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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 Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	ImageLab (Bio-Rad). This is listed in the Methods section.
Data analysis	FlowJo, BioAnalyzer, CRISPR Genome Analyzer, GraphPad's Prism7, and Image J (NIH). They are listed in the Methods section.

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/reviewers upon request. 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

The authors declare that all data supporting the findings of this study are available within the paper and its Supplementary Information.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-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 our sample sizes are similar to those generally employed in the field.
Data exclusions	None of the data were excluded for the analysis.
Replication	Each experiment was replicated multiple times and the results were successfully reproduced.
Randomization	Control and injected mice were chosen randomly. We randomized the injection side (left or right side of the brain) for Thy1-YFP or Ai9 mice.
Blinding	The investigator was not blinded to the group of allocation during the experiment and when assessing the outcome. However, behavioral experiments were performed and analyzed as blind.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

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

Antibodies

Antibodies used	The mouse monoclonal RFP antibody (6G6) was purchased from ChromoTek; the chicken polyclonal GFP antibody (GFP-1020) from Aves Labs (Tigard, OR); the rabbit polyclonal GFAP antibody (AB5804) and the mouse monoclonal NeuN antibody (MAB377) from Millipore (Burlington, MA) the rabbit polyclonal Iba1 antibody (019-19741) from Wako Chemicals (Richmond, VA); and the rabbit polyclonal mGluR5 antibody (AGC-007) from Alomone Labs (Israel). The goat anti-mouse IgG2a-Cy3, goat anti-chicken-Cy2, goat anti-rabbit-Cy5, goat anti-mouse IgG1-Cy5, and donkey anti-rabbit IgG-Alexa Fluor 647 antibodies were purchased from Jackson ImmunoResearch Laboratories, Inc (West Grove, PA).
Validation	All antibodies were commercially available and were validated by manufacturers. All antibodies were also validated in immunostaining for mouse brain section in this study.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HEK293T cells from the Cell Culture Facility at UC Berkeley.
Authentication	HEK293T cell line was authenticated using short tandem repeat (STR) profiling.
Mycoplasma contamination	Mycoplasma test was conducted and the result was negative.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Animals and other organisms

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

Laboratory animals	Ai9 (in C57BL/6J background), Thy1-YFP (in C57BL/6J background), mdx, wild-type (in FVB background: FVB.129P2-Pde6b+ Tyrc-ch/AntJ), and Fmr1 KO (in FVB background: FVB.129P2-Pde6b+ Tyrc-ch Fmr1tm1Cgr/J) mice were obtained from Jackson Laboratory. The use and care of animals in this study follow the guidelines of the UTHSCSA and UC Berkeley Institutional Animal Care and Use Committee.
Wild animals	This study did not involve wild animals.
Field-collected samples	This study did not involve sample collected in field.

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Prepared as described in Methods.
Instrument	Attune NxT Flow Cytometer
Software	FlowJo
Cell population abundance	Cells were abundant
Gating strategy	FSC/SSC gating, live cell gating

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.