

Reporting Summary

Nature Portfolio 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 Portfolio 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 (<i>n</i>) 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 <i>d</i> , Pearson's <i>r</i>), 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

- Single-nucleus RNA-seq: sequences from an ultra-high-throughput DIPSEQ T1 sequencer (BGI Genomics, China) were de-multiplexed using PISA, and reads were aligned to the GRCh38 mouse 606 genome using STAR (v2.7.4a) and sorted by Sambamba (v0.7.0).
-Fiber photometry: commercialized software from ThinkerTech Version 2022
-Single-unit data: commercialized Plexon Software Version 5.0
-Whole-cell recording data: Commercialized Software Clampex 10.4.
-Confocal data: Zeiss Commercialized Software Zen 2010.
-Olympus scanner data: Olympus VS200 ASW 3.2.1 (Olympus)
-Behavioral data: Biobase tracking system

Data analysis

For single-cell sequencing:

- Rstudio (version 2022)
- Seurat (v4.1.0) R toolkit (<https://github.com/satijalab/seurat>)
- STAR 2.7.4a

For behavior, imaging, and electrophysiological analysis:

- BIOBSERVE, for behavior experiments.
- Clampex 10.4 for in-vitro electrophysiological recordings
- NeuroExplorer v5.0 and Offline Sorter v4.0 (Plexon, Inc.) for in-vivo electrophysiological recordings
- Zeiss Commercialized Software Zen 2010 for confocal image analysis
- Olympus OlyVIA 3.2.1, Fiji ImageJ for tissue imaging analysis
- GraphPad Prism 8 for statistical analysis

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 Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

All data supporting the findings of this study are provided within the paper and its supplementary information. We have updated the single-nucleus sequencing data to the Gene Expression Omnibus (GEO) database. The data could be viewed at <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE273782>. All additional information will be made available upon reasonable request to the authors. Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

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. Sample sizes in behavior tests and electrophysiological recordings were based on work in previous publications (PMID: 27217145; PMID: 36924980). For imaging experiments, at least three animals per genotype or condition were used.
Data exclusions	For behavioral analyses, the mice with incorrect AAV injections/optical fiber implantations were excluded for further analyses. For whole-cell recordings, the neurons with $R_a > 18 \text{ M}\Omega$ or a 20% increase in R_a were excluded from further analyses, because stable $R_a (< 18 \text{ M}\Omega)$ is required for high-quality patch-clamp recordings. For single-unit recordings, the units with spike-to-noise ratio lower than 3/1 were excluded from further analyses, because lower spike-to-noise ratio would interfere with accurate reading of spikes.
Replication	All replicates reproduced the phenotypes. At least three independent cohorts were performed. The total number of animals and cells is reported for all experiments.
Randomization	All mice were randomly assigned to different groups.
Blinding	All investigators were blinded to group allocation during data collection and analysis.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used	-Rabbit polyclonal anti-Calbindin 1: Proteintech, CAT# 14479-1-AP; dilution 1:500 -Mouse monoclonal anti -NeuN: Millipore; CAT# MAB377; dilution 1:1000 -Guinea pig polyclonal anti-c-fos: Synaptic systems, CAT# 226004; dilution 1:1000 -Rabbit anti-RGS14: Proteintech, CAT# 16258-1-AP; dilution 1:1000 -Rat monoclonal anti-mCherry: Thermo Fisher Scientific, CAT# M11217; dilution 1:1000 -Rabbit polyclonal anti-GFP: Thermo Fisher Scientific, CAT# A-11122; dilution 1:1000 -Goat anti-mouse Alexa Fluor 647: Thermo Fisher Scientific, CAT# A-21236; dilution 1:1000 -Goat anti-guinea Pig Alexa Fluor 633: Thermo Fisher Scientific, CAT# A-21105; dilution 1:1000 -Goat anti- rabbit Alexa Fluor 488: Thermo Fisher Scientific, CAT# A-11034; dilution 1:1000 -Goat anti-rat Alexa Fluor 546: Thermo Fisher Scientific, CAT# A-11081; dilution 1:1000
Validation	-Calbindin 1: Website states the Rabbit polyclonal anti-Calbindin 1 antibody (14479-1-AP) has been tested in IHC, IF, IP, and WB. Reference: PubMed: 33762741; PubMed: 32272060; -NeuN: Website states the Mouse monoclonal anti -NeuN antibody (MAB377) has been tested in FC, IC, IF, IH, IH(P), IP and WB. Reference: PMID: 32369733 -c-fos: Website states the Guinea pig polyclonal anti-c-fos antibody (226004) works perfectly in ICC, IHC and IHC-P. Reference: PMID: 30801002 -RGS14: Website states the Rabbit polyclonal anti-RGS14 antibody(16258-1-AP) has been tested in WB, IP, IHC, ELISA. Reference: PMID: 38237897; PMID: 28776200 -mCherry: Website states the Rat monoclonal anti-mCherry antibody (M11217) has been tested in ICC, IHC, FC, IP, and WB. Reference: PMID: 27749828 -GFP: Website states the Rabbit polyclonal anti-GFP antibody (A-11122) has been tested in ICC, IHC, FC, IP, and WB. Reference: PMID: 32369733

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals

The C57BL/6 mice were purchased from the Animal Center of Huazhong University of Science and Technology. SST-Cre (JAX stock#: 013044), SST-Flp (JAX stock#: 028579), CB-Cre (JAX stock#: 028532), Esr1-Cre (JAX Stock#:0017913), Ai14 (JAX stock#: 007914), LSL-H2B-GFP (JAX stock#: 036761) mouse lines were bred in house. All mouse lines bred in-house were maintained on the C57BL/6J background, and heterozygotes were used in behavior tests. Mice (3–5 per cage) were maintained in standard cages under a 12-h light/dark cycle, with ambient temperature of 20–24 °C and relative humidity of 30–70%. Food and water provided ad libitum. Male mice aged 5–6 weeks were used for virus injection and, after 2–4 weeks of recovery, were used for the following experiments. To avoid sex-specific variance, we only used male mice. All animals were handled daily for 3 days in advance and habituated for 3 h in the test room before behavioral tests. All behavioral tests were conducted in the light phase (10:00–19:00).

Wild animals

No wild animals were used in this study

Reporting on sex

We have only used male mice in this study because the social behaviors of laboratory mice exhibit sex- and strain-dependent behavioral parameters (PMID: 35098101; 4744471)

Field-collected samples

No field-collected samples were used in this study.

Ethics oversight

All protocols and husbandry conditions were approved by the Animal Care and Use Committee of Huazhong University of Science and Technology, China.

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

Plants

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.