

Supplementary Fig. 1. Skeletal muscle SOD1 expression and late muscle denervation in fast and slow progressing SOD1<sup>G93A</sup> mice. (A and B) Representative Immunoblot image and relative densitometric analysis of soluble and aggregated human and murine SOD1 protein expression in GCM muscles of C57SOD1<sup>G93A</sup> and 129SvSOD1<sup>G93A</sup> mice compared with NTG littermates (n = 4). Protein levels were normalised on the total amount of protein loaded. Data are expressed as the mean (± SEM) and analysed by 2-way ANOVA with uncorrected Fisher's LSD post-analysis.



Supplementary Fig. 2. Nicotinic Acetylcholine receptor morphology in fast and slow progressing mice. (A) Representative confocal micrographs and morphometric analysis of  $\alpha$ -Bungarotoxin (BTX) positive endplates on longitudinal sections of GCM in C57SOD1<sup>G93A</sup> mice, 129SvSOD1<sup>G93A</sup> mice and NTG littermates at 12 weeks of age. (B-F) Average area clusters (B), AChR area (C), AChR perimeter (D), Endplate area (E) and Endplate perimeter (F) have been analysed through NMJ-Morph (n = 4). Data are expressed as the mean (± SEM). Significance was calculated with Two-way ANOVA with uncorrected Fisher's LSD post-analysis (\* $P \le 0.05$ ; \*\* $P \le 0.01$ ; \*\*\* $P \le 0.001$ ).



Supplementary Fig. 3. Ex-vivo muscle-derive satellite cells proliferation in fast and slow-progressing mice. (A) Representative confocal micrographs showing the immunostaining for Ki67 (red) and DAPI (blue) on primary satellite cell (SC) cultures of C57SOD1<sup>G93A</sup> and 129SvSOD1<sup>G93A</sup> mice in growing medium for 72 h, compared with NTG littermates. Scale bar = 100 µm. (B) The proliferation index was calculated as No. of Ki67 and DAPI positive cells (n = 3). Data are reported by means ± SEM. Statistics were calculated by One-way ANOVA with uncorrected Fisher's LSD post-analysis. (C-E) Real-time qPCR for MyoD (C), AchRy (D) and AchRa1 (E) mRNA transcripts in primary SC cultures of C57SOD1<sup>G93A</sup> and 129SvSOD1<sup>G93A</sup> mice compared with NTG littermates (n = 3). Data are expressed as the mean (± SEM). Data were analysed by Two-way ANOVA with uncorrected Fisher's LSD post-analysis.



Supplementary Fig. 4. Muscle fibre composition of the two ALS murine models. (A and D) Representative confocal micrograph and longitudinal analysis of Lectin immunostained muscle fibre cross-sectional area (CSA) on GCM coronal sections of C57SOD1<sup>G93A</sup> mice 129SvSOD1<sup>G93A</sup> mice and relative NTG littermates (n =6). For each section, the percent of fibre dimension was calculated relative to the total number of muscle fibres counted by Muscle J. Data are expressed as the mean (± SEM). Significance was calculated with 2-way ANOVA with uncorrected Fisher's LSD post-analysis (\* $P \le 0.05$ ; \*\*\* $P \le 0.001$ ; \*\*\*\* $P \le 0.0001$ ). (E and H) Representative confocal micrograph and longitudinal analysis of fibre type composition on GCM coronal sections of C57SOD1<sup>G93A</sup> mice 129SvSOD1<sup>G93A</sup> mice and NTG littermates (n = 6). A mix of antibodies against I (red), IIA (green), IIB (blue), MyHCs and Lectin (white) were used; IIX muscle fibres are unstained (black). Percent of fibre types was calculated relative to the total number of muscle fibres counted by Muscle J. Data are expressed as the mean (± SEM). Significance was calculated with Two-way ANOVA with uncorrected Fisher's LSD post-analysis (\*\* $P \le 0.01$ ).



Supplementary Fig. 5. Muscle inflammatory signals in fast and slow progressing mice. (A-D) Real-time qPCR for IGF1 (A), TGF $\beta$ 1 (B), IFN $\gamma$  (C), CD11c (D) and CD8 (E) mRNA transcripts in GCM muscle of C57SOD1<sup>G93A</sup> and 129SvSOD1<sup>G93A</sup> mice compared with NTG littermates (n = 4). Data are expressed as the mean (± SEM). Significance was calculated with Two-way ANOVA with uncorrected Fisher's LSD post-analysis (\* $P \le 0.05$ ; \*\* $P \le 0.001$ ; \*\*\*\* $P \le 0.0001$ ).