

## **Supplementary Materials**

**Title:** RNAi-mediated silencing of SOD1 profoundly extends survival and functional outcomes in ALS mice

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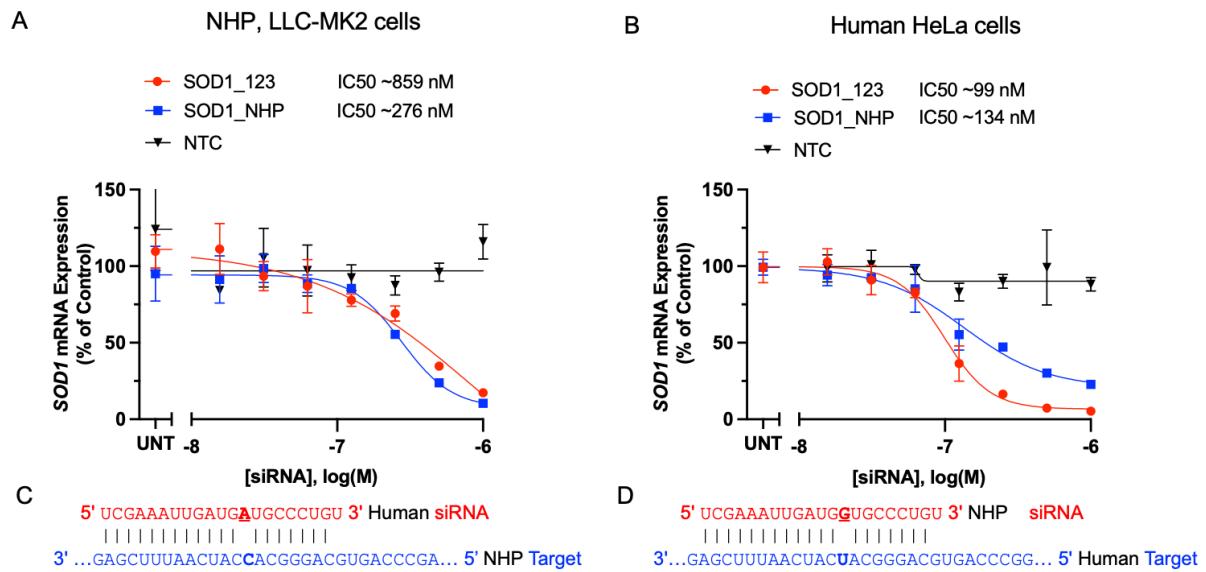
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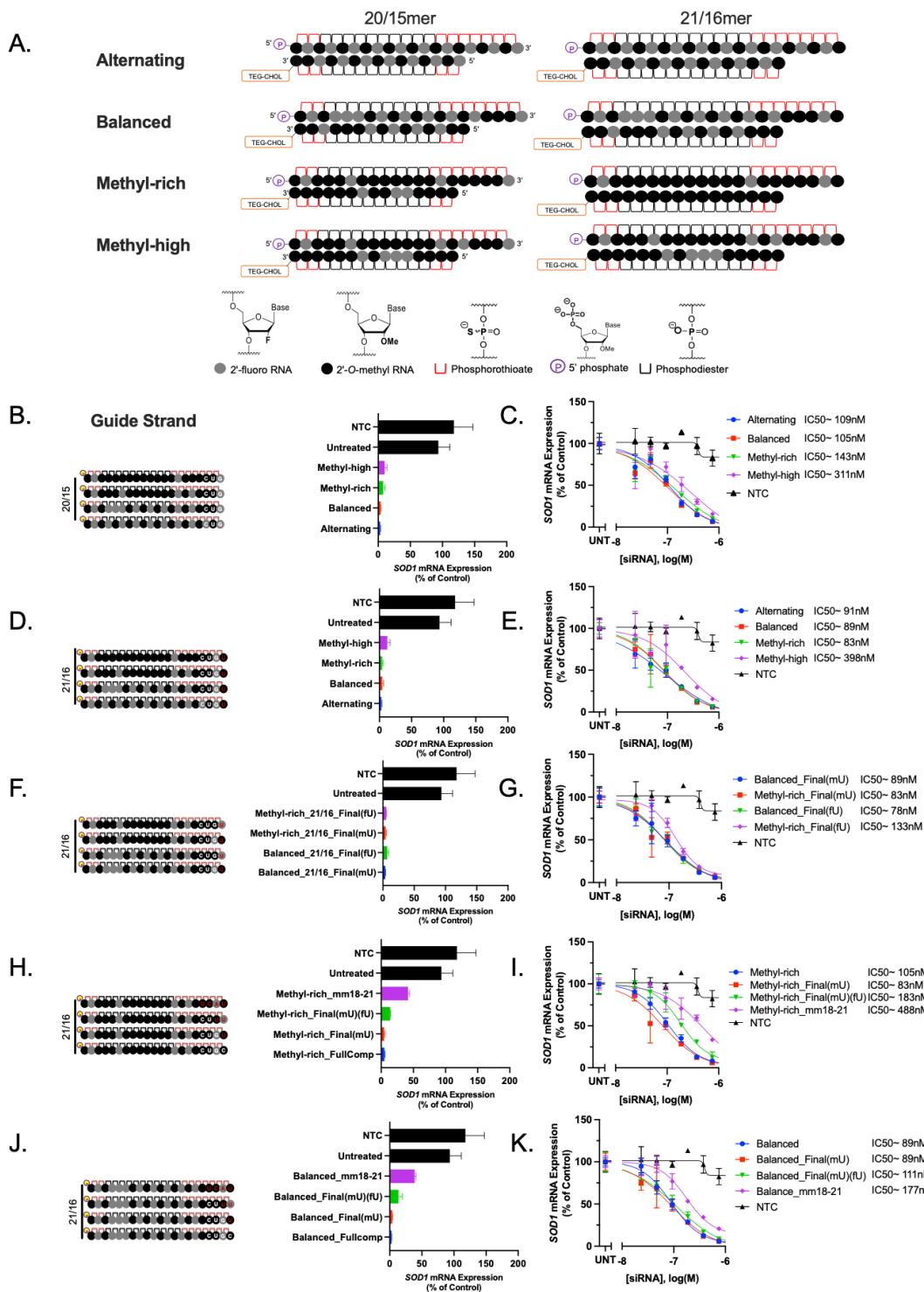
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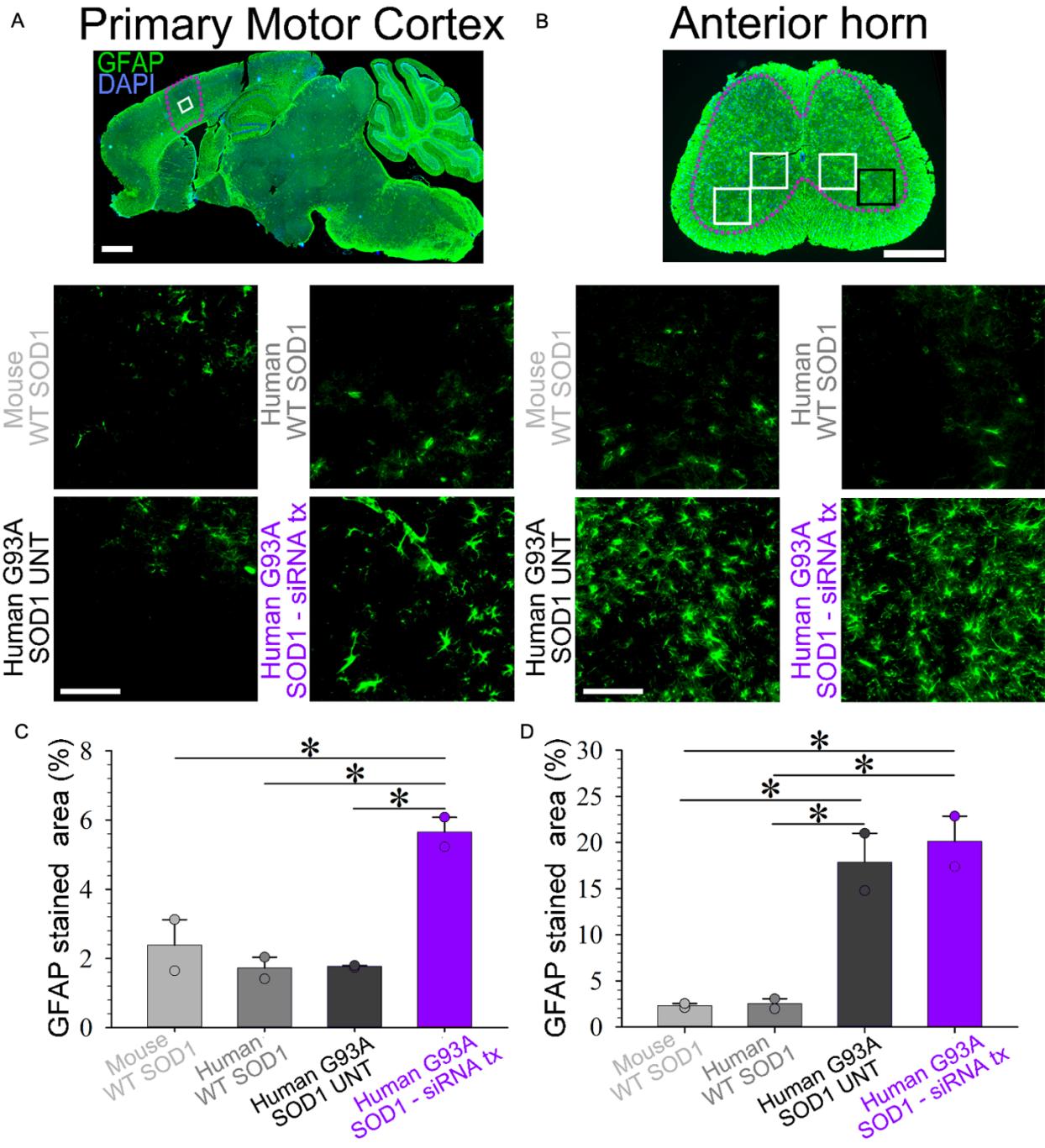


**Supplemental Figure 1: SOD1\_123 silences both human and non-human primate mRNA *in vitro*.** (A, B) 7-point dose-response curves for SOD1\_123 and SOD1\_NHP in (A) LLC-MK2 cells (NHP-derived) or (B) HeLa cells (human-derived) ( $n = 3$ , mean  $\pm$  SD). HeLa and LLC\_MK2 cells were treated with siRNAs at concentrations shown for 72 h (Passive uptake). mRNA levels were measured using QuantiGene, ( $n=3$ , mean  $\pm$  SD), UNT (untreated), NTC (non-targeting control). (C) Sequence of the human-targeting siRNA guide (red) against the NHP target mRNA (blue). Mismatch shown in bold. (D) Sequence of the NHP-targeting guide strand (red) against the human target mRNA (blue). Mismatch shown in bold. IC<sub>50</sub> values are shown above the graph. IC<sub>50</sub> values were calculated using the nonlinear least squares method (GraphPad Prism).



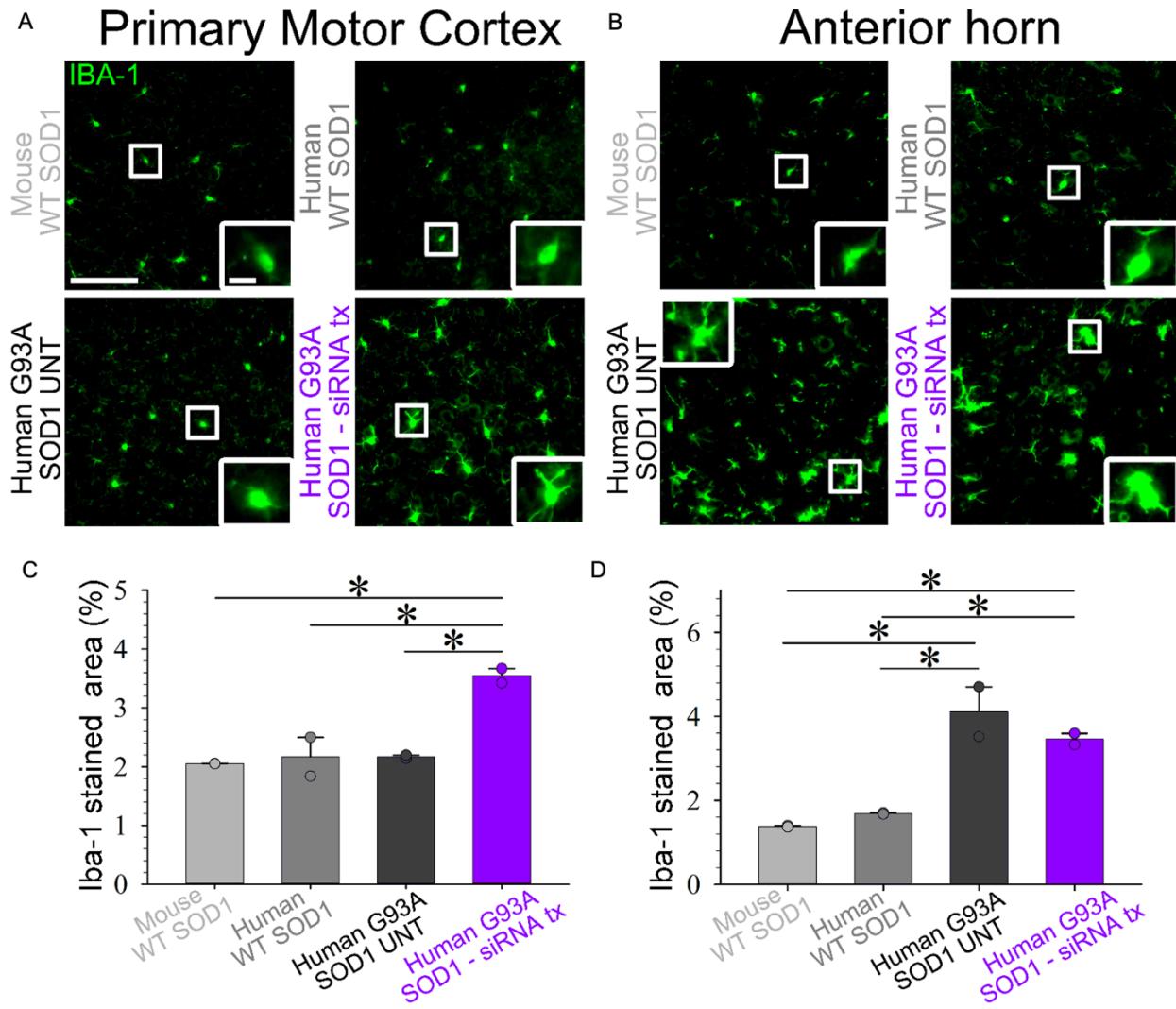
**Supplemental Figure 2: Chemical optimization of SOD1\_123 reveals multiple potent configurations. (A)** Schematic of siRNA patterns (top), and chemical modifications (bottom). **(B)**

HeLa cells treated by passive uptake with SOD1\_123 in four distinct patterns. The left panel shows diagram of the guide strands. **(C)** 7-point dose-reponse curves for siRNAs in B. **(D)** HeLa cells treated (by passive uptake) with SOD1\_123 **(E)** 7-point dose-response curves for siRNAs described in D. **(F)** HeLa cells treated (by passive uptake) with the modification patterns shown **(G)** 7-point dose-response curves for siRNAs described in F. **(H)** HeLa cells treated (by passive uptake) with four SOD1\_123 siRNAs in the Methyl-rich pattern, **(I)** 7-point dose-response curves for siRNAs described in F. **(J)** As in H but in the Balanced pattern. **(K)** Dose-dependent analysis of siRNAs described in H but in the Balanced pattern. Top dose 1.5  $\mu$ M, SOD1 mRNA evaluated at 72 hours, QuantiGene, (n=3, mean  $\pm$  SD). NTC (nontargeting control siRNA), UNT (untreated). The target site and IC<sub>50</sub> values are shown in the graphs. IC<sub>50</sub> values were calculated using the nonlinear least squares method (GraphPad Prism).



**Supplemental Figure 3: Astrogliosis in the cortex but not lumbar spinal cord of di-siRNA treated G93A mice versus untreated G93A mice. (A, B)** GFAP-stained sagittal section of brain (A) and transverse lumbar spinal cord (B) images with rectangles indicate the regions of interest (ROIs) used for quantification. **(C)** Representative images of layer V of primary motor cortex

and anterior horn. Scale bar=100  $\mu$ m. **(D, E)** Quantification of GFAP signal in layer V of primary motor cortex **(D)** and anterior horn of lumbar spinal cord **(E)**. Data in the bar graphs are shown as mean  $\pm$ SEM n=2 per group. One-way ANOVA with post hoc Holm-Šídák test.



**Supplemental Figure 4: Di-siRNA treatment activates cortical microglia and attenuates microgliosis in the anterior horn.** **(A)** Representative images and insets of Iba-1 stained microglia in Motor cortex. Scale bar=100  $\mu$ m Scale bar=15  $\mu$ m (inset). **(B)** Representative images and insets of Iba-1 stained microglia in anterior horn. Scale bar=100  $\mu$ m, scale bar in inset=15  $\mu$ m. **(C)** Quantification of Iba-1 stained microglia in layer V of primary motor cortex and **(D)** anterior horn of lumbar spinal cord. Data in the bar graphs are shown as mean  $\pm$ SEM n=2 per group. One-way ANOVA with post hoc Holm-Šídák test.

