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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 (*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	Software used for data collection included VisuTrack Animal Behavior Analysis Software (Shanghai XinRuan), The Accurate 96 Real Time PCR System (DLAB), The Olympus VS200 Research Slide Scanner (Olympus), The Olympus Ixplore SpinSR confocal microscope (Olympus), A MultiClamp 700B amplifier and pCLAMP10 software(Axon Instruments), Tecnai G2 Spirit 120 kV transmission electron microscopy and Illumina HiSeq platform.
Data analysis	For behavior tests, data were analyzed using VisuTrack Animal Behavior Analysis Software (Shanghai XinRuan). For Real time-PCR experiments, data were analyzed using The Accurate 96 Real Time PCR System (DLAB). For imaging experiments, data were analyzed using CellSens (Olympus) and ImageJ (NIH, USA). For electrophysiology experiment, data analysis was performed using Minianalysis software. For RNA-sequencing, gene expression levels were quantified and differential expression analysis was performed using DESeq2. Data visualization and downstream analysis were conducted using R, with functional enrichment analysis performed using the ClusterProfiler package. Graphpad Prism 9.0 was used 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

RNA-seq and ChIP-seq data in this manuscript have been deposited in the NCBI GEO database under the accession number GSE282099 (reviewer token: yfaliyyijhkhdeb) and GSE282098 (reviewer token: wzibcscgdviptqp), respectively.

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	n/a
Reporting on race, ethnicity, or other socially relevant groupings	n/a
Population characteristics	n/a
Recruitment	n/a
Ethics oversight	n/a

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 method was used in deciding sample sizes. The sample size per group was determined from previous publications with similar methodologies.
Data exclusions	No data were excluded from analyses.
Replication	Each experiment has been conducted for at least three times.
Randomization	In the genetic knockout of BAF155 experiments, for behavioral test, no randomization was applicable because all knockout mice and their littermate control were included in the experiments; for histological and acute brain slice experiment, half male and half female mice were randomly allocated for each group; for RNAseq experiments, half male and half female mice were randomly allocated for each group.
Blinding	Investigators were blinded to group allocation during data 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
[ ]	[x] Antibodies
[x]	[ ] Eukaryotic cell lines
[x]	[ ] Palaeontology and archaeology
[ ]	[x] Animals and other organisms
[x]	[ ] Clinical data
[x]	[ ] Dual use research of concern
[x]	[ ] Plants

Methods

n/a	Involved in the study
[ ]	[x] ChIP-seq
[x]	[ ] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used

Primary antibodies used are PDGFRα antibody (Abcam, ab96569); anti-DIG-AP Fab fragments antibody (Sigma-Aldrich, 11093274910); Rat anti-MBP (Millipore, MAB395); Mouse anti-CC1 (Calbiochem, OP80); Guinea anti-vGlut1 (Synaptic Systems, 135304); Mouse anti-vGAT (Synaptic Systems, 131011); Rabbit anti-Homer1 (Synaptic Systems, 160003); Mouse anti-Synapsin-1 (Cell Signaling Technology, 5297); Goat anti-PDGFRα (R&D, AF1062); Mouse anti-Olig2 (Millipore, MABN50); Rabbit anti-Olig2 (Millipore, AB9610); Rabbit anti-Ki67 (Thermo, MA514520); Goat anti-GFP (Abcam, ab5450); BAF155 antibody (Cell Signaling Technology, 11956); Rabbit-anti-NG2 (Millipore, AB5320).

Validation

PDGFRα antibody (Abcam, ab96569): Validated for mouse and human, ICC/IF/Flow Cyt/IHC-P, manufacturer's website.
anti-DIG-AP Fab fragments antibody (Sigma-Aldrich, 11093274910): for the detection of digoxin labeled compounds, manufacturer's website.
Rat anti-MBP (Millipore, MAB395): Validated for mammals, IHC-Frozen section/ELISA, manufacturer's website.
Mouse anti-CC1 (Calbiochem, OP80): Validated for mouse, rat and human, IHC-Frozen section/ICC/IF, manufacturer's website.
Guinea anti-vGlut1 (Synaptic Systems, 135304): Validated for mouse and rat, WB/ICC/IHC/ IHC-P, manufacturer's website.
Mouse anti-vGAT (Synaptic Systems, 131011): Validated for mouse, rat and human, ICC/IF/IHC/ IH(P)/IP/WB, manufacturer's website.
Rabbit anti-Homer1 (Synaptic Systems, 160003): Validated for mouse, rat and human, ICC/IF/IHC/ IH(P)/IP/WB, manufacturer's website.
Mouse anti-Synapsin-1 (Cell Signaling Technology, 5297): Validated for mouse, rat and human, IF/IHC/IP/WB, manufacturer's website.
Goat anti-PDGFRα (R&D, AF1062): Validated for mouse, IF/WB, manufacturer's website.
Mouse anti-Olig2 (Millipore, MABN50): Validated for mouse, rat and human, ICC/IF/IHC/IP/WB, manufacturer's website.
Rabbit anti-Olig2 (Millipore, AB9610): Validated for mouse, rat and human, ICC/IF/IHC/ IH(P)/IP/WB, manufacturer's website.
Rabbit anti-Ki67 (Thermo, MA514520): Validated for mouse, rat and human, IHC(P/F)/ICC/IF/WB/Flow Cyt, manufacturer's website.
Goat anti-GFP (Abcam, ab5450): ICC/IF/WB/IHC-P, manufacturer's website.
BAF155 antibody (Cell Signaling Technology, 11956): Validated for mouse, rat, monkey and human, WB/IP/ChIP, manufacturer's website.
Rabbit-anti-NG2 (Millipore, AB5320): Validated for mouse, rat and human, IHC/WB, manufacturer's website.

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

PdgfrαCreER mice were acquired from Dr. Stephen Fancy at the University of California, San Francisco. PlpCreERT mice (JAX lab, Catalog #005975) were purchased from The Jackson Laboratory (US). Baf155-flox mice were generated by Biocytogen Pharmaceuticals (Beijing) Co., Ltd (China). PdgfrαCreER; Rosa-YFP reporter mice (JAX lab, Catalog #006148) were acquired from Dr. Stephen Fancy at the University of California, San Francisco. NestinCreERT2 (JAX lab, Catalog #016261) were purchased from The Jackson Laboratory (US).

Wild animals

The study did not involve wild animals

Reporting on sex

The finding does not apply to only one sex. Our study examined male and female animals, and similar findings are reported for both sexes.

Field-collected samples

The study did not involve samples collected from the field

Ethics oversight

All procedures were performed under the ethical approval of the Army medical University Institutional Animal Care and Use Committee (AMUWEC20223052).

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

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a

ChIP-seq

Data deposition

☒ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☒ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE282098
Files in database submission	GSM8635957;GSM8635958; GSM8635959; GSM8635960
Genome browser session (e.g. UCSC)	https://genome.ucsc.edu/s/Niu%20Lab/WXR

Methodology

Replicates	OPC, 1day, BAF155 ChIP; OPC, 1day, Input; OPC, 5day, BAF155 ChIP; OPC, 5day, Input
Sequencing depth	OPC 1day ChIP: The number of total raw read pairs was 35017484; the number of mapped reads was 65133894; the number of high-quality mapped read pairs was 17684684. OPC 1day input: The number of total raw read pairs was 31390877; the number of mapped reads was 59672647; the number of high-quality mapped read pairs was 21827035. OPC 5day ChIP: The number of total raw read pairs was 35374962; the number of mapped reads was 65320502; the number of high-quality mapped read pairs was 17485832. OPC 5day input: The number of total raw read pairs was 33750286; the number of mapped reads was 64276472; the number of high-quality mapped read pairs was 23093051.
Antibodies	BAF155 antibody (Cell Signaling Technology, 11956)
Peak calling parameters	Peak-calling: MACS2. Peak filtering: IDR. Peak annotation: ChIPseeker. High-quality mapped reads with a mean Phred quality score (MPAQ) of 30 or greater were used for subsequent analysis.
Data quality	Following ChIP-seq sequencing, raw reads were obtained and filtered to remove junctions using Cutadapt. Trimmomatic was then used to remove low quality reads, followed by quality control by FastQC.
Software	Illumina HiSeq platform was used to sequence. The software used for the analysis included cutadapt, Trimmomatic-0.35, FastQC, Bowtie2, samtools, macs2 callpeak and ChIPseeker.