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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	No custom code was used to collect data. All data were collected using the commercial programs provided with the instruments used as discussed in the manuscript methods.
Data analysis	No custom code was used to analyze data. Analysis was primarily done in Microsoft Excel and Prism. ImagJ, Flowjo, NMRviewJ, and IMARIS were also used as detailed in the manuscript methods.

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 manuscript and its supplementary files and are available from the authors on reasonable request.

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	Sample sizes were determined based on the number of samples required for statistical comparisons between groups.
Data exclusions	None.
Replication	All attempts at replication were successful.
Randomization	No randomization was required for non-animal work. For animal experiments, mice were randomized prior to handling, and all mice were treated with identical measures prior to selection.
Blinding	Blinding was not relevant to this work as no experimental treatments requiring this method were used.

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	Anti-mouse CD45-BV-510 (30-F11, BD Biosciences, San Jose, CA), F4/80-PerCP-Cy5.5 (BM8, Biolegend, San Diego, CA), CD11b-APC (M1/70, Biolegend, San Diego, CA), Ly6C-FITC (AL-21 Biolegend, San Diego, CA), Ly6G-PE (IA8, Biolegend, San Diego, CA), CD31-PE-Cy7 (390, Biolegend, San Diego, CA), CD326-APC-Cy7 (G8.8, Biolegend, San Diego, CA), and DAPI (Biolegend, San Diego, CA) were used for flow cytometry analysis.
Validation	Validation statements were provided by the manufacturer, and fluorescence intensities were further validated by absorption onto AbC control beads (Thermo Fisher, Waltham, MA).

Animals and other organisms

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

Laboratory animals	For PK and SPECT analysis, 7 week old female athymic nude mice were purchased from Charles River. For cell infiltration analysis, 7 week old female C57BL/6 mice were purchased from Charles River.
Wild animals	None.
Field-collected samples	None.

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	Excised right hind injections (n=3-4) were transferred to 2ml PBS and digested with 0.5mg/ml Collagenase IV (Sigma, St. Louis, MO) and 50 units of DNase I (Sigma, St. Louis, MO) at 37˚C for 45min. Digested tissue was filtered through a 70um cell strainer and repeatedly washed with sterile 2% FBS (Thermo Fisher, Waltham, MA) in PBS. After ACK (Thermo Fisher, Waltham, MA) lysis, cells were counted using a hemocytometer. Cells were stained as previously described by others. Briefly, cells were blocked with 2.4 G2 antibody (BD Biosciences, San Jose, CA) and stained antibody mixture.
Instrument	Cell type analysis was done on a FACSCANTO II (BD Biosciences, San Jose, CA).
Software	Flow cytometry data was gated and quantified with FlowJo (FlowJo LLC, Portland, Oregon) and exported for analysis.
Cell population abundance	Flow cytometry was used for analysis purposes only, not to isolated cell populations for further use. Relative abundance of specific cell types changes between experimental groups and is discussed withing the main text and supplemental information of the manuscript.
Gating strategy	Cell debris was removed using SSC-A vs FSC-A, singlets were isolated using FSC-A vs FSC-H, and live cells were isolated using DAPI vs FSC-A. >50k live cells were quantified for each experiement before cell analysis was stopped.

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