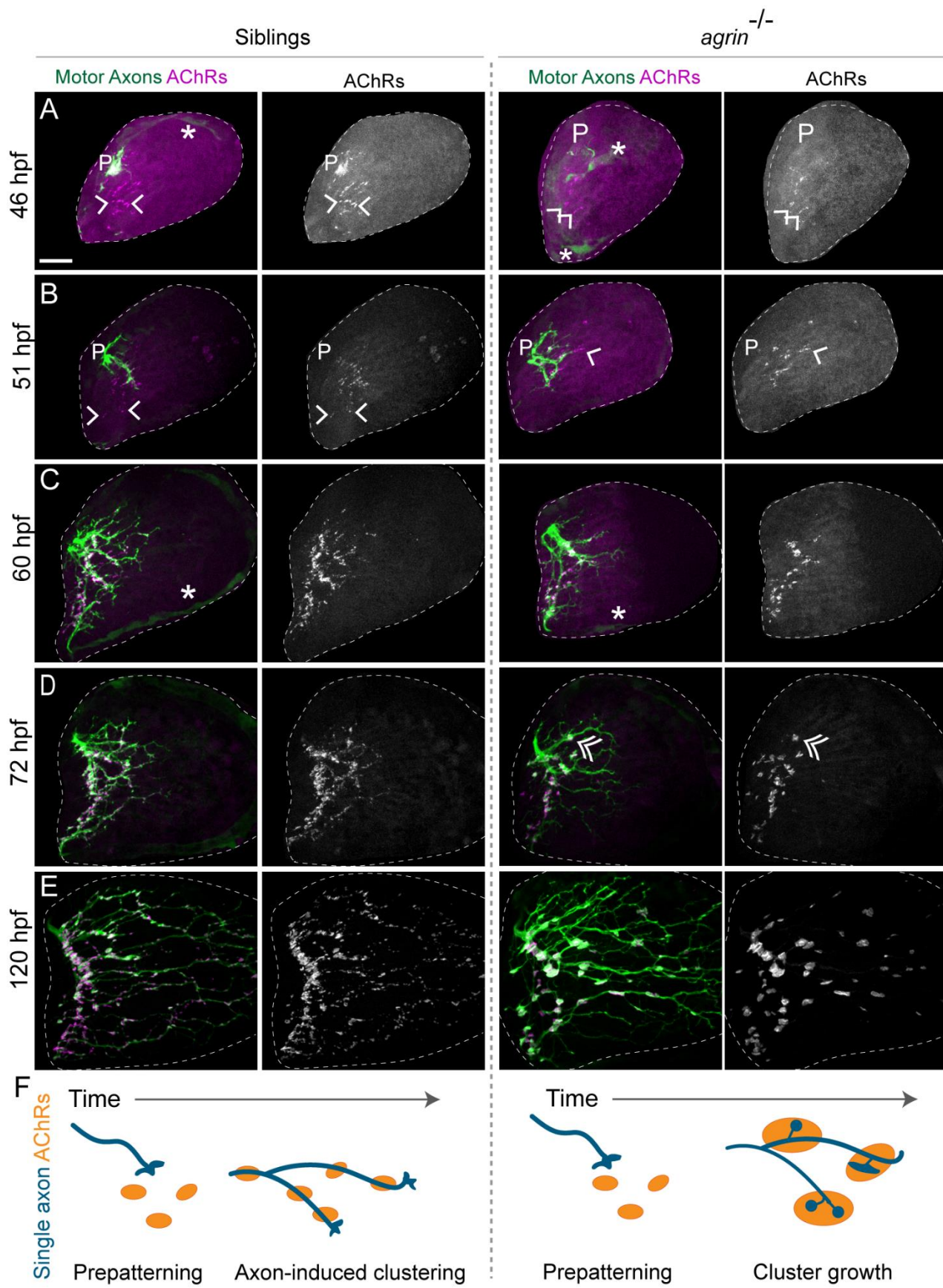


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Figure 8



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