

Figure S1. The effect of chronic corticosterone (CORT) treatment on behaviors, NSC apoptosis and neuronal BDNF. (A) Timeline of the experimental procedure. **(B)** Line chart showing body weight gain. Control (n = 17), CORT (n = 6), $P < 0.001$. **(C)** Body weight gain in the eighth week. Control (n = 17), CORT (n = 16), $P = 0.0002$. **(D)** Distance

moved while assessing locomotor activity. $n = 12$ per group, $P = 0.4033$. **(E)** Time spent in the closed arms of the EPM. $n = 12$ per group, $P = 0.0003$. **(F)** Distance moved in the EPM. $n = 12$ per group, $P = 0.6474$. **(G)** Exploration time for object A1 in the training stage of the NOR test. $n = 12$ per group, $P = 0.6176$. **(H)** Exploration time for object A2 in the training stage of the NOR test. $n = 12$ per group, $P = 0.4432$. **(I)** Preference index in the training stage of the NOR test. Control ($n=12$), $P = 0.4330$. **(J)** Representative images of control and CORT DG with triple immunostaining of SOX2⁺ (gray), GFAP⁺ (green), and cleaved-caspase 3⁺ (red) cells. Arrowheads indicate SOX2⁺/GFAP⁺/cleaved-caspase 3⁺ cells. **(K)** Quantification of SOX2⁺GFAP⁺cleaved-caspase 3⁺ cells. $n = 4$ mice per group, $P = 0.0182$. Scale bar = 20 μm . Data are presented as the mean \pm SEM. Two-tailed unpaired t -test was used to identify statistically significant differences between datasets ($*P < 0.05$, $**P < 0.01$, $***P < 0.001$ compared to the control group). n.s., non-significant difference.

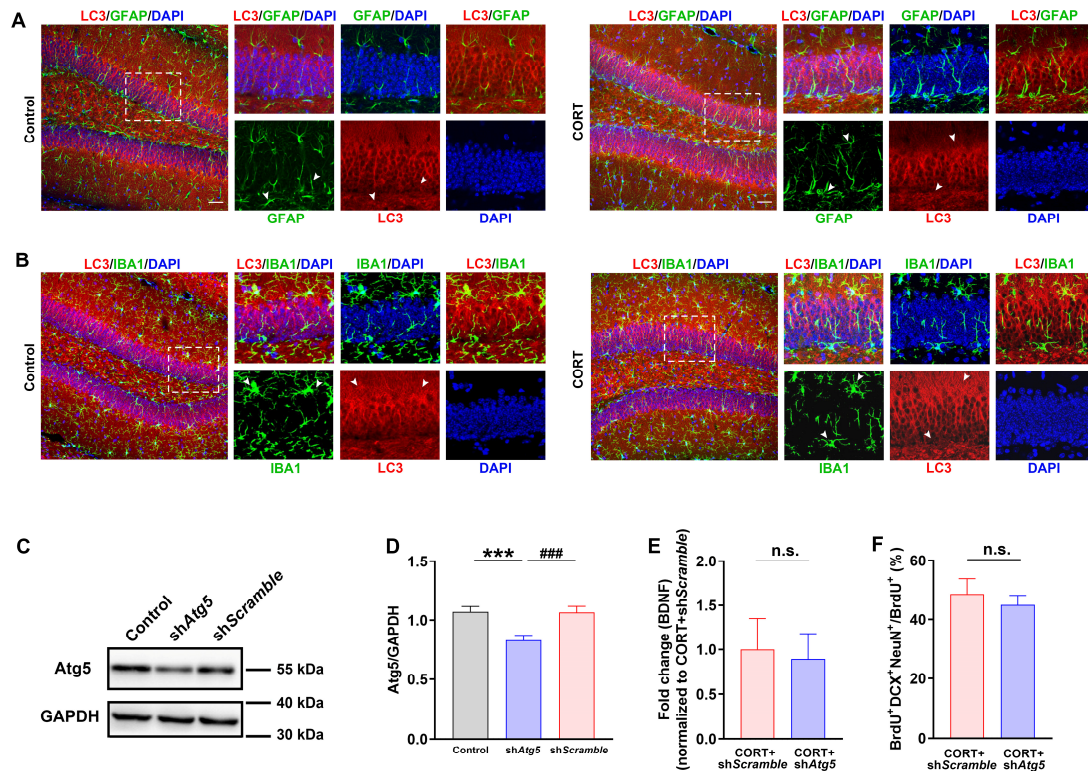


Figure S2. The effect of chronic CORT on autophagy in astrocytes and microglia in mice. (A) Representative images of control and CORT DG with double immunostaining of LC3⁺ (red) and GFAP⁺ (green) cells. The boxed areas are enlarged in the right panels. White arrowheads indicate LC3⁺/GFAP⁺ cells. (B) Representative images of control and CORT DG with double immunostaining of LC3⁺ (red) and IBA1⁺ (green) cells. The boxed areas are enlarged in the right panels. White arrowheads indicate LC3⁺/IBA1⁺ cells. (C) Representative western blots analyzing protein expression in control, control+sh*Atg5* and control+sh*Scramble* groups. (D) Quantification of *Atg5* expression. $n = 3$ mice per group, $P < 0.0001$. (E) Quantification of BDNF gene mRNA expression. $n = 4$ mice per group, $P = 0.8135$. (F) Quantification of BrdU⁺DCX⁺NeuN⁺/BrdU⁺ cells. $n = 3$ mice per group, $P = 0.5394$. Data are presented as mean \pm SEM. The two-tailed unpaired *t*-test was used to identify statistically significant differences between datasets (*** $P < 0.001$ compared

to control group, $###P < 0.001$ compared to CORT+sh*Scramble* group). n.s., non-significant difference.