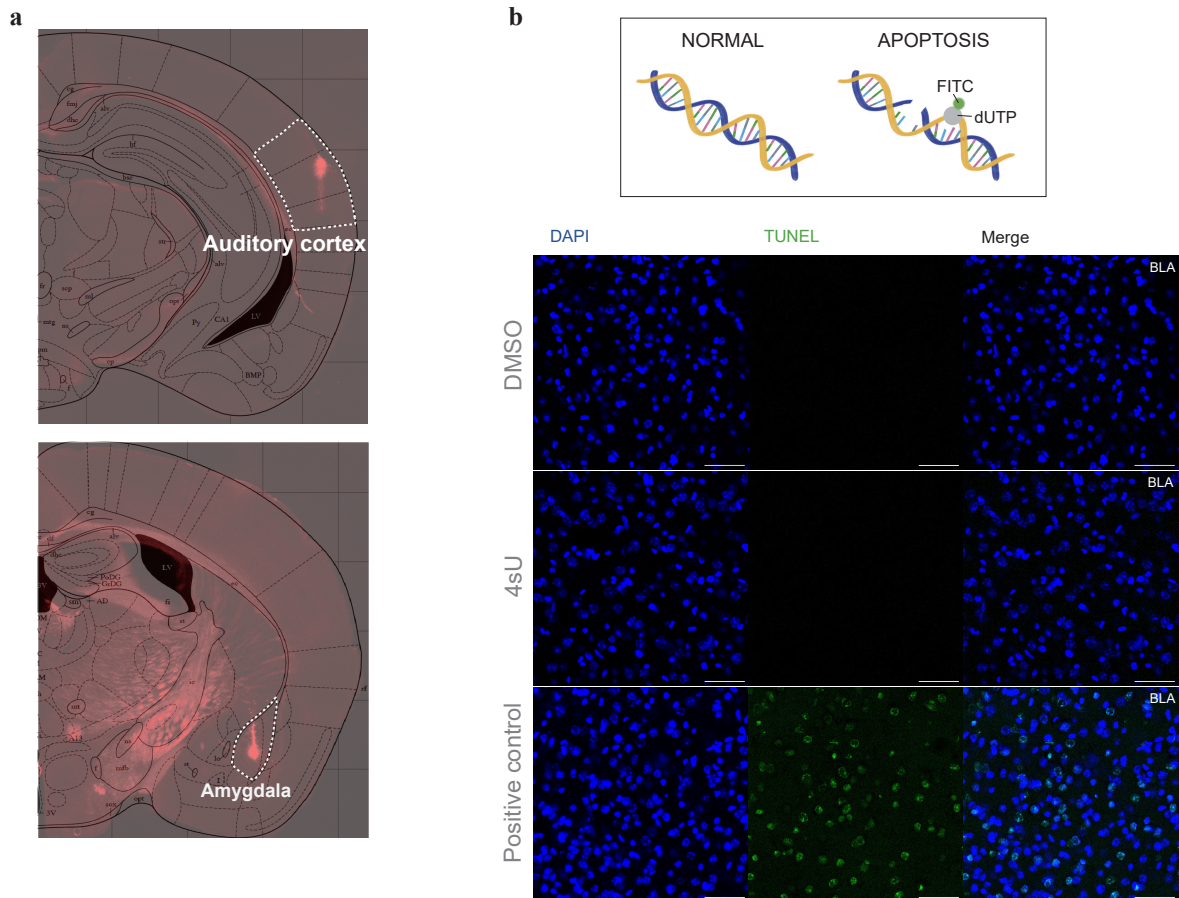


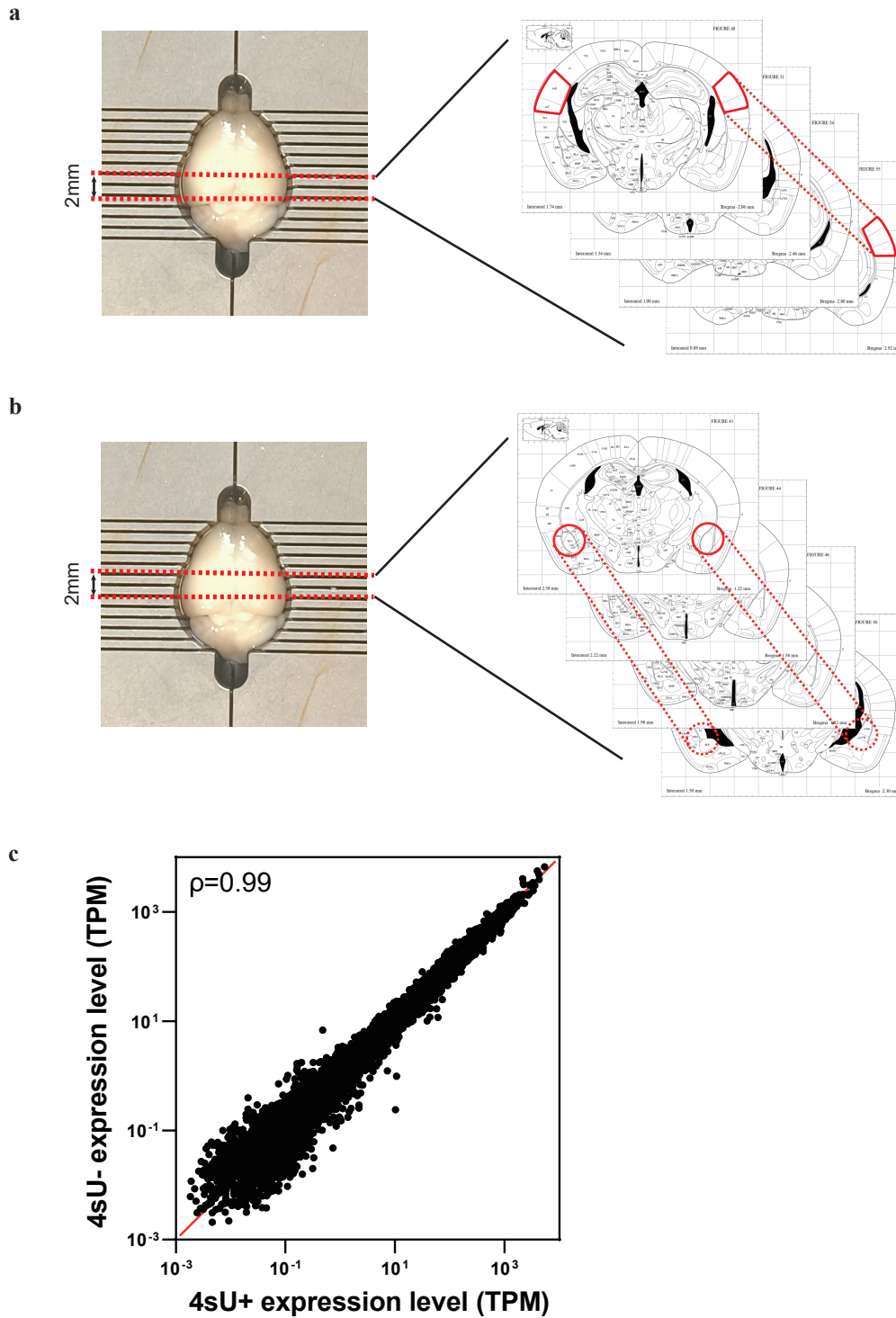
Supp. Fig. 1



(a) Injection sites of DMSO or 4 sU in the auditory cortex and amygdala. Signal of Dil denoted the injection trajectory.

(b) TUNEL staining of brain slices for positive control (top panels), and brain slices with DMSO (middle) and 4sU (bottom) injections in the amygdala. Green signals denoted dead cells. Scale bar = 50 μ m.

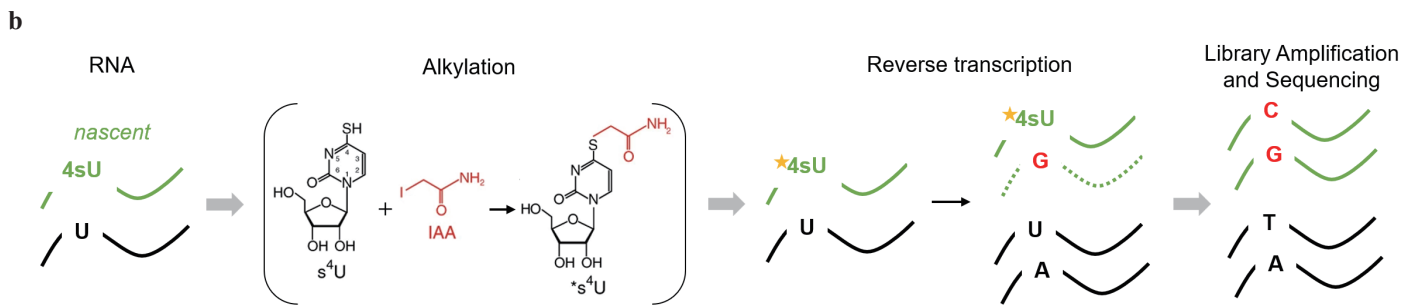
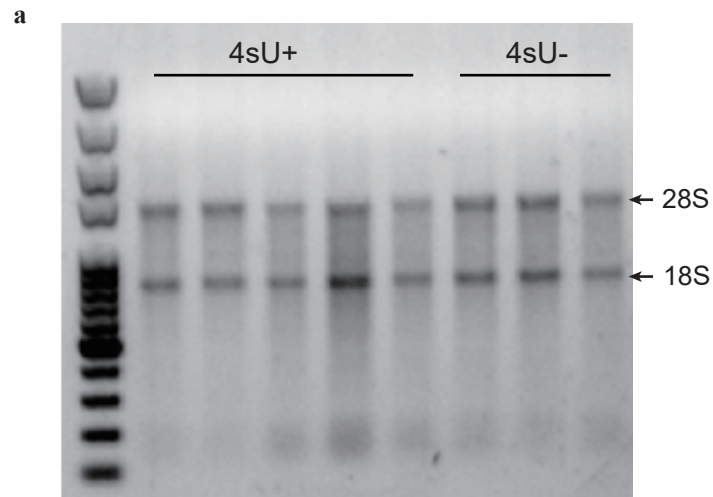
Supp. Fig. 2



(a) Schematic showing position of auditory cortex tissue for RNA extraction.

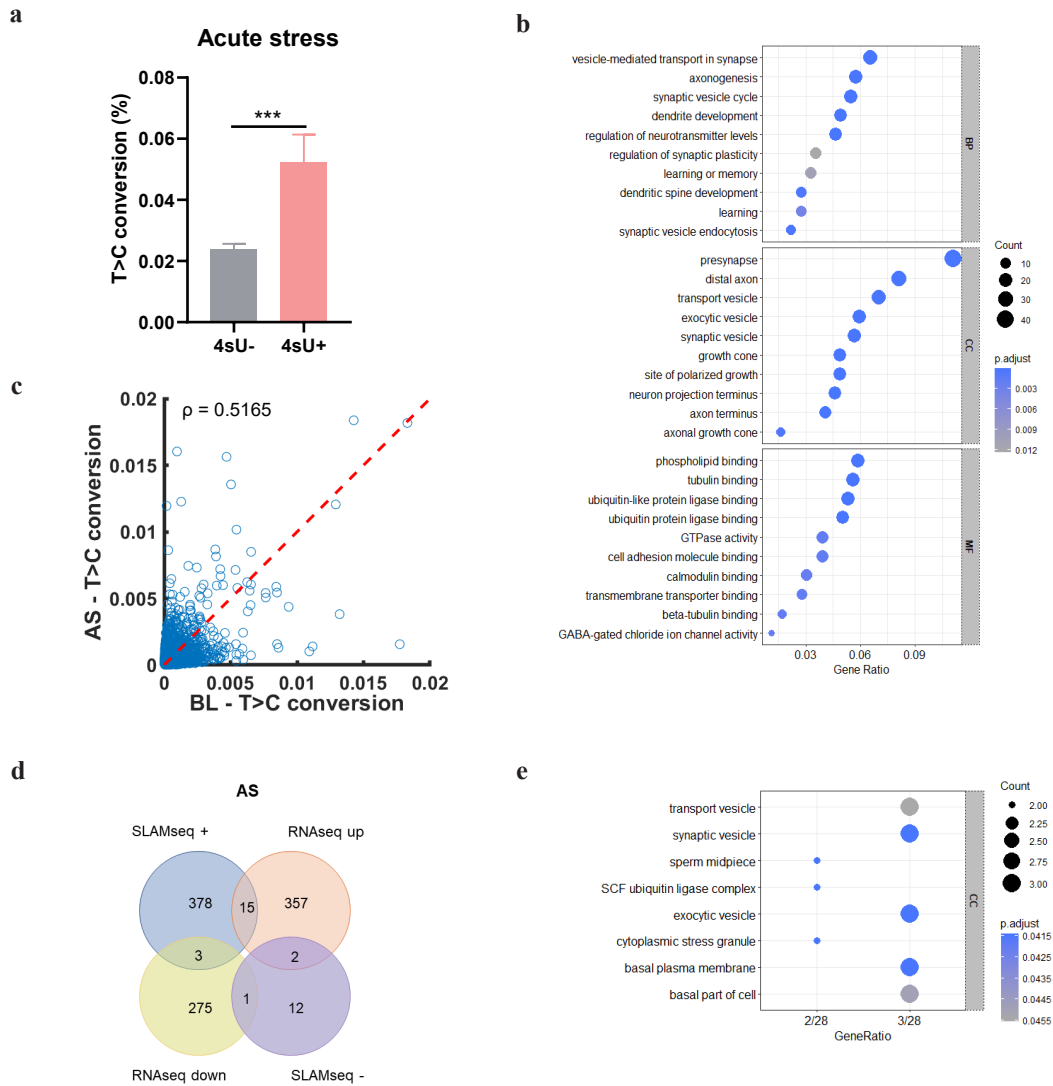
(b) Schematic showing position of amygdala tissue for RNA extraction.

(c) Correlation of RNA levels extracted from DMSO and 4sU injected amygdala samples. ρ , spearman correlation coefficient.



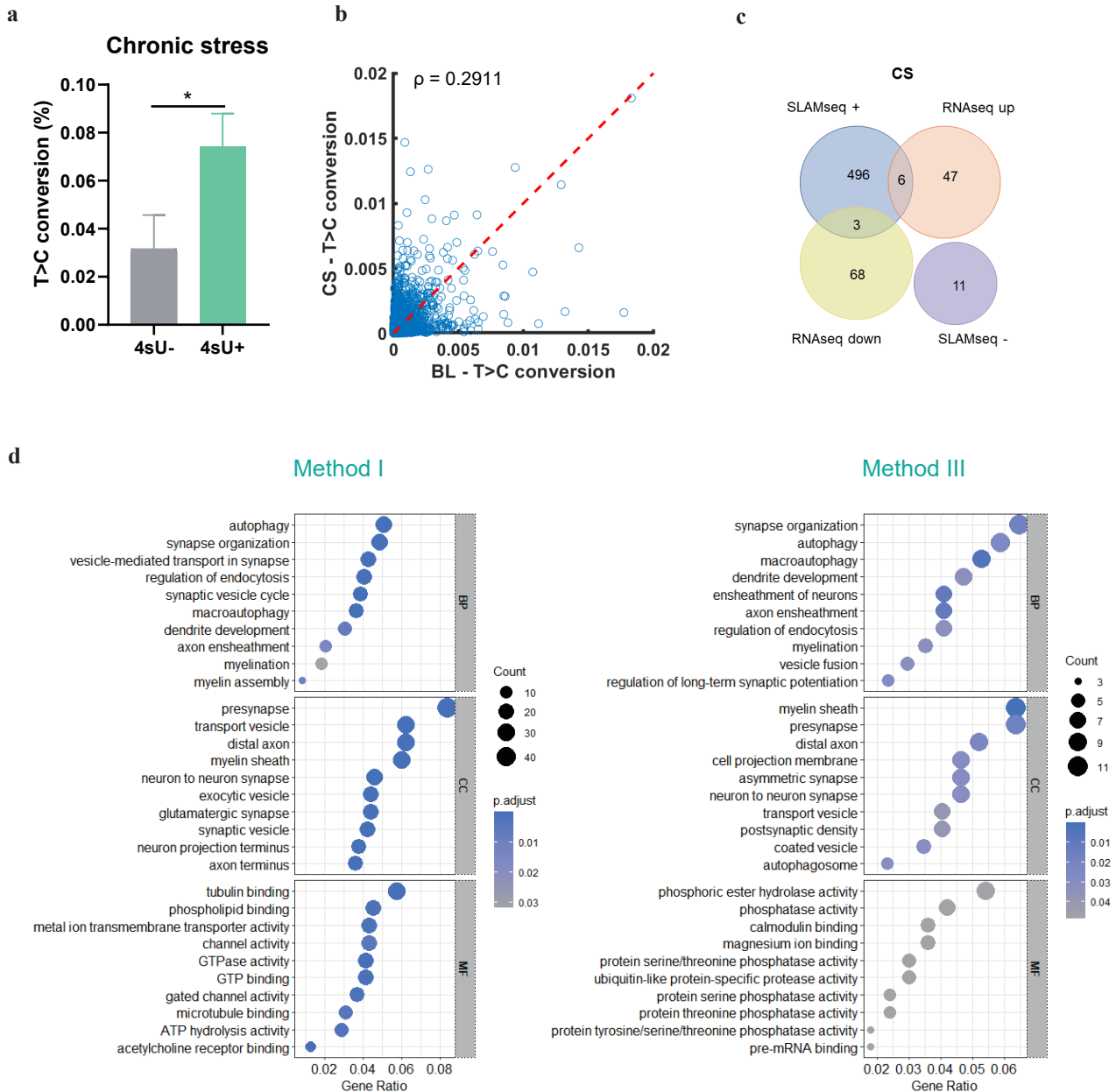
(a) Example RNA gel for 5 amygdala RNA samples injected with 4sU and 3 samples injected with DMSO after IAA treatment.
(b) Schematic showing IAA treatment and library preparation for SLAM-seq.

Supp. Fig. 4



- (a) T>C Conversion rates of total mRNA extracted from DMSO (n=5) and 4sU (n=5) injected amygdala under AS condition (two-tailed unpaired t-test, $p < 0.001$).
- (b) GO term analysis for genes specifically detected by SLAM-seq under AS (Method I), including BP, CC and MF.
- (c) Correlation of T>C conversion between BL and AS DMSO-injected samples. ρ , spearman correlation coefficient.
- (d) Venn diagram showing intersection of AS-specific genes identified by SLAM-seq (SLAMseq+: 4sU+ > 4sU-; SLAMseq-: 4sU+ < 4sU-) and RNA-seq (upregulated and downregulated).
- (e) GO term analysis for genes detected by SLAM-seq under AS (Method III), including CC.

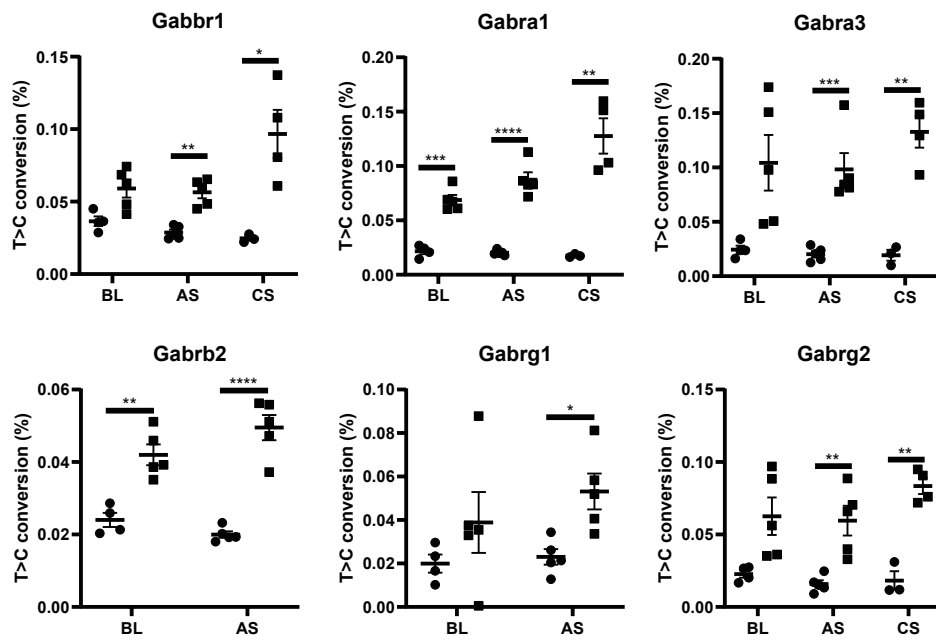
Supp. Fig. 5



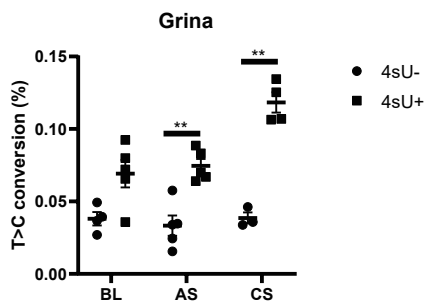
- (a) T>C Conversion rates of total mRNA extracted from DMSO (n=4) and 4sU (n=3) injected amygdala under CS condition (two-tailed unpaired t-test, $p < 0.05$).
- (b) Correlation of T>C conversion between BL and CS DMSO-injected samples. ρ , spearman correlation coefficient.
- (c) Venn diagram showing intersection of CS-specific genes identified by SLAM-seq (SLAMseq+: 4sU+ > 4sU-; SLAMseq-: 4sU+ < 4sU-) and RNA-seq (upregulated and downregulated).
- (d) GO term analysis for genes specifically detected by SLAM-seq (Method I/III) under CS, including BP, CC and MF.

Supp. Fig. 6

GABA receptor



Glutamate receptor



T>C conversion rates for GABA and glutamate receptors detected by SLAM-seq.