Transcriptome Dynamics in Mouse Amygdala under Acute and Chronic Stress Revealed by Thio-labeled RNA Sequencing

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Abstract

Both acute and chronic stress have significant impact on brain functions. The amygdala is essential in mediating stress responses, but how its transcriptomic dynamics change under stress remains elusive. To overcome the difficulties in detecting subtle stress-induced changes by evaluating total RNA using classic RNA sequencing, we conducted thio-labeled RNA sequencing (SLAM-seq). We injected 4-thiouridine (4sU) into mouse amygdala followed by SLAM-seq to detect nascent mRNA induced by acute and chronic restraint stress, and found that SLAM-seq could label actively transcribed genes in the major neuronal and glial subtypes. We also found that acute stress induced active transcription of 6 gamma-aminobutyric acid (GABA) receptors and only 1 glutamate receptor, indicating an imminent increase of inhibitory control in the stressed amygdala. Conversely, chronic stress led to active transcription of 3 glutamate receptors and 4 GABA receptors, suggesting a release of inhibitory control after prolonged stress. SLAM-seq also identified genes associated with myelination under chronic stress, and this finding is validated by immunostaining showing increased myelination in chronically stressed amygdala. Additionally, genes detected by SLAM-seq and RNA-seq only partially overlapped, with SLAM-seq particularly sensitive to transcriptional changes in genes with high basal transcription levels. Thus, by applying SLAM-seq *in vivo*, we obtained a rich dataset of nascently transcribed genes in the amygdala, and revealed distinct transcriptional dynamics associated with acute and chronic stress.

Introduction

The impact of stress on the brain is profound and has been linked to an increased risk of mental illnesses, including depression and anxiety disorders [1, 2]. Both acute and chronic stress can

30 induce adaptive changes in various brain regions [3-9], including the amygdala, which plays a key
31 role in processing physiological and behavioral responses to stress [10, 11]. In its resting state, the
32 amygdala is tightly regulated through inhibitory mechanisms mediated by gamma-aminobutyric
33 acid (GABA) [12]. Previous research showed that stress leads to amygdala disinhibition, resulting
34 in its heightened activity [13, 14]. While many studies have demonstrated that stress affects
35 amygdala function, the underlying molecular mechanisms responsible for these changes remain
36 elusive. To understand the stress-induced effects in the amygdala at the molecular level, it is
37 essential to study how gene expression in amygdala is influenced by acute and chronic stress.
38
39 It has long been established that neuronal activities lead to fast expression of immediate early
40 genes, which further regulates transcription of thousands of downstream genes over an extended
41 period [15-17]. Such activity-dependent transcription dynamics are crucial for modulating
42 neuronal functions and long-term connectivity changes [18, 19]. Studies have shown that glial
43 cells in the brain also exhibit significant functional changes induced by neuronal activities. For
44 example, oligodendrocytes undergo activity-dependent myelination [20, 21]. However, the
45 abundance of gene transcripts for maintaining cellular functions, and the complex morphology of
46 neurons and glia, made the classic RNA sequencing (RNA-seq) method unsuitable for studying
47 the dynamic transcriptomic changes of these cells [22].
48
49 The thio-labeled RNA sequencing (SLAM-seq) method specifically label newly transcribed
50 mRNAs [23], and has been widely applied in cultured cells [24, 25]. Recently, SLAM-seq has also
51 been extended to *in vivo* studies to explore genomic changes during zebrafish embryo development
52 [26], and to identify cell type-specific transcriptome in mouse tissues in a Cre-dependent manner
53 (SLAM-ITseq, [27]). Although SLAM-ITseq provides a solution to metabolically label RNA with
54 4-thiouracil (4-TU) in a specific cell type *in vivo*, this method requires usage of double-transgenic
55 mouse lines to achieve cell type-specific expression of uracil phosphoribosyltransferase (UPRT),
56 to transform 4-TU to 4-thiouridine (4sU) in Cre-expressing cells, limiting the applicability.
57
58 By conducting SLAM-seq with direct stereotactic injection of 4sU, we detected newly transcribed
59 genes in the amygdala under acute and chronic stress. Bioinformatic analyses showed that the
60 injected 4sU was integrated into the transcription of genes expressed in major brain cell types. In

addition, acute stress and chronic stress induced differential transcription of GABA and glutamate receptors, indicating diverse inhibitory control in the amygdala under acute and chronic stress. Furthermore, compared to RNA-seq, SLAM-seq is more sensitive to transcriptional changes in genes expressed in high basal levels.

Results

Adapt SLAM-seq for the brain through stereotactic injection of 4sU

Neuronal activity is known to quickly trigger the transcription of many genes [15-17]. Seeking to detect gene transcription in response to diverse conditions of neuronal activity in different brain regions, we adapted the SLAM-seq protocol *in vivo* by injecting 4sU directly into the brain region of interest. The stereotactic injection method was used to ensure the target delivery of 4sU, a nucleotide analog that can be imported into animal cells by equilibrate nucleoside transporters [28], in selected brain regions (See Methods for details). To estimate the 4sU incorporation rate in brain cells, we first injected 4sU (100mM, dissolved in 10% DMSO, 1uL) into the mouse auditory cortex (**Fig. 1a**), and performed biotin dot blot essay with mRNAs extracted from the cortex at 2 h, 8 h, and 24 h after 4sU injection [29]. The labeling strength increased with labeling time (**Fig. 1b**), and at 24 h post injection, the labeling is highly efficient. Thus, we determined that 24 h is a sufficient duration to allow 4sU diffusion into brain cells to support SLAM-seq.

To evaluate the extent of tissue damage potentially caused by the injection of 4sU, we used TUNEL (Terminal deoxynucleotidyl transferase dUTP Nick End Labeling) staining to assess cell death in the injected brain region [30]. We injected 4sU (100mM, dissolved in 10% DMSO, 1uL) and DMSO (10%, 1uL) into the mouse auditory cortex and amygdala, and 24 h later, extracted the mouse brains for slicing and TUNEL staining (Methods). We did not see dead cells in the brain slices near the injection sites, for both 4sU and DMSO injections, suggesting that neither 4sU nor DMSO induced detectable cell death or tissue damage in the injected brain regions (**Fig. 1c, Supp. Fig. 1**).

We also assessed whether the presence of 4sU had any impact on the transcriptome by performing 150bp paired-end sequencing of total mRNA extracted from the isolated mouse auditory cortex and amygdala at 24 h after stereotactic 4sU or DMSO injections (**Supp. Fig. 2a, 2b**). By comparing

the read counts for all genes [23], we did not observe any significant difference in gene expression levels between 4sU (denoted as 4sU+) and DMSO (denoted as 4sU-) groups (**Fig.1d, Supp. Fig. 2c**). These findings support that local injection of 4sU into specific brain regions enables efficient incorporation into transcription in brain cells, without obviously affecting the gene expression.

Identify 4sU-incorporated mRNA with SLAM-seq under basal conditions

Recently, in addition to cultured cells [24, 25], SLAM-seq has also been applied *in vivo* by injecting 4sU into zebrafish embryo [26], or injecting 4-thiouracil (4-TU) intraperitoneally into transgenic mice expressing UPRT in selected cell types [27]. Given that local injection of 4sU into the mouse brain has never been reported, we needed to empirically determine whether the delivered 4sU can be incorporated into the nascently transcribed RNA molecules. We injected 4sU (100mM, 1uL, dissolved in 10% DMSO) and DMSO (10%, 1uL) into the mouse amygdala 24 h prior to tissue dissection and RNA extraction (**Fig. 2a**), to establish a baseline (BL) for nascent RNA transcription in normal behaving mice. We then subjected the aforementioned total RNA extracts to iodoacetamide (IAA) treatment (Methods, **Supp. Fig. 3a**), to covalently attach a carboxyamidomethyl group to 4sU by nucleophilic substitution [23], and then performed 150bp paired-end RNA-seq (**Supp. Fig. 3b**). During the reverse transcription step of RNA-seq library preparation, a guanine (G), instead of an adenine (A), is base paired to an alkylated 4sU, leading to the thymine (T) to cytosine (C) base conversion (T>C conversion) at the corresponding T position in mRNA [23]. To control for the background T>C conversion rate without 4sU, RNA obtained from DMSO-injected amygdala was subjected to the same procedures before RNA-seq.

We calculated the T>C conversion rates for each gene in both the 4sU-injected and DMSO-injected samples using SLAM-DUNK software [31]. At the whole transcriptome level, the average T>C conversion rate of the 4sU-injected group was significantly higher than that of DMSO-injected group (**Fig. 2b**), indicating that the injected 4sU was incorporated into transcription. We identified 414 genes with significantly higher T>C conversion rates in the 4sU group than in the DMSO group (**Fig. 2c**), which can be plausibly interpreted as genes undergoing active transcription. Note that these mice were not subjected to any behavioral or physiological perturbations, therefore, the 414 differentially 4sU-labeled genes were actively transcribed under normal baseline conditions. Indeed, these genes included sodium channels (*Scn1b*), potassium channels (*Kcnab2, Kcnc2*),

cation transport ATPases (*Atp1a2, Atp1b2)*, calcium channels (*Cacng7*) and Calmodulin (*Calm3*), all of which are essential for maintaining basic neuronal functions [32].

Determine the 4sU labeling efficiency in distinct cell types

Identification of genes encoding neuron-specific ion channels indicated that 4sU was successfully incorporated into transcription of genes in the amygdala neurons. To additionally evaluate the efficiency of 4sU incorporation into the transcription of other cell types in amygdala, we cross-referenced the 414 differentially 4sU-labeled genes with known marker genes of major cell types as reported in single-cell RNA sequencing studies [33, 34]. We found that the 414 differentially labeled genes under baseline conditions covered marker genes of excitatory (*Slc17a7, Camk2a*) and inhibitory neurons (*Gad1, Gad2*), astrocytes (*Gfap, S100b*), microglia (*Fcer1g, Lyz2*) and oligodendrocytes (*Mobp, Plp1*). The T>C conversion rates of these genes were significantly higher in 4sU-injected than DMSO-injected amygdala (**Fig. 2d**). These results indicate that 4sU has been imported into major neuronal and glial cell types of the amygdala, and could be effectively incorporated into the transcription of these cells to signal nascent transcription.

Transcriptome dynamics of the amygdala under acute stress

The amygdala has been extensively implicated in stress responses [10, 11]. To identify genes that were actively transcribed upon acute stress (AS), we subjected 4sU- and DMSO-injected mice to 1.5 h of restraint stress [35], and immediately after the stress treatment, we isolated the amygdala and extracted total RNAs (Methods, **Fig. 3a**). We treated the RNA samples with IAA for SLAM-seq, and identified the differentially 4sU-labeled genes using SLAM-DUNK by comparing T>C conversion rates between 4sU- and DMSO-injected amygdala samples (**Supp. Fig. 4a**). Meanwhile, we conducted a separate bulk RNA-seq analysis, using DESeq2 software package [36] to identify differentially expressed genes (DEGs) in acute stress condition, compared to baseline.

By comparing the T>C conversion rates of genes between the 4sU and DMSO groups under AS, we identified 728 differentially 4sU-labeled genes with significantly higher T>C conversion rates in the 4sU group (FDR<0.05, $\log_2$FC>1, **Fig. 3b**. FDR: false discovery rate. FC: fold change). A gene ontology (GO) analysis of the differentially 4sU-labeled genes in the AS samples indicated enrichment for terms including “vesicle-mediated transport in synapse”, “regulation of

154 neurotransmitter levels", and "synaptic vesicle cycle", all of which are closely associated with
155 synaptic vesicle functions (**Fig. 3c, Supp. Fig. 4b**). Among these are genes tightly linked to
156 synaptic vesicle release, including *Git1, Syn1, Synj1* [37-39] (**Fig. 3b**). GO analysis also revealed
157 enrichment for terms such as "regulation of synaptic plasticity" and "learning or memory", and
158 related genes included *Vgf, Prkcg, Snap25, Snap47* [40-42] (**Fig. 3b**).
159
160 A KEGG pathway analysis showed that the most significant pathways include "glutamatergic
161 synapse" and "GABAergic synapse", suggesting that AS had a strong influence on both excitatory
162 and inhibitory synaptic functions (**Fig. 3d**). Comparing genes identified under BL condition with
163 genes identified under AS, we found only one GABA receptor gene (*Gabra1*) among the
164 differentially 4sU-labeled genes under BL, in contrast to 6 GABA receptor genes under AS
165 (*Gabbr1, Gabra1, Gabra3, Gabrb2, Gabrg1, Gabrg2*), representing a higher transcription rate for
166 GABAergic receptors in the amygdala after acute stress. Conversely, only one glutamate receptor
167 gene (*Grina*) was detected under AS, and none under BL (**Fig. 3e**). Consistent with previous
168 studies linking amygdala GABAergic inhibitory control to stress response [14, 43], our results
169 suggested a strong influence on GABAergic neurons in the amygdala by acute stress, in the form
170 of quickly elevating GABA receptor expression.
171
172 **Sensitivity of SLAM-seq vs. RNA-seq**
173 Neurons require high abundance of transcripts for maintaining normal functions, while also exhibit
174 highly dynamic activity-induced transcription, making it hard to detect the subtle changes by
175 evaluating the total RNA amount using classic RNA-seq [22]. Indeed, none of the differentially
176 4sU-labeled GABA receptor and glutamate receptor genes identified by SLAM-seq were detected
177 using the differential gene expression analysis, even with a lenient standard (FDR<0.1,
178 $Log_2FC>0.1$, **Fig. 3f, Supp. Fig. 4c**). In total, 374 significantly upregulated and 279 downregulated
179 genes were identified using DESeq2 by comparing RNA read counts between AS and BL
180 conditions. 44 overlapping genes were identified by intersecting these AS-upregulated genes with
181 differentially 4sU-labeled genes under AS (**Fig. 3g**). These genes include known stress-related
182 genes such as *Cldn11, Vamp1, Glud1* and *Etnppl* [44-47]. For all of the overlapped genes, fold
183 change is bigger for SLAM-seq analysis than RNA-seq (**Fig. 3h**).
184

185 Further investigation revealed that the overlapped genes detected by SLAM-seq and RNA-seq had
186 relatively high expression levels (**Fig. 3i, Supp. Fig. 4d**). In fact, the genes with very high
187 expression levels that were marginally upregulated as determined by DESeq2 (Log_2FC <0.5) were
188 detected by SLAM-seq (red data points in **Fig. 3i**) with bigger fold changes and higher significance
189 levels (**Fig. 3h, k**). In addition, genes identified by SLAM-seq had higher expression levels than
190 genes detected by RNA-seq (**Fig. 3j**, Kolmogorov-Smirnov test, $p < 0.05$). These results suggest
191 that compared to RNA-seq, SLAM-seq is more sensitive to genes with high expression levels, and
192 is therefore useful for detecting the increased active transcription of genes that can be masked by
193 the high abundance of transcripts required for normal functioning. This is of particular importance
194 for neurons, given the high basal expression level of many genes [22].
195
196 **Transcriptome dynamics of amygdala under chronic stress**
197 Chronic stress (CS) poses prolonged impact in the brain [48]. For chronic stress experiments, we
198 subjected mice to 7 days of restraint stress, 2 h each day [49, 50] (Methods, **Fig. 4a**). To examine
199 the long-lasting transcriptomic changes under CS, we extracted the amygdala at 10 h after the final
200 restraint stress session on day 7. We reasoned that by shifting 10 h, we reduced the possibility of
201 detecting acute changes induced by the last session of restraint stress. 4sU was injected into the
202 amygdala 24 h before brain extraction, same as BL and AS experiments. By comparing T>C
203 conversion rates between 4sU and DMSO injected groups, we identified 815 differentially 4sU-
204 labeled genes under CS (**Fig. 4b, Supp. Fig. 5a**). We performed a GO analysis for these genes,
205 and found that in addition to terms associated with neuronal functions such as "synaptic vesicle
206 cycle" and "neurotransmitter secretion", there is also enrichment for terms closely linked to glial
207 cells, especially oligodendrocytes and microglia (**Fig. 4c**). These terms include "myelination",
208 "ensheathment of neurons" and "axon ensheathment", which are tightly linked to the function of
209 oligodendrocytes, as well as "autophagy" and "autophagosome", which are associated with
210 microglia (**Supp. Fig. 5b**). Among these genes, *Mag* and *Dag1* are associated with myelination,
211 and *Rragb* and *Usp36* are associated with autophagy [51].
212
213 Regarding sensitivity for SLAM-seq vs. RNA-seq, we noted a similar trend for CS data to AS.
214 DESeq2 analysis detected 53 significantly up-regulated and 11 down-regulated genes for CS
215 (FDR<0.1, Log_2FC>0.1, **Fig. 4d**). Intersection of the differentially 4sU-labeled genes identified

216 by SLAM-seq and upregulated genes identified by RNA-seq revealed 11 overlapping genes (**Fig.**
217 **4e**), all with high expression levels (**Fig. 4f, Supp. Fig. 5c**). Expression of six out of the 11
218 overlapped genes is affected by chronic stress (*Esrrg, Gabarapl2, Cct8, Vamp1, Nrsn1, Cplx1*) [47,
219 52-54]. These genes all show bigger fold changes and 9 out of 11 genes also show higher
220 significance levels for SLAM-seq than for RNA-seq (**Fig. 4h, 4i**). Similar to AS, genes identified
221 by SLAM-seq in CS also had higher expression levels (**Fig. 4g**, Kolmogorov-Smirnov test, $p <$
222 0.05), again demonstrating the sensitivity of SLAM-seq for detecting actively transcribed genes
223 with high abundance. The GO analysis of the genes identified by SLAM-seq indicated enrichment
224 for terms closely linked to glial functions, but these terms did not show in GO analysis of genes
225 identified by RNA-seq (**Supp. Fig. 6**). Thus, the low-magnitude yet persistent transcriptome
226 changes associated with CS are more likely to be captured by SLAM-seq.
227
228 **Comparison of differentially 4sU-labeled genes among BL, AS and CS conditions**
229 By comparing the differentially 4sU-labeled genes under BL, AS and CS conditions, we found that
230 a majority of genes (363 out of 413) labeled under BL were also identified in either AS or CS
231 conditions, including known housekeeping genes such as *Sdha, Ywhaz*, *Gfap* [55] (**Fig. 5a**). These
232 genes were actively transcribed regardless of stress conditions, indicating their important roles in
233 maintaining normal cellular functions. In contrast to BL, we identified many more condition-
234 specific genes after stress treatments, namely, 224 AS-specific genes and 333 CS-specific genes
235 (**Fig. 5a**). Among the 172 AS-CS overlapped genes, 29 were associated with synaptic transmission,
236 synaptic vesicle cycle and synaptic regulations (**Fig. 5a**). Thus, both acute and chronic stress
237 strongly affected synaptic functions in amygdala neurons. Notably, compared to CS, AS triggered
238 active transcription of a higher proportion of synapse-related genes, among which were genes
239 associated with protein localization to postsynaptic membrane (*Git1, Mapk10, Stx1b, Kif1a*) [39,
240 56, 57], highlighting immediate postsynaptic plasticity caused by acute stress (**Fig. 5b**).
241
242 As described in an earlier section, we detected 6 GABA receptor genes (*Gabbr1, Gabra1, Gabra3,*
243 *Gabrb2, Gabrg1, Gabrg2*) and 1 glutamate receptor gene (*Grina*) under AS, representing an
244 imminent effect of AS on GABAergic inhibitory control of the amygdala. In comparison, we found
245 4 GABA receptor genes (*Gabbr1, Gabra1, Gabra3, Gabrg2*) and 3 glutamate receptor genes
246 (*Gria3, Gria4, Grina*) among the differentially 4sU-labeled genes under CS (**Fig. 5c**). The increase

247 in excitatory receptor transcription and relatively lower transcription of GABAergic receptors
248 might underlie hyperactivity of the amygdala [13, 14], caused by stress-induced removal of
249 GABAergic inhibitory control.
250
251 **Validation of SLAM-seq results by quantitative immunofluoresence**
252 Recent studies suggested that elevated neuronal and axonal activity could trigger myelination [20,
253 21], a phenomenon known as "activity-dependent myelination". In line with these findings, CS-
254 specific genes detected by SLAM-seq included a set of genes related to myelination, such as *Fyn,*
255 *Dag1, Mag, Epb41l3,* and *Ndrg1* (**Fig. 5d**), and the enriched GO terms included "myelination",
256 "positive regulation of myelination", and "myelin sheath" (**Fig. 5e**). These genes were not detected
257 by RNA-seq (**Supp. Fig. 7**), possibly due to their high baseline expression levels. To examine
258 whether the increased transcription of myelination-related genes after CS is indicative of increased
259 myelination, we stained brain slices of chronically stressed mice and control mice with a myelin
260 marker, the myelin basic protein (MBP), and compared the immunofluorescence signals between
261 the two groups (**Fig. 5f**). We found that the MBP signal is indeed significantly stronger in the
262 amygdala of chronically stressed mice than the control mice ($p<0.01$, Student's t-test, **Fig. 5g**),
263 demonstrating increased myelination after CS. Therefore, consistent with the SLAM-seq result
264 that chronic stress led to active transcription of myelination-related genes.
265
266 **Discussion**
267 By directly injecting 4-sulfuridine (4sU) into the amygdala followed by SLAM-seq, we were able
268 to identify newly transcribed genes under acute and chronic stress. By cross-referencing these
269 genes with known cell type-specific marker genes, we found that the injected 4sU was integrated
270 into the transcription of major subtypes of neurons and glia cells in the amygdala. Analyses
271 revealed that acute stress resulted in increased transcription of GABA receptors in neurons, while
272 chronic stress had a stronger impact on transcription of glutamate receptors and genes associated
273 with myelination, both in line with heightened activity of the amygdala [14]. Furthermore, we
274 observed that SLAM-seq exhibited greater sensitivity to transcriptional changes in genes with high
275 expression levels compared to RNA-seq. Thus, by applying SLAM-seq to the amygdala, we
276 generated a rich dataset which can be used in future studies to dissect the functions of genes related
277 to stress responses.

Neurons have highly specialized morphology, including axons and dendrites that can span long distances, with functional subcellular compartments such as dendritic spines and axonal boutons [58]. The transcriptional networks in neurons are dynamically modulated by synaptic activities, through coupling of a small subset of active synapses to the nucleus [59, 60]. Given the abundance of gene transcripts for maintaining fundamental neuronal functions such as action potential firing [19], the transcriptional modulation that lead to activation of relevant gene expression may not alter the total mRNA of these genes [22]. Therefore, the most common method for gene expression profiling, RNA-seq, may not be suited for accessing the highly dynamic transcriptional changes under fast-varying physiological, behavioral or pathological conditions.

SLAM-seq, a metabolic RNA labeling method for identifying newly synthesized RNA molecules, is an alternative approach to gain insights into the transcriptional regulation regardless of the steady-state abundance of genes [24-26]. A previously published method, SLAM-ITseq, extended SLAM-seq to mouse tissues by crossing Cre-dependent UPRT mice with Cre lines [27]. This method requires usage of transgenic animals, and the cell types that can be investigated are restricted by available Cre lines. Instead of intravenously injecting 4-thiouracil and relying on Cre-dependent UPRT expression for cell-specific labeling, we used stereotactic 4sU injection to target all cell types in selected brain regions. Our data showed that 4sU can be effectively imported into major cell types [28], and incorporated into the transcription, without causing detectable tissue damage or cell death. This is a simplified method that can be applied to any brain region in mice and possibly other species using stereotaxic injection, without the need for transgenic animals.

We used this method to investigate the RNA dynamics of a key brain region involved in stress conditions, the amygdala, under acute and chronic restraint stress. We found partial overlap in genes detected by SLAM-seq and RNA-seq, and over half of the overlapped up-regulated genes under CS condition had been implicated in chronic stress by previous studies [52-54, 61-64]. Notably, for all these genes, SLAM-seq showed higher sensitivity than RNA-seq, shown by higher fold changes and significance levels. The upregulated genes with high abundance were detected by SLAM-seq with high significance level, while barely meets the lenient criteria in RNA-seq. It supports the notion that for genes with high expression rate, physiological condition (restraint

stress) may not cause a noticeable change in the total amount of mRNA for relevant genes. One such example is the ensemble of genes related to myelination. The high abundance of these genes precluded detection by RNA-seq following CS treatment, although immunostaining of myelin-specific protein revealed increased myelination, consistent with the SLAM-seq results. Therefore, SLAM-seq serves as a better method for screening the dynamics of highly expressed genes.

Competition and cooperation between excitation and inhibition is crucial for balancing neural activity[65, 66]. Using SLAM-seq, we identified 6 GABA receptors under AS, compared to 1 under BL and 4 under CS, suggesting an imminent inhibition drive induced by AS. Conversely, 3 glutamate receptors were identified under CS, while only 1 under AS and 0 under BL, suggesting an increase in elevated activity of the amygdala. Furthermore, CS also induced transcription of many genes associated with myelination. Myelination has been shown to be initiated by neuronal activities [20, 21], and can in turn facilitate signal transduction in neurons [51, 67]. These results are consistent with previous findings that stress could cause hyperactivity of the amygdala [14, 68, 69]. Therefore, our findings indicated that acute and chronic stress could differentially modulate the transcription level of GABA and glutamate receptors as well as proteins constituting the myelin sheath, and in turn influence the excitation-inhibition balance of the amygdala neurons.

We provided a rich dataset of molecular responses of amygdala to acute and chronic stress, and confirmed that CS can induce increased myelination through immunostaining. Future studies will be essential for understanding the functions of other genes identified in this study.

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489 **Figure legends**

490 **Fig. 1：SLAM-seq for mouse brain cells by stereotactic injection of 4sU into the brain.**

491 **(a)** Schematic showing SLAM-seq procedure, including stereotactic 4sU injection, RNA
492 extraction, iodoacetamide (IAA) treatment, RNA sequencing and T-C conversion detection.

493 **(b)** Dot blot essay of RNA extracted from mouse brain labeled with 4sU for different durations.
494 Left to right: biotin-oligo (positive control); RNA samples extracted from mouse auditory
495 cortex with no 4sU injection (negative control); 2 h, 8 h, and 24 h after 4sU injection.

496 **(c)** TUNEL staining of brain slices for positive control (top panels), and brain slices with DMSO
497 (middle) and 4sU (bottom) injections in auditory cortex. Green signals denoted dead cells.
498 Scale bar, 50 μm.

499 **(d)** Correlation of RNA levels extracted from DMSO (denoted as 4sU-) and 4sU (denoted as 4sU+)
500 injected auditory cortex samples. ρ, spearman correlation coefficient.

501

502 **Fig. 2：Identifying 4sU-labeled genes with SLAM-seq and match to different cell types**

503 **(a)** Time line showing stereotactic 4sU injection and brain extraction under baseline (BL)
504 condition. Shading demonstrates nascent mRNA that can be detected by SLAM-seq.

505 **(b)** T>C Conversion rates of total mRNA extracted from DMSO (n=5) and 4sU (n=4) injected
506 amygdala under baseline condition.

507 **(c)** Volcano plots showing T>C conversion rates of transcripts under baseline, with or without
508 4sU injection. Red dots represent transcripts with significant higher T>C conversion rates in
509 the 4sU+ group (FDR < 0.05 and $\log_2$FC > 1); blue dots represent transcripts with significant
510 lower T>C conversion rates in the 4sU+ group (FDR < 0.05 and $\log_2$FC < -1).

511 **(d)** T>C Conversion rates of marker genes for multiple neuron and glia cell types.

512

513 **Fig. 3：Transcriptome dynamics of mouse amygdala under acute stress.**

514 **(a)** Time line of acute stress experiment, including time points for 4sU injection and brain
515 extraction.

516 **(b)** Volcano plots showing T>C conversion rates of transcripts under AS, with or without 4sU
517 injection. Red dots represent transcripts with significant higher T>C conversion rates in the
518 4sU+ group (FDR < 0.05 and $\log_2$FC > 1); blue dots represent transcripts with significant lower
519 T>C conversion rates in the 4sU+ group (FDR < 0.05 and $\log_2$FC < -1).

520 **(c)** GO term analysis for genes detected by SLAM-seq.

521 **(d)** KEGG analysis for genes detected by SLAM-seq.

522 **(e)** Fold changes of T>C conversion rates for GABA and glutamate receptors detected by SLAM-
523 seq. Student's t-test, *** $P < 0.001$.

524 **(f)** Volcano plots showing differentially expressed genes (DEGs) under AS compared to BL. Red
525 dots represent significantly AS-upregulated genes (FDR < 0.1 and $\log_2FC > 0.1$); blue dots
526 represent significantly AS-downregulated genes (FDR<0.1 and $\log_2FC < -0.1$). ns, no
527 significant difference; up, significantly upregulated; down, significantly downregulated.

528 **(g)** Venn diagram showing intersection of AS-specific genes identified by SLAM-seq (red dots in
529 **b**) and RNA-seq (red dots in **f**).

530 **(h)** Fold changes of T>C conversion rates for 4sU+ vs. 4sU- (SLAM), and of expression levels for
531 AS vs. BL (DEG) of all overlapped genes in (**g**). Paired t-test, *** $P < 0.001$.

532 **(i)** Correlation between FC-DEG and expression levels of AS-upregulated genes in **3g**, with the
533 color and size of each data point denoting the significance level (FDR-SLAM) and fold change
534 (FC-SLAM) of each AS-upregulated gene.

535 **(j)** Distribution for expression levels of genes detected by SLAM-seq and RNA-seq under AS.
536 Two-sample Kolmogorov-Smirnov test, $p < 0.05$

537 **(k)** Significance levels of T>C conversion rates for 4sU+ vs. 4sU- (SLAM), and of expression
538 levels for AS vs. BL (DEG) of all overlapped genes in (**g**). Paired t-test, *** $P < 0.001$.

539

540 **Fig. 4：Transcriptome dynamics of mouse amygdala under chronic stress.**

541 **(a)** Time line of chronic stress experiment, including time points for 4sU injection and brain
542 extraction.

543 **(b)** Volcano plots showing T>C conversion rates of transcripts under CS, with or without 4sU
544 injection. Red dots represent transcripts with significant higher T>C conversion rates in the
545 4sU+ group (FDR < 0.05 and $\log_2FC > 1$); blue dots represent transcripts with significant lower
546 T>C conversion rates in the 4sU+ group (FDR < 0.05 and $\log_2FC < -1$).

547 **(c)** GO term analysis for genes detected by SLAM-seq.

548 **(d)** Volcano plots showing differentially expressed genes (DEGs) under CS compared to BL. Red
549 dots represent significantly AS-upregulated genes (FDR < 0.1 and $\log_2FC > 0.1$); blue dots
550 represent significantly AS-downregulated genes (FDR<0.1 and $\log_2FC < -0.1$).

551 **(e)** Venn diagram showing intersection of AS-specific genes identified by SLAM-seq (red dots in
552 **b**) and RNA-seq (red dots in **d**).
553 **(f)** Correlation between FC-DEG and expression levels of AS-upregulated genes in **e**, with the
554 color and size of each data point denoting the significance level (FDR-SLAM) and fold change
555 (FC-SLAM) of each CS-upregulated gene.
556 **(g)** Distribution for expression levels of genes detected by SLAM-seq and RNA-seq under CS.
557 Two-sample Kolmogorov-Smirnov test, $p < 0.05$.
558 **(h)** Fold changes of T>C conversion rates for 4sU+ vs. 4sU- (SLAM), and of expression levels for
559 AS vs. BL (DEG) of all overlapped genes in (**e**). Paired t-test, *** $P < 0.001$.
560 **(i)** Significance levels of T>C conversion rates for 4sU+ vs. 4sU- (SLAM), and of expression
561 levels for AS vs. BL (DEG) of all overlapped genes in (**e**). Paired t-test, * $P < 0.05$.
562
563 **Fig. 5: Comparison of AS and CS-associated genes and validation of SLAM-seq results**
564 **(a)** Venn diagram showing intersections of genes identified by SLAM-seq under BL, AS and CS
565 conditions. Genes associated with synapse, postsynaptic plasticity, autophagy and myelination
566 are listed.
567 **(b)** GO term analysis for AS-specific genes detected by SLAM-seq.
568 **(c)** Fold changes of T>C conversion rates for GABA and glutamate receptors detected by SLAM-
569 seq under CS. Student's t-test, *** $P < 0.001$.
570 **(d)** Fold changes of T>C conversion rates for myelination related genes detected by SLAM-seq
571 under CS. Student's t-test, *** $P < 0.001$.
572 **(e)** GO term analysis for CS-specific genes detected by SLAM-seq.
573 **(f)** Example images showing immunostaining of myelin basic protein (MBP) in the amygdala of
574 control (BL) and chronically stressed (CS) mice. Scale bar, 20 μm.
575 **(g)** Increased MBP signal intensity in CS mice (n=5) compared to BL mice (n=5), measured by
576 mean gray value. Student's t-test, ** $p<0.01$.
577
578

579 **Materials and methods**

580 **Animals**

581 C57BL/6 mice were purchased from Slac Laboratory Animals. Mice were housed and bred in a 12
582 h light-dark cycle (7 am - 7 pm light) in the animal facility of ShanghaiTech University. Eight- to
583 ten-week-old male mice were used for the experiments. All procedures were approved by the
584 Animal Committee of ShanghaiTech University.

585

586 **4sU Injection**

587 The 4sU powder was dissolved in dimethyl sulfoxide (DMSO) to reach a concentration of 1 M,
588 and the solution was aliquoted, frozen, and stored at -20°C. Before injection, the solution was 1:10
589 diluted with phosphate-buffered saline (PBS). For injection, mice were anesthetized with
590 isoflurane (1.5-2 %) and positioned in a stereotaxic frame (RWD Life Science Co.). Body
591 temperature was maintained at 37 °C using a heating pad. 4sU solution (1 μL) were injected using
592 a glass micropipette with a tip diameter of 15–20 μm, through a small skull opening (<0.5 mm2),
593 with a microinjector (Nanoject III), at a rate of 1 nL/s. In baseline, acute stress and chronic stress
594 experiments, 4sU was injected into bilateral amygdala 24 h before brain extraction.

595

596 **TUNEL Staining**

597 The TUNEL assay was performed following the one-step method outlined in the Promega TUNEL
598 Cell Apoptosis Detection Kit. Mice were intracranially injected with 1 μL of 100 mM 4sU into the
599 auditory cortex (M/L=-4.4 mm, A/P=-2.2 mm, D/V=-1.1 mm) or amygdala (M/L=±3.25 mm,
600 A/P=-1.1 mm, D/V=-3.95 mm), as described above. After 24 h, mice were deeply anesthetized and
601 transcardially perfused with PBS and paraformaldehyde (PFA), followed by brain extraction. The
602 extracted brains were postfixed in PFA at 4°C for 12 hours and embedded in agarose for vibratome
603 sectioning at 70 μm per slice. Brain slices were collected for TUNEL staining, in which terminal
604 deoxynucleotidyl transferase (TdT) labels DNA strand breaks with fluorophore-labeled
605 nucleotides. Stained brain slices were mounted on glass slides and imaged using confocal
606 fluorescence microscopy (Leica).

607

608 **Tissue RNA Extraction**

609 Mice were deeply anesthetized and transcardially perfused with cold PBS. Each mouse was then
610 quickly decapitated, and the head was immersed in ice-cold PBS for rapid cooling for 10 seconds.
611 The mouse brain was then carefully extracted using forceps, placed in a pre-chilled mouse brain
612 mold (RWD Life Science Inc.), and a 2 mm-thick brain tissue block containing the target region
613 (auditory cortex or amygdala) was sliced using a razor blade. The brain slice was then placed on a
614 6 mm petri dish and dropped into liquid nitrogen briefly for 7-8 s. Then, the auditory cortex or
615 amygdala was cut out using a 15 G needle, and promptly transferred to cryotubes for rapid freezing
616 in liquid nitrogen, and subsequent storage at -80°C.
617
618 RNA extraction from mouse brain tissue was performed using the Trizol method. The frozen tissue
619 in cryotubes was thawed, and 1 mL of Trizol (MagZol Reagent R4801-02) was added to each tube.
620 Tissue homogenization was performed using an electric homogenizer, with a 10-second pause
621 every 10 seconds to prevent overheating. The mixture was then left at room temperature for 5
622 minutes for tissue digestion, and the liquid was transferred to 1.5 mL centrifuge tubes. To each
623 tube, 200 μL of chloroform (one-fifth of the Trizol volume) was added, and after thorough vortex
624 mixing, the mixture was left at room temperature for 15 minutes. The mixture was then centrifuged
625 at 12,000 rpm for 15 minutes at 4°C. Then, the supernatant containing RNA was carefully aspirated
626 into new tubes, an equal volume of pre-cooled isopropanol was added, along with 1/100 volume
627 of 10 mM DTT (final concentration 0.1 mM) and 1 μL glycogen (20 mg/mL). After thorough
628 mixing, the mixture was left at -20°C for 1 hour for RNA precipitation. Subsequently, it was
629 centrifuged at 12,000 rpm for 30 minutes at 4°C, resulting in a white gel-like RNA substance at
630 the bottom. The RNA pellet was washed once with pre-cooled 75% ethanol (containing 5 μL 10
631 mM DTT), and after removing the supernatant, the RNA pellet was air-dried for approximately 3-
632 5 minutes. Finally, the RNA was dissolved in 20 μL RNase-free water, and the concentration was
633 determined using Nanodrop 2000.
634
635 **Dot Blot Assay**
636 Four RNA samples with different 4sU injection conditions were used in this experiment: 1) RNA
637 extracted from cortex with no 4sU injection, 2) RNA extracted from cortex dissected 2 h after 4sU
638 injection, 3) RNA extracted from cortex dissected 8 h after 4sU injection, 4) RNA extracted from
639 cortex dissected 24 h after 4sU injection. Positive control was 5′-biotin labeled DNA oligo.

640 Positive control and the extracted RNA samples (1 μg for each sample) were used for dot blot
641 essay following the standard protocol for Chemiluminescent Biotin-labeled Nucleic Acid
642 Detection Kit (Beyotime, D3308), using EZ-Link™ HPDP-Biotin (Thermo Scientific, 21341).
643
644 **Restraint Stress Experiment**
645 Mice were acclimated in the animal facility for at least one week before the initiation of restraint
646 stress experiments.
647 *Acute stress group:*
648 Each mouse was carefully removed from its home cage and put in a Falcon 50 mL centrifuge tube,
649 with 8 small ventilation holes drilled on the tube walls. Once the mouse entered the tube, the rear
650 was sealed with a clean tissue, and the tube was capped with the lid, preventing forward or
651 backward movements. Following the 1.5-hour restraint, the mouse was perfused and the brain was
652 extracted.
653 *Chronic stress group:*
654 Each mouse was carefully removed from its home cage and put in a 50 mL tube, as described in
655 the acute stress experiment. Daily restraint sessions lasting 2 hours (from 10:00 am to 12:00 pm)
656 were conducted for one week. On the 7th day, 10 hours after the final restraint session ended, the
657 mouse was perfused and the brain was extracted.
658 *Baseline group:*
659 Mice did not undergo any restraint stress, and remained in their home cages until they were
660 perfused.
661
662 **IAA treatment**
663 Extracted RNA was reacted with IAA to alkylate the thiol group following [1]. For a 50 μL
664 reaction: 2-3 μg RNA, 25 μL DMSO, 5 μL 100 mM iodoacetamide (IAA), and 5 μL 500 mM
665 sodium phosphate (pH=8), and RNase-free water. IAA was freshly prepared and diluted with
666 anhydrous ethanol. The prepared mixture was incubated at 50°C for 15 minutes, followed by the
667 addition of 1 M dithiothreitol (DTT) to terminate the reaction. Then, 125 μL anhydrous ethanol,
668 1 μL glycogen (20 mg/mL), and 5 μL sodium acetate (3 M, pH=5.2) were added to the reaction
669 system. After thorough mixing, the solution was left at -80°C for 30 minutes, followed by
670 centrifugation at 12,000 rpm for 30 minutes at 4°C, resulting in a white gel-like RNA substance

671 at the bottom. The RNA pellet was washed once with pre-cooled 75% ethanol. After removing
672 the supernatant, the RNA pellet was air-dried for approximately 3-5 minutes, and dissolved in 20
673 μL RNase-free water.
674
675 **RNA sequencing**
676 The IAA-methylated RNA was stored in a -80°C freezer, and library construction and
677 sequencing were conducted by Suzhou Geneseeq Technology Inc. The libraries were sequenced
678 using the Illumina NovaSeq for 150-base pair paired-end sequencing, generating approximately
679 6 GB of sequencing data for each RNA sample.
680
681 **Bioinformatics Analysis**
682 *Preprocessing of RNA-Seq Data:*
683 Raw data obtained from RNA-Seq was preprocessed using Cutadapt v3.1. Adapter sequences in
684 paired-end sequencing were eliminated, and sequences shorter than 15 nucleotides were
685 discarded. The preprocessed data was then aligned to the NCBI reference mouse genome
686 (mm10) using Hisat2 v2.1.0. The resulting alignment data in SAM format was converted to
687 BAM format using Samtools v1.9.
688
689 *SLAM-Seq Analysis:*
690 The software SLAM-DUNK v0.2.4 (tneumann.github.io/slamdunk/), designed for SLAM-Seq
691 analysis, was used to compute the T>C mutation counts for each sample [2]. Annotation data for
692 3' UTR regions were obtained from the RefSeq and Ensembl databases. To identify significantly
693 4sU-labeled transcripts, a two-step filtering process was implemented. Firstly, genes with zero T
694 read counts were excluded. Secondly, only genes with read counts > 5 in all samples were kept
695 for further analyses. Statistical analysis was performed using the ibb R package (version 13.06),
696 as described in [3]. To control for the false discovery rate (FDR), adjusted P-values were
697 calculated using the Benjamini-Hochberg method. Transcripts with an FDR below 0.05 were
698 considered significantly labeled.
699
700 *Differential Gene Expression (DEG) Analysis:*

701 Quantification of gene expression was performed using FeatureCounts (v2.0.1). The Transcripts
702 Per Million (TPM) values for each gene were calculated using the formula:

703 $$TPM=RPK/\sum RPK\times 10^6$$

704 Here, RPK (Reads Per Kilobase) represents the reads per thousand base pairs, and ∑RPK is the
705 sum of RPK values for all genes in the sample. Differential expression analysis was performed
706 using the DESeq2 package in R 3.6.1. The standard DESeq2 workflow was followed for data
707 normalization, variance estimation, and statistical modeling. Identification of significantly
708 differentially expressed genes was based on the criterion of adjusted P-values < 0.05 or < 0.1.
709

710 **GO term enrichment analysis**

711 List of genes was used as input for PANTHER 13.1 (pantherdb.org/) to perform 'Statistical
712 enrichment test' with GO terms for biological processes, cellular components and molecular
713 functions. The enriched GO terms obtained were further selected based on the P-values for
714 visualization.
715

716 **Immunofluorescence**

717 Chronic stressed mice were perfused 2 weeks after the final restraint session ended, with 0.01M
718 PBS and 4% PFA. Control mice were perfused without any stress treatment. Brains were sliced
719 (at 50 μm) using a vibratome (Leica VT1200S) after post-fixed for 5 d in 4% PFA at 4 °C. Brain
720 slices including the amygdala were permeabilized with 0.4% Triton X-100 in PBS for 30
721 minutes, blocked with 5% bovine serum albumin (BSA) in PBS for 1 h at RT, and incubated with
722 rat anti-MBP (1:200; MCA409S, Serotec) in 0.1% Triton X-100 and 1% BSA in PBS for 40 h at
723 4°C, then washed with PBS 3 × 10 minutes. Sections were incubated with DAPI (1:2500) and
724 fluorophore-conjugated secondary antibodies (1:500; AB150165, abcam) in 0.1% Triton X-100
725 and 1% BSA in PBS for 2h at RT, then washed with PBS 3 × 10 minutes. Images were acquired
726 at a Leica STELLARIS 8 FALCON, with a HC FLUOTAR L VISIR 25x/0.95 water objective;
727 pinhole was set to 1 AU, pixel size to 113.55nm × 113.55nm and z-stack interval to 1 μm.
728 Image processing and quantification were performed using FIJI. For the quantitative
729 immunofluorescence analysis, the mean grey value of each field of view was first thresholded for
730 identification of myelin structures, and then calculated for 11 optical planes of acquired z-stacks

(step 1 μm). For each mouse, the mean grey value is averaged across two sections containing the amygdala, one from each hemisphere.

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Figure 1

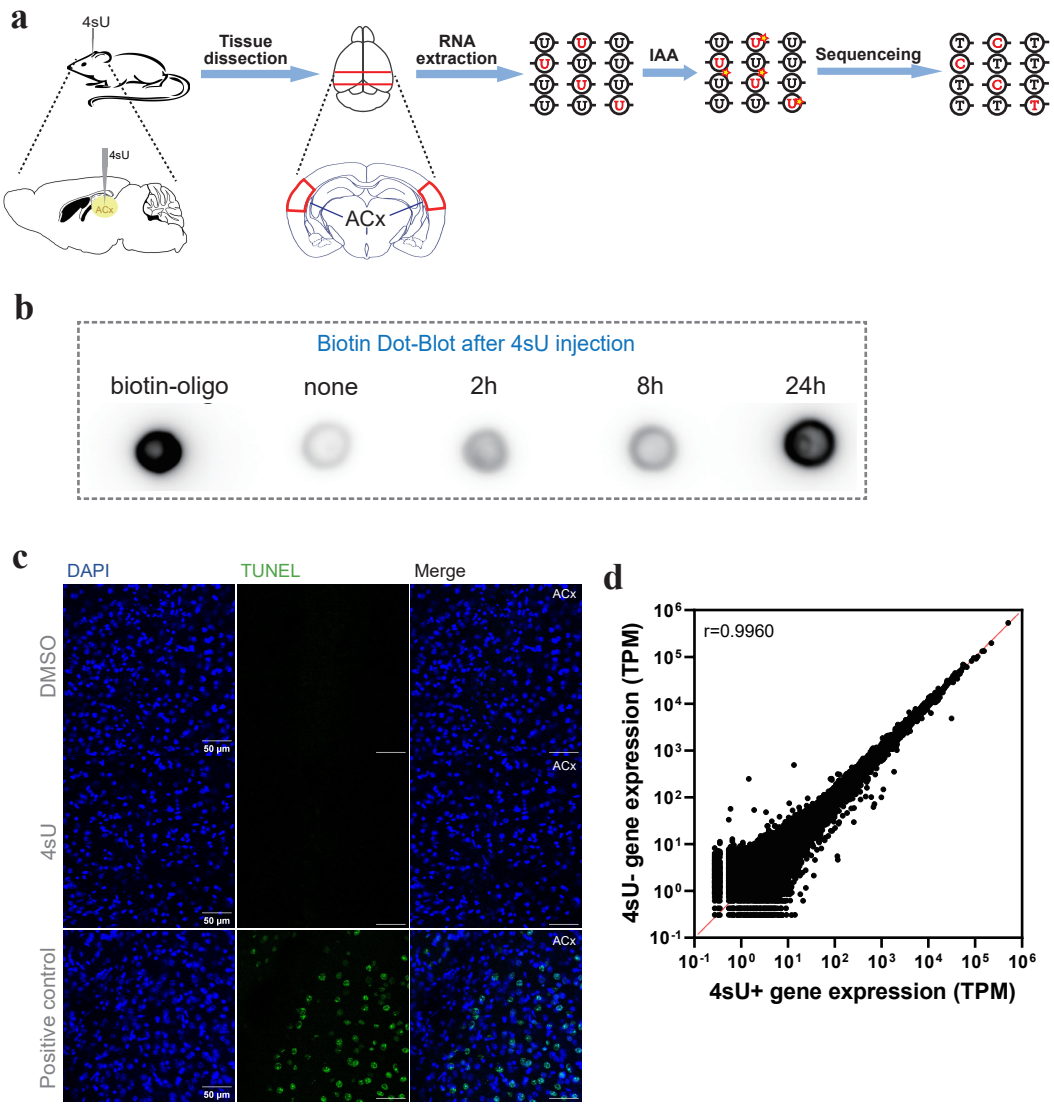
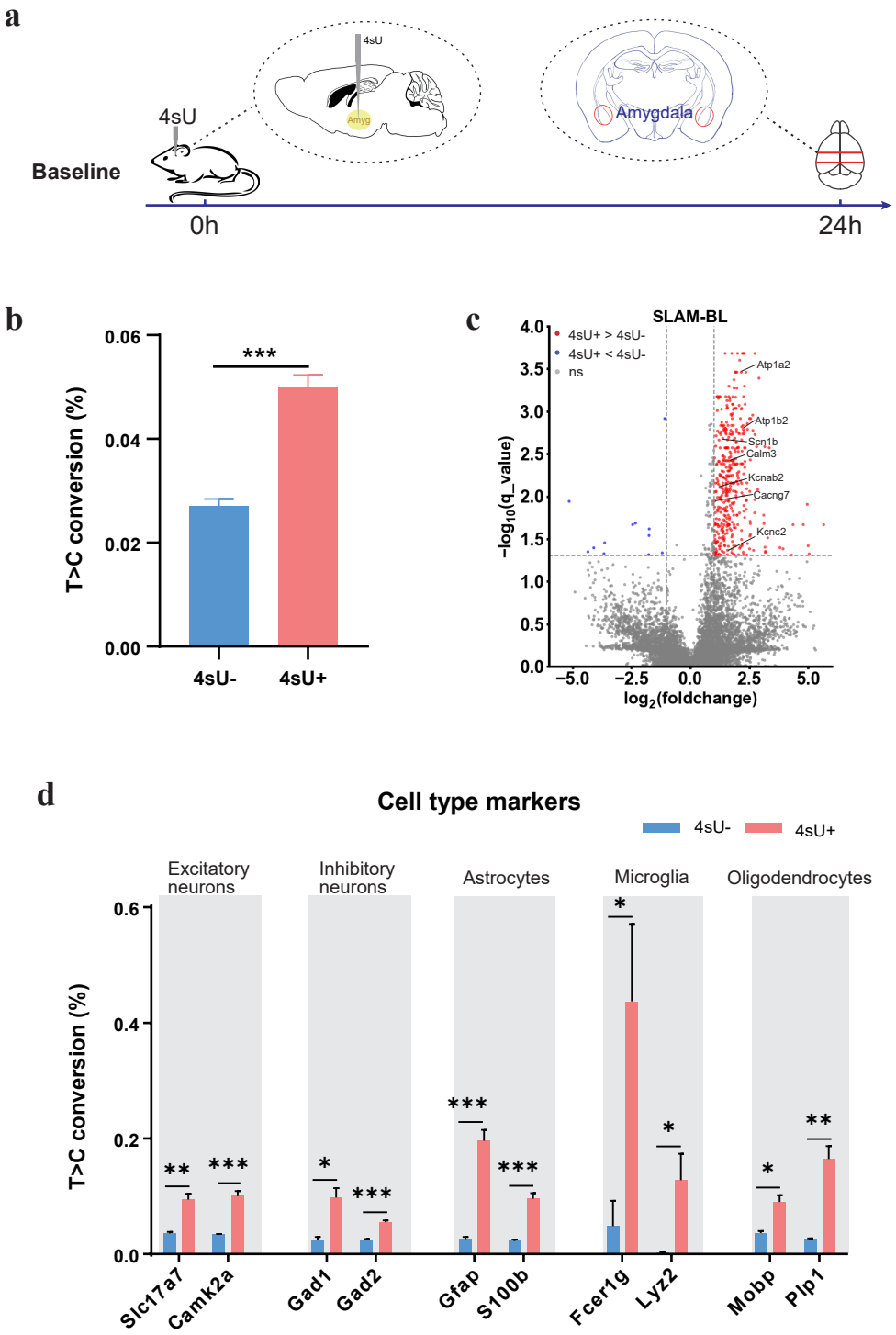

a
4sU
Tissue dissection
RNA extraction
IAA
Sequenceing
ACx
b
Biotin Dot-Blot after 4sU injection
biotin-oligo
none
2h
8h
24h
c
DAPI
TUNEL
Merge
DMSO
4sU
Positive control
ACx
50 μm
d
r=0.9960
4sU- gene expression (TPM)
4sU+ gene expression (TPM)

Figure 2


a
4sU
Baseline
4sU
Amyg
Amygdala
0h
24h
b
T>C conversion (%)
0.06
0.04
0.02
0.00
***
4sU-
4sU+
c
SLAM-BL
4sU+ > 4sU-
4sU+ < 4sU-
ns
Atp1a2
Atp1b2
Scn1b
Calm3
Kcnab2
Cacng7
Kcnc2
−log10(q_value)
log2(foldchange)
d
Cell type markers
4sU-
4sU+
Excitatory neurons
Inhibitory neurons
Astrocytes
Microglia
Oligodendrocytes
T>C conversion (%)
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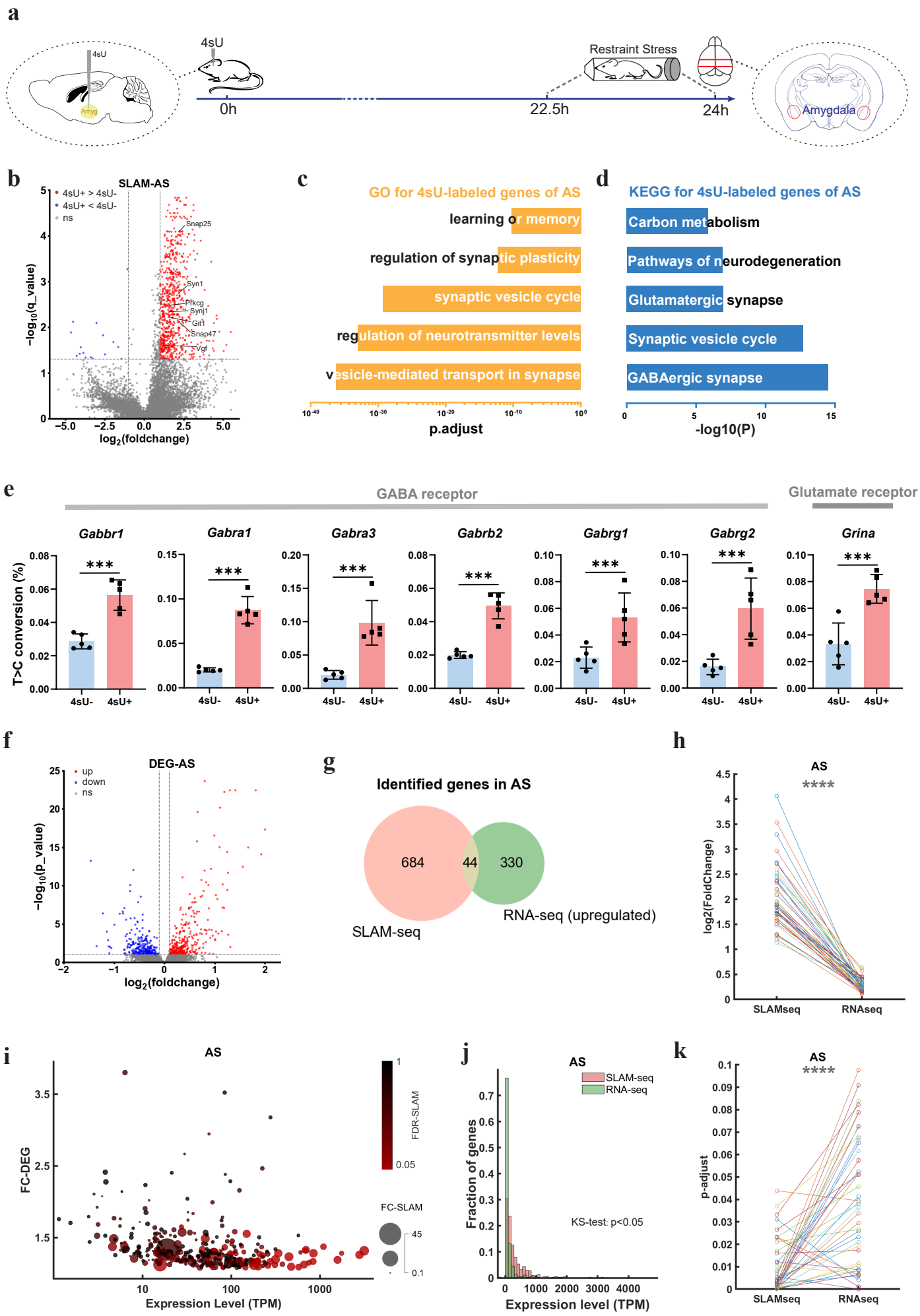
Camk2a
Gad1
Gad2
Gfap
S100b
Fcer1g
Lyz2
Mobp
Plp1

Figure 3


a
4sU
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4sU
0h
Restraint Stress
22.5h
24h
Amygdala
b
SLAM-AS
4sU+ > 4sU-
4sU+ < 4sU-
ns
Snap25
Syn1
Pfkcg
Synj1
Git1
Snap47
Vgf
−log10(q_value)
log2(foldchange)
c
GO for 4sU-labeled genes of AS
learning or memory
regulation of synaptic plasticity
synaptic vesicle cycle
regulation of neurotransmitter levels
vesicle-mediated transport in synapse
p.adjust
d
KEGG for 4sU-labeled genes of AS
Carbon metabolism
Pathways of neurodegeneration
Glutamatergic synapse
Synaptic vesicle cycle
GABAergic synapse
-log10(P)
e
GABA receptor
Glutamate receptor
Gabbr1
Gabra1
Gabra3
Gabrb2
Gabrg1
Gabrg2
Grina
T>C conversion (%)
4sU-
4sU+
f
DEG-AS
up
down
ns
−log10(p_value)
log2(foldchange)
g
Identified genes in AS
684
44
330
SLAM-seq
RNA-seq (upregulated)
h
AS
log2(FoldChange)
SLAMseq
RNAseq
i
AS
FC-DEG
Expression Level (TPM)
FDR-SLAM
FC-SLAM
j
AS
SLAM-seq
RNA-seq
Fraction of genes
KS-test: p<0.05
Expression level (TPM)
k
AS
p-adjust
SLAMseq
RNAseq

Figure 4

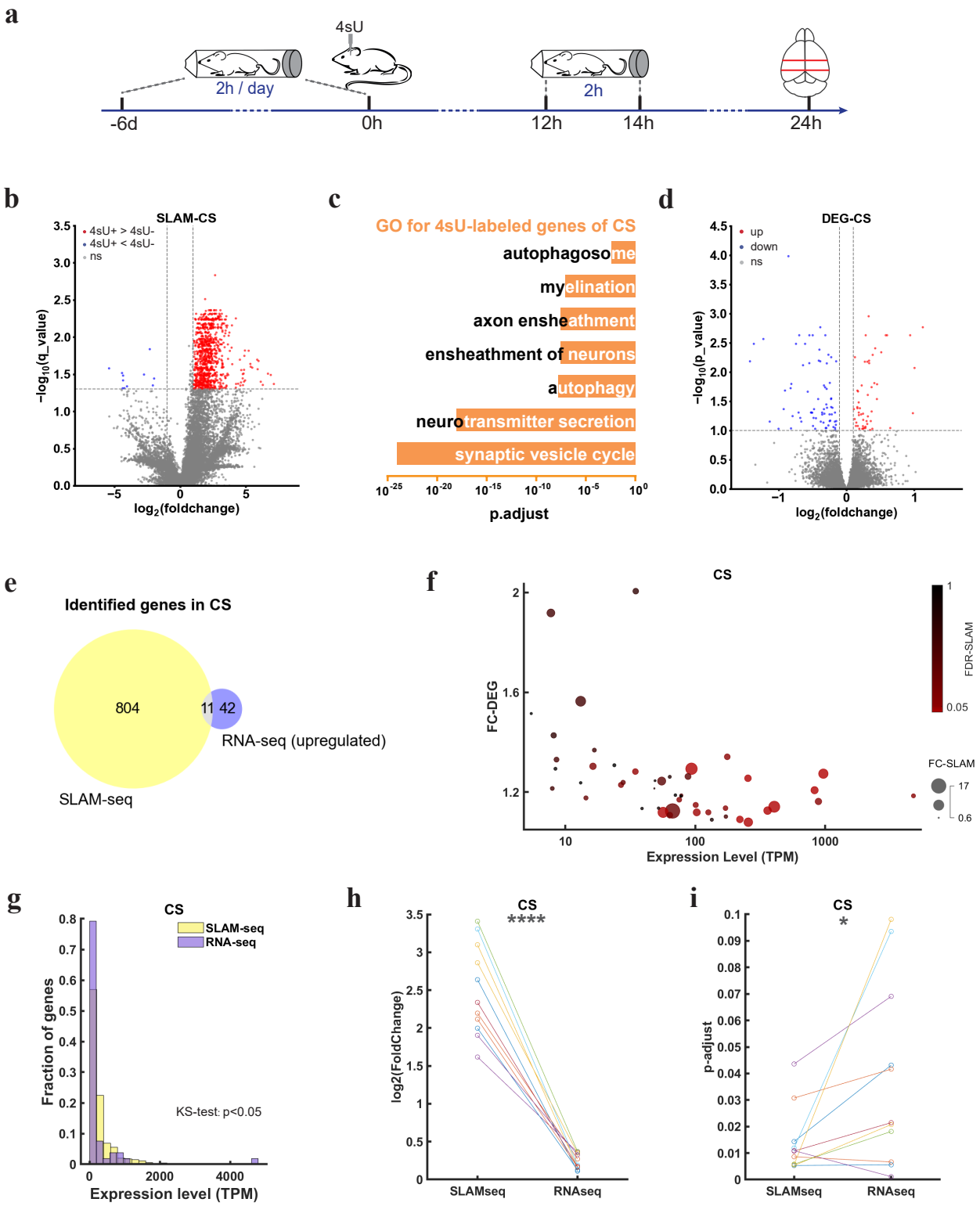
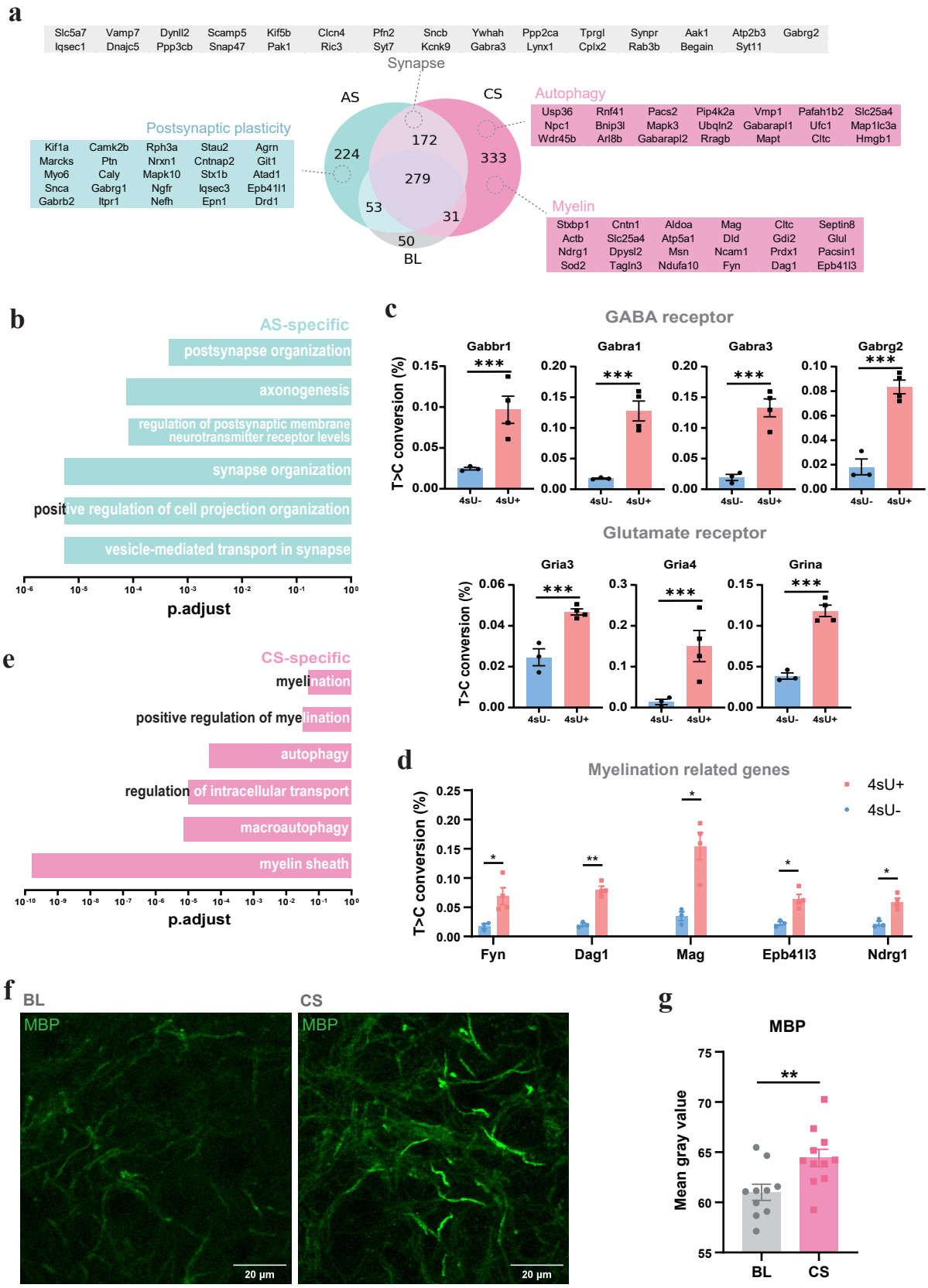

a
4sU
2h / day
2h
-6d
0h
12h
14h
24h
b
SLAM-CS
4sU+ > 4sU-
4sU+ < 4sU-
ns
−log10(q_value)
log2(foldchange)
c
GO for 4sU-labeled genes of CS
autophagosome
myelination
axon ensheathment
ensheathment of neurons
autophagy
neurotransmitter secretion
synaptic vesicle cycle
p.adjust
d
DEG-CS
up
down
ns
−log10(p_value)
log2(foldchange)
e
Identified genes in CS
804
11
42
RNA-seq (upregulated)
SLAM-seq
f
CS
FC-DEG
Expression Level (TPM)
FDR-SLAM
FC-SLAM
g
CS
SLAM-seq
RNA-seq
Fraction of genes
KS-test: p<0.05
Expression level (TPM)
h
CS
****
log2(FoldChange)
SLAMseq
RNAseq
i
CS
*
p-adjust
SLAMseq
RNAseq

Figure 5


a
Slc5a7 Vamp7 DynII2 Scamp5 Kif5b Clcn4 Pfn2 Sncb Ywhah Ppp2ca Tprgl Synpr Aak1 Atp2b3 Gabrg2
Iqsec1 Dnajc5 Ppp3cb Snap47 Pak1 Ric3 Syt7 Kcnk9 Gabra3 Lynx1 Cplx2 Rab3b Begain Syt11
Synapse
AS
CS
BL
224
172
333
279
53
31
50
Postsynaptic plasticity
Kif1a Camk2b Rph3a Stau2 Agrn
Marcks Ptn Nrxn1 Cntnap2 Git1
Myo6 Caly Mapk10 Stx1b Atad1
Snca Gabrg1 Ngfr Iqsec3 Epb41l1
Gabrb2 Itpr1 Nefh Epn1 Drd1
Autophagy
Usp36 Rnf41 Pacs2 Pip4k2a Vmp1 Pafah1b2 Slc25a4
Npc1 Bnip3l Mapk3 Ubqln2 Gabarapl1 Ufc1 Map1lc3a
Wdr45b Arl8b Gabarapl2 Rragb Mapt Cltc Hmgb1
Myelin
Stxbp1 Cntn1 Aldoa Mag Cltc Septin8
Actb Slc25a4 Atp5a1 Dld Gdi2 Glul
Ndrg1 Dpysl2 Msn Ncam1 Prdx1 Pacsin1
Sod2 Tagln3 Ndufa10 Fyn Dag1 Epb41l3
b
AS-specific
postsynapse organization
axonogenesis
regulation of postsynaptic membrane neurotransmitter receptor levels
synapse organization
positive regulation of cell projection organization
vesicle-mediated transport in synapse
p.adjust
c
GABA receptor
Gabbr1
Gabra1
Gabra3
Gabrg2
T>C conversion (%)
4sU-
4sU+
Glutamate receptor
Gria3
Gria4
Grina
e
CS-specific
myelination
positive regulation of myelination
autophagy
regulation of intracellular transport
macroautophagy
myelin sheath
p.adjust
d
Myelination related genes
4sU+
4sU-
Fyn
Dag1
Mag
Epb41l3
Ndrg1
f
BL
CS
MBP
20 μm
g
MBP
Mean gray value
BL
CS