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Corresponding author(s): Jinye Dai and Thomas C. Südhof

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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	QuantStudio (Applied Biosystems) Image Studio ver 5.2 (LI-COR Biosciences) Clampex 10.5.0.9 data acquisition software (Molecular Devices) Multiclamp 700B amplifier commander (Molecular Devices) NIS-Elements AR 5.21.01 (Nikon) VS-ASW FL 2.7 (Olympus)
Data analysis	Clampfit 10.5.0.9 (Molecular Devices) SigmaPlot 11.0.0.75 (Systat Software) Igor Pro 6.2.1.0 (Wavemetrics) Image Studio ver 5.2 (LI-COR Biosciences) NIS-Elements AR Analysis 5.21.01 (Nikon) QuantStudio Design&Analysis software v1.4.1 (Applied Biosystems)

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

All source data with statistic p-values in this study is available.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No statistical methods were used to predetermine sample sizes, but sample sizes in this study are similar to those generally used in the field (ref. 5, 6, 20, 23-31).
Data exclusions	No data were excluded from the analyses.
Replication	All results were independently replicated at least 3 times, as described in the figure legends.
Randomization	P0 pups were randomly picked up for making hippocampal cultures. Within litters, P21 animals received the same injections of ΔCre or Cre AAV viruses. In culture experiments, cover slips were assigned randomly.
Blinding	All data collection and analysis procedures were blinded with the exception of the experiment of CRISPR-mediated GluD1 deletion in the subiculum in vivo. These could not be blinded because the identification of mCherry expression was used to group control and infected neurons in Fig. 1j-1l. Moreover, qRT-PCR, immunoblotting, HA- and Flag-immunostaining measurements of expression levels were not blinded. Because these experiments provide a readout over which the experimentalist has no control.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

Primary antibodies: anti-Tuj1 mouse (1:2000; Covance; Cat# MMS-435P), anti-GluD1 rabbit (1:1000; Frontier Institute; Cat# Af1390), anti-HA mouse (1:1000; Covance; Cat# MMS101R), anti-HA rabbit (1:1000; Cell Signaling Technologies; Cat# 3724), anti-Flag mouse (1:1000; Sigma; Cat# F3165), anti-vGluT1 guinea pig (1:1000; Millipore; Cat# AB5905), anti-MAP2 rabbit (1:1000; Millipore; Cat# AB5622), anti-Homer1 rabbit (1:1000, Millipore, Car# ABN37).

Secondary antibodies: For immunocytochemistry and immunohistochemistry, anti-rabbit/anti-mouse/anti-guinea pig (1:1000, Alexa 647, Alexa 488, Alexa 405, Invitrogen) were applied accordingly in each experiment. For immunoblotting, donkey anti-rabbit/anti-mouse (1:10000, IRDye 800CW/680LT, Li-COR) were applied accordingly in each experiment.

Validation	All antibodies have been validated in previous papers (ref. 2, 5, 17, 23, 25, 28, 30).

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HEK 293T (CRL11268)
Authentication	HEK 293T cells were directly purchased from ATCC
Mycoplasma contamination	Cell lines were tested negative for mycoplasma contamination using the fluorochrome Hoechst DNA stain and the direct culture method.
Commonly misidentified lines (See ICLAC register)	None of the cell lines used is listed as commonly misidentified.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Cbln2 conditional KO mice were described previously (ref. 19). CRISPR/CAS9 knockin mice were obtained from Jackson Laboratory (Jax stock no: 024858). All studies used littermate male or female mice with the same age. Day0 pups were used for all cultured hippocampal neurons. Day21 mice were used for virus injections and were analyzed 2-4 weeks after virus injection.
Wild animals	This study did not involve wild animals.
Field-collected samples	This study did not involve field-collected samples.
Ethics oversight	All mice described in this study were maintained using established procedures according to protocols approved by the Stanford University Administrative Panel on Laboratory Animal Care.

Note that full information on the approval of the study protocol must also be provided in the manuscript.