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	Synergy LX Multimode reader (BioTek Instruments), Helios™ mass cytometer (Fluidigm), DxFLEX flow cytometer (B73415, Beckman Coulter, Inc.) or sorted using a BD FACSAria II (643180, Becton Dickinson), Zeiss AxioScan7 (Germany), Protein Simple Imager (ProteinSimple, Santa Clara), Transmission electron microscope (H-7650 electron microscope, Hitachi) .
Data analysis	Cytosplore software, R (4.2.0), flowjoVX10 (BD Biosciences), Image-pro Plus (Media Cybernetics; Rockville), Cuffdiff v2.1.1, Prism software version 8.3.0 (GraphPad Software).

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 fecal microbiome data generated in this study have been deposited in the National Microbiology Data Center of China (https://data.mendeley.com/datasets/

j8bw86mc5h/1, DOI: 10.17632/j8bw86mc5h.1). Mass cytometry data generated in this study have been deposited in the Flow Repository (https://data.mendeley.com/datasets/vm5rkkk96d/1, DOI: 10.17632/vm5rkkk96d.1). RNA-sequencing data generated in this study have been deposited in the Genome Sequence Archive (GSA, https://bigd.big.ac.cn/gsa/) under project PRJCA034212 (accession number CRA021908).

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	The sex and gender were not considered in the study design. As shown in the last point-by-point response to the reviewers' comments, we found that there was no significant difference in the number of cDC1 cells between different sex.
Reporting on race, ethnicity, or other socially relevant groupings	Race/ethnicity was not considered in the study design as a covariate and neither as an inclusion nor exclusion criteria.
Population characteristics	This information was shown in Supplementary Table 1.
Recruitment	We studied biopsy specimens of patients undergoing a liver biopsy for medical reasons. Written informed consent was obtained from each participant.
Ethics oversight	The human studies were approved by the Ethical Committee of The First Bethune Hospital of Jilin University (No. 2023-573) and were performed in accordance with the ethical guidelines on the participation of human subjects in the Declaration of Helsinki.

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	We determined the sample size based on similar studies and a reliable calculation tool (https://www.bu.edu/researchsupport/compliance/animal-care/working-with-animals/research/sample-size-calculations-iacuc). For flow cytometry and mass cytometry, we calculated that at least 5 mice per group were needed to detect a predicted twofold difference in the quantity of c-kit+cDC1 between WD and NCD groups (P=0.01, 90% power), with an additional 3 mice per group for flow cytometry to account for potential losses. For H&E staining and ELISA, we used all 15 mice from the same cohort for a comprehensive assessment.
Data exclusions	No data were excluded from the analyses.
Replication	The number of biological replicates and experiments were provided in the figure legends.
Randomization	Samples/mice were randomly allocated to different groups.
Blinding	The value of NAS was assessed blindly with no group information.

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

CD45-89Y, BioLegend; CD3e-15in, BioLegend; CD117(c-kit)-141Pr, BioLegend; cleaved caspase 3-142Nd, CST; B220(CD45R)-143Nd, BioLegend; CD183(CXCR3)-144Nd, BioLegend; CD36-145Nd, BioLegend; CD27-146Nd, BioLegend; Ly-6G-147Sm, BioLegend; Ly-6C-148Nd, BioLegend; CX3CR1-149Sm, BioLegend; CD62L-151Eu,BioLegend; CD11C-152Sm, BioLegend; CD14-156Gd, BioLegend; Ki67-154Sm, eBioscience;CD103-155Gd, BioLegend; CD19-158Gd,BioLegend; TCRγ8-158Gd, Homemade; F4/80-159Tb, BiO-RAD; CD206-160Gd, BioLegend; CD25(IL-2R)-163Dy, BioLegend; TRB-161Dy, BioLegend; CD69-162Dy, BioLegend; CD182(CXCR2)-164Dy, BioLegend; CD64(FcYRI)-165HO, BioLegend; CD194(CCR4)-166ErCD192(CCR2)-167Er, R&D; FoxP3-168Er, eBioscience; CD127(1L-7Ra)-169Tm, BioLegend; CD161C(NK1.1)-170Er, BioLegend; CD86-171Yb, BioLegend; CD71-172Yb, BioLegend; CD49d-174Yb, BioLegend; CD196(CCR6)-175Lu, BioLegend; MHC 1l-176Yb, Xcel; CD4-197Au, BioLegend; CD8-198Pt, BioLegend; cD11b-20gBi, Homemade; Annexin V Apoptosis Detection Kit (556547, BD Biosciences); Rabbit anti-c-kit (1:200, AF6153, AffinityBiosciences); Rabbit ant-CD103(1:100,ab224202, Abcam); Rabbit anXCR1 (1:50,NBP1-02343, NOVUSBiologicals); HRP-coupled goat anti-rabbit lgG (1:1000, ab6721, Abcam); Cyto-lD@ Autophagy Detection Kit 2.0 (ENZ-KIT175-0050, Enz0 Life science Inc); Lc3 (1:1000, ab48394, Abcam); sequestosome-1 (p62, 1:1000, 23214Cell Signaling Technology); B-actin (1:2000, ab8226, Abcam); horseradish peroxidase (HRP)-conjugated antirabbit (1:5000, SA00001-2, ProteinTech Group); antimouse (1:5000, SA000011, ProteinTech Group) immunoglobulin; Fc Block, BioLegend; 7-AAD, BioLegend; CD45 Briliant Violet 51o", BioLegend; CD11c BriliantViolet 6o5"m, BioLegend; CD3 APC/Cyanine7, BioLegend; CD19 APC/Cyanine7, BioLegend; NK1.1 APC/Cyanine7, CD11bPE/Cyanine7, BioLegend; c-kitPE, BioLegend; cD103Brilliant Violet 421, BioLegend; CD172a FITC, BioLegend; XCR1 APC, BioLegend; IL-10 FITC, Biolegend; CD45.1 PE/Dazzle™ 594, Biolegend; CD45.2 PerCP-Cyanine5.5, Biolegend; CD44 FITC, Biolegend; CD62L PE, Biolegend; CD4 FITC, Biolegend; CD8 FITC, Biolegend; CD3 BV421, Biolegend; CD107a PE, Biolegend; INF-γ PE, Biolegend; Atg5 (1:1000, DF6010, Affinity).

Validation

Antibodies were quality checked and validated by the respective manufacturers and informations regarding the validation can be found on the companies' websites.

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

Six-week-old male C57BL/6 mice weighing 18-20 g were purchased from Vital River Laboratories. zDC-Cre (B6. Cg Zbtb46tm3.1(cre)Mnz/J, 028538) mice carrying the Zbtb46-driven Cre recombinase transgene were obtained from The Jackson Laboratory. The control c-kitflox/flox (C57BL/6J-Kitem1 flox Cya, S-CKO-03726) mice were obtained from Cyagen biological company. Lyz2-Cre mice (B6.129P2-Lyz2tm1(cre)Ifo/J, 004781) were purchased from the Jackson Laboratory. Atg5flox/flox mice (C57BL/6Smoc-Atg5em2(flox)Smoc, NM-CKO-0013) were obtained from Shanghai Model Organisms Center. T-cell receptor (TCR)-transgenic OT-I mice and OT-II mice were purchased from Jackson Laboratories.

Wild animals

No wild animals were used in this study.

Reporting on sex

Male mice were used for the experiments.

Field-collected samples

No field-collected samples were used in this study.

Ethics oversight

The protocol was approved by the Ethics Committee on the Use and Care of Animals of Jilin University (No. SY202012022 and SY202302019) and performed in accordance with the institutional guidelines.

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

Plants

Seed stocks	NA
Novel plant genotypes	NA
Authentication	NA

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 specific process was provided in the Method in our manuscript.
Instrument	Helios™ mass cytometer (Fluidigm), DxFLEX flow cytometer (B73415, Beckman Coulter, Inc.), BD FACSAria II (643180, Becton Dickinson).
Software	Cytosplore software, R (4.2.0), flowjoVX10 (BD Biosciences).
Cell population abundance	The purity of sorted cells was >90% and the cell populations were sufficient for downstream.
Gating strategy	Gating strategies were provided in Fig 2 and Fig S1, S3, S4, and S10.

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