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	BD FACSDiva Software, ZEN software (Zeiss), QuantStudio Real-Time PCR software version 1.0 (Thermo Fisher Scientific).
Data analysis	FlowJo V10.6.2 software (TreeStar), GraphPad Prism V9 software (GraphPad Software, Inc.), ZEN software (Zeiss), QuantStudio Real-Time PCR software version 1.0 (Thermo Fisher Scientific), R V4.0.2 and V4.0.3..

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

The RNA-seq data are deposited in the Sequence Read Archive (SRA) repository database, the accession codes are included in the manuscript.

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	Three to nine mice per group were used in each experiment. Each experiment is shown in dot plots acknowleging each biologic replicate.
Data exclusions	No data were excluded from the analysis.
Replication	Experiments were repeated so that our data are based on at least two to three independent experiments with similar results. The precise number of repeats are given in the figure legend.
Randomization	We did not use randomization to assign animals to experimental groups.
Blinding	Blinding was not performed.

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	All antibody information and company source are provided in the method section
Validation	Antibodies were validated by the manufacturers' Quality control system (Biolegend) and were titrated in our lab.

Animals and other research organisms

Laboratory animals	This information is included in the Methods section, page.
Wild animals	N/A
Reporting on sex	Both sexes were used in the current study and not specifically reported. Similar results were obtained in both genders.
Field-collected samples	N/A
Ethics oversight	All animal experiments were approved and are in accordance with the local animal care committees (LAGeSo Berlin).

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

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	The biological source of the cells and the tissue processing steps are included in the Methods section on pages: .
Instrument	BD LSRFortessa™ X-20 Cell Analyzer and BD FACS Aria™ Fusion Flow Cytometer
Software	BD FACSDiva™ Software (BD Bioscience) and FlowJo V10.6.2 software (TreeStar)
Cell population abundance	We routinely achieved >98% purity of sorted populations
Gating strategy	The gating information is provided in figure legends.

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