nature portfolio

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Last updated by author(s): Jun 21, 2025

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 sequence data: fastp v0.20.1, BWA v0.7.17, Picard v2.25.5, SAMtools v1.17, Pilon v1.24. The qRT-PCR data: CFX Maestro Software 2.3 on CFX96. The western blot data: ChemiDoc MP and Tanon 5200. The ELISA and lactate assay data: Thermo Scientific Multiskan FC. The metabolites data: Multiquant (v3.0.2). The confocal image: Nikon A1HD25 system with NIS-Elements AR software. The growth curve: UVmini-1240. The histological imaging: TEKSQRAY SQS40P slide scanner, Olympus DP72 microscope equipped with a DS-Ri2 camera, and analyzed using DPVIEW (v2.0.4) and ImageJ (v1.53t). The flow cytometry data: FlowJo Software 10.9.0. The Structural prediction: AlphaFold2, PyMOL (v2.6.2), and AutoDock (v4.2). The RNA-seq data: fastp (v0.20.1), HISAT2 (v2.0.5), featureCounts (v1.5.0-p3), and DESeq2 (v1.20.0).
Data analysis	GraphPad Prism software 9.4.1 was used for all analyses.

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 generated in this study have been deposited in the Gene Expression Omnibus (GEO) database under accession number GSE291007. The metabolite profiling data generated in this study are provided in the Supplementary Data 1. Further information and requests for resources or reagents should be directed to and will be fulfilled by Yanlin Zhao (zhaoyl@chinacdc.cn) or Xiangmei Zhou (zhouxm@cau.edu.cn). Source data are provided with this paper.

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	No formal statistical methods were employed to predetermine sample sizes. Sample sizes were selected based on established standards in the field and historical experimental experience. Specifically, murine experiments utilized 5 animals per group, while cell-based assays employed 3 biological replicates. These sample sizes are consistent with those commonly employed and reported in comparable studies within the research area.
Data exclusions	Outliers were identified using Grubb's test in GraphPad Prism software. A data point was excluded in Figure 5b, as it was identified as an outlier. Exclusion criteria were pre-established.
Replication	All attempts at replication were successful as indicated in the figure legends.
Randomization	For animal experiments, mice were randomly chosen from 6-8 weeks old female mice in each group. For cellular experiments, cells were randomly cultured in the plate, infection or treatment were randomly applied to the cells.
Blinding	Blinding was not required for most quantitative measurements, as data were objectively recorded. However, histopathological evaluation of lung sections was performed by two board-certified veterinary pathologists blinded to group allocations to ensure unbiased assessment.

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

The following antibodies were used in this study: rabbit anti-HIF-1α antibody (Bioss, bs-0737R/polyclonal, 1:1000 for immunoblot analysis, 1:200 for immunofluorescence), rabbit anti-IL-1β antibody (Abmart, P01583/ polyclonal, 1:1000 for immunoblot analysis), rabbit anti-α-Tubulin antibody (Proteintech, 11224-1-AP/polyclonal, 1:2000 for immunoblot analysis), donkey anti-Rabbit lgG(H+L) Secondary Antibody, YSFluor™594 (Yeasen, 34212ES60, 1:400 for immunofluorescence), anti-mouse IL-1R (Bio X Cell, BE0256), polyclonal Armenian hamster IgG (Bio X Cell, BE0091), anti-mouse CD4-FITC (Elabscience, E-AB-F1353C, clone RM4-5, 5 μL/test), anti-mouse CD69-PE (Elabscience, E-AB-F1187D, clone H1.2F3, 5 μL per test), anti-mouse IFNγ-PECy7 (LIANKE, F21IFNG05, clone XMG1.2, 5 μL per test) , and anti-mouse IL-17A-Elab Fluor® 647 (Elabscience, E-AB-F1199M, clone TC11-18H10.1, 5 μL per test). They are described in Methods section.

Validation

All antibodies used in this study were obtained commercially and their validation was done by the individual companies.
Validation information:
Rabbit anti-HIF-1α antibody (Bioss, bs-0737R/polyclonal, 1:1000 for immunoblot analysis, 1:200 for immunofluorescence): http://www.bioss.com.cn/SpeNew01.asp?id=433&pro37=1&pro33=101&guige01=50ul
Rabbit anti-IL-1β antibody (Abmart, P01583/ polyclonal, 1:1000 for immunoblot analysis): http://www.ab-mart.com.cn/page.aspx?node=%2065%20&id=%2050298
Rabbit anti-α-Tubulin antibody (Proteintech, 11224-1-AP/polyclonal, 1:2000 for immunoblot analysis): https://www.ptglab.co.jp/products/TUBA1B-Antibody-11224-1-AP.htm
Donkey anti-Rabbit lgG(H+L) Secondary Antibody, YSFluor™594 (Yeasen, 34212ES60, 1:400 for immunofluorescence): https://www.yeasen.com/products/detail/118
Anti-mouse IL-1R (Bio X Cell, BE0256): https://bioxcell.com/invivomab-anti-mouse-il-1-r-cd121a-be0256
Polyclonal Armenian hamster IgG (Bio X Cell, BE0091): https://bioxcell.com/invivomab-polyclonal-armenian-hamster-igg-be0091
Anti-mouse CD4-FITC (Elabscience, E-AB-F1353C, clone RM4-5, 5 μL per test): http://wbm.elabscience.cn/p-fitc_anti_mouse_cd4_antibody_rm4_5-e_ab_f1353c
Anti-mouse CD69-PE (Elabscience, E-AB-F1187D, clone H1.2F3, 5 μL per test): http://wbm.elabscience.cn/p-pe_anti_mouse_cd69_antibody_h1_2f3-e_ab_f1187d
Anti-mouse IFNγ-PECy7 (LIANKE, F21IFNG05, clone XMG1.2, 5 μL per test): https://www.liankebio.com/product/anti-mouse-ifn-gamma-pe-cy7-clone-xmg1-2-15700.html
Anti-mouse IL-17A-Elab Fluor® 647 (Elabscience, E-AB-F1199M, clone TC11-18H10.1, 5 μL per test): https://www.elabscience.com/p/elab-fluor-647-anti-mouse-il-17a-antibody-tc11-18h10-1--e-ab-f1199m

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

6–8 weeks old female C57BL/6 mice were purchased from SPF Biotechnology Co.,Ltd. (Beijing). Mice are housed in ABSL-3 containment facilities under SPF conditions (12 h light/dark cycle, 25–27°C, 50% relative humidity) with ad libitum access to food and water.

Wild animals

No wild animals were used in the study.

Reporting on sex

Only female mice were used in this study as sex was not a consideration in this study.

Field-collected samples

No field collected samples were used in the study.

Ethics oversight

All experimental protocols and procedures were carried out in accordance with all relevant ethical regulations and guidelines, and were approved by the animal care and use committee (IACUC) protocols (20,110,611–01) at China Agricultural University. The animal experimental manipulations and protocols were approved by the Laboratory Animal Ethical Committee of China Agricultural University (permit number: AW02110202-2).

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	All cells were obtained from female C57BL/6 mice. Lymph nodes were passed through a 40um nylon membrane filter directly. Red blood cells were lysed by treating with red blood cell lysis buffer (Solarbio, R1010) and washed with PBS to obtain single cells.
Instrument	Samples were acquired using the BD Biosciences LSRFortessa X-20.
Software	Samples were analyzed using Flow Jo,v10.9.0. Raw numbers for each group were exported to excel. Following additional calculations, GraphPad Prism, v9.4.1 was used to plot and statistically analyze the percent and total number of the selected populations.
Cell population abundance	The number of single cells (identified as those cells with appropriate SSC-A,FSC-A and FSC-H parameters in Flow Jo, (as shown) was used to calculate the percent of population abundance for each cell population. Total number of cells for each subpopulation was then calculated using the percentage obtained as described and then multiplied by the calculated number of cells for each sample as counted under the microscope at a known dilution.
Gating strategy	Gating strategy can be found in Supplementary Fig.5.

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