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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.

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 LSRFortessa (BD Biosciences), BD FACSAria™ (BD Biosciences) and ABI-Prism 7900 (Thermo Fisher Scientific).
Data analysis	FlowJo (Treestar Inc., VX), Prism (GraphPad Inc., V6) and SDSv2.4 (Applied Biosystems)

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. 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

Data 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

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No sample size calculation was performed as no information on the experimental outcome was available at the time when this study was designed. Group sizes of 5-6 mice were chosen for experiments with 2-3 times replication, because we realized that these setups were sufficiently large to identify differences between groups.
Data exclusions	No data was excluded from any results.
Replication	All experiments were replicated successfully. A sufficiently high number of animals was used in each group to demonstrate statistical significance, as indicated in the figure legends.
Randomization	Mice were randomly allocated for immunization, infection and treatment. All animals were bred and kept under specific-pathogen-free conditions in the local animal facility, thus they have similar baseline immune condition.
Blinding	Investigators were not blinded to genotypes or treatment groups prior to data collection as non-subjective measures were used (i.e. antibody titer, viral load or body weight) to describe observations.

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used

The following fluorescence-labeled antibodies were used for flow cytometry:
CD4 (1:200, AF700, clone RM4-5, #4324114, eBioscience),
CD19 (1:200, PerCP/5.5, clone 1D3/CD19, #152406, BioLegend),
B220 (1:200, PE, clone RA3-6B2, #103208, eBioscience),
CD16/32 (1:100, clone 93, #101320, BioLegend),
CD45 (1:200, FITC, clone 30-F11, #103108, BioLegend),
CD45 (1:200, PE, clone 30-F11, #103108, BioLegend),
CD45 (1:200, AF700, clone 30-F11, #103108, BioLegend),
CD45 (1:200, APC, clone 30-F11, #103108, BioLegend),
CD45 (1:200, PerCP/5.5, clone 30-F11, #103108, BioLegend),
CD45 (1:200, BV421, clone 30-F11, #103108, BioLegend),
CD45 (1:200, APC-Cy7, clone 30-F11, #103108, BioLegend),
EpCAM (1:100, AF488, clone G8.8, #118210, BioLegend),
EpCAM (1,100, BV421, clone G8.8, #118225, BioLegend),
NKM16-2-4 (1:50, APC, clone NKM16-2-4, # 30102149, Miltenyi Biotec),
PD1 (1:100, FITC, clone 29F.1A12, #135214, BioLegend),
CXCR5 (1:100, APC, clone L138D7, #145506, BioLegend),
CD44 (1.100, BV421, clone IM7, # 103040, BioLegend),
FAS (1:100, PerCP/5.5, clone SA367H8, #152610, BioLegend),
GL7 (1:100, PB, clone GL7, #144614, BioLegend),
TSLP (1:30, biotinylated, #BAF555, R&D Systems),
Streptavidin (1:500, PE, #405204, Biolegend)
IgG1 (1.100, FITC, clone A85-1, #553533, BD Biosciences).
P-STAT1 (1:30, PE, clone 4a, #562069, BD Biosciences)
CD8a (1:100, FITC, clone 53-6.7, #100706, BioLegend)
CD11c (1:100, AF700; clone N418, #117320, BioLegend)
CD11b (1:100, PE-Cy7, clone M1/70, #101216, Biolegend)
CD103 (1:100, PE, clone 2E7, #121406, Biolegend)
MHC-II (1:100, I-A/I-E), BV421, clone M5/114.15.2, #107632, BioLegend)
CD3 (1.100, APC, clone 17A2, #100236, BioLegend)

CD3 (1:100, PE-Cy7, clone 17A2, #100220, BioLegend)

The following horseradish peroxidase-labeled antibodies were used for ELISA:
IgG (1:2,000, #62-6520, Invitrogen)
IgG1 (1:2,000, #A10551, Invitrogen)
IgG2c (1:7,000, #1078-05, Southern Biotech)
IgA (1:2,000, #626720, Invitrogen)

For in vivo neutralization of TSLP, anti-TSLP (R&D Systems MAB555, 25 µg per treatment) and IgG isotype control (R&D Systems MAB006, 25 µg per treatment) were used.

Validation

All antibodies used in this study were purchased from commercial sources and were validated by the vendors. Validation data are available on the manufacturer's websites. We further verified specificity by using isotype control antibodies when performing experiments.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Madin-Darby Canine Kidney (MDCK) cell lines were purchased from ATCC.
Authentication	MDCK cell lines were not authenticated.
Mycoplasma contamination	MDCK cell lines were not tested for Mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in this study.

Animals and other organisms

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

Laboratory animals	C57BL/6J wildtype and the following mutant mice having C57BL/6J genetic background were used: B6.A2G-Mx1 carrying intact Mx1 alleles (designated Mx1-WT), B6.A2G-Mx1-Ifnαr1-/- lacking functional IFN-α receptors (designated Mx1-Ifnαr1-/-), B6.A2G-Mx1-Ifnlr1-/- lacking functional IFN-λ receptors (designated Mx1-Ifnlr1-/-), Tslpr-/- mice, and Batf3-/- mice. In addition, BALB/c and DBA/2J mice were used for virus transmission studies. Male and female mice of 6-12 weeks of age were used.
Wild animals	Our study did not involve wild animals.
Field-collected samples	Our study did not involve samples collected from the field.
Ethics oversight	All experiments with mice were carried out in accordance with the guidelines of the Federation for Laboratory Animal Science Associations (FELASA) and the national animal welfare body. Experiments were in compliance with the German animal protection law and were approved by the animal welfare committee of the Regierungspräsidium Freiburg (permits G-16/177 and G-17/74).

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

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 details of sample preparation for flow cytometry are demonstrated in the Methods section.
Instrument	We used a BD LSRFortessa machine (BD Biosciences; 4 lasers - blue, red, violet and Yellow-Green; 14 fluorescent parameters) for analysing cells. For cell sorting, we used a BD FACSAria™ Fusion cell sorter machine (BD Biosciences)
Software	We used the software FACSDiva 6.2 and FACSD 8.0.1 (BD Biosciences) to collect the data and the software FlowJo (Treestar Inc., VX) to analyze the data.

Cell population abundance	After cell sorting, we obtained between 3x10e5 and 1x10e6 cells from each target population (which were used for RNA extraction). Post-sort analysis showed >93% to purity of target subpopulations.
Gating strategy	For cell sorting, we first selected cells based on FSC-A x SSC-A; then, we selected the singlets based on FSC-W x FSC-A; SSC-W x SSC-A and FSC x Live-Dead gating. Afterwards, we selected CD45 single positive cells and EpCAM single postive cells. M positve cells were further gated on EpCAM positive cells using NKM16-2-4 maker, as indicated in the Fig. S5. For Tfh and GC B cells gating, among single and live cells, Tfh cells were gated as: CD19-CD4+CD44+CXCR5+PD1+; GC B cells were gated as: CD4-B220 +GL7+Fas+.

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