

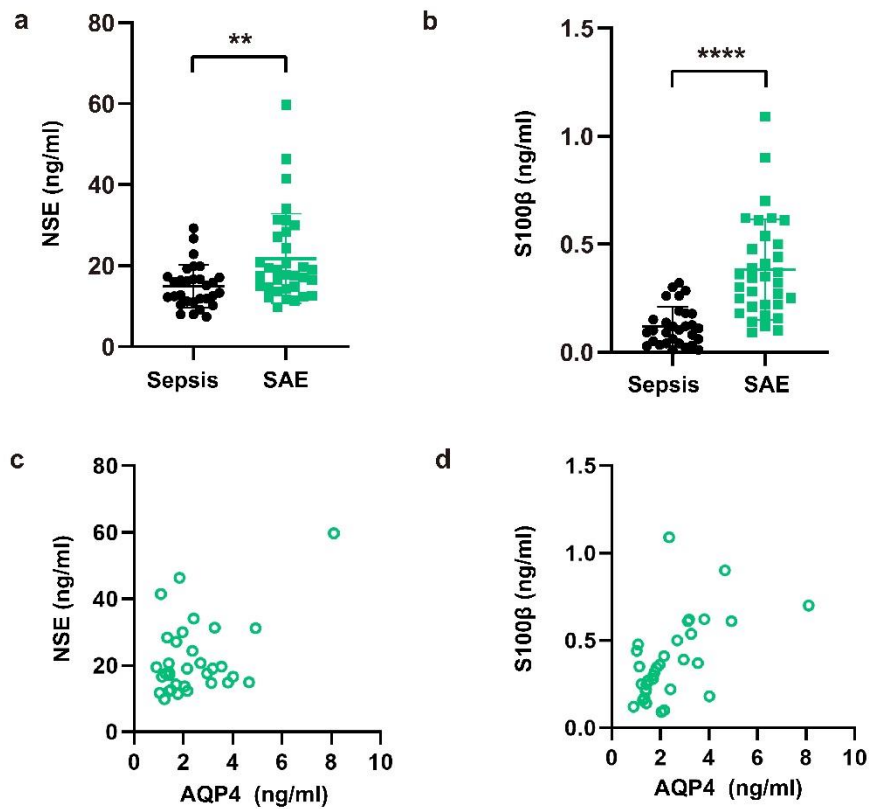
**Table S1 Participant Characteristics**

Characteristics	Sepsis group (n=27)	SAE group (n=33)	P
Sex, (male/female)	10/17	20/13	0.069
Age, median (IQR), y	70 (21-90)	76 (40-90)	0.144
Temperature, °C	37.76±1.13	37.65±1.21	0.719
Heart rate, /min	105.4±21.27	98.48±19.97	0.202
Shock (yes/no)	11/16	18/15	0.287
APACHEII score <sup>a</sup>	16.74±6.24	21.42±6.46	0.006
SOFA score <sup>b</sup>	7.30±4.39	8.36±4.23	0.343
Length of ventilator, d	5.68±4.60	76.2±182.5	0.049
Length of ICU stay, median (IQR), d	12 (5-26)	16 (8-38)	0.005
Mortality at 28 d, No. (%)	9 (33.3%)	22 (66.7%)	0.010
Mortality at 60 d, No. (%)	12 (44.4%)	22 (66.7%)	0.084

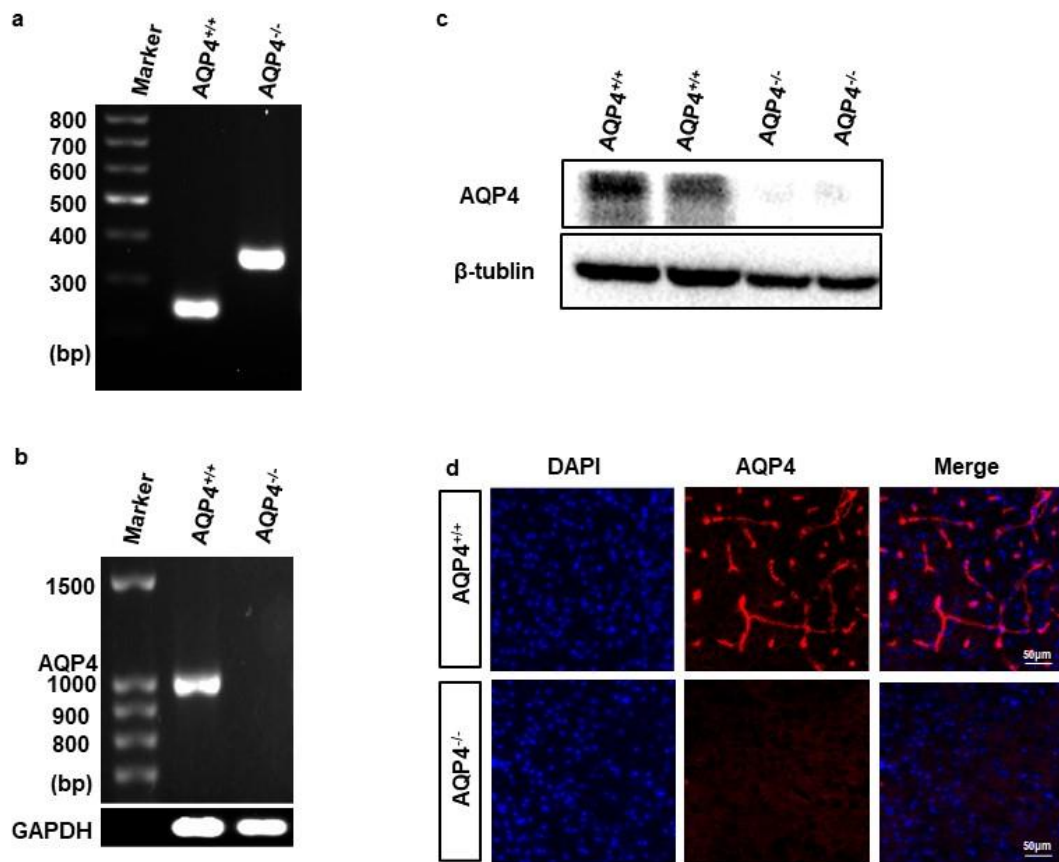
**Table S1:** Abbreviations: IQR, interquartile range.

<sup>a</sup>The Acute Physiology and Chronic Health Evaluation (APACHE) II score ranges from 0 to 71, with higher scores indicating greater risk of hospital death. A score of 25 indicates a mortality probability of approximately 50%.

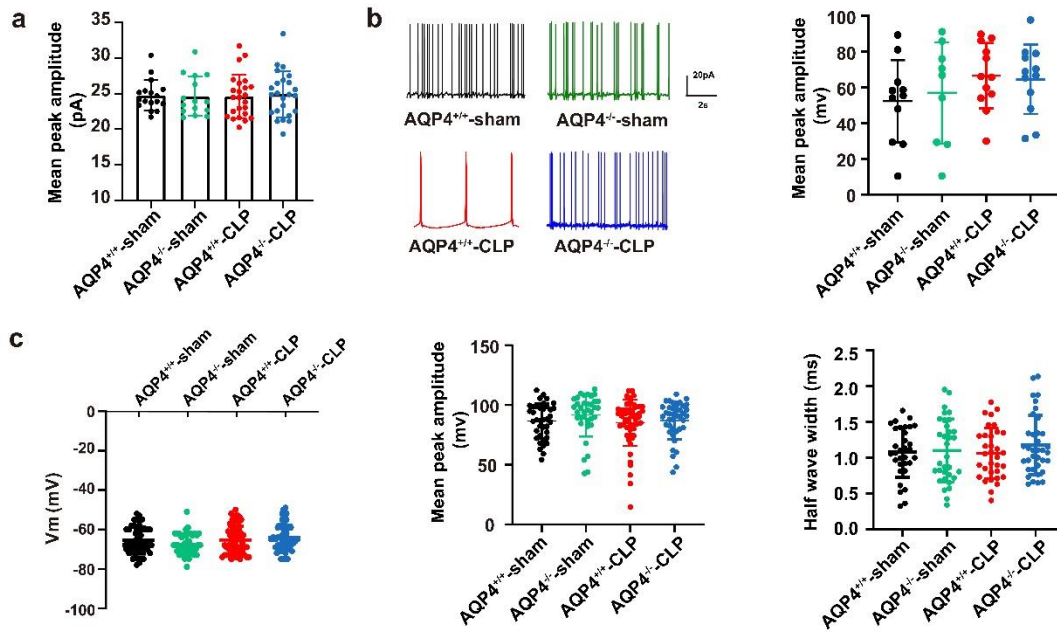
<sup>b</sup>The Sequential Organ Failure Assessment (SOFA) score ranges from 0 to 24, with higher scores indicating greater severity of organ dysfunction. SOFA scores between 7 and 9 are associated with a 40% to 50% mortality risk.



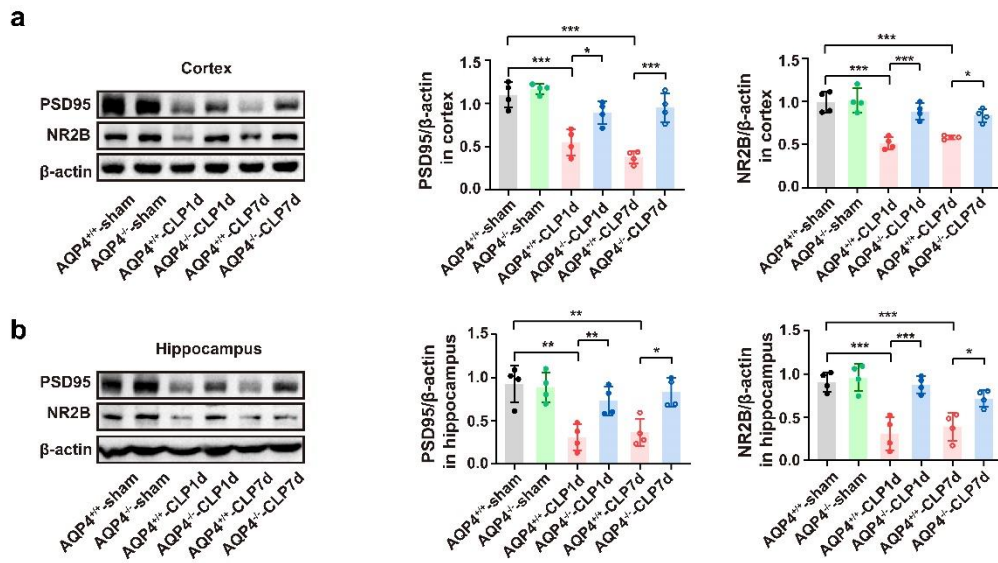
**S1. NSE, S100β was elevated in peripheral blood of patients with sepsis associated encephalopathy. a, b.** The change of NSE, S-100β levels in peripheral blood of sepsis patients and SAE patients were detected by ELSA. Sepsis patients without encephalopathy (n=27), sepsis related encephalopathy (n=33). Data are represented as the mean  $\pm$  SD. \*\*  $p < 0.01$ , \*\*\*\*  $p < 0.0001$ , Mann–Whitney test. **c, d.** Pearson correlation analysis between AQP4 and NSE, S-100β in patients with sepsis associated encephalopathy.



**S2. The genotyping of AQP4<sup>+/+</sup> and AQP4<sup>-/-</sup> mice at gene level, protein level and morphological level.** **a.** Genotyping of AQP4<sup>+/+</sup> and AQP4<sup>-/-</sup> mice. The size of the AQP4<sup>+/+</sup> amplicon is 240 bp, and the size of the AQP4<sup>-/-</sup> amplicon is 320 bp. **b.** The mRNA levels of AQP4 were determined by RT-PCR in AQP4<sup>+/+</sup> and AQP4<sup>-/-</sup> mice. AQP4<sup>-/-</sup> mice have no band on the agarose gel. **c.** The representative Western blot band of AQP4 in AQP4<sup>+/+</sup> and AQP4<sup>-/-</sup> mice. AQP4<sup>-/-</sup> mice have no AQP4 protein band. **d.** Representative immunofluorescence images of AQP4<sup>+/+</sup> and AQP4<sup>-/-</sup> mice. AQP4<sup>+/+</sup> and AQP4<sup>-/-</sup> mice were stained with anti-AQP4 antibody (red), with nuclei stained with DAPI (blue). Scale bar, 50μm.

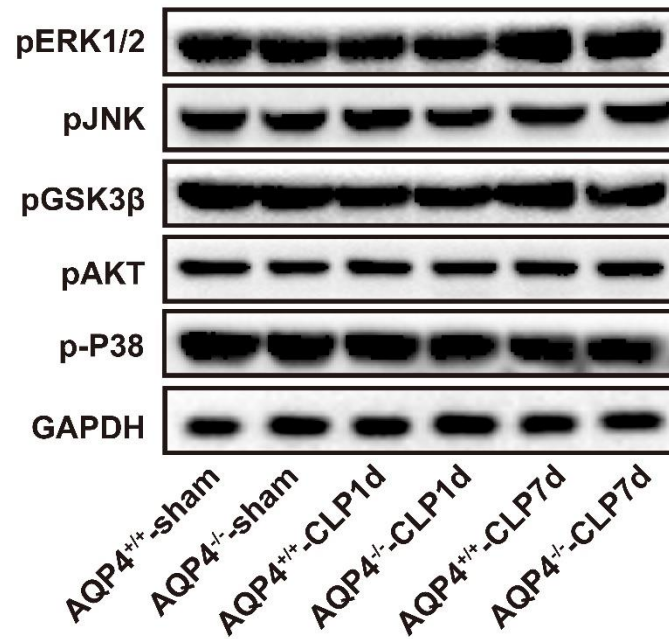


**S3. No significant different data of electrophysiology and recording. a.** Quantification of the mean peak amplitude of sEPSC. Neurons from 6 mice. **b.** Representative sAP of different groups (*left*) and quantification of sAP mean peak amplitude (*right*). Neurons from 6 mice. **c.** Quantification of eAP membrane potential(*left*) and quantification of the mean eAP peak amplitude(*middle*), quantification of the eAP half wave width (*right*). Neurons from 6 mice for each group. Data are presented as mean  $\pm$  SD. There were no statistically significant differences among groups.  $p > 0.05$ , two-way ANOVA with Tukey's post hoc test.



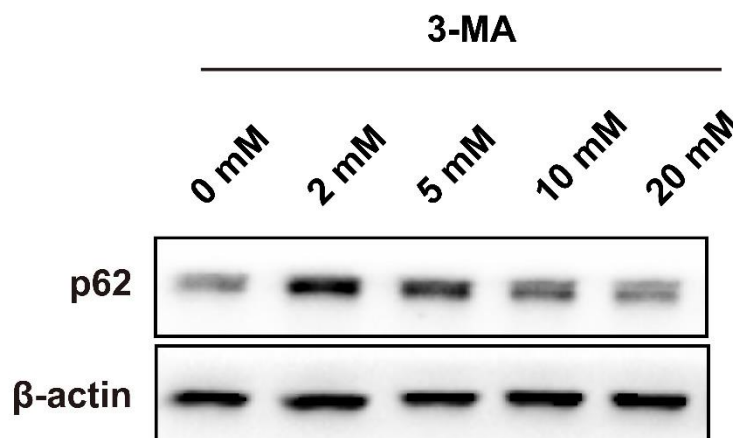
#### S4. AQP4 knockout alleviate the decline of cognitive function-related molecules

**in septic mice. a.** Expressions of PSD95 and NR2B in cortex were analyzed by western blots.  $n=4$  mice for each group. **b.** Expressions of PSD95 and NR2B in hippocampus were analyzed by western blots.  $n=4$  mice for each group. Data are presented as mean  $\pm$  SD. \*  $p<0.05$ , \*\*  $p<0.01$ , \*\*\*  $p<0.001$ , one-way ANOVA with Tukey's post hoc test.



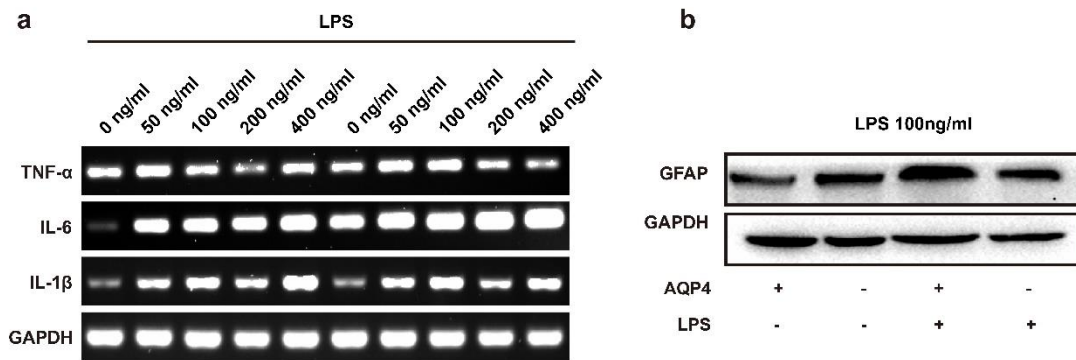
**S5. AQP4 has no regulatory effect on other autophagy signaling pathways.**

Representative Western blot band for p-ERK1/2, pJNK, pGSK3 $\beta$ , pAKT, p-P38.



**S6. 3-MA drug concentration fumble.** Representative bands of p62 protein expression levels of primary astrocytes treated with 3-MA at different concentrations.

At 2 $\mu$ M, the expression level of p62 was the highest.



**S7. To explore LPS stimulated primary astrocyte concentration. a.** Representative bands of TNF- $\alpha$ , IL-6 and IL-1 $\beta$  mRNA expression levels in astrocytes which stimulated by different concentrations of LPS. **b.** Representative Western blot band of GFAP of primary astrocytes treated with 100ng/ml LPS. The GFAP expression level of AQP4<sup>+/+</sup>-LPS significantly increased, while AQP4 knockout, the GFAP expression level was decreased.