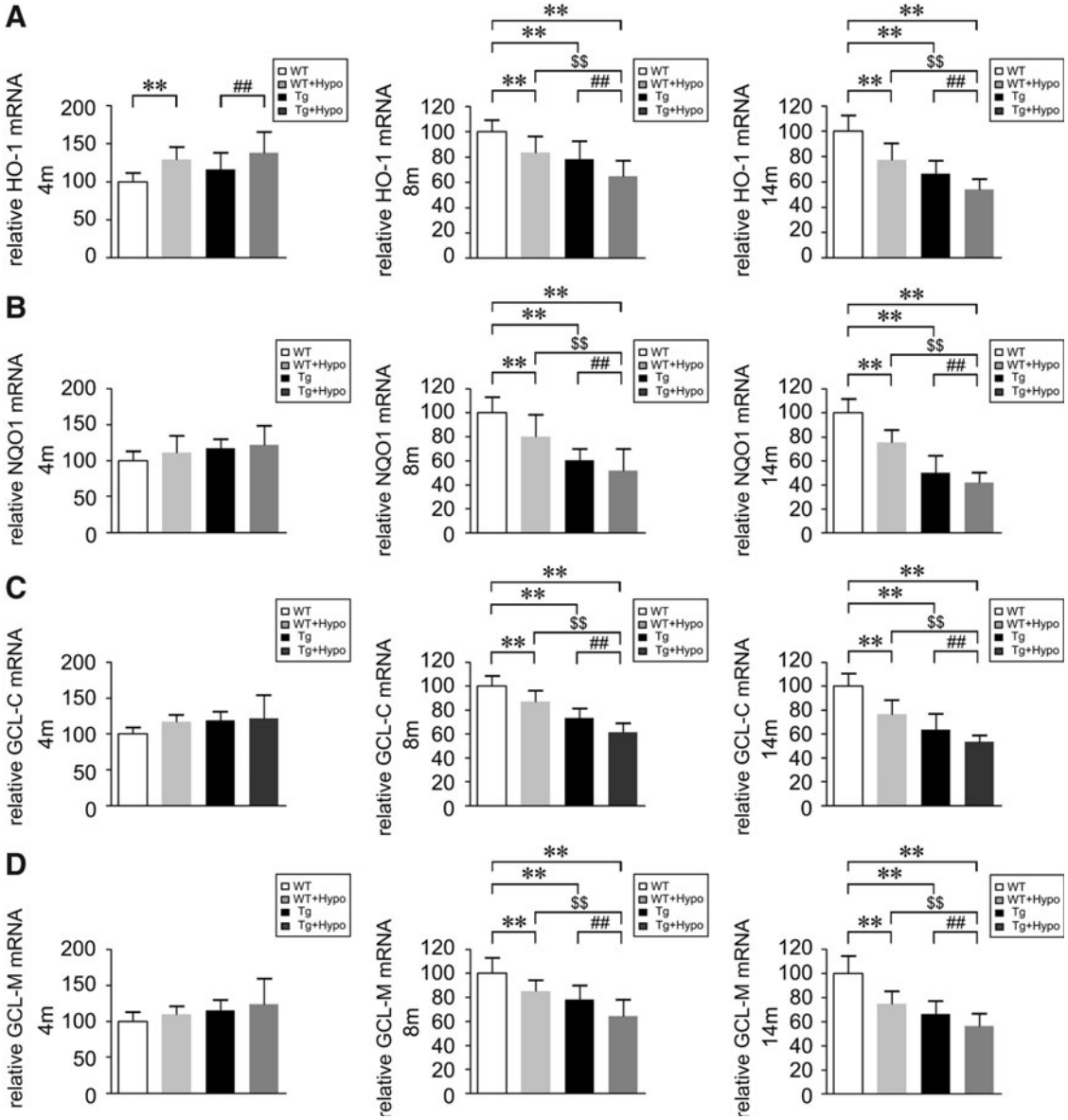

SUPPLEMENTARY FIG. S2. Chronic hypoxia intervention impaired Nrf2 target genes mRNA expression in the aging mouse brain. After 2 months of hypoxia treatment, the relative alterations of mRNA expression of Nrf2 target genes, heme oxygenase-1 (HO-1), nicotinamide adenine dinucleotide phosphate quinone oxidoreductase-1 (NQO1), catalytic subunits of γ-glutamyl cysteine ligase (γGCL-C), and modulatory subunits of γ-glutamyl cysteine ligase (γGCL-M) were analyzed by RT-PCR. **(A)** An elevation of HO-1 mRNA expression was observed in both 4-month-old transgenic (Tg) APP/PS1 and age-matched WT mice brain. However, at 8 and 14 months of age, HO-1 mRNA expression was reduced in the Tg group compared with WT mice. Hypoxia triggered significant decreases of HO-1 mRNA expression in both the WT and Tg mice brain at 8- and 14 months of age. The decreases of HO-1 mRNA levels in Hypoxia-treated Tg mice were significantly aggravated. **(B–D)** There was no statistical difference in the mRNA expression of NQO1, γGCL-C, and γGCL-M in both genotypes between Hypoxia and control groups at 4 months of age. Hypoxia was significantly reduced in the mRNA expression of NQO1, γGCL-C, and γGCL-M in 8- and 14-month-old WT and Tg mice. NQO1, γGCL-C, and γGCL-M and mRNA levels were less in the Tg group than in the WT group, and hypoxia exposure exacerbated the down-regulation of the expression in the Tg mice brain. $^{**}p < 0.01$ *versus* WT group, $^{\#\#}p < 0.01$ *versus* Tg group, and $^{\$\$}p < 0.01$ *versus* WT + Hypo group by two-way ANOVA, $n = 6$–8 in each group. Values represent the mean ± SEM.