nature portfolio

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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	The raw sequencing data (fastq files) were collected at the Single Cell Genomics Core, Baylor College of Medicine, USA. Fastq raw data are available at https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE228974. Data for Immunofluorescent staining, Fluoro-Jade C staining, western blot and pain behavior were collected at Shao-jun Tang's lab at the Department of Neurobiology, University of Texas Medical Branch, Galveston, TX, USA.
Data analysis	The raw sequencing data were pre-processed using Cell Ranger (v.3.1.0) (10X Genomics). The resulting filtered single-cell expression matrices files from the WT, gp120Tg, gp120Tg/Gal3-/-, and Gal3-/- mice were imported into R for Seurat snRNA-seq integration analysis. Seurat R package (v.4.0.5) was utilized for dimension reduction and cluster analysis. R code for snRNA-seq can be available at github.com/tang-lab/astrocyte-critical-for-hiv-pain-pathogenesis.

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

All data which supports the findings here can be found in the manuscript and supplementary information. Source data for all experiments are provided with this study. The accession number for the snRNA-seq reported in this paper is GSE228974. The code used for the analysis described in this paper can be accessed upon requested.

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	no human participants in this study.
Reporting on race, ethnicity, or other socially relevant groupings	no human participants in this study.
Population characteristics	no human participants in this study.
Recruitment	no human participants in this study.
Ethics oversight	no human participants in this study.

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	Sample sizes were determined based on published work in literature. There are 4 groups (WT, gp120Tg, gp120TgGal3-/-., and Gal3-/-) for snRNA-seq study. Each group has 1 sample pooled from 3 mice. For all other studies, the sample sized are: n=4 for the WT group, n=6 for the gp120Tg group; n=3 for the gp120TgGal3-/- group.
Data exclusions	For snRNA-seq data, we set the filter criteria of nFeature_RNA > 200 and nFeature_RNA < 5000 as a QC control to remove the dead, low-quality nuclei, and doublets.
Replication	Except the snRNA-seq, all other experiment were replicated at least three times.
Randomization	Age- and sex-matched mice were randomly chosen for control and experimental groups.
Blinding	The pain behavioral tests were performed by experimenters who were not notified with the information about animal groups.

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
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Antibodies

Antibodies used	anti-GFAP antibody (Millipore, cat. no. AB5541), anti-Iba1 antibody (Wako, cat. no. 016–20001), anti-Vimentin antibody (Abcam, cat. no. ab137321), anti-NeuN antibody (Millipore, cat. no. ABN90), and anti-vGlut1 antibody (Synaptic systems, cat. no. 35 303).
Validation	Antibody were validated by bands of the expected molecular weight(s) for the target protein.

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	C57/BL mice; transgenic mice
Wild animals	No wild animals were used.
Reporting on sex	Male animals were used in this study. Because snRNA-seq experiments were expensive, we avoided complex experimental designs that involved both sexes.
Field-collected samples	No field-collected samples were used.
Ethics oversight	University of Texas Medical Branch and Stony Brook University

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