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Corresponding author(s): Nahrendorf

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	Imaris (version 7.7.2) or Matlab (version R2015a) softwares were use to reconstruct images. Affinity designer (version 1.6.1) software was used to stich 4X images for microscopy. MicroCT images were generated with Horos (version 1.1.7, https://www.horosproject.org) and Osirix software (version 3.8.1). MicroCT image renderings were performed in the Amira software (version 5.3) environment. FlowJo software (version X 10.0.7r2) was use to generate flow cytometry dotplots.
Data analysis	Imaris software (version 7.7.2) was used to analyze images. FlowJo sofware (X 10.0.7r2) was used to anayze flow cytometry data. Statistical analyses were performed using Graphpad Prism 7 software.

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 data that support the findings of this study are available from the corresponding authors upon 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 chosen based on prior imaging and flow cytometry data. No statistical predetermination of sample size was done.
Data exclusions	No data were excluded.
Replication	All experiments were done in duplicate the least unless specified otherwise. Certain experiments were done only once: costly experiments (e.g. electron microscopy, microCT), pilot experiments for technical optimization of the micro-injection technique (cell tracker titration, sub-dural cell tracker injection), or experiments performed for illustrative purpose (e.g. 1d).
Randomization	Mice were randomly allocated to experimental groups. There are no treatment studies in this manuscript.
Blinding	The investigator was not blinded to group allocation as this was obvious during the experiments (e.g. stroke vs sham).

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	Commercially available antibodies were used and are described appropriately in the method section and Supplemental Table 1.
Validation	Antibodies were commercially available and validated by the vendors.

Animals and other organisms

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

Laboratory animals	We used 4 week and 3 month old male C57BL/6 from Jackson laboratories, and bred heterozygous Cx3cr1GFP (3-6 month old males were used in experiments).

Wild animals	None
Field-collected samples	None

Human research participants

Policy information about studies involving human research participants

Population characteristics	Three patients that underwent cranial surgery were consented to provide a specimen. These were the three first available skull specimen available during the revision period.
Recruitment	The first three consecutively available patients undergoing craniotomy, that consented to participate, were recruited to investigate if skull channels are present in humans. There were no exclusion criteria.

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	Brain and tissue samples from mice were prepared by digestion, washing and staining as previously described and as listed in the method section.
Instrument	LSR2 flow cytometer
Software	Vendor software from BD
Cell population abundance	No cell sorting was done. All analyzed cell populations were abundant enough for analysis.
Gating strategy	The entire gating strategy is reported in supplemental data, and the appropriate staining controls for proper gate placements.

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