nature portfolio

Corresponding author(s): Yunlong Huo

Last updated by author(s): Mar 19, 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	Flow cytometry was performed using BD FACSDiva v9.0 Software and CytExpert v2.3. Bruker 3D.SUITE was used for Micro-CT data collection.
Data analysis	Flowjo (ver.10.0) was used for flow cytometry analysis; Olyvia (ver.4.1) and Fiji(ImageJ) were used for histology analysis. DataViewer and CTAn (version 1.15) were used in Micro-CT analysis. For proteomic research, the DIA MS data were analyzed using DIA-NN 1.8.1. MS data that were searched against the UniProtKB reviewed (Swiss-prot) database (uniprot-Mus musculus (Mouse) [10090]-88473-20230717.fasta). Softwares for scRNA-seq: R 4.0.3;R package;Seurat 3.1.1;DoubletFinder 2.0;FindVariableFeatures; FindNeighbors; Findclusters; FindAllMarkers; FindMarkers; GO analysis; KEGG analysis; Matrix 1.2.14 ;fields 9.6 ;KernSmooth 2.23-15 ;ROCR 1.0-7 ;parallel 3.5.1;Slingshot 2.5.2; RNA velocity.

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 scRNA-seq data have been deposited in the Gene Expression Omnibus database under accession code GSE283267.
[https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE283267]
The proteomics data have been submitted to ProteomeXchange via the PRIDE database with Project accession code PXD053333.
[http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD053333]

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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	In vitro cell studies, sample size for cell lines' experiments and particle physical analysis were at least 3 to ensure repeatability during material preparation; sample size for in vitro transfection experiments were at least 5 to ensure the stability of transfection. For in vivo studies, sample size for particle distribution experiments were 4 and for disease model experiments were at least 10 in order to guarantee the confidence of the results between different independent mice.
Data exclusions	There was no data exclusions.
Replication	All samples used in experiments and sample size marked in manuscript means the independent biological replicates.
Randomization	For the same in vitro experiment, all samples from different groups were collected at the same time and were analyzed following the same

protocol. For in vivo experiments, the mice were randomly grouped. Subjects were randomly selected during detection, and data were classified according to group markers after detection. The tissue samples of different groups were collected and the experiments were carried out at the same time following the same protocol.

Blinding: During Ashcroft score analysis, single-blind strategy was used to assess and score the degree of fibrosis.

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: purified rat anti-mouse CD5, clone 53-7.3 (#100602,BioLegend); anti-mouse IgG (H+L) and F(ab')2 Fragment (PE Conjugate) (#8887S, CST); FVS 700 (live/death dye, #564997, BD Bioscience); CD3e (#562600, BD Bioscience); CD8a (#557654, BD Bioscience); anti-mouse FAP antibody (#ab218164, Abcam); CD3e (#78588T, Cell Signaling Technology); Anti-Claudin 5 (#ab131259, Abcam); anti-Calponin (#CL594-13938, Proteintech); anti-PKC zeta (aPKC; #CL488-26899, Proteintech); F4/80 (#565411, BD Bioscience); CD86 (#558703, BD Bioscience); CD163 (#12-1631-82, Thermo Fisher); FAP (#FAB9727G, R&D system); Pdgfra (#12-1401-81, Thermo Fisher); CD11c (#64804, Cell Signaling Technology); CD19 (#3574, Cell Signaling Technology); F4/80 (#30325, Cell Signaling Technology); CD163 (#ab316218, Abcam); iNos (#CL594-18985, Proteintech); Krt8 (#ab53280, Abcam); Sftpc (#ab90716, Abcam); Cdc42 (#10155-1-AP, Proteintech)

Validation: Verify statements are available on manufacturer's websites.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s): NIH/3T3 (#CRL-1658, ATCC), 293T cells (#CRL-3216, ATCC); NCTC1469 (#CCL-9.1, ATCC);AML12 (#CRL-2254, ATCC)

Authentication: All cell lines were authenticated by the supplier's according to STR profiling.

Mycoplasma contamination: All cell lines tested negative for mycoplasma contamination.

Commonly misidentified lines (See ICLAC register): *Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

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: C57BL/6J mice (males, 8 weeks and 16 months) were used in research.

Wild animals: The study did not involve wild animals.

Reporting on sex: Only male mice were used in research.

Field-collected samples: The model and control animals were raised in the laboratory animal center and housed at 21-25 ℃, with 40-50% humidity, 12 h light:12 h dark cycle, and free access to water and food for 28 days.

Ethics oversight: The animal care and experimental protocols conformed to the recommendations in the 8th Edition of the Guide for the Care and Use of Laboratory Animals of the National Institutes of Health (NIH, revised 2011) and were in accordance with the Animal Management Rules of China (Documentation 55, 2001, Ministry of Health, China). The study was approved by the Animal Research Committee of Shanghai Jiao Tong University.

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

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*

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	Primary t cells are centrifuged to remove culture medium and re-suspended with PBS. The mouse spleen and lung were carefully milled and filtered through 70 μm mesh to form single-cell suspension in cold PBS.
Instrument	Cytoflex (Beckman Coulter, Brea, CA, USA) and BD LSRFortessa (BD Bioscience)
Software	BD FACSDiva v9.0 Software, CytExpert v2.3, Flowjo (ver.10.0)
Cell population abundance	*Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.*
Gating strategy	First, FSC-A/SSC-A gating strategy was used for screening lymphocytes; then FSC-A/FSC-H was used for selecting single cells; last, FVS 700 was used for excluding dead cells from lymphocytes.

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