

CORRECTION

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# Correction: Immune-mediated myogenesis and acetylcholine receptor clustering promote a slow disease progression in ALS mouse models

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Following publication of the original article [1], the authors reported that Fig. 7 needed to be amended.

The correct Fig. 7 has been provided in this Correction.

The original article [1] has been corrected.

## Reference

1. Margotta C, Fabbrizio P, Ceccanti M, et al. Immune-mediated myogenesis and acetylcholine receptor clustering promote a slow disease progression in ALS mouse models. *Inflamm Regen*. 2023;43:19. <https://doi.org/10.1186/s41232-023-00270-w>.

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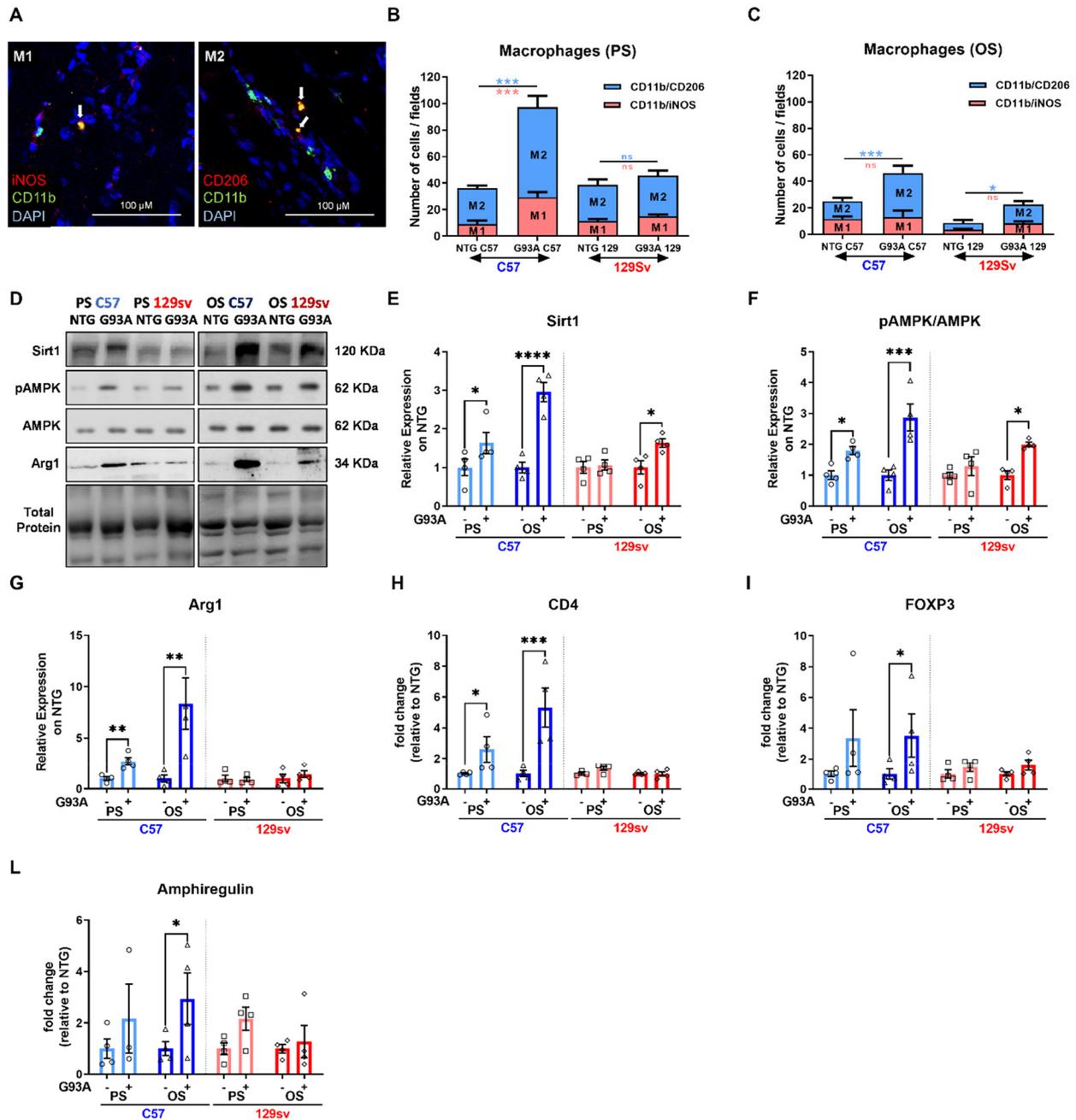
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**Fig. 7** The macrophage transition from M1- to M2-biased phenotype drives myogenesis in slow-progressing mice. **A** Representative confocal micrographs showing the immunostaining for M1 (iNOS + /CD11b + /DAPI +) and M2 (CD206 + /CD11b + /DAPI +) macrophages (MΦ) in longitudinal GCM sections of transgenic mice. **B** and **C** Percentage of M1 and M2 MΦ in the GCM of transgenic and NTG littermates at the presymptomatic (PS) (**B**) and onset (OS) (**C**) disease stages, calculated relative to the total number of CD11b + /DAPI + cells counted on five stereological 0.6 × 0.6 mm fields analysed for each slice. Data are expressed as the mean ± SEM (n = 4). Significance was calculated with one-way ANOVA with uncorrected Fisher's LSD post-analysis (\*p ≤ 0.05, \*\*\*p ≤ 0.001). **D–F** Representative immunoblot images (full blots images in Additional file 2) and relative densitometric analysis of **D** and **E** Sirt1-, **D** and **F** pAMPK/AMPK, **D** and **G** Arg1 protein expression in GCM muscles of C57SOD1G93A and 129SvSOD1G93A mice compared with NTG littermates (n = 4). Data are expressed as the mean (± SEM). Significance was calculated with 2-way ANOVA with uncorrected Fisher's LSD post-analysis (\*p ≤ 0.05; \*\*\*\*p ≤ 0.0001). **H–L** Real-time qPCR for CD4 (**H**), FOXP3 (**I**), amphiregulin (**L**) mRNA transcripts in GCM muscle of C57SOD1G93A and 129SvSOD1G93A mice compared with NTG littermates (n = 4). Data are expressed as the mean (± SEM)-fold change ratio between NTG C57 mice, C57SOD1G93A mice, 129SvSOD1G93A mice, and NTG 129 Sv mice. Significance was calculated with 2-way ANOVA with uncorrected Fisher's LSD post-analysis (\*p ≤ 0.05, \*\*p ≤ 0.01)