

1 **Title 1: A CRMP4-Dependent Retrograde Axon-to-Soma Death Signal in**
2 **Amyotrophic Lateral Sclerosis**

3
4 **Running Title:** – Retrograde Axonal Death Signal in ALS

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28
29 **Key Words:**

30 Retrograde Signaling, CRMP4, Axonal Transport, ALS, Dynein

31 **Abstract**

32 Amyotrophic Lateral Sclerosis (ALS) is a fatal non-cell-autonomous
33 neurodegenerative disease characterized by the loss of motor neurons (MNs).
34 Mutations in CRMP4 are associated with ALS in patients, and elevated levels of

This is the author manuscript accepted for publication and has undergone full peer review but has not been through the copyediting, typesetting, pagination and proofreading process, which may lead to differences between this version and the Version of Record. Please cite this article as doi: [10.15252/EMBJ.2020107586](https://doi.org/10.15252/EMBJ.2020107586)

35 CRMP4 are suggested to affect MN health in the SODG93A-ALS mouse model.
36 However, the mechanism by which CRMP4 mediates toxicity in ALS MNs is poorly
37 understood. Here, by using tissue from human patients with sporadic ALS, MNs
38 derived from C9orf72-mutant patients, and the SOD1G93A-ALS mouse model, we
39 demonstrate that subcellular changes in CRMP4 levels promote MN loss in ALS.
40 First, we show that while expression of CRMP4 protein is increased in cell bodies of
41 ALS-affected MN, CRMP4 levels are decreased in the distal axons. Cellular
42 mislocalization of CRMP4 is caused by increased interaction with the retrograde
43 motor protein, dynein, which mediates CRMP4 transport from distal axons to the
44 soma and thereby promotes MN loss. Blocking the CRMP4-dynein interaction
45 reduces MN loss in human-derived MNs (C9orf72) and in ALS model mice. Thus, we
46 demonstrate a novel CRMP4-dependent retrograde death signal that underlies MN
47 loss in ALS.

48
49

50 Introduction

51 Amyotrophic lateral sclerosis (ALS) is a lethal neurodegenerative disease that is
52 characterized by degeneration of upper and lower motor neurons (MN). This process
53 leads to spasticity, muscle atrophy, and paralysis, which develop into respiratory
54 failure and patient death (Peters *et al*, 2015; Fischer *et al*, 2004; Frey *et al*, 2000;
55 Moloney *et al*, 2014; Boillée *et al*, 2006). The most common mutations responsible
56 for familial ALS (fALS) include expansions of a repeated DNA element (GGGGCC) in
57 the C9orf72 gene, and point mutations in the superoxide dismutase 1 (SOD1) gene
58 (Rosen *et al*, 1993; Renton *et al*, 2011; DeJesus-Hernandez *et al*, 2011).

59 A hallmark finding in ALS patients, as well as in ALS mouse models, is
60 alterations in axonal transport (Perlson *et al*, 2010; De Vos & Hafezparast, 2017;
61 Gershoni-Emek *et al*, 2015; Bilslund *et al*, 2010). In order to survive and function,
62 MNs depend upon the propagation of signalling events along the axons between the
63 synapse and soma (cell body) (Millecamps & Julien, 2013; Harrington & Ginty, 2013;
64 Terenzio *et al*, 2017; Zahavi *et al*, 2017). Retrograde and anterograde axonal
65 transport are mediated by the dynein/dynactin and kinesin motor protein families,
66 respectively (Paschal & Vallee, 1987; Howard *et al*, 1989; Guedes-Dias & Holzbaur,
67 2019). Notably, mutations in kinesin and dynein/dynactin are also associated with
68 ALS in humans (LaMonte *et al*, 2002; Nicolas *et al*, 2018; Steinberg *et al*, 2015;
69 Münch *et al*, 2004). Several studies have suggested that alterations in cross-talk and
70 long-distance signaling pathways between neurons and their diverse extracellular

71 cues, which are mediated by axonal transport, contribute to ALS pathology (Perlson
72 *et al*, 2009; Gibbs *et al*, 2018; Boillée *et al*, 2006).

73 Collapsin Response Mediator Proteins (CRMPs) constitute a family of
74 developmentally-regulated phosphoproteins known for their intracellular mediation of
75 class 3 Semaphorin signaling (Goshima *et al*, 1995; Ziak *et al*, 2020). There are 5
76 known CRMPs in vertebrates, all of which share ~75 percent sequence similarities
77 (Schmidt & Strittmatter, 2007). The semaphorin/CRMP signaling pathway involves
78 phosphorylation of CRMPs via various kinases including Rho-kinase, CDK5 or
79 GSK3 β , which leads to microtubule destabilization and axon retraction (Yamashita &
80 Goshima, 2012; Sasaki *et al*, 2002; Balastik *et al*, 2015). In addition to their role in
81 mediating semaphorin intrinsic cell responses, CRMPs have been reported to bind
82 dynein and kinesin, and modulate their function (Arimura *et al*, 2009; Rahajeng *et al*,
83 2010). Several studies have demonstrated the involvement of CRMPs in
84 neurodegenerative diseases and neuronal injury (Charrier *et al*, 2003; Nagai *et al*,
85 2017; Yamashita & Goshima, 2012; Jang *et al*, 2010). Specifically, CRMP4
86 expression levels were found to be elevated in the SOD1^{G93A} mouse spinal cord, and
87 were suggested to promote MN death (Duplan *et al*, 2010; Valdez *et al*, 2012; Nagai
88 *et al*, 2015). Interestingly, mutations in CRMP4 are associated with ALS (Blasco *et al*,
89 2013). However, the mechanism of CRMP4 mediated-MN cell death in ALS is
90 unknown.

91
92 Here, we identify a novel mechanism by which CRMP4 mediates MN toxicity
93 in ALS. We discover a CRMP4-dependent retrograde signal in ALS motor neurons
94 that facilitates MN loss. This process is mediated by alterations of CRMP4
95 expression and the formation of a CRMP4-dynein complex via a specific motif in the
96 CRMP4 protein in a subtype of ALS diseased axons.

97

98 **Results**

99 **Alterations in CRMP4 protein levels along ALS diseased motor unit**

100 Increased CRMP4 levels in MN cell bodies of the SOD1^{G93A} ALS mouse model were
101 previously reported to be toxic to MNs and lead to cell death (Duplan *et al.*, 2010).
102 Specific mutations in the N-terminus of CRMP4 are associated with ALS in patients
103 (Duplan *et al*, 2010; Valdez *et al*, 2012; Nagai *et al*, 2015). However, how CRMP4
104 mediates its toxicity in ALS MNs remains unknown. To address this, we first
105 measured CRMP4 protein levels in the spinal cord of human ALS patients (Figure 1
106 A-B). Consistent with the published results from the SOD1^{G93A} ALS mice model
107 (Duplan *et al.*, 2010), we observed a significant 2.5-fold increase in the relative

108 CRMP4 expression in sALS patient compared to non-diseased controls (mean:
109 healthy 1.285 ± 0.184 ; sALS patient 2.571 ± 0.137) (Figure 1 A, B). This increase
110 was also prevalent in SOD1^{G93A} mice spinal cord, as the total number of cells
111 expressing CRMP4 in the SOD1^{G93A} P90 spinal cord compared to their littermate
112 control was elevated (Figure 1C, D) (mean: WT $4.54\% \pm 4.4\%$; SOD1^{G93A} $26.43\% \pm$
113 3.04%). Next, we determined the expression levels of CRMP4 in the distal part of the
114 motor neuron: I) Intra muscular axons and II) NMJs. Unexpectedly, our analysis in
115 human intra-muscular nerves from sALS patients, revealed a significant 28%
116 decrease in CRMP4 levels within neurofilament heavy chain (NFH) positive axons
117 compared to healthy controls and a similar non-significant trend in MBP positive
118 Schwann cells (Figure 2 A,B) (Appendix Figure S1 A,B) (mean intensity: Non-ALS
119 1.00 ± 0.097 ; ALS 0.719 ± 0.108). Furthermore, analysis of P90 gastrocnemius
120 muscles (GC) revealed a decrease in the number of NMJs expressing CRMP4 in
121 SOD1^{G93A} mice compared to the WT control (Figure 2 C,D) (the mean percentage of
122 P90 NMJs expressing CRMP4: WT $90.6595\% \pm 4.78\%$; SOD1^{G93A} $60.29\% \pm 9.00\%$).
123 Interestingly, we detected early partial NMJ degeneration in CRMP4-negative NMJs,
124 suggesting an active role for CRMP4 in preservation of distal axons (Figure 2 C,E)
125 (the mean percentage of P90 partially-innervated SOD1^{G93A} NMJs: CRMP4 positive
126 $33.33\% \pm 16.67\%$; CRMP4 negative $91.67\% \pm 8.33\%$). Lastly, we monitored CRMP4
127 expression levels in WT and SOD1^{G93A} P90 sciatic nerves by immunostaining. We
128 detected a 3-fold increase in CRMP4 signal in sciatic nerve axons (NFH-positive),
129 and a moderate 70% increase in CRMP4 signal also in GFAP positive cells in
130 SOD1^{G93A} mice compared to the controls (Figure 2 F,G; Appendix Figure S1 C,D)
131 (mean area: WT 1.00 ± 0.146 ; SOD1^{G93A} 2.817 ± 0.32) (mean area: WT $0.763 \pm$
132 0.127 ; SOD1^{G93A} 1.415 ± 0.25). Western blot analysis of SOD1^{G93A} and WT P90
133 sciatic axoplasm confirmed this overall increase in CRMP4 levels in ALS sciatic
134 nerves (Figure 2 H,I) (mean: WT 0.56 ± 0.11 ; SOD1^{G93A} 1.22 ± 0.14). Thus, our data
135 thus far reveal that, while the expression levels of CRMP4 increase in MN cell bodies
136 and proximal nerves, the opposite trend occurs in the distal/terminal parts of the MN
137 and in NMJ of ALS-diseased MNs. This suggests that in ALS, distal-CRMP4 is
138 mislocalized into proximal axons and cell bodies.

139

140 **CRMP4 protein mislocalization via Dynein dependent activity**

141 To investigate the potentially disease-relevant function of this intracellular
142 mislocalisation of CRMP4, we utilized human iPSC-derived MNs (iPS-MN) from
143 healthy controls and C9orf72-ALS patients (Tank *et al*, 2018) and plated them in
144 microfluidic chambers (MFCs). First, we immunostained for the neuronal/axonal

145 markers NFH and Tau, along with the MN-specific marker HB9, to validate the MN
146 cell identity (Appendix Figure S2 A-F). Then, we performed immunostaining for
147 CRMP4 to assess changes in its levels in distal axons (Figure 3 A-D). Our analysis
148 revealed no difference in CRMP4 intensity levels between healthy and C9orf72 iPS-
149 MN axons in this system (Figure 3 A,B). In our previous study, we demonstrated that
150 muscle-secreted Sema3A leads to NMJ disruption and axonal degeneration in ALS
151 (Maimon *et al*, 2018). The canonical pathway for CRMP activation involves Sema3A-
152 NRP-PlexinA interactions. Therefore, we considered whether CRMP4 requires stress
153 activation for differential, disease-relevant mislocalization in MNs cultures and asked
154 whether Sema3A treatment might differentially affect CRMP4 levels in ALS iPS-MNs
155 versus Healthy iPS-MNs. We found that exposing distal axons to Sema3A for 8 hours
156 led to significant increase in CRMP4 intensity specifically in axons of C9orf72 MNs
157 (mean: Healthy 0.7 ± 0.05 ; Healthy+Sema3A 0.75 ± 0.047 ; C9orf72 0.61 ± 0.03 ;
158 C9orf72+Sema3A 1.27 ± 0.16) (Figure 3 A,B). Given that CRMP4 levels were
159 specifically high in somata and proximal axons of ALS patients and SOD1^{G93A} mice,
160 we tested the CRMP4 levels in somata and proximal axons of C9orf72 and healthy
161 iPSC-MNs following distal Sema3A treatment. We used Cholera toxin B-647 (CTX)
162 retrograde tracing to specifically examine CRMP4 levels in proximal axons and soma
163 parts of neurons that send their axons into distal compartment of MFC (Figure 3C).
164 Looking specifically at this neuronal population, we detected an increase in CRMP4
165 intensity post Sema3A treatment in C9orf72 iPS-MN soma and proximal axons but
166 not in healthy iPS-MN controls (Figure 3 D-G)(CRMP4 mean intensity in somata
167 area, measured by GAPDH outline: Healthy 1.00 ± 0.128 ; Healthy+Sema3A $1.222 \pm$
168 0.148 ; C9orf72 1.00 ± 0.078 ; C9orf72+Sema3A 1.258 ± 0.068 ;) (CRMP4 mean
169 intensity proximal axons: Healthy 1.00 ± 0.066 ; Healthy+Sema3A 1.048 ± 0.059 ;
170 C9orf72 1.00 ± 0.093 ; C9orf72 +Sema3A 1.302 ± 0.11).

171
172 CRMPs have been reported to bind to the dynein motor protein and modulate its
173 function (Arimura *et al*, 2009; Rahajeng *et al*, 2010). Since distal exposure to
174 Sema3A led to CRMP4 elevation in the ALS diseased MN soma, we speculated that
175 CRMP4 undergoes retrograde transport mediated by dynein. Therefore, we
176 examined CRMP4 levels in the cell bodies and proximal axons of healthy and
177 C9orf72 iPS-MNs that were distally exposed to Sema3A with or without the presence
178 of the dynein inhibitor, Ciliobrevin D (Herein: Dyn-In)(Firestone *et al*, 2012) (Figure 3
179 D-G). Inhibiting dynein completely blocked Sema3A-induced increase in CRMP4
180 levels in C9orf72 iPS-MNs axons and somata (Figure 3 D-G; Appendix Figure S3
181 A,B) (CRMP4 mean intensity somata - measured by GAPDH outline:

182 Healthy+Sema3A 1.222 ± 0.148 ; Healthy+Sema3A+Dyn in 1.161 ± 0.067 ;
183 C9orf72+Sema3A 1.258 ± 0.068 ; C9orf72+Sema3A+Dyn in 0.787 ± 0.088) (CRMP4
184 mean intensity proximal axons: Healthy+Sema3A 1.048 ± 0.059 ;
185 Healthy+Sema3A+Dyn in 1.087 ± 0.089 ; C9orf72 +Sema3A 1.302 ± 0.11 ; C9orf72
186 +Sema3A+Dyn in 0.655 ± 0.036). We did not observe this effect in the presence of
187 Dyn-In alone (Appendix Figure S3 A,B). Furthermore, to validate that distal Sema3A
188 treatment has effect on MN soma, we quantified the cell body area (by measuring
189 CTX signal outline) and found that C9orf72 Sema3A-treated MNs exhibit smaller
190 soma areas compared to untreated or healthy MNs cultures (Appendix Figure S3 C).
191 Here again, when dynein activity was inhibited prior to Sema3A application, this
192 effect was abolished (mean area: Healthy untreated 302 ± 29 ; Healthy+Sema3A 285
193 ± 15 ; Healthy+Sema3A+Dyn-In 296 ± 18 ; C9orf72 untreated 314 ± 10 ;
194 C9orf72+Sema3A 263 ± 10 ; C9orf72+Sema3A+Dyn-In 318 ± 12) (Appendix Figure
195 S3 C). Importantly, no differences were monitored post application of Dyn-In alone in
196 both healthy and disease conditions. These data indicate that the elevation in
197 CRMP4 in cell bodies and in proximal axons of ALS-diseased neurons is mediated
198 by dynein, likely by binding to axonal CRMP4 and subsequent retrograde transport to
199 the cell body.

200

201 **A specific CRMP4 motif mediates the CRMP4-dynein-dynactin interaction**

202 CRMP2 members were previously found to bind the dynein motor protein (Arimura *et al*,
203 *et al*, 2009). Arimura *et al*. also characterized two specific domains in the CRMP2
204 protein that are responsible for dynein binding (Arimura *et al*, 2009). Since CRMP2
205 and CRMP4 share substantial sequence similarity, we hypothesized that the dynein-
206 binding domains (100aa-150aa) of CRMP2 would play a similar role in CRMP4.
207 Following this, and on the basis of the CRMP4 protein 3D structure (PDB code
208 4CNT) (Ponnusamy *et al*, 2014) (Figure 4A), we overexpressed full length GFP-
209 CRMP4 or CRMP4 lacking amino acids 100-150 (GFP-CRMP4 Δ 100-150) in COS7
210 cells, and immunoprecipitated the endogenous dynein intermediate chain (DIC).
211 Western blot analysis of these fractions revealed a clear interaction of DIC with full-
212 length GFP-CRMP4 but not with GFP-CRMP4 Δ 100-150 (Figure 4B) (mean: GFP-
213 CRMP4 1.473 ± 0.373 ; GFP-CRMP4 Δ 100-150 0.009 ± 0.001). Since a large deletion
214 in the CRMP4 protein sequence may result in its misfolding and dysfunction, we
215 pursued an alternative strategy by generating small peptides to cover the potential
216 dynein-binding motif, and test if this could block dynein binding to CRMP4. We
217 designed four short peptides within the 50 amino acid domain, which exhibit the
218 potential to block CRMP4-dynein interaction, based on the protein structure.

219 Importantly, the peptide sequences were designed to avoid an overlap with CRMP4
220 homo-tetramer interfaces, likely preventing a disturbance to the protein's homomeric
221 assembly (Figure 4A). To test the peptides activity, we pre-incubated a mixture of
222 peptides 1-4 with lysate from GFP-CRMP4 overexpressing COS7 cells. This process
223 significantly reduced the CRMP4-DIC interaction (Figure 4 B,C; mean: GFP-CRMP4
224 1.473 ± 0.373 ; GFP-CRMP4 + peptides 0.3 ± 0.05). We also examined CRMP4
225 interaction with dynactin (p150), a dynein activator, in COS7 cells overexpressing
226 Flag-tagged CRMP4. After an overnight incubation of cell lysate with peptides 1-4,
227 we pulled-down Flag-CRMP4 and blotted for dynactin (p150). Application of the
228 peptide mixture resulted in a dramatic decrease in CRMP4 binding to dynactin
229 (Figure 4 D,E)(mean: control 0.77 ± 0.1 ; All Pep 0.17 ± 0.06). We also determined
230 whether introducing the individual peptides might be sufficient to also block the
231 CRMP4-dynactin interaction. Using the same assay, we incubated each peptide
232 separately, and found that only peptide-4 had a mild but significant ability to block
233 CRMP4 interaction with dynactin (Figure 4F,G) (mean: control 1.92 ± 0.2 ; peptide-1
234 1.44 ± 0.3 ; peptide-2 1.34 ± 0.3 ; peptide-3 1.8 ± 0.8 ; peptide-4 1.13 ± 0.14). Hence,
235 although peptide-4 was sufficient to block CRMP4-dynactin binding, blocking
236 CRMP4-dynactin complex formation requires a combination of all four peptides.
237 Lastly, we generated a genetic tool to block the CRMP4-dynein interaction using a
238 plasmid with the CRMP4-dynein binding motif sequence (corresponding to a.a 100-
239 150 of CRMP4) and determined whether it could act in a dominant-negative manner.
240 We transfected COS7 cells with GFP or GFP-expressing the 50aa sequence (GFP-
241 50aa), then extracted the cells and assayed for CRMP4 that co-purified with the
242 dynein intermediate chain (DIC) via immunoprecipitation. Our Western blot analysis
243 revealed weaker interaction of CRMP4 with dynein in the presence of GFP-50aa
244 overexpressing cells compare to the control (mean: GFP CRMP4 1.00 ± 0.10 ; GFP-
245 50aa 0.54 ± 0.11) (Figure 4 H,I). Thus, amino acids 100-150 in the CRMP4 protein
246 are sufficient and essential for CRMP4/dynein/dynactin binding.

247

248 **Enhanced CRMP4-dynein complex formation in ALS Diseased MNs**

249 Our data thus far suggest that CRMP4 levels are: 1) increased in the cell soma and
250 2) decreased in the NMJs and distal axons of ALS diseased MNs (Figure 1, Figure
251 2). We further demonstrated that CRMP4 mislocalization in ALS-diseased MNs can
252 be facilitated by Sema3A and is mediated by dynein (Figures 3 and Figure 4). Since
253 our previous report suggests elevations in Sema3A secretion from ALS muscles
254 (Maimon *et al*, 2018), we predicted an increase in CRMP4-dynein complex formation
255 along the axons of ALS models. To test this, we first extracted sciatic nerves

256 axoplasm from WT and SOD1^{G93A} P90 mice, and measured the levels of CRMP4 that
257 co-purified with the dynein intermediate chain (DIC) *in vivo* using
258 immunoprecipitation. We found a stronger interaction of DIC with CRMP4 in the
259 SOD1^{G93A} mice compared with the control (Figure 5 A, B) (mean: WT 0.28 ± 0.11 ;
260 SOD1^{G93A} 1.48 ± 0.62). Notably, transfecting cells with CRMP4 that carries an ALS-
261 associated mutation, I141V, also enhanced the formation of the CRMP4-dynein
262 complex (Figure 5 C,D) (mean: WT CRMP4 1.00 ± 0.207 ; Mutated CRMP4 $1.625 \pm$
263 0.116). Importantly, I141V is located in the same dynein binding motif in the CRMP4
264 protein, suggesting a CRMP4 gain of toxic function in ALS.

265
266 To further characterize CRMP4-dynein interactions in ALS, we attempted to track
267 CRMP4-GFP retrograde movement in healthy and ALS diseased MN axons.
268 However, overexpressing CRMP4-GFP resulted in a uniformly diffuse distribution
269 (Appendix Figure S4). Thus, in order to demonstrate retrograde transport of
270 endogenous CRMP4 we immunostained distinct cellular compartments (dynein and
271 CRMP4) using Proximity Ligation Assay (PLA), as previously performed (Olenick *et*
272 *al*, 2019). First, by using PLA, we observed that indeed there is an increase in the
273 CRMP4-dynein colocalization along cultured WT MNs axons, post Sema3A
274 treatment compared to untreated WT cultures (Figure 5E). Importantly, this
275 colocalization was twice as high in the Sema3A-treated SOD1^{G93A} MNs axons
276 (Figure 5 E,F). Furthermore, when comparing co-localization patterns of the CRMP4-
277 dynein puncta in human iPS-MNs in the presence or absence of Sema3A, we
278 obtained similar results: In naive, untreated axons, the number of CRMP4-dynein
279 puncta was similar between healthy and C9orf72 iPS-MNs. However, following
280 Sema3A treatment, the number of CRMP4-dynein puncta in C9orf72 axons was
281 significantly higher compared to treated healthy control (Figure 5 G,H) (mean puncta
282 per axon: Healthy untreated 0.032 ± 0.004 ; Healthy+Sema3A 0.062 ± 0.006 ; C9orf72
283 untreated 0.082 ± 0.004 ; C9orf72+Sema3A 0.344 ± 0.026). Next, in order to
284 determine whether the formation of CRMP4-dynein complexes in MN axons is
285 reversible, we aimed to block the CRMP4-dynein interaction in iPS-MN distal axons.
286 To this end, we plated healthy and C9orf72 iPS-MNs in MFCs and exclusively
287 introduced a mix of all peptides (1-4) into axons in the distal compartment. Using
288 TAMRA peptides as a positive control for uptake, we observed that peptides 1-4
289 peptides were successfully taken up by distal axons (Appendix Figure S5 A,B).
290 Strikingly, application of peptides 1-4 significantly interfered with the interaction of
291 CRMP4 and dynein in distal C9orf72 iPS-MN axons as determined by PLA. CRMP4-
292 dynein interaction in healthy iPS-MN remained unaffected by either Sema3A,

293 peptides 1-4, or by both (Figure 5 G,H)(mean puncta per axon: Healthy+Sema3A
294 0.062 ± 0.006 ; Healthy+Sema3A+peptide 0.063 ± 0.006 ; C9orf72+ Sema3A $0.344 \pm$
295 0.026 ; C9orf72+ Sema3A+ peptide 0.067 ± 0.009). No differences were monitored
296 when peptides were inserted without Sema3A activation in both conditions (Figure 5
297 G,H)(mean puncta per axon: Healthy untreated 0.032 ± 0.004 ; Healthy+peptides
298 0.056 ± 0.004 ; C9orf72 untreated 0.082 ± 0.004 ; C9orf72+peptides 0.080 ± 0.005).
299 Together, we have demonstrated both *in vivo* and *in vitro* that the CRMP4-dynein
300 interaction is elevated in ALS-mutated MN axons. Importantly, this strong interaction
301 can be blocked in ALS MN axons by interfering with the CRMP4-dynein binding
302 domain using both genetic and pharmacological tools.

303

304 **The CRMP4-dynein complex facilitates selective neuronal loss in ALS**

305 MNs undergo apoptosis and degenerate in ALS (Reyes et al, 2010). Downregulation
306 of CRMP4 was previously suggested to inhibit neurodegeneration *in vitro* and *in vivo*
307 in ALS models (Charrier et al, 2003; Duplan et al, 2010). Thus, we examined whether
308 enhancement of the CRMP4-dynein interaction by Sema3A would lead to neuronal
309 cell death in ALS. Similar to the experimental design in Figure 3C, we applied CTX to
310 the distal compartment of the MFCs in order to label only the cell bodies of neurons
311 whose axons traversed into the distal compartment. The number of CTX⁺ iPS-MNs
312 were quantified before and 2 days after Sema3A was applied to the distal
313 compartment. Our analysis did not detect any significant loss of CTX⁺ cells in healthy
314 iPS-MNs in response to Sema3A, whereas in C9orf72 iPS-MNs we detected a ~25
315 percent decrease in CTX⁺ MNs upon treatment with Sema3A (Figure 6A-C).
316 Similarly, applying Sema3A to spinal cord cultures from SOD1^{G93A} embryos resulted
317 in a ~30% reduction in CTX⁺ MNs 3 days after treatment, compared with ~5% in the
318 control and WT explants (Figure 6D-E; Appendix Figure S6) (mean fold change over
319 control: Sema3A 0.68 ± 0.06 ; control 1 ± 0.04). In order to determine whether distal
320 stress such as Sema3A application triggers MN loss in ALS-diseased MNs via
321 retrograde signaling, we used dynein inhibitor to block all retrograde transport events
322 (Firestone et al, 2012). Inhibiting retrograde transport in the distal axon prevented
323 MN loss in the SOD1^{G93A} primary cultures (Figure 6D,E; Appendix Figure S6 A-E)
324 (mean fold change over control: Sema3A + Dyn-In 0.92 ± 0.09 ; control 1 ± 0.04).
325 Sema3A was previously shown to internalize together with its receptor, Plexin A1
326 (PLXNA1) in a dynamin-dependent manner (Castellani et al, 2004; Fournier et al,
327 2000). To further determine whether endocytosis of Sema3A is important for the
328 apparent retrograde death signal, as shown before in different neurons (Wehner et
329 al., 2016), we applied Dynasore, a dynamin-dependent endocytosis inhibitor (Macia

330 *et al*, 2006), to the distal axons prior to application of Sema3A. Inhibiting
331 Sema3A+PLAXNA1 (Appendix Figure S7) internalization did not inhibit the loss of
332 SOD1^{G93A} CTX⁺ MNs (Figure 6E; Appendix Figure S6) (mean fold change over
333 control: Sema3A + Dynasore 0.71 ± 0.01 ; control 1 ± 0.04). Thus, Sema3A
334 internalization at the distal axons, is not required for the observed toxicity.
335 Importantly, interfering with the CRMP4-dynein interaction by introducing peptides 1-
336 4 into diseased iPS-MN axons prior to applying Sema3A completely abolished the
337 CTX⁺ signal loss (mean: Control 0.97 ± 0.009 ; Sema3A 0.813 ± 0.036 ; Sema3A + Pep
338 0.94 ± 0.019) (Figure 6 F,G). Our findings demonstrate that death of ALS MNs
339 following Sema3A application can be prevented by inhibiting the formation of
340 CRMP4-dynein complexes.

341

342 We further examined whether impairing the CRMP4-dynein interaction *in vivo*
343 reduces MN death, which is a hallmark in the SOD1^{G93A} mouse model. To this
344 end, we chose to prevent CRMP4-dynein interaction using intrathecal
345 injections of AAV9 viruses to insert CRMP4 dominant negative construct
346 (Figure 4 H,I) into spinal cord MNs. First, to demonstrate injection efficacy, we
347 immunostained spinal cord and sciatic nerve tissues that were infected with a
348 control AAV9-GFP, by intrathecal injections (Appendix Figure S8 A) and
349 monitored the percentage of infected neurons by analyzing colocalization of
350 the neuronal markers NeuN or NFH with GFP in spinal cords and axons along
351 the sciatic nerves (Appendix Figure S8 B,D). We found that 65% of spinal
352 cord neurons as well as 50% sciatic nerve axons expressed GFP signal in
353 AAV9-GFP injected mice compared to non-injected control (Appendix Figure
354 S8 C,D) (Infected SC mean: Non injected $0.25\% \pm 0.19\%$; AAV9-GFP $70.31\% \pm 0.97\%$;
355 Infected SN mean: Non injected $0.25\% \pm 0.163\%$; AAV9-GFP $53.98\% \pm 4.233\%$). We then delivered
356 AAV9-GFP-50aa/AAV-GFP as a dominant negative approach, into pre-symptomatic ~P60 SOD1^{G93A} CSF by
357 lumbar intrathecal injection and monitored for the activation of the apoptotic
358 marker caspase 3 (Pasinelli *et al*, 1998; Porter, 1999; Reyes *et al*, 2010) 4
359 weeks post injection (Figure 7A-E). Importantly, GFP signal was detected in
360 similar number of spinal cord neurons and in similar intensity in both AAV
361 treatments, meaning no difference in infection effectiveness between the GFP
362 and GFP-50aa constructs (Appendix Figure S8 E,F)(Infected cells mean:
363 AAV9-GFP $70.31\% \pm 4.024\%$; 50aa-AAV9-GFP $76.38\% \pm 2.965\%$) (GFP
364

365 intensity mean: AAV9-GFP 3955 ± 318 ; 50aa-AAV9-GFP 3625 ± 383). We
366 measured the degree of activated caspase 3 in P90 SOD1^{G93A} and compared
367 it to the age matched control. As expected, ~90% of NeuN positive cells with
368 MN morphology in the ventral horn were positive for activated caspase 3 in
369 the spinal cord of SOD1^{G93A} mice, while only few caspase 3 positive neurons
370 were detected in the control mice (Figure 7A,B) (mean: WT 12.18 ± 5.666 ;
371 SOD1^{G93A} 92.67 ± 3.167). Injection with AAV9-GFP-50aa resulted in a ~25%
372 decrease in the percentage of activated caspase 3 positive cells in the spinal
373 cord of SOD1^{G93A} mice, compared to injection with AAV9-GFP (Figure 7
374 C,D)(mean: AAV9-GFP $84.44\% \pm 1.47\%$; AAV9-GFP-50aa $73.24\% \pm 0.39\%$).
375 Additionally, the number of NeuN positive cells in the ventral horn of the spinal
376 cord was significantly higher in the 50 aa injected group compared with GFP
377 control (Figure 7 E) (mean: AAV9-GFP 1 ± 0.12 AAV9-GFP-50aa $1.37 \pm$
378 0.12).

379

380 Taken together, our *in vivo* and *in vitro* data demonstrate that a CRMP4-dynein
381 complex contribute to motor neuron loss in ALS disease. Importantly, this process is
382 reversible and can be prevented by blocking the CRMP4 and dynein interaction.

383

384 Discussion

385 Duplan et al., previously reported that CRMP4 is elevated in SOD^{G93A} MNs both *in vivo*
386 and *in vitro* and lead to their loss. By reducing CRMP4 levels the group demonstrated
387 protective effect on MN health (Duplan *et al*, 2010). However, the mechanism by
388 which CRMP4 mediates MN toxicity, its involvement in other ALS models and its
389 relevance to human ALS disease were unknown. In this work we discover subcellular
390 alterations in CRMP4 levels in sALS human patients, C9orf72 human derived MNs
391 and in the SOD^{G93A} mice CRMP4 alterations dependent on dynein activity.
392 Specifically, CRMP4-dynein interactions are mediated by amino acids 100-150 in the
393 CRMP4 protein, a region in which mutation was indeed correlated with ALS (Blasco
394 *et al*, 2013). Notably, CRMP4-dynein complexes are enriched in ALS diseased MNs,
395 and lead to ~25% cell death observed in ALS diseased spinal cord. Finally, we show
396 that blocking the CRMP4-dynein interaction rescued this MN population, both *in vitro*
397 and *in vivo* (Figure 7F). These results pose many important open questions:

398

399 What is the cause for CRMP4 alterations in ALS-diseased MN axons?

400 Here, we reported that CRMP4 is elevated in the soma of several ALS model MNs
401 but is decreased near distal axons. We further demonstrated that Sema3A facilitates
402 an increase in CRMP4 protein levels specifically in ALS diseased MN somata and
403 proximal axons. Since in our previous report we demonstrated that ALS disease
404 muscles secrete Sema3A, we assume that CRMP4 elevations in somata and
405 proximal axons are due to the nearby presence of Sema3A. However, the
406 mechanism responsible for the permanent elevation of CRMP4 specifically in ALS-
407 diseased MNs is unknown. miRNA downregulation and defects in local protein
408 synthesis are common features in several ALS models (Haramati *et al*, 2010; Costa
409 & Willis, 2018). Along with that, Sema3A was shown to induce axonal local synthesis
410 in several neuronal systems (Manns *et al*, 2012; Wu *et al*, 2005; Campbell & Holt,
411 2001; Cagnetta *et al*, 2019, 2018). Thus, we hypothesize that the permanent
412 elevation in CRMP4 that we observed in diseased MN somata and proximal axons
413 are possibly due to increase in axonal protein synthesis. Specifically, our recent
414 published work suggests that miR126-5p is downregulated in both muscles and MN
415 axons in several ALS models (Rotem *et al*, 2017; Maimon *et al*, 2018). Thus, it is
416 tempting to speculate further that miR126-5p downregulation mediates CRMP4
417 increases in ALS-diseased MNs via local protein synthesis and consolidation of
418 retrograde death signals in ALS models. Another possibility for CRMP4 alterations in
419 ALS disease is a proteolytic degradation of CRMP4 at the injured site of the neuron,
420 as has been shown before (Jang *et al*, 2010). Further experiments are needed to test
421 the probability of those ideas.

422

423 How does CRMP4-dynein activate caspase 3 in ALS diseased MNs?

424 Our data further suggest that CRMP4 forms complexes with dynein along ALS-
425 diseased MNs and leads to their loss via a caspase 3-dependent cascade. However,
426 it is still not clear whether CRMP4 itself activates the apoptotic program or whether it
427 plays a regulatory role in recruiting the death complex. Since CRMP members have
428 not yet been reported to act as transcription factors, we assume that CRMP4 is
429 indeed a critical part of a retrograde signaling complex that might contain additional
430 proteins. For example, DLK regulation of JNK and c-Jun might also be a part of this
431 death signal mediated by Sema3A in ALS MNs, since it was previously shown that
432 both DLK and JNK signaling are elevated in ALS models and that they are part of a
433 retrograde death signal (Ghosh *et al*, 2011; Siu *et al*, 2018; Escudero *et al*, 2019;
434 Perlson *et al*, 2010). Another possibility is that the neurotrophic receptor p75^{NTR} is
435 also involved in this process. p75^{NTR} regulates a diverse range of cellular functions
436 including axon pruning (Singh *et al*, 2008) and neuronal death (Bamji *et al*, 1998;

437 Kenchappa *et al*, 2010; Pathak *et al*, 2018). p75^{NTR} is retrogradely transported along
438 the axon (Deinhardt *et al*, 2006; Cosker & Segal, 2014; Harrington & Ginty, 2013)
439 and plays a role in generating a retrograde apoptotic signal that activates JNK
440 (Kenchappa *et al*, 2010). It is noteworthy that the activity of Semaphorin 3A and its receptor
441 was previously linked to p75^{NTR} (Ben-Zvi *et al*, 2007). Another possible candidate that
442 was shown to be coupled with Semaphorin 3A is PTEN (Chadborn *et al*, 2006).
443 Furthermore, it was established that the p75^{NTR}-dependent apoptosis signal is
444 promoted by PTEN activation (Song *et al*, 2010). Thus, future experiments should
445 examine whether PTEN, p75^{NTR}, and JNK indeed participate in Semaphorin 3A-dependent
446 retrograde death signals in ALS.

447

448 CRMP4 gain of toxicity in ALS disease

449 CRMP4 overexpression has been suggested to cause MN death in ALS models
450 (Charrier *et al*, 2003; Duplan *et al*, 2010). Furthermore, a *CRMP4* mutation was
451 associated with ALS in patients (Blasco *et al*, 2013). However, the mechanism of
452 CRMP4 toxicity in ALS MNs is unknown. Here, we demonstrate a specific
453 mechanism by which CRMP4 toxicity to MNs is dependent on dynein activity.
454 Moreover, we demonstrate that amino acids 100-150 of CRMP4 are responsible for
455 the CRMP4 and dynein interaction. Importantly, the ALS associated mutation in
456 CRMP4 is located in this motif. Our data show a stronger dynein interaction for the
457 mutant CRMP4, which is in accordance with CRMP4 gain of toxicity. Alternatively,
458 CRMP4 has been documented before, in a number of experimental models to
459 elevate post neuronal injury (near injury site). Thus, it is possible that the results in
460 this manuscript reflect a response of motor neurons to stress rather than an ALS-
461 specific mechanism (Jang *et al*, 2010). Additional studies will be needed to dissect in
462 detail the mutant CRMP4 activity in ALS-diseased MNs.

463

464 **Materials and Methods**

465

466 **Animals**

467 SOD1^{G93A} (Stock No. 002726) mice were originally obtained from Jackson
468 Laboratories, and maintained by breeding with C57BL/6J mice.
469 B6;129S6-ChAT^{tm2(cre)Lowl/J} (Stock No. 006410) and B6;129S6Gt(ROSA)26
470 Sor^{tm14(CAG-tdTomato)Hze/J} (Stock No. 007908) mice were originally obtained from
471 Jackson Laboratories. Animals were cross-bred in the Tel-Aviv SPF animal unit to
472 yield homozygous ChAT::Rosa^{tdTomato} mice. The ChAT::Rosa^{tdTomato} colony was

473 maintained by in-breeding males and females from the colony. The
 474 ChAT::Rosa^{tdTomato} colony was cross-bred with SOD1^{G93A} to yield
 475 SOD1^{G93A/ChAT::tdTomato} mice. C57BL/6 J mice were used as a WT mouse strain. Mice
 476 were genotyped using the PCR reaction (KAPA Bio Systems - Wilmington, MA,
 477 USA). DNA samples were generated from mouse ear or tail. Animal experiments
 478 were performed under the supervision and approval of the Tel-Aviv University
 479 Committee for Animal Ethics.

480

481 iPSc Cultures

482 Healthy/Control iPSC lines, provided by Dr. Sami Barnada, were created and
 483 characterized as before (Tank *et al*, 2018). Two lines from fALS patients carrying the
 484 C9orf72 mutation, and two lines from healthy controls, were used for all experiments.

Name	Age donated	Age of onset	Gender	
ALS883	51	49 (Lumbar)	M	(>44 repeats per Athena 7/26/2012)
ALS312	54	52 (Lumbar)	M	(44 and 2 repeats) by Athena Diagnostics 10/03/2012
Control746	58		M	Healthy
Control1021	54		F	Healthy

485

486 Colonies were groomed daily until each well of the 6-well plate was between 30%
 487 and 40% confluence and no spontaneously differentiated cells were observed. At this
 488 point, we used the direct iMN" (diMN) differentiation in monolayers from hiPSCs
 489 protocol published by Cedar Sinai and approved by Dhruv Sareen (Protocol number:
 490 CSMNC-SOP-C-005) for our experiments. Briefly, we induced MN differentiation by
 491 MN Differentiation Stage 1 media: prepared with – IMDM (LifeTech), F12 (LifeTech),
 492 NEAA (Gibco), B27 (LifeTech), N2 (LifeTech), PSA (LifeTech), LDN193189 0.2 μM
 493 (Selleck), SB431542 10 μM (Tocris), and CHIR99021 3 μM (Cayman Chemicals).
 494 The media was gently added to the wells, and colonies were grown with it for 5 days.
 495 MN differentiation Stage 2: At day 6 the colonies were dissociated, using accutase,
 496 and 100K cells were plated in the proximal compartment of our micro fluidic device.
 497 Stage 2 media, which contains IMDM, F12, NEAA, B27, N2, PSA, LDN193189 0.2
 498 μM (Selleck), SB431542 10 μM (Tocris), and CHIR99021 3 μM (Cayman Chemicals),
 499 All-trans RA 0.1 μM (Stemgent), and SAG 1 μM (Sonic Hedgehog Agonist – Cayman
 500 Chemicals) media was added to both the distal and proximal compartments of the

501 MFC and refreshed every 2 days until day 11. MN differentiation Stage 3: At day 12
 502 the media was changed to stage 3 media prepared with IMDM, F12, NEAA, B27,
 503 N2, PSA, Compound E 0.1 μ M (Calbiochem), DAPT 2.5 μ M (Cayman Chemicals),
 504 db-cAMP 0.1 μ M (Millipore), Alltrans RA 0.5 μ M (Stemgent), SAG 0.1 μ M,
 505 Ascorbic Acid 200 ng/ml (Sigma), BDNF 10 ng/ml (Alomone lab), and GDNF 10
 506 ng/ml (Alomone lab) and was refreshed every 2 days until cells exhibited MN
 507 neuronal morphology and positive markers. Human iPSC experiments were
 508 performed under the supervision and approval of the Tel-Aviv University Committee
 509 for Human Ethics.

510

511 **Microfluidic chamber preparation**

512 Polydimethylsiloxane (PDMS) microfluidic chambers (MFCs) were designed and cast
 513 as described previously (Ionescu *et al*, 2016). Briefly, MFCs were fabricated from our
 514 designed templates and made from PDMS mixture at 70°C. After the wells were
 515 punched, a small 'cave' was made in the explant well near the grooves using a 25G
 516 needle, keeping the explant in place. Microfluidic devices were cleaned of surface
 517 particles using adhesive tape and were sterilized in 70% ethanol for 15 minutes.
 518 Devices were completely dried under sterile conditions using UV radiation, attached
 519 to a sterile 60-mm plastic dishes (Nunc) with gentle pressure and margins were
 520 sealed with PDMS before incubation at 60°C for 30 minutes to prevent the chamber
 521 from detaching. The wells and channels were filled with 150 μ L of 1.5 ng/mL
 522 polyornithine (P-8638, Sigma) in PBS overnight, and then replaced with 150 μ L
 523 laminin (L-2020, Sigma), 1:333 in deionized distilled water (DDW) overnight. One day
 524 before plating the spinal cord explant, laminin was replaced with explant medium
 525 containing Neurobasal (Life Technologies) supplemented with 2% B27 (Invitrogen),
 526 1% penicillin-streptomycin (Biological Industries), 1% Glutamax (Life Technologies),
 527 25 ng/mL brain-derived neurotrophic factor (Alomone Labs), until the day on which
 528 co-culturing began.

529

530 **Motor neuron cell culture**

531 Primary spinal cord neurons were cultured using E12.5 mouse embryos of either sex
 532 as previously described (Zahavi *et al*, 2015). Briefly, spinal cords were excised,
 533 trypsinized, and triturated. Supernatant was collected and centrifuged through a 4%
 534 BSA cushion. The pellet was resuspended and centrifuged through an Optiprep
 535 gradient (10.4% Optiprep (Sigma-Aldrich), 10 mM Tricine, 4% glucose) for 20 min at
 536 760 x g with the brake turned off. Cells were collected from the interface, washed
 537 once in complete medium, and then plated in coated growth chambers. Cells were

538 maintained in Complete Neurobasal Medium (Gibco) containing B27 (Gibco), 10%
539 (v/v) horse serum (Biological Industries), 25 nM beta-mercaptoethanol, 1% Penicillin-
540 Streptomycin (PS; Biological Industries), and 1% GlutaMAX (Gibco) supplemented
541 with 1 ng/mL Glial-Derived Neurotrophic Factor (GDNF), 0.5 ng/mL Ciliary
542 Neurotrophic Factor (CNTF), and 1 ng/mL Brain-Derived Neurotrophic Factor
543 (BDNF), (Alomone Labs). Prior to plating, growth plates were coated with 1.5 g/mL
544 poly D-L-ornithine (PLO; Sigma-Aldrich) overnight at 37 °C and with 3 µg/mL Laminin
545 (Sigma-Aldrich) for 2 hours at 37 °C. For immunofluorescence staining, 10,000 cells
546 were plated on cover slides in 24-well plates. Cells were grown at 37 °C in 5% CO₂.

547

548 **Spinal cord explants**

549 Spinal cords were dissected from E12.5 mouse embryos of both sexes, either using
550 HB9::GFP or SOD1^{G93A} stripped of meninges and dorsal root ganglia. The ventral
551 horn was separated from the dorsal horn by longitudinal cuts along the spinal cord,
552 and transverse sections up to 1 mm were placed in the explant well. Prior to plating,
553 growth chambers were coated with 1.5 g/mL PLO overnight at 37 °C and 3 µg/mL
554 Laminin overnight at 37 °C. Explants were maintained in Spinal Cord Explant
555 Medium containing Neurobasal, 2% B27, 1% PS, and 1% GlutaMAX, supplemented
556 with 25 ng/mL BDNF. Explants were grown at 37 °C in 5% CO₂.

557

558 **Fluorescence microscopy and image analysis**

559 All confocal images were captured using a Nikon Ti microscope equipped with a
560 Yokogawa CSU X-1 spinning disc and an Andor iXon897 EMCCD camera controlled
561 by Andor IQ3 software. All live-imaging assays were performed in a humidified
562 incubation chamber at 37°C, 5% CO₂. Images were analyzed using ImageJ software.

563

564 **Retrograde labeling of cell bodies in the MFC**

565 Alexa Fluor 647-conjugated Cholera toxin subunit B (CTX; Thermo-Fisher C-347777)
566 at 500 ng/mL was applied to the distal compartment of an MFC system while
567 maintaining a higher liquid volume in the proximal compartment to prevent unspecific
568 labeling by diffusion. After 8 hours, only somata whose axons traversed to the distal
569 compartment were labeled.

570

571 **Recombinant Sema3A application**

572 Recombinant Sema3A (R&D,1250-S3-025) at 500 ng/mL was used in our
573 experiments. We dilute the Sema3A in poor neurobasal (PNB) containing Neurobasal
574 medium (Gibco) with 1% PS and 1% Glutamax.

575

576 Retrograde transport inhibition

577 In order to inhibit dynein-dependent retrograde transport, Cillibrevin-D (Merck-
578 Millipore, 250401) at 10 μ M was applied to the distal compartment of the MFC while
579 maintaining a proximal-to-distal volume gradient.

580

581 Inhibition of dynamin-dependent endocytosis

582 Dynasore (Sigma Aldrich, D7693) at 100nM was added to the distal compartment of
583 the MFC while maintaining a proximal-to-distal volume gradient.

584

585 Pull down assays

586 For the cell cultures pull downs experiments, 2 x 10⁶ COS7 cells were plated in 10
587 cm culture dishes. The following day, cells were transfected using calcium phosphate
588 protocol with Flag-CRMP4/ GFP-CRMP4/ GFP-Delta-CRMP4/ Mutated-Flag-
589 CRMP4/ AAV9-GFP/ AAV9-GFP-50aa vector. The next day, cells were lysed, and
590 proteins were extracted using lysis buffer containing PBS, 1% Triton- 100X, and 1%
591 protease and phosphatase inhibitors (Roche), followed by centrifugation and
592 collection of the supernatant. At this point, immunoprecipitation preparation of the
593 lysate was precleared with protein-A-agarose beads (Roche). Following overnight
594 incubation with primary anti-flag antibody/anti DIC antibody, complexes were
595 incubated with protein A agarose beads for 2 h at 4 °C and then precipitated and
596 washed with PBS with 0.1% Triton X-100 (Sigma). Proteins were eluted by boiling in
597 sample buffer and then subjected to western blot precipitation analysis with
598 CRMP4/dynactin p150/Flag antibody(Sigma-Aldrich F3165)/DIC. We used mouse
599 IgG antibody as a control (SC-2025). For sciatic nerve pull downs, 12 sciatic nerves
600 were pooled for each experiment. Here as well, the P90 sciatic nerve samples were
601 first excised and homogenized in lysis buffer containing PBS and 1% protease and
602 phosphatase inhibitors (Roche), followed by centrifugation and collection of the
603 supernatant. Then we performed the pull-down assay using the technique described
604 above. Under these conditions, pull downs were performed using DIC (Millipore
605 MAB1618) and CRMP4 (Millipore AB5454) antibodies.

606

607 Western blotting

608 Sciatic nerve axoplasm was isolated by excising and cutting sciatic nerves into short
609 segments, followed by detergent-free buffer homogenized with PBS X1 protease and
610 phosphatase inhibitors (Roche), followed by centrifugation and collection of the
611 supernatant. Complete sciatic nerve extracts were achieved in the same manner with

612 the exception of adding 1% Triton X-100. The protein concentration was determined
613 using the Bio-Rad Protein Assay. Protein samples were denatured by boiling in SDS
614 sample buffer and then electrophoresed in 8% polyacrylamide gels (SDS-PAGE).
615 Proteins were transferred to a nitrocellulose membrane and then immunoblotted with
616 appropriate primary antibodies: anti-CRMP4 - 1:2000 (Millipore AB5454) anti-DIC –
617 1:1000 (Millipore MAB1618) anti-p150 1:250 (BD Bioscience 611003) anti-Flag
618 1:4000 (Sigma-Aldrich F3165) anti-Tubulin 1:10,000 (ab7291); and anti-tERK
619 1:10,000 (M5670), diluted in 5% (w/v) Skim-milk (BD Difco) in TBS-T, followed by
620 species-specific HRP-conjugated secondary antibodies (Jackson Laboratories) and
621 visualized using a myECL imager (Thermo), according to the manufacturer's
622 instructions. ImageJ software was used for quantification.

623

624 **AAV production**

625 We used AAV serotype 9 (AAV9) for overexpression experiments. The AAV9
626 produced in AAVpro 293T cells (Takara-Clontech, #632273), with the AAVpro®
627 Purification Kit (All Serotypes) from TaKaRa (#6666). For each construct four 15 cm
628 plates were transfected with 20 µg of DNA (AAVplasmid containing the construct of
629 interest and two AAV9 helpers plasmids) using jetPEITM (Polyplus-transfection) in
630 DMEM medium without serum or antibiotics. pAdDeltaF6 and pPHP.S helper vectors
631 were kind gift from Prof. Fainzilber. Medium (DMEM, 20 % FBS, 1 mM sodium
632 pyruvate, 100 U/mL penicillin 100 mg/mL streptomycin) was added on the following
633 day to a final concentration of 10% FBS and extraction was done at three days post
634 transfection. Purification was performed according to the manufacturer's instructions.
635 For all constructs, we obtained titers in the range of 10^{13} - 10^{14} viral genomes/ml.

636

637 **Vector injections**

638 The injection procedure was performed on pre-symptomatic ~P60 mice. Mice were
639 first anesthetized using a mixture of Xylasin and ketamine. Then, a thin incision was
640 performed in the mouse skin in order to expose the area of the L-5 and L-6
641 vertebrae. Next, 5 µL of AAV9-GFP (6.5×10^{14} vg /ml) or AAV-GFP-50aa (1.21×10^{13}
642 vg /ml), were injected by intrathecal injection to L5-L6 vertebrae in the spinal cord
643 using a 25 µL Hamilton syringe and a 30G Hamilton needle. All animal
644 experimentations were approved by the Tel-Aviv University Animal Ethics
645 Committee. This method was conducted with the help of Dr. Michael Tolmasov. All
646 the tissues were taken 4 weeks post injection.

647

648 **Human muscle biopsy for intra-muscular nerve staining**

649 Intra-muscular nerve staining was performed on muscle biopsies from ALS patients
650 and non-ALS patients. All clinical and muscle biopsy materials used in this study
651 were obtained with written informed consent during 2016-2020 for diagnostic
652 purposes followed by research application, approved by the institutional review
653 board. Deltoid, quadriceps or gastrocnemius skeletal muscle samples were excised
654 via open biopsies and pathological analysis was performed at the neuromuscular
655 pathology laboratory at Sheba Medical Center, Ramat-Gan, Israel. All ALS patients
656 were diagnosed with clinically definite or probable ALS according to Awaji criteria (de
657 Carvalho *et al*, 2008) Control muscles included a variation of findings, which were
658 consistent with a diagnosis of normal muscle, severe, chronic ongoing denervation
659 and reinnervation due to spinal stenosis, necrotic autoimmune myopathy, type 2 fiber
660 atrophy due to disuse and overlap myositis syndrome.

661 Frozen muscle biopsies were cryo-sectioned to 10 μ m thick slices, mounted
662 onto slides and air dried for 30 minutes in room temperature (RT). Sections were
663 washed in PBS, fixed in 4% PFA for 20 min, and permeabilized with 0.1% Triton, and
664 blocked with 5% goat serum (Jackson Laboratories) and 1 mg/mL BSA (Amresco).
665 Sections were then incubated with appropriate antibodies overnight at 4°C in
666 blocking solution Rabbit anti CRMP4 (Millipore AB5454, 1:250), Chicken anti NFH
667 (Abcam, 1:1,000). Sections were washed again and incubated for 2 hours with
668 secondary antibodies (1:1,000, Jackson Laboratories and ThermoFisher), washed
669 and mounted with ProLong Gold (Life Technologies).

670

671 **IHC of CRMP4 in human spinal cord tissue**

672 The Dako Autostainer Link 48 (Agilent, USA) was used for all human spinal cord
673 immunohistochemistry. The CRMP4 antibody (Millipore AB5454) was used at 1:700
674 for 30 minutes at room temperature. Heat induced epitope retrieval was used prior to
675 staining with Dako's EnV Flex Low pH TRS. The Dako Envision Flex Plus Mouse
676 Link Kit (Agilent, USA) to detect the antibody along with the Dako DAB (Agilent,
677 USA). CRMP4 relative expression was semi-quantified by scoring IHC spinal cord
678 sections between 1-3, blindly. 1= Low expression, 2= Middle expression 3= High
679 expression

680

681 **Sciatic nerve sectioning and immunostaining**

682 Sciatic nerves of P90 mice were isolated and immediately fixed by using 4% PFA
683 followed by 20% sucrose incubation. Then the samples were embedded by freezing
684 in Tissue-Tek® OCT. Next, 10 μ m lumbar sciatic nerve sections were prepared using
685 Cryotome™ FSE cryostat (Thermo-Fisher Scientific). Sections were rinsed in PBS,

686 and then permeabilized with 0.1% Triton X-100, 5% Goat Serum (GS), 1 mg/mL
687 Bovine Serum Albumin IgG, and protease free (BSA) in PBS. Primary antibodies
688 against NFH 1:500(Abcam ab72996/ Covance smi31p/ Covance smi32p) / CRMP4
689 1:400 (Millipore AB5454) /GFP 1:400 (Abcam ab13970) were diluted in blocking
690 solution, 5% GS, 1 mg/mL BSA in PBS, and incubated overnight at 4°C. Samples
691 were incubated with species-specific fluorescent secondary antibodies for 2 hours at
692 room temperature. ProLong antifade medium (Molecular Probes) was added and the
693 samples were covered with a #1.5, 18×18 mm cover slide.

694

695 **Spinal cord sectioning and immunostaining**

696 Spinal cord of P90 mice were isolated and immediately fixed by using 4% PFA
697 followed by 20% sucrose incubation. Then the samples were embedded by freezing
698 in TissueTek® OCT. Next, 10 µm lumbar spinal cord sections were prepared using
699 Cryotome™ FSE cryostat (Thermo-Fisher Scientific). Sections were rinsed in PBS,
700 and then permeabilized with 0.1% Triton X-100, 5% Goat Serum (GS), 1 mg/mL
701 Bovine Serum Albumin IgG, and protease free (BSA) in PBS. Primary antibodies
702 against NeuN 1:500 (Millipore MAB377)/ CRMP4 1:400 (Millipore AB5454)/ GFP
703 1:400(Abcam ab13970)/ activated Caspase 3 1:15 (Biovision 3015-100) were diluted
704 in blocking solution, 5% GS, 1 mg/mL BSA in PBS, and incubated overnight at 4°C.
705 Samples were incubated with species-specific fluorescent secondary antibodies for 2
706 hours at room temperature. ProLong antifade medium with Dapi (Molecular Probes)
707 was added and the samples were covered with a #1.5, 18×18 mm cover slide.

708

709 **Immunostaining of cell cultures**

710 Cultures were fixed in 4% paraformaldehyde and permeabilized with 0.1% Triton X-
711 100, 5% GS, 1 mg/mL BSA in PBS. Samples were blocked for 1 hour with blocking
712 medium containing 5% GS and 1 mg/mL BSA in PBS. Primary antibodies against
713 Tau 1:100 (abcam, ab80579) NFH - 1:500 (Sigma-Aldrich N4142), PlexinA1 - 1:100
714 (Alomone lab, APR-081-F), CRMP4- 1:100 (Millipore, AB5454), GAPDH 1:500
715 (abcam, ab9484), Tubulin 1:500 (abcam, ab7291), HB9 1:100 (IMGENEX, IMG-
716 6549A) were diluted in blocking solution and incubated overnight at 4°C. Samples
717 were incubated with species-specific fluorescent secondary antibodies for 2 hours at
718 room temperature. For visualizing nuclei in myotubes, DAPI was used. In the MFC,
719 after the staining protocol was completed, the MFC was peeled from the dish by
720 gently pulling it from the proximal to the distal side.

721

722 **Whole mount NMJ Immunofluorescence staining**

723 Gastrocnemius muscles of P60/ P90 SOD1^{G93A/ChAT::tdTomato} or WT^{ChAT::tdTomato} mice
724 were dissected from mice, washed with cold PBS and cut in longitudinal sections
725 along the fiber before fixed in 4% paraformaldehyde (PFA) in PBS for 15 min at room
726 temperature, while rocking. From fixation until the end of staining protocol
727 (mounting), muscle fibers were washed three times with PBS after each step, except
728 between blocking and primary antibodies staining. After been fixated, muscle fibers
729 were further dissected into smaller section, along fiber orientation. For postsynaptic
730 AChR labelling, the fibers were then stained with α BTX (TMR- α -bungarotoxin; T0195
731 Sigma) 2 μ g/mL in PBS for 15min at RT while rocking. Fibers were then
732 permeabilized in -20oC methanol for 5min, then blocked for 1 hour at RT with
733 blocking solution (2% BSA, 0.4% Triton X-100 in PBS), followed by the application of
734 primary antibodies diluted in blocking solution; NFH (1:500; ab72996, Abcam) and
735 CRMP4 (1:250; Millipore, AB5454) and incubation overnight at RT while rocking. On
736 the next day, samples were incubated with species-specific fluorescent secondary
737 antibodies for 4 hours at room temperature while rocking. Muscle fibers were then
738 placed on a cover slide suitable for imaging, mounted with Vectashield (Vector
739 Laboratories) and sealed with clear nail polish. Slides were kept in RT until
740 completely dried, then stored at 4oC until imaged in the microscope.

741 **Proximity ligation assay**

742 The proximity ligation assay (PLA) was used to visualize the co-localization of
743 selected proteins; it was performed as previously described (Söderberg *et al*, 2008).
744 Briefly, iPSc-derived MNs and murine-MN cultures were grown in the MFC on glass
745 dishes for 18 and 5 DIV, respectively, and were then fixed in 4% PFA, at 4°C for 20
746 minutes. Subsequently, the samples were blocked and permeabilized with 5%
747 Donkey Serum, 1% BSA, and 0.1% Triton X-100 in PBS for 1h and incubated with
748 anti-CRMP4 and anti-DIC antibodies overnight at 4°C. Interactions (range ~40nm)
749 were detected by the proximity ligation assay Duolink kit (Sigma: PLA probe anti-
750 mouse minus DUO92004, anti-rabbit plus DUO92002, and the detection kit Far Red).
751 PLA was performed according to the manufacturer's instructions. Coverslips were
752 washed, mounted, and imaged by confocal microscopy. Half ligation samples were
753 used as a negative control. The axonal PLA signal was quantified with ImageJ
754 software using an axonal mask based on an endogenous mCherry/Rosa signal. The
755 PLA puncta signal was quantified with the analyzed particle function of the software.

756

757 **CRMP4-like Peptide design and insertion into MNs**

758 The Dynein-CRMP4 blocking peptide design was based on previous findings by
759 Amrimura et al., which pointed to 50 specific amino acid sequences responsible for

760 CRMP2 binding to dynein (Arimura *et al*, 2009). Peptides were prepared by Alomone
 761 labs and GL Biochem. Peptide sequences are as follows:
 762

Name	Sequence	MW (Da)
Peptide-1	TTMIIDHVVPEPE	1480 Da
Peptide-2	SSLTEAYEKWREWADGKS	2143 Da
Peptide-3	CCDYALHVDI	1151 Da
Peptide-4	THWNDSVKQ	1114 Da

763 The peptides were inserted into axons by harsh pipetting. Final concentration of
 764 10uM of each peptide were inserted. Tamra peptide was generously donated by Dr.
 765 Mike Fainzilber's lab (10uM final concentration).

766

767 **Vectors**

768 CRMP4 and CRMP4 Δ 100-150 (containing deletion of the coding sequence 301-
 769 450bp) were sub-cloned in frame into the pLL3.7-GFP (Addgene) mammalian
 770 expression vector. Flag-CRMP4 and mutated Flag-CRMP4-I141V, used in the pull-
 771 down assays, was cloned into pCDNA3 vector (Invitrogen). GFP and GFP-50aa
 772 (containing the coding sequence of CRMP4 301-450bp) were sub-cloned in frame
 773 into the pAAV-CBh (Vector Builder) mammalian gene expression vector.

774

775 **Experimental design and statistical analysis**

776 All statistical analyses were performed using GraphPad Prism v6.0. For two-group
 777 analysis, Student's t-test or the Mann-Whitney test was used, as determined by a
 778 normality test. For multiple comparisons, Anova was used with the Tukey or Holm-
 779 Sidak post-hoc tests. All experiments include at least 3 biologically independent
 780 repeats, Significance was set at $p < 0.05$.

781 **Data Availability**

782 This study includes no data deposited in external repositories. All data generated or
 783 analyzed during this study are included in this published article.

784

785 **Acknowledgments**

786 This work was supported by IsrALS Foundation, the Israel Science Foundation
 787 (735/19), and the European Research Council (grant number 309377) to E.P, Czech
 788 Health Research Council grant no. NV18-04-00085 to MB, Czech Science
 789 Foundation grant no. 21-24571S to MB and RW, and Grant Agency of the Charles

790 University grants no. 524218 to RW. We thank Prof. Mike Fainzilber for the Tamra
791 peptides, and help in AAV9. We thank Prof. Eva Feldman and Prof. Stephen
792 Goutman for obtaining the fibroblasts for the iPSC lines. We thank Dr. Michael
793 Tolmasov for performing the intrathecal injections. We thanks Michigan Brain Bank
794 ([5P30 AG053760](#) University of Michigan Alzheimer's Disease Core Center) for
795 providing patients spinal cord sections. Immunohistochemistry (IHC) was performed
796 at the Rogel Cancer Center Tissue and Molecular Pathology Shared Resource
797 Laboratory (funding support: NIH P30 CA04659229).

798

799 **Abbreviations**

800

801 ALS - Amyotrophic Lateral Sclerosis

802 BDNF - Brain-Derived Neurotrophic Factor

803 CNTF - Ciliary Neurotrophic Factor

804 CTX – Alexa Fluor 647-conjugated Cholera toxin subunit B

805 C9orf72 - Chromosome 9 open reading frame 72

806 CRMPs – Collapsin Respond Mediator Proteins

807 DIV - Days In Vitro

808 Dyn-In - Ciliobrevin-D (Dynein Inhibitor)

809 GFP-CRMP4 Δ 100-150

810 GDNF - Glial-Derived Neurotrophic

811 iPSC – Induced Pluripotent Stem Cells

812 JNK - c-Jun N-terminal kinases

813 MFC - Microfluidic Chambers

814 MNs - Motor Neurons

815 NMJ - Neuromuscular Junction

816 NRP1 - Neuropilin 1

817 PTEN - Phosphatase and tensin homolog

818 PLO - Poly D-L-ornithine

819 PLA - Proximity Ligation Assay

820 PDMS - Polydimethylsiloxane

821 PNB - Poor Neurobasal medium (neurotrophin- and serum-free medium)

822 SOD1 - Cu/Zn Superoxide Dismutase 1

823 Sema3A - Semaphorin3A

824 SN – Sciatic Nervep75^{NTR} - low-affinity nerve growth factor receptor

825

826 **Ethics approval and consent to participate**

827 Animal experiments were performed under the supervision and approval of the Tel-
828 Aviv University Committee for Animal Ethics. Human iPSC experiments were
829 performed under the supervision and approval of the Tel-Aviv University Committee
830 for Human Ethics.

831 **Conflict of Interest**

832 The authors declare that they have no conflict of interest point.

833

834 **Author Contribution**

835 Project conceptualization by RM, LA, TGP, MB, and EP; Data curation by RM, LA,
836 TGP, TA, AI; Formal analysis by RM, LA, TGP, AI, MO, EP; Investigation by RM, LA,
837 TGP, TA, RW, MO, ET, GA, NS, AD, SB; Methodology by RM, LA, TGP, TA, AI, RW,
838 MO, ET, GA, NS, YA, AD, SB, MB, EP; Resource obtain from ET, GA, NS, AD, SB;
839 Funding acquisition MB, EP; Supervision MB, EP; Writing—original draft, review and
840 editing by RM, LA, TGP, TA, AI, YA, AD, SB, MB, EP and approved by all.

841

842

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1074
 1075 **Figure Legends**

1076

1077 **Figure 1 –CRMP4 is elevated in ALS diseased spinal cord neurons**

1078 (A, B) (A) Representative IHC images and (B) semi quantification of CRMP4 protein
 1079 in human spinal cords (SC) cross sections from 2 control patients and 3 ALS
 1080 patients. We analyzed total of 7 SC sections of controls and 14 SC sections of ALS
 1081 patients, Data presented as mean \pm SE. DAB: labeled CRMP4. Scale bar: left images
 1082 20 μ m, right insets 10 μ m. Mann-Whitney test ***p = 0.0003.

1083 (C) Representative images of P90 SC cross sections of SOD1^{G93A} and WT mice.
 1084 Red: denotes NeuN, Green: denotes CRMP4. Scale bar: 10 μ m.

1085 (D) Quantification of the percentage of CRMP4 positive SC neurons in
 1086 3 WT VS. 3 SOD1^{G93A} mice. We monitored CRMP4 expression in total of 108 cells in
 1087 WT condition and 123 cells in SOD1^{G93A}, an average of 36 or 41 cells in each repeat
 1088 respectively. Student's t-test, n = 3, Data presented as mean \pm SE, *p = 0.0161.

1089

1090 **Figure 2 –CRMP4 is mis localized in ALS motor units**

1091 (A) Representative images of ALS patient or non-ALS human control intra-muscular
 1092 nerves. Red: denotes NFH, Green: denotes CRMP4, White: denotes co-localization
 1093 area using Imaris software. Scale bar: 20 μ m.

1094 (B) Quantification of CRMP4 intensity levels in NFH positive intra-muscular distal
 1095 nerves from 5 non-ALS controls and 4 sALS patients. We analyzed 40 terminal
 1096 axons from the healthy samples (~8 axons per sample) and 36 terminal axons from
 1097 sALS samples (~8 axons per sample). Data presented as mean \pm SE. Student's t-
 1098 test, *p = 0.0475.

1099 (C) Representative images of SOD1^{G93A/ChAT::tdTomato} or WT^{ChAT::tdTomato} neuromuscular
 1100 junctions at P90. White: denotes BTX, Red: denotes direct ChAT, Green: denotes
 1101 CRMP4, Yellow: denotes Z projection of 3D Imaris co-localization of CRMP4 and
 1102 ChAT. Scale bar: 10 μ m.

1103 (D) Quantification of CRMP4 positive NMJs in gastrocnemius muscles from 3 WT or
 1104 3 SOD1^{G93A} P90 mice. Total of 44 NMJ's in WT condition and 60 NMJ's in SOD1^{G93A}
 1105 condition. Student's t-test, n=3, Data presented as mean \pm SE, *p = 0.0157.

1106 (E) Quantification of the percent of partially denervated NMJ's in the presence or
 1107 absence of CRMP4 immunostaining in 3 different SOD1^{G93A} mice. We counted 24
 1108 NMJ's in SOD1^{G93A} CRMP4 negatives and 67 NMJ's in SOD1^{G93A} CRMP4 positives.
 1109 Student's t-test, n=3, Data presented as mean \pm SE, *p = 0.0352.

1110 (F) Representative images of P90 SOD1^{G93A} and WT sciatic nerves. Red: denotes
 1111 NFH, Blue: denotes GFAP and green denotes CRMP4, Yellow: denotes the Z
 1112 projection of 3D Imaris co-localization of CRMP4 and NFH. Scale bar: 5 μ m.

1113 (G) Quantification of the co-localization area of CRMP4 with NFH in the sciatic nerve
 1114 in 3 SOD1^{G93A} mice compared to 3 WT mice using Imaris analysis. 14 WT sciatic
 1115 nerve sections and 11 SOD1^{G93A} sections were monitored. Data presented as mean
 1116 \pm SE. Student's t-test, n=3, ****p<0.0001.

1117 (H-I) Western blot analysis and quantification of 3 independent repeats of P90 SN
 1118 tissues for CRMP4 expression levels (size of ~64 KDa) in SOD1^{G93A} compared to

1119 WT. tERK was used as a loading control (size of ~44 KDa). Student's t-test, n=3,
1120 Data presented as mean \pm SE, *p = 0.0215.

1121

1122 **Figure 3 –CRMP4 protein levels are altered via a dynein-dependent activity**

1123 (A) Representative images of healthy or *C9orf72* iPSC-derived MNs treated with
1124 *Sema3A* or untreated in the distal compartment, 6 hours post treatment. Red:
1125 denotes Tubulin, Green: denotes CRMP4. Scale bar: 5 μ m.

1126 (B) Quantification of CRMP4 intensity levels in healthy or *C9orf72* iPSC-derived MNs
1127 with *Sema3A* treatment or untreated. 14 untreated healthy axons, 12 healthy axons
1128 with *Sema3A* treatment, 49 untreated *C9orf72* axons and 31 *C9orf72* axons with
1129 *Sema3A* treatment were monitored from 3 different chambers. One-way ANOVA,
1130 Tukey's multiple comparisons test, n = 3, Data presented as mean \pm SE, *p = 0.0338;
1131 ****p<0.0001.

1132 (C) Illustration of the experimental procedure for MNs in an MFC treated with the
1133 fluorescently tagged retrograde tracer CTX in the distal compartment. Neuronal cell
1134 bodies in the primary neuron whose axons have traversed into the distal
1135 compartment were also labeled by the retrograde tracer.

1136 (D) Representative images of healthy or *C9orf72* human-derived MN cell somata with
1137 *Sema3A* treatment, *Sema3A* + dynein inhibitor treatment, or untreated. Gray:
1138 denotes CTX, Green: denotes CRMP4. Scale bar: 5 μ m.

1139 (E) Quantification of CRMP4 intensity (normalized to GAPDH+mCherry/area) levels
1140 at the somata of healthy or *C9orf72* human-derived MN after *Sema3A* treatment,
1141 *Sema3A* + dynein inhibitor treatment, or untreated. Analysis performed in 3
1142 independent chambers per condition. 19 healthy untreated cell somata, 26 healthy
1143 cell somata with *Sema3A* treatment, 20 healthy cell somata with *Sema3A* + dynein
1144 inhibitor treatment and 14 *C9orf72* cell somata from each condition were monitored.
1145 One-way ANOVA, Newman-Keuls multiple comparisons test, n=3, Data presented as
1146 mean \pm SE, *p=0.0207; ***p=0.0004.

1147 (F) Representative images of healthy or *C9orf72* human-derived MN proximal axons
1148 with *Sema3A* treatment, *Sema3A* + dynein inhibitor treatment or untreated control.
1149 Green: denotes CRMP4, Red: denotes GAPDH. Scale bar: 5 μ m.

1150 (G) Quantification of CRMP4 intensity levels (normalized to GAPDH+mCherry/area)
1151 at the proximal axons in healthy or *C9orf72* human-derived MN after *Sema3A*
1152 treatment, *Sema3A* + dynein inhibitor treatment, or untreated control. Analysis
1153 performed from 3 independent chambers in each condition. 21 healthy untreated
1154 proximal axons, 24 healthy proximal axons with *Sema3A* treatment, 16 healthy
1155 proximal axons with *Sema3A* + dynein inhibitor treatment, 12 *C9orf72* untreated

1156 proximal axons, 8 *C9orf72* proximal axons with Sema3A treatment and 13 *C9orf72*
1157 proximal axons with Sema3A + dynein inhibitor treatment were monitored. One-way
1158 ANOVA, Newman-Keuls multiple comparisons test, $n = 3$, Data presented as mean
1159 \pm SE, * $p = 0.0334$, **** $p < 0.0001$.

1160

1161 **Figure 4 –CRMP4 binds dynein via a specific 50 amino acid motif**

1162 (A) Crystal structure (PDB code 4CNT) of a CRMP4 monomer (upper panel)
1163 and biological tetramer assembly (lower panel). The peptides that were selected to
1164 inhibit binding are highlighted and color coded as indicated.

1165 (B) Upper panel represent the binding site domain of dynein in CRMP4 and its
1166 deletion. These constructs were used in the IP that was performed in the middle
1167 panel. Middle panel - Immunoprecipitation of DIC followed by western blot analysis of
1168 CRMP4 in COS7 cells overexpressing either GFP-CRMP4, or GFP-CRMP4 with
1169 deletion of amino acid 100-150, or GFP-CRMP4 overexpressing cells that were pre-
1170 incubated with a 10 μ m mixture of peptides 1-4 (size of \sim 91 KDa). Lower panel -
1171 Western blot analysis of total protein levels before the pull-down assay (DIC size:
1172 \sim 75 KDa).

1173 (C) Quantification of the Western blot in B from 3 independent repeats. The dynactin
1174 intensity band was normalized to the Flag-CRMP4 intensity band in each technical
1175 repeat. One-way ANOVA, Tukey's multiple comparisons test, $n=3$, Data presented as
1176 mean \pm SE, ** $p=0.007$, * $p=0.0261$.

1177 (D) Upper panel - immunoprecipitation assay with anti-Flag antibody followed by
1178 Western blot analysis of dynactin (p150) in COS7 cells overexpressing Flag-CRMP4
1179 (size of \sim 65 KDa). Lower panel - total protein input (size of \sim 150 KDa).

1180 (E) Quantification of the blot in D from 3 independent repeats. The dynactin intensity
1181 band was normalized to the Flag-CRMP4 intensity band in each repeat. Student's t-
1182 test, $n=3$, Data presented as mean \pm SE, ** $p=0.01$.

1183 (F) Upper panel - Immunoprecipitation assay with anti-Flag antibody followed by
1184 Western blot analysis of dynactin (p150) in COS7 cells overexpressing Flag-CRMP4
1185 (size of \sim 65 KDa). Lower panel - Total input (size of \sim 150 KDa).

1186 (G) Quantification of the blot in F. The dynactin intensity band was normalized to the
1187 Flag-CRMP4 intensity band in each repeat. Student's t-test, $n=3$, Data presented as
1188 mean \pm SE, * $p=0.0299$.

1189 (H) Immunoprecipitation of DIC (size of \sim 75 KDa) followed by Western blot analysis
1190 of CRMP4 (size of \sim 64 KDa) in COS7 cells that were transfected with CRMP4 and
1191 AAV9-50aa or its control. IgG antibody was used as a control.

1192 (I) Quantification of the blot in H from 3 independent repeats. The CRMP4 intensity
 1193 band was normalized to the DIC intensity band in each repeat. Student's t-test, n=3,
 1194 Data presented as mean \pm SE, *p=0.0479.

1195

1196 **Figure 5 –CRMP4-dynein interaction is enhanced in ALS motor neuron axons**

1197

1198 (A) Immunoprecipitation of DIC followed by Western blot analysis of CRMP4 in
 1199 SOD1^{G93A} compared to WT P90 sciatic nerves under physiological conditions. IgG
 1200 antibody was used as a control.

1201 (B) Quantification of the blot in A. 3 repeats, 12 sciatic nerves per condition were
 1202 used in each repeat. The CRMP4 intensity band was normalized to the DIC intensity
 1203 band in each repeat. Data presented as mean \pm SE (Ratio Paired t-test, *p = 0.0416).

1204 (C) Immunoprecipitation of DIC followed by Western blot analysis of CRMP4 in Cos7
 1205 cells that were transfected with mutant CRMP4 I141V compared to control. IgG
 1206 antibody was used as a control.

1207 (D) Quantification of four repeated pull down in C. The CRMP4 intensity band
 1208 was normalized to the DIC intensity band for each repeat. (Student's t-test, n=4, Data
 1209 presented as mean \pm SE, *p=0.0393).

1210 (E) Representative images from the proximity ligation assay (For explanation of PLA
 1211 technique; please refer to method section) for CRMP4 and dynein in SOD^{G93A} and
 1212 WT primary MNs axons that were exposed to either control or Semaphorin 3A 8h post
 1213 treatment. Scale bar: 5 μ m.

1214 (F) Quantification of the CRMP4-DIC puncta number per primary motor neuron axon
 1215 in each condition. We analyzed ~20 axons per condition from 3 independent
 1216 chambers per group (One-way ANOVA, Tukey's multiple comparisons test, n=3,
 1217 Data presented as mean \pm SE, **p=0.01 *p=0.04)

1218 (G) Representative images of proximity ligation assay for CRMP4 and dynein in
 1219 healthy and C9orf72 human-derived proximal axons post peptides treatment,
 1220 Semaphorin 3A treatment, Semaphorin 3A + peptides treatment or untreated controls. Scale bar:
 1221 5 μ m.

1222 (H) Quantification of the CRMP4-DIC puncta number per axon in healthy or C9orf72
 1223 human-derived MN proximal axons after Semaphorin 3A treatment, Semaphorin 3A + peptides
 1224 treatment or untreated controls. Data collected from 3 independent chambers in each
 1225 condition. Total of 37 healthy untreated proximal axons, 61 healthy proximal axons
 1226 with peptides treatment, 59 healthy proximal axons with Semaphorin 3A treatment and 52
 1227 healthy proximal axons with Semaphorin 3A + peptides treatment. 67 C9orf72 untreated

1228 proximal axons, 63 *C9orf72* proximal axons with peptides treatment, 41 *C9orf72*
1229 proximal axons with Sema3A treatment and 50 *C9orf72* proximal axons with Sema3A
1230 + peptides treatment monitored. Data presented as mean \pm SE. One-way ANOVA,
1231 Tukey's multiple comparisons test, $n=3$, **** $p<0.0001$.

1232

1233 **Figure 6 – Retrograde CRMP4-dynein complex formation mediates MN loss in**
1234 **ALS**

1235

1236 (A) Representative images of CTX signal in healthy and *C9orf72* human iPSC-
1237 derived MNs before and after Sema3A application. Green: denotes CTX-positive
1238 cells. Yellow circles are numbered CTX positive cells. Purple circles are cells that are
1239 missing post Sema3A treatment. Scale bar: 40 μ m.

1240 (B-C) Quantification of CTX signal in healthy and *C9orf72* iPSC-derived MNs before
1241 and 3 days after applying Sema3A to distal compartment, compared with untreated
1242 control. 3 independent chambers in each condition were analyzed. Average of \sim 150
1243 neurons per condition monitored. Student's t-test, $n=3$, Data presented as mean
1244 \pm SE, * $p<0.05$.

1245 (D) Representative images of CTX signal in WT or *SOD1^{G93A}* primary MNs before
1246 and 2 days after Sema3A application to the distal compartment in the presence of
1247 either Dynein inhibitor+Sema3A, Dynasore+Sema3A or untreated. Green: denotes
1248 CTX-positive cells. Yellow circles are numbered CTX positive cells. Purple circles are
1249 cells that are missing post Sema3A treatment. Scale bar: 30 μ m.

1250 (E) Quantification of CTX signal in a *SOD1^{G93A}* explant before and 2 days after
1251 Sema3A application to the distal compartment in the presence of either Dynein
1252 inhibitor+Sema3A, Dynasore+Sema3A. 3 independent chambers in each condition
1253 were analyzed. \sim 200 neurons were monitored per each condition. One-way ANOVA,
1254 Tukey's multiple comparisons test, $n = 3$, Data presented as mean \pm SE, * $p<0.05$,
1255 ** $p<0.01$. Dynein inhibitor and Dynasore treatments were used as a negative control.

1256 (F-G) Representative images and quantification of *C9orf72* iPSC-derived MNs in the
1257 proximal compartment of an MFC before and after Sema3A treatment with and
1258 without 10 μ g peptides 1-4. Green: denotes CTX-positive cells. Yellow circles are
1259 numbered CTX positive cells. Purple circles are cells that are missing post Sema3A
1260 treatment. 3 independent chambers in each condition were analyzed. \sim 200 neurons
1261 per condition monitored. Scale bar: 40 μ m. One-way ANOVA Tukey's multiple
1262 comparisons test, $n = 3$, Data presented as mean \pm SE, ** $p = 0.004$.

1263

1264 **Figure 7 – Blocking the formation of the CRMP4-dynein complexes reduces**
1265 **motor neuron toxicity *in vivo***

1266

1267 (A) Representative images and insets of P90 WT and SOD1^{G93A} SC cross sections at
1268 P90. Blue: denotes DAPI, Red: denoted NeuN, and White: denotes activated
1269 caspase 3. Scale bar: 20 μ m.

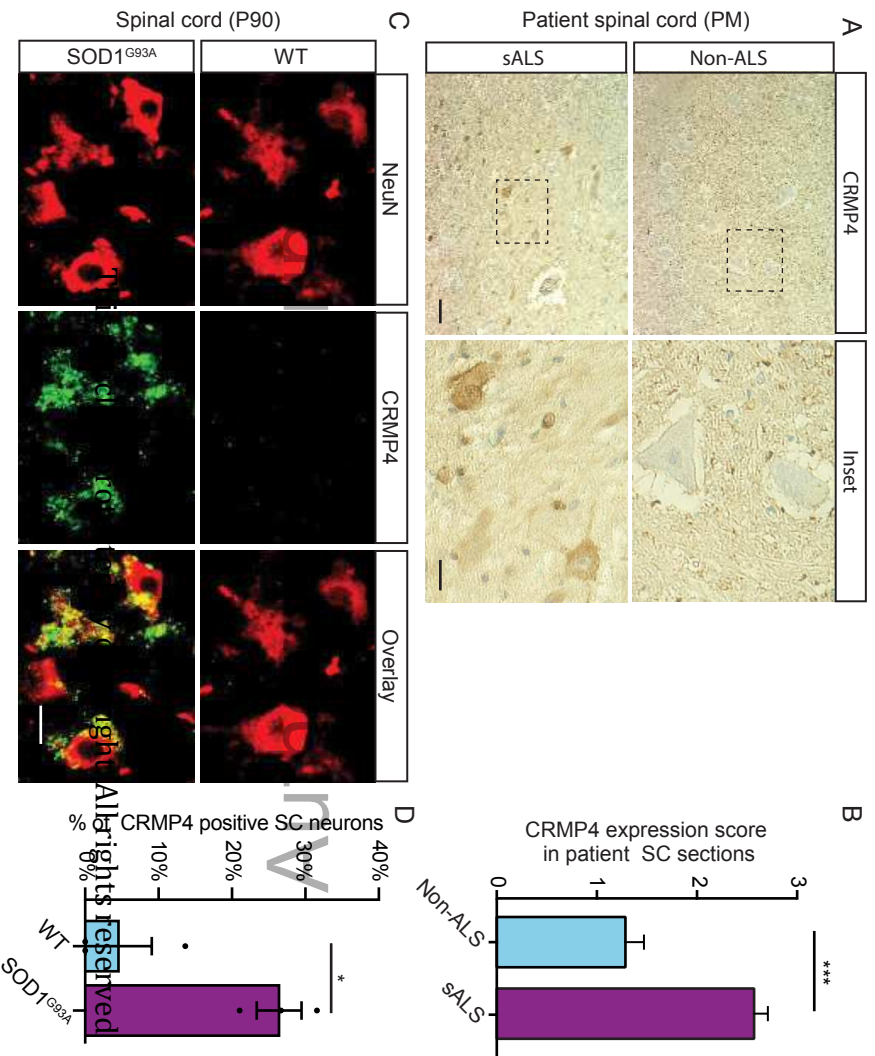
1270 (B) Quantification of active caspase 3 positive cells in P90 WT and SOD1^{G93A} SC. 3
1271 different mice in each condition analyzed. We monitored active caspase 3 expression
1272 in total of 108 cells in WT SC and 123 cells in SOD1^{G93A}. Student's t-test, n=3, Data
1273 presented as mean \pm SE, ****p<0.0001.

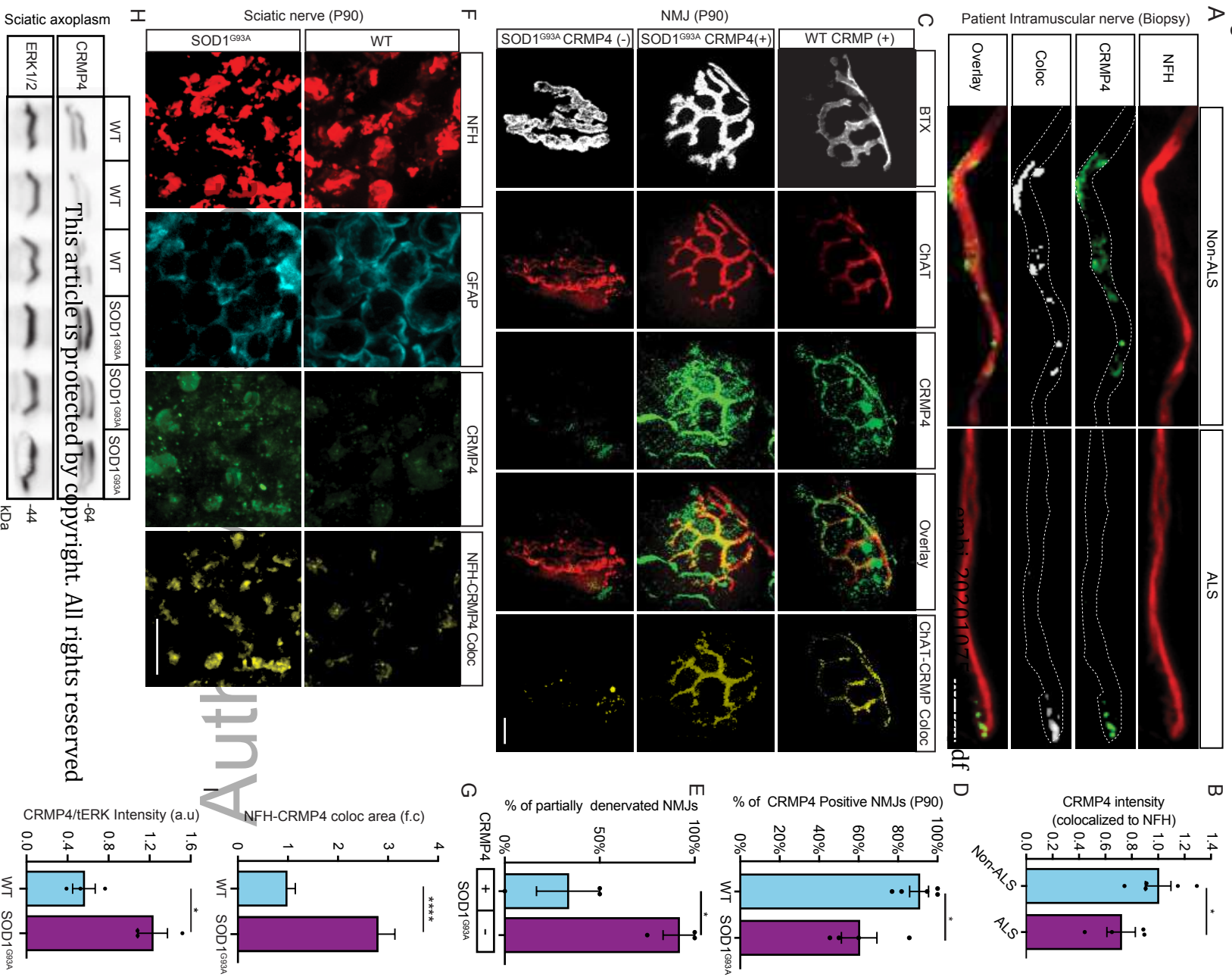
1274 (C) Representative images of P90 SOD1^{G93A} mice SC cross sections that were
1275 injected with AAV9-GFP/AAV9-50aa-GFP. Blue: denotes DAPI, Red: denoted NeuN,
1276 and White: denotes activated caspase 3. Scale bar: 10 μ m.

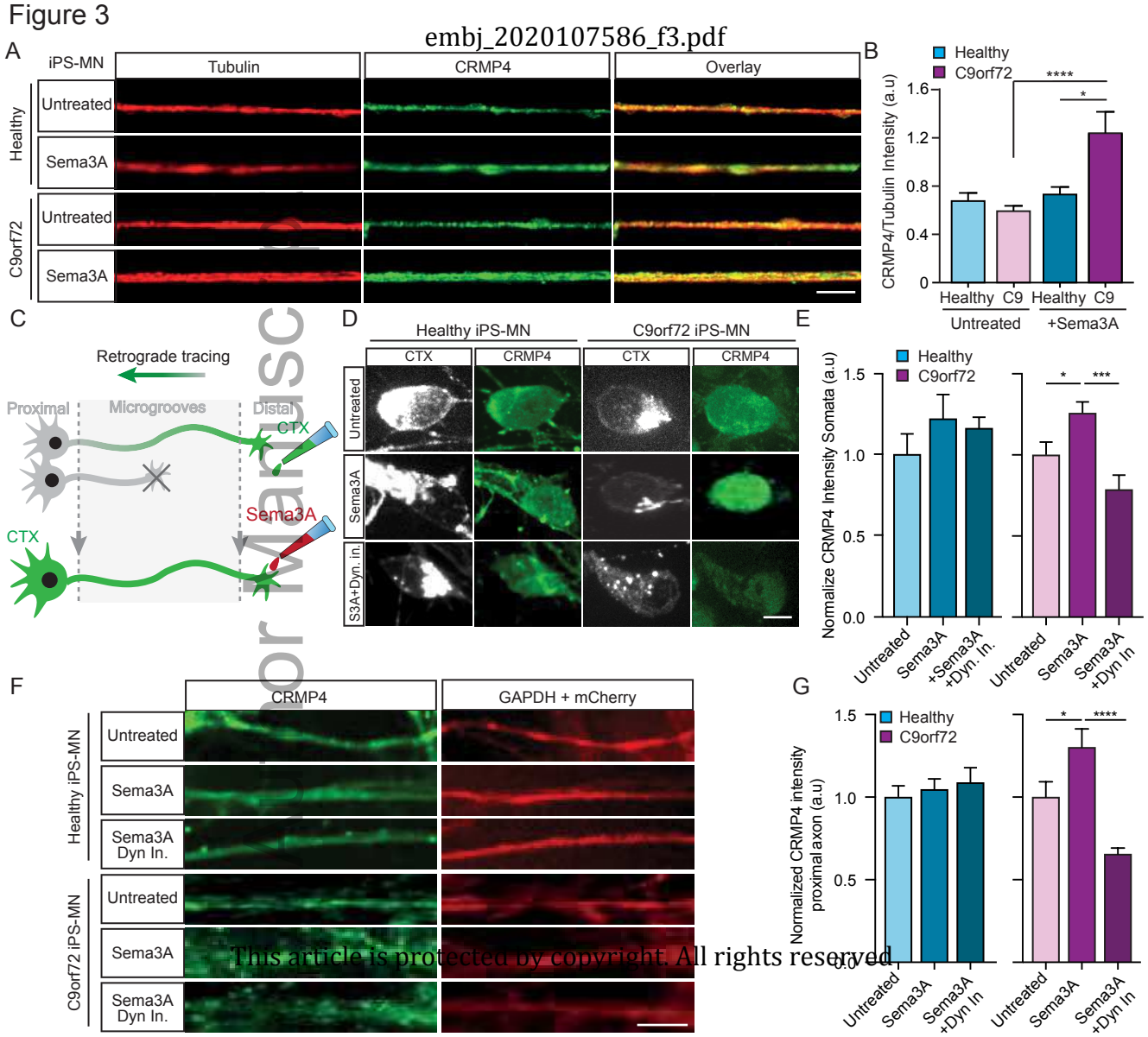
1277 (D) Quantification of caspase 3 positive cells in P90 SOD1^{G93A} mice SC cross
1278 sections that were injected with either AAV9-GFP or AAV9-50aa-GFP. Data collected
1279 from 3 different mice in each condition. We monitored active caspase 3 expression
1280 in total of 228 cells in in P90 SOD1^{G93A} mice SC cross sections that were injected
1281 with AAV9-GFP and 179 cells P90 SOD1^{G93A} mice SC cross sections that were
1282 injected with AAV9-50aa-GFP. Student's t-test, n=3, Data presented as mean \pm SE, **
1283 p=0.0019.

1284 (E) Quantification of the number of NeuN positive cells in P90 SOD1^{G93A} mice SC
1285 cross sections that were injected with either AAV9-GFP or AAV9-50aa-GFP. Data
1286 collected from 3 different mice in each condition. We monitored the number of NeuN
1287 positive cells from total of 228 cells in P90 SOD1^{G93A} mice SC cross sections that
1288 were injected with AAV9-GFP and 179 cells P90 SOD1^{G93A} mice SC cross sections
1289 that were injected with AAV9-50aa-GFP. Unpaired t test with Welch's correction,
1290 n=3, Data presented as mean \pm SE, * p=0.0484.

1291 (F) Working model – CRMP4-dynein complex formation is enhanced in ALS disease
1292 and leads to subtype-specific neuronal loss.







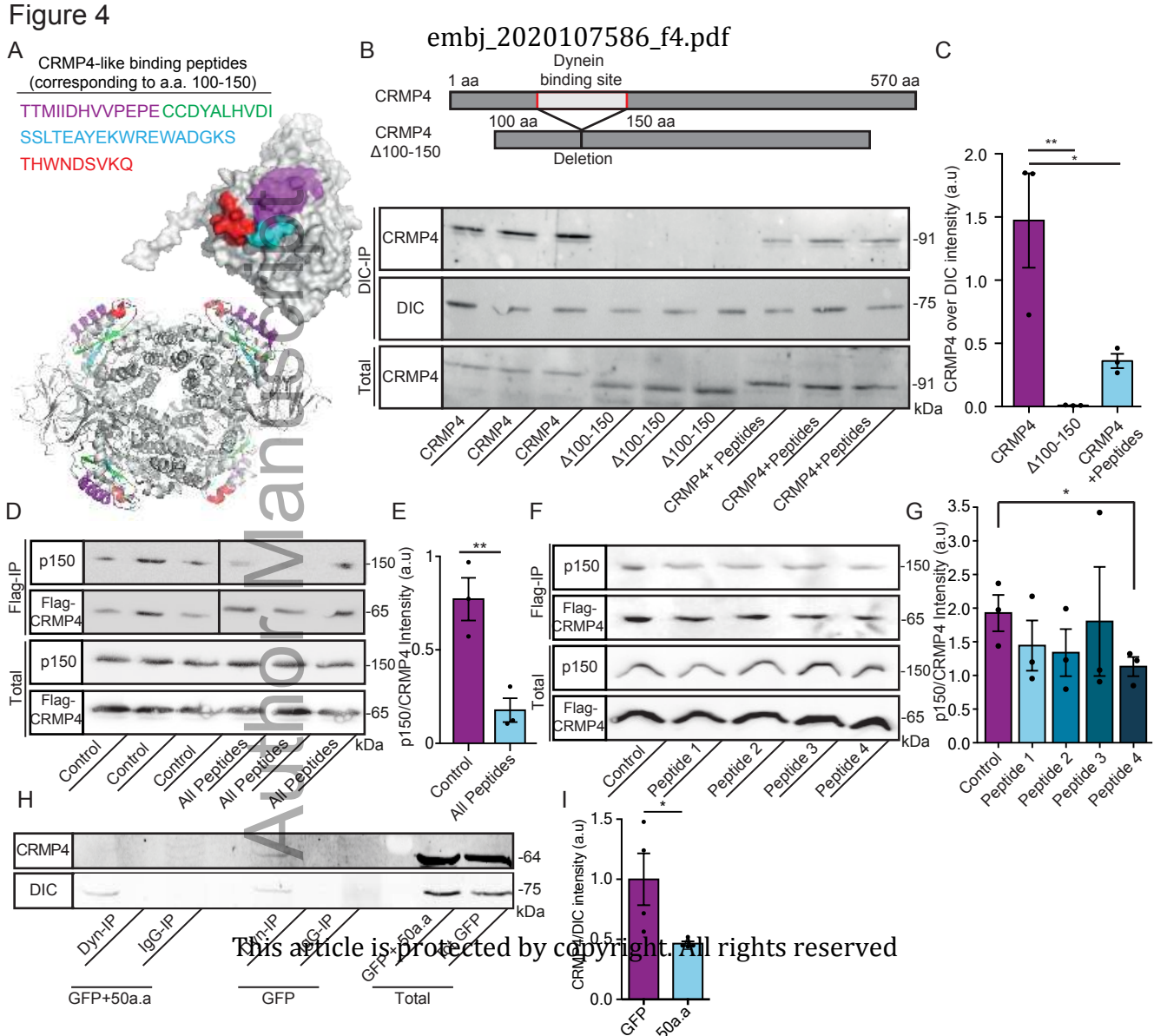
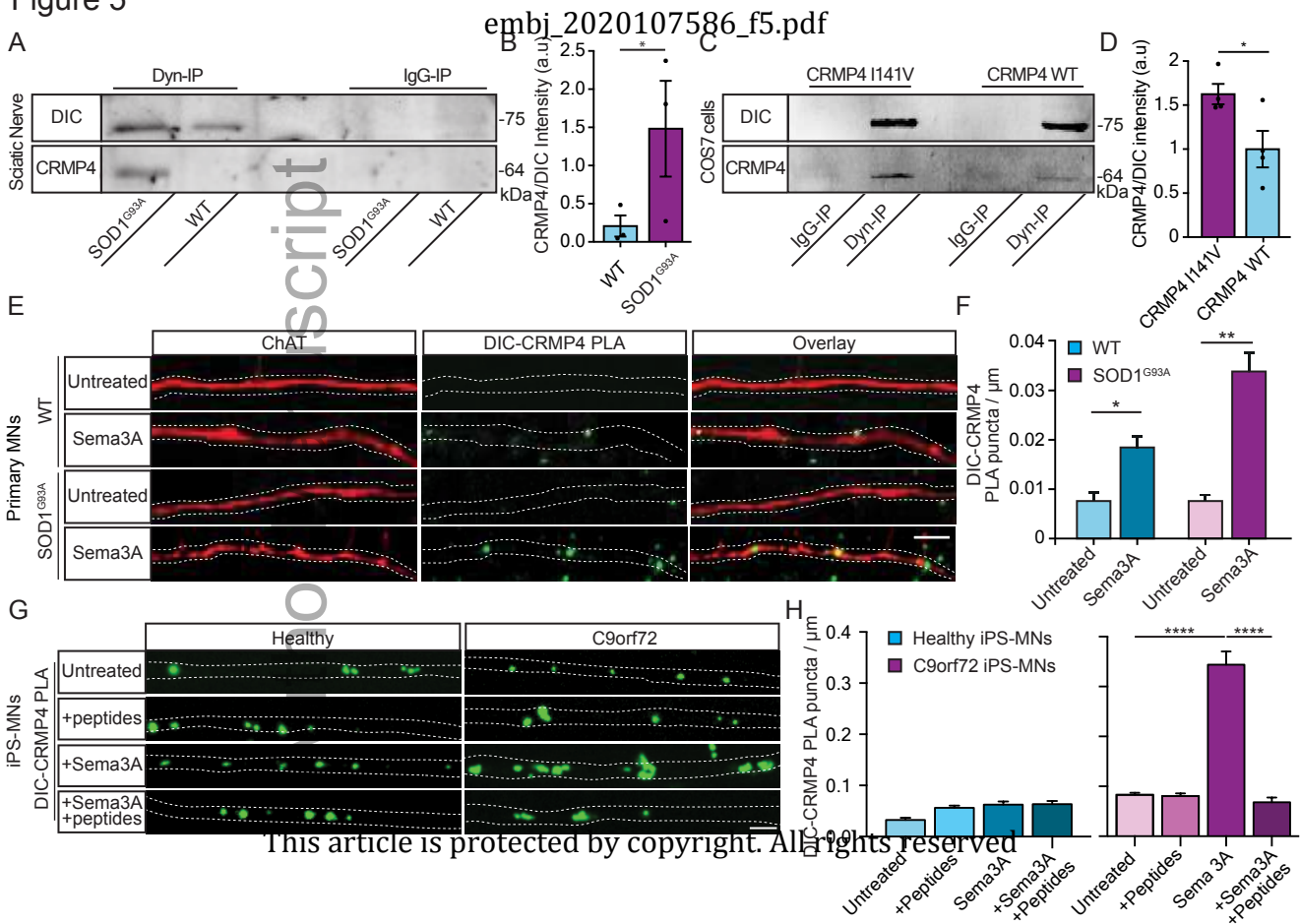
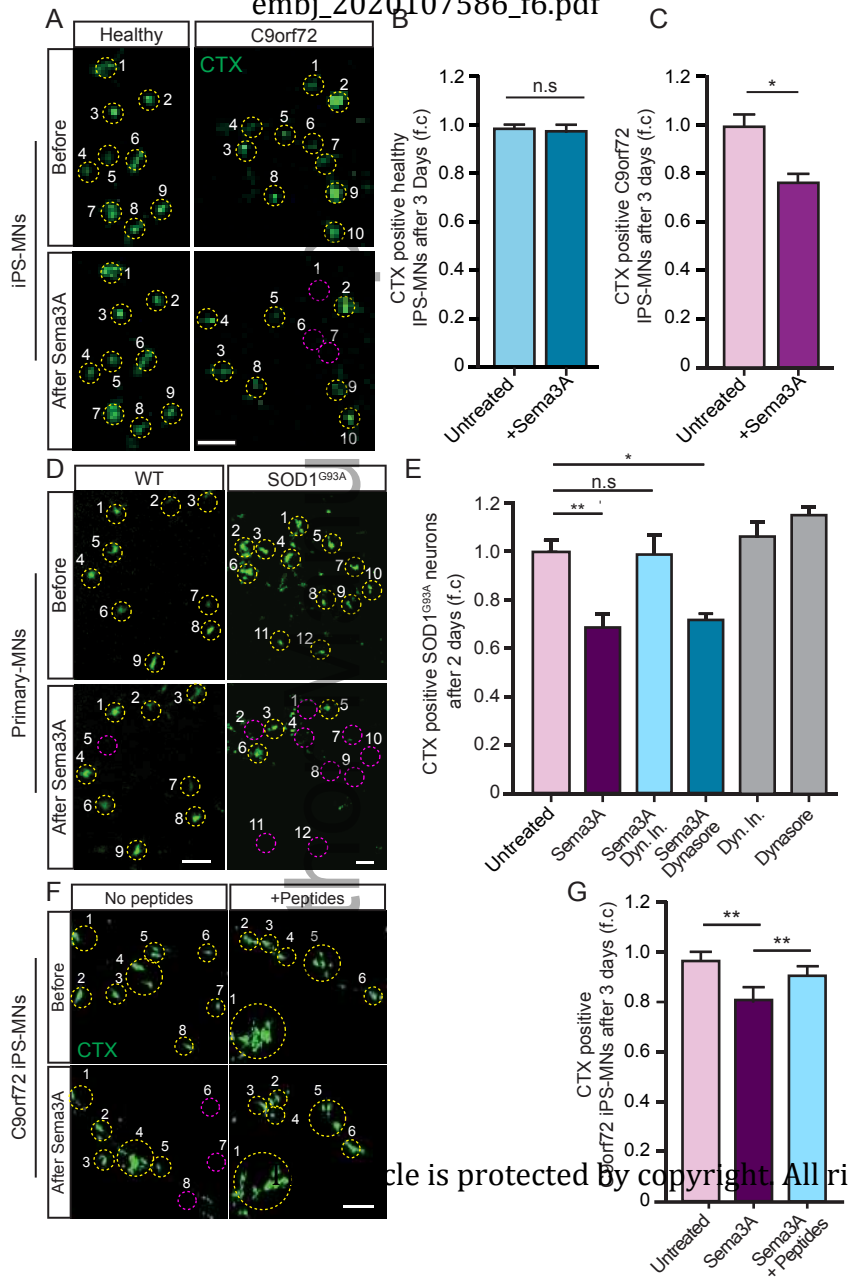


Figure 5





ALS MNs

