

Figure S1: Enhanced level of Nrf2 in the hippocampus in the APP/PS1 mice. (A) Nrf2 mice genotype (upper, n=3/genotype) and APP/PS1 mice genotype (lower, n=3/genotype). (B) Immumohistochemical staining with anti-Nrf2 in hippocampus CA1, CA3 and DG in the WT (APP/PS1<sup>-/-</sup>, Nrf2<sup>+/-</sup>) and AT (APP/PS1<sup>+/-</sup>, Nrf2<sup>+/-</sup>) genotype mice (scale=50 $\mu$ m). (C) Average optical density of Nrf2 immunoreactivity in hippocampus was significantly different between WT (APP/PS1<sup>-/-</sup>, Nrf2<sup>+/-</sup>) and AT (APP/PS1<sup>+/-</sup>, Nrf2<sup>+/-</sup>) genotype mice (n=3/genotype, \*P < 0.05). (D) qRT-PCR determination of hippocampus Nrf2 mRNA levels showed significantly between WT (APP/PS1<sup>-/-</sup>, Nrf2<sup>+/-</sup>) and AT (APP/PS1<sup>+/-</sup>, Nrf2<sup>+/-</sup>) genotype mice (n=5/genotype, \*P < 0.05). Data is represented as means±SD and were analysed by t-test (C, D).

	MWM		IHC/IF		qRT-PCR		ELISA	
	М	F	М	F	М	F	Μ	F
WT	4	2	4	2	4	2	0	0
Nrf2-KO	6	2	4	2	4	2	0	0
AT	6	6	3	3	3	3	3	2
AT/Nrf2-KO	6	7	3	3	3	3	2	3

Table.S1 The information of mice and their use for various protocols

Table S1: We generated four genotypes (WT, Nrf2-KO, AT and AT/Nrf2-KO). The number represented the number of mice with different genotypes in the corresponding expriments. MWM: Morris water maze test; IHC/IF: Immunohistochemistry/ immunofluorescence; qRT-PCR: quantitative real-time PCR; ELISA: enzyme-linked immunosorbent assay; M: male; F: female; WT: wild-type mice (APP/PS1<sup>-/-</sup>, Nrf2<sup>+/-</sup>); Nrf2-KO: Nrf2-knockout mice (APP/PS1<sup>-/-</sup>, Nrf2<sup>-/-</sup>); AT: APP/PS1 transgenic mice (APP/PS1<sup>+/-</sup>, Nrf2<sup>+/-</sup>); AT/Nrf2-KO: APP/PS1/Nrf2-knockout mice (APP/PS1<sup>+/-</sup>, Nrf2<sup>-/-</sup>).