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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	All software used is reported in the methods under the "Flow cytometry," "DNA sequencing and isolation," or "RNA sequencing" sections.
Data analysis	All software used is reported in the methods under the "Flow cytometry," "DNA sequencing and isolation," "RNA sequencing, differential gene expression analysis and enrichment," or "Statistical analysis" sections.

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

All relevant data are available from the authors. DNA sequencing data have been submitted under BioProject ID PRJNA353361. RNA sequencing data have been deposited in the Gene Expression Omnibus (GEO) database (accession number GSE115495).

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 following empirical statistical power analysis based on previous pilot studies (Khader et al. 2007 Nat Immunol, Griffiths et al, 2016 etc).
Data exclusions	One data point in Figure 1d and Supplementary Figure 1 (same mouse) was excluded based on Graphpad Prism's Grubb's outliers test (p<0.05)
Replication	Experiments were replicated at least twice to ensure reproducibility. All attempts at replication were successful.
Randomization	No method of randomization was used.
Blinding	J.R-M. was blinded during the histological analyses.

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	All antibodies are described in the methods under "Flow cytometry" or "in vitro Mtb infection" sections.
Validation	All antibodies were validated for the species and application by the manufacturer.

Animals and other organisms

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

Laboratory animals	The strain, sex, and age of all mice (Mus musculus) used in the study are reported in the methods in the "mice" section.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve field-collected samples.

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	Sample preparation is described in methods in the "Flow cytometry" section.
Instrument	Becton Dickinson (BD) Fortessa flow cytometer using FACS Diva software, or the BD FACSJazz flow cytometer using FACS Sortware software (BD).
Software	Flow cytometry experiments were analyzed using FlowJo (Tree Star Inc) and percentages were calculated using previously published gating strategies (Griffiths et al, Nat Comm 2016; Treerat et al, 2017, Mucosal Immunol)
Cell population abundance	N/A
Gating strategy	Reported in the methods in the "Flow cytometry" section. Percentages of different cell types were gated based on published gating strategies (Griffiths et al, 2016, Nature Comm; Treerat Et al, Mucosal Immunol 2017) and total cell numbers/lung were back calculated based on counted lung cell numbers.

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