

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 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 The images on animal study were collected using Bruker 11.7T MRI and Paravision 6.0.1 software.

Data analysis The images were processed using custom code on MATLAB platform (www.mathworks.com, version 9.4.0.813654). The code for generating the images was deposited to GitHub.

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 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 source data underlying Figs. 8a–b, 9c, 10g–h, 11c are provided as a Source Data file. The other data that support the findings of this study are available from the corresponding author upon reasonable request.

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](https://www.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	Power analysis was performed to determine the appropriate sample size to draw the conclusion. Assume we accept a $p < 0.05$ as acceptable and a study with 95% power, the sample size for the study will be about 4. In this study, the minimal data size for one group is 5, which is sufficient.
Data exclusions	No data was excluded for analysis.
Replication	All subjects were measured successfully.
Randomization	For the purpose of this protocol on image-guided BBBO, the therapeutic arm is not involved. Having imaging readout prior to opening of the BBB including sham group is not necessary. The untreated contralateral hemisphere of the brain was sufficient and appropriate control to determine mannitol-induced local BBBO in the ipsilateral hemisphere by histology and MR imaging.
Blinding	The images of T1 post Gd and T2* perfusion were blindly processed by Guanshu Liu.

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used	Primary antibodies including anti-GFAP (1:250, Dako, cat. Z0334) ; anti-IBA-1 (1:250, Wako, cat. 019-19741); anti-NeuN (1:100, Cell Signaling Technology, cat. 94403S) were used in this study to evaluate the activation of astrocyte and microglia as well as the loss of neurons in the brain.
Validation	anti-GFAP, reactivity: cat, cow, dog, mouse, rat and sheep, application: immunohistochemistry, precipitation. anti-IBA-1, reactivity: human, mouse and rat, application: immunohistochemistry. anti-NeuN, reactivity: human, mouse and rat, application: western blot, immunoprecipitation, immunohistochemistry, chromatin immunoprecipitation, immunofluorescence, flow cytometry.

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	6-8-week-old male SCID/NCr mice (CB17/Icr-Prkdcscid/IcrCr, Charles River, cat. no. 561) were used in this study.
Wild animals	The study did not involve wild animals
Field-collected samples	The study did not involve samples collected from field.

Ethics oversight

All experimental protocols described in the protocol were approved by the Institutional Animal Care and Use Committee (IACUC) of the Johns Hopkins University

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