

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ | 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ | 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: BD LSRFortessa X-20 cytometer (BD Biosciences), Beckman CytoFLEX cytometer (Beckman Coulter) Fluorescence-activated cell sorting: BD FACSAriaTM II cell sorter (BD biosciences) Western blotting: EC3TM 510 Imaging System (UVP, US) Light microscope (Olympus, Japan) Whole-slide fluorescence scanner: Panoramic MIDI (3DHISTECN) ELISA: Multiskan FC microplate photometer (Thermo Fisher Scientific)
Data analysis	GraphPad Prism (9.4.1), R package (4.0.3), Image J(1.8.0), FlowJo (V10), CellRanger (v7.1.0), Seurat (v3.2), Monocle2 R package software were used to analyze data.

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 mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the iProX partner repository with the dataset identifier PXD051763 [<https://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PX051763>]. The Single-Cell RNA-seq data generated in this study have been deposited in the GEO database under accession code GSE266493 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE266493>]. The ChIP-seq data generated in this study have been deposited in the GEO database under accession code GSE266492 [<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE266492>]. Uncropped western blots for data in the main and Supplementary Figures are provided in the Source data file. 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	No gender specific analyses were performed in this study. The trial recruited female and male patients without any prejudice. Specifically, among the six patients with sepsis, three were male and three were female. Among the non-septic patients, there were two males and four females.
Reporting on race, ethnicity, or other socially relevant groupings	There was no bias of recruitment in terms of race, ethnicity, or other socially relevant.
Population characteristics	Septic and non-septic patients were matched for age (range 45–87 years old), sex and ethnicity in the discovery. septic patients were eligible if they had evidence of infection along with acute organ dysfunction as defined by an increase in the Sequential [Sepsis-related] Organ Failure Assessment (SOFA) score of 2 points or more at study entry.
Recruitment	Septic and non-septic patients were recruited sequentially from the Intensive Care Units (ICU) of Wuhan Union Hospital, Tongji Medical College, Huazhong University of Science and Technology. Study candidates were identified by treating physicians at ICU of Wuhan Union Hospital. All participants included in this study signed an informed consent.
Ethics oversight	This project was reviewed and proved by the Ethics Committee of the Huazhong University of Science and Technology (2023-0143-01)

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](https://www.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	For mouse and human assays, common samples sizes of n=6 with a minimum of n=3 was chosen based on the statistical power of detecting meaningful effects. all experiments were conducted at least three times using biological replicates to ensure the reproducibility of the results.
Data exclusions	No data was excluded from the analysis.
Replication	All attempts at replication were successful. Data were representative of at least three independent experiments.
Randomization	All identified patient samples meeting diagnostic criteria were included in this study. For mouse experiments, animals were randomized.
Blinding	Investigators were blinded to group allocation during data collection, image quantification and data analysis.

Behavioural & social sciences study design

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

Study description	Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).
Research sample	State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.
Sampling strategy	Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.
Data collection	Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.
Timing	Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.
Data exclusions	If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.
Non-participation	State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.
Randomization	If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.

Ecological, evolutionary & environmental sciences study design

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

Study description	Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested, hierarchical), nature and number of experimental units and replicates.
Research sample	Describe the research sample (e.g. a group of tagged <i>Passer domesticus</i> , all <i>Stenocereus thurberi</i> within Organ Pipe Cactus National Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.
Sampling strategy	Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.
Data collection	Describe the data collection procedure, including who recorded the data and how.
Timing and spatial scale	Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken
Data exclusions	If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.
Reproducibility	Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.
Randomization	Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.
Blinding	Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.

Did the study involve field work? ☐ Yes ☐ No

Field work, collection and transport

Field conditions	<i>Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).</i>
Location	<i>State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).</i>
Access & import/export	<i>Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).</i>
Disturbance	<i>Describe any disturbance caused by the study and how it was minimized.</i>

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

CCL1 R&D Systems Cat# MAB845; RRID: AB_2070618
 CCL1 ABclonal Cat# A10670; RRID: AB_2768750
 IL-17A Santa Cruz Cat# sc-374218; RRID: AB_10988239
 β-actin Proteintech Cat# 66009-1-Ig; RRID: AB_2687938
 GAPDH Proteintech Cat# 60004-1-Ig; RRID: AB_2107436
 IL-6 Abcam Cat# ab229381; RRID: AB_2861234
 IL-1β ABclonal Cat# A1112; RRID: AB_2758416
 MUC-2 Proteintech Cat# 27675-1-AP; RRID: AB_2880943
 ZO-1 Proteintech Cat# 21773-1-AP; RRID: AB_10733242
 Occludin Proteintech Cat# 27260-1-AP; RRID: AB_2880820
 Wnt5a Zen Bio Cat# 619919; RRID: AB_2927750
 FZD5 Zen Bio Cat# 222996; RRID: AB_3075327
 β-Catenin Proteintech Cat# 51067-2-AP; RRID: AB_2086128
 Lef1 Proteintech Cat# 14972-1-AP; RRID: AB_2265677
 Lef1 Cell Signaling Technology Cat# 76010; RRID: AB_2799877
 TCF1/7 Abclonal Cat# A20835; RRID: AB_3066057
 HRP-goat anti-mouse IgG (HL) AntGene Cat# ANT019; RRID:
 PerCP-Cy™5.5 anti-mouse CD45 BD Biosciences Cat# 550994; RRID: AB_394003
 FITC anti-mouse CD11b BD Biosciences Cat# 561688; RRID: AB_10898180
 PE-Cy™7 anti-mouse Ly-6G BD Biosciences Cat# 560601; RRID: AB_1727562
 APC anti-mouse CD86 BD Biosciences Cat# 558703; RRID: AB_2075114
 BV421 anti-mouse F4/80 BD Biosciences Cat# 565411; RRID: AB_2734779
 BV650 anti-mouse CD11c BD Biosciences Cat# 564079; RRID: AB_2725779
 PE-CF594 anti-mouse Siglec-F BD Biosciences Cat# 552125; RRID: AB_394340
 BV605 anti-mouse CD206 Biolegend Cat# 141721; RRID: AB_2562340
 Fixable Viability Stain 510 BD Biosciences Cat# 564406; RRID: AB_2869572
 FITC anti-mouse CD45 BD Biosciences Cat# 553079; RRID: AB_394609
 PE-Cy™7 anti-mouse CD3e BD Biosciences Cat# 552774; RRID: AB_394460
 APC anti-mouse TCR γ/δ Biolegend Cat# 118115; RRID: AB_1731824
 Brilliant Violet 421™ anti-mouse IL-17A Biolegend Cat# 506925; RRID: AB_10900442
 APC/Fire750 anti-mouse CD8a Biolegend Cat# 100766; RRID: AB_2572113
 Purified rat anti-mouse CD16/CD32 BD Biosciences Cat# 553141; RRID: AB_39465

BV786 anti-mouse CD44 BD Biosciences Cat# 563736, RRID: AB_2738395
 Alexa Fluor 700 anti-Mouse Ly-6C (AL-21) BD Biosciences Cat# 561237, RRID: AB_10612017
 FITC anti-mouse IFN- γ (XMG1.2) BD Biosciences Cat# 554411, RRID: AB_395375
 PE anti-mouse CD198 (CCR8) Biolegend Cat# 150312, RRID: AB_2617032
 PE anti-mouse CD185 (CXCR5) Biolegend Cat# 145504, RRID: AB_2561968
 BV421 anti-mouse CD192 (CCR2) Biolegend Cat# 150605, RRID: AB_2571913
 BV421 anti-mouse Ki67 Biolegend Cat# 652411, RRID: AB_2562663
 Purified hamster anti-mouse TCR $\gamma\delta$ (GL4) BD Biosciences Cat# 553180, RRID: AB_394690
 BV605 anti-mouse IL-7R Thermo Fisher Scientific Cat# 416-1271-82, RRID: AB_2929104
 FITC anti-mouse/human CD11b Biolegend Cat# 101205, RRID: AB_312788
 PerCP-CyTM5.5 anti-human CD45 Biolegend Cat# 304027, RRID: AB_1236444
 PE-CyTM7 anti-human HLA-DR Biolegend Cat# 361611, RRID: AB_2783278
 APC anti-human CD169 (Siglec-1) Biolegend Cat# 307609, RRID: AB_314688
 Goat anti-rabbit IgG H&L (Alexa Fluor[®] 488) Abcam Cat# ab150077, RRID: AB_2630356
 Goat anti-mouse IgG H&L (Alexa Fluor[®] 594) Abcam Cat# ab150116, RRID: AB_2650601
 Goat anti-rabbit IgG H&L (HRP) Abcam Cat# ab205718, RRID: AB_2819160
 Cith3 Abcam Cat# ab5103, RRID: AB_304752
 MPO Abcam Cat# ab208670, RRID: AB_2864724

Validation

Similar results with validation results in relevant citations: Mouse CCL1/I-309/TCA-3 Antibody R&D Systems Cat# MAB845; RRID: AB_2070618 - Li L, Ni L, Heary RF, Elkabes S. J Neuroinflammation. 2020;17(1):73.
 CCL1 Rabbit pAb ABclonal Cat# A10670; RRID: AB_2768750. Supplier validation: "Species reactivity, Reacts with: Human, applications suitable for: WB, ELISA".
 IL-17 Antibody (G-4) Santa Cruz Cat# sc-374218, RRID: AB_10988239 - Yao Z, Fanslow WC, Seldin MF, et al. J Immunol. 2011;187(9):4392-4402.
 Beta Actin Monoclonal antibody Proteintech Cat# 66009-1-Ig, RRID: AB_2687938 - Qian H, Kang X, Hu J, et al. Nature. 2020;582(7813):550-556.
 GAPDH Monoclonal antibody Proteintech Cat# 60004-1-Ig, RRID: AB_2107436 - Zhou R, Wang G, Li Q, et al. Nature. 2022;612(7940):519-527.
 Recombinant Anti-IL-6 antibody Abcam Cat# ab229381, RRID: AB_2861234 - Cui L, Xu F, Xu C, Ding Y, Wang S, Du M. J Biomed Sci. 2022;29(1):101. Published 2022 Nov 24.
 IL1 β Rabbit pAb ABclonal Cat# A1112, RRID: AB_2758416. Supplier validation: "Species reactivity, Reacts with: Human, applications suitable for: WB, IF/ICC, ELISA".
 TNF- α Rabbit pAb Abclonal Cat# A11534, RRID: AB_2758597 - Cui L, Xu F, Xu C, Ding Y, Wang S, Du M. J Biomed Sci. 2022;29(1):101.
 MUC2 Polyclonal antibody Proteintech Cat# 27675-1-AP, RRID: AB_2880943 - Zhang Y, Tu S, Ji X, et al. Nat Commun. 2024;15(1):1333.
 ZO-1 Polyclonal antibody Proteintech Cat# 21773-1-AP, RRID: AB_10733242 - Yang J, Yang X, Wu G, et al. Cell Metab. 2023;35(9):1548-1562.e7.
 Occludin Polyclonal antibody Proteintech Cat# 27260-1-AP, RRID: AB_2880820 - Wang S, Fu W, Zhao X, et al. Microbiome. 2022;10(1):234.
 Wnt5a Rabbit pAb Zen Bio Cat# 619919, RRID: AB_2927750 - Wu DM, Zhang T, Liu YB, et al. Cell Death Dis. 2019;10(5):349.
 FZD5 Mouse mAb Zen Bio Cat# 222996, RRID: AB_3075327. Supplier validation: "Species reactivity, Reacts with: Human, applications suitable for: WB, FC, ELISA".
 Beta Catenin Polyclonal antibody Proteintech Cat# 51067-2-AP, RRID: AB_2086128 - Zhong X, Cui P, Cai Y, et al. Cell Metab. 2019;29(4):979-992.e4.
 LEF1 Polyclonal antibody Proteintech Cat# 14972-1-AP, RRID: AB_2265677 - Jing Y, Kang D, Liu L, et al. J Allergy Clin Immunol. 2019;144(5):1377-1390.e4.
 LEF1 (D6J2W) Rabbit mAb Cell Signaling Technology Cat# 76010, RRID: AB_2799877 - Sayed S, Song J, Wang L, et al. Br J Pharmacol. 2023;180(13):1748-1765.
 TCF1/TCF7 Rabbit mAb Abclonal Cat# A20835, RRID: AB_3066057. Supplier validation: "Species reactivity, Reacts with: Human, Mouse, Rat, applications suitable for: WB, ELISA".
 PerCP-CyTM5.5 Rat Anti-Mouse CD45 BD Biosciences Cat# 550994, RRID: AB_394003 - Trowbridge IS, Thomas ML. Annu Rev Immunol. 1994;12:85-116.
 FITC Rat Anti-CD11b BD Biosciences Cat# 561688, RRID: AB_10898180 - Lub M, van Kooyk Y, Figdor CG. J Leukoc Biol. 1996;59(5):648-655.
 PE-CyTM7 Rat Anti-Mouse Ly-6G BD Biosciences Cat# 560601, RRID: AB_1727562 - Fleming TJ, Fleming ML, Malek TR. J Immunol. 1993;151(5):2399-2408.
 APC Rat anti-Mouse CD86 BD Biosciences Cat# 558703, RRID: AB_2075114 - Bluestone JA. Immunity. 1995;2(6):555-559.
 BV421 Rat Anti-Mouse F4/80 BD Biosciences Cat# 565411, RRID: AB_2734779 - Austyn JM, Gordon S. Eur J Immunol. 1981;11(10):805-815.
 BV650 Hamster Anti-Mouse CD11c BD Biosciences Cat# 564079, RRID: AB_2725779 - Fagarasan S, Muramatsu M, Suzuki K, Nagaoka H, Hiai H, Honjo T. Science. 2002;298(5597):1424-1427.
 Purified Rat Anti-Mouse Siglec-F BD Biosciences Cat# 552125, RRID: AB_394340 - Angata T, Hingorani R, Varki NM, Varki A. J Biol Chem. 2001;276(48):45128-45136.
 Brilliant Violet 605TM anti-mouse CD206 (MMR) Antibody Biolegend Cat# 141721, RRID: AB_2562340 - Yang X, Zhang Y, Hosaka K, et al. Proc Natl Acad Sci U S A. 2015;112(22):E2900-E2909.
 Fixable Viability Stain 510 BD Biosciences Cat# 564406, RRID: AB_2869572 - Charles ED, Green RM, Marukian S, et al. Blood. 2008;111(3):1344-1356.
 FITC Rat Anti-Mouse CD45 BD Biosciences Cat# 553079, RRID: AB_394609 - Lagasse E, Connors H, Al-Dhalimy M, et al. Nat Med. 2000;6(11):1229-1234.

PE-Cy™7 Hamster Anti-Mouse CD3e BD Biosciences Cat# 552774, RRID: AB_394460 - sakov N, Wange RL, Burgess WH, Watts JD, Aebbersold R, Samelson LE. J Exp Med. 1995;181(1):375-380.

APC Anti-mouse TCR γ/δ Antibody Biolegend Cat# 118115, RRID: AB_1731824 - Garo LP, Ajay AK, Fujiwara M, et al. Nat Commun. 2021;12(1):2419.

Brilliant Violet 421™ anti-mouse IL-17A Antibody Biolegend Cat# 506925, RRID: AB_10900442 - Sanchez-Felipe L, Vercruysse T, Sharma S, et al. Nature. 2021;590(7845):320-325.

APC/Fire™ 750 anti-mouse CD8a Antibody Biolegend Cat# 100766, RRID: AB_2572113 - Cibrian D, Castillo-González R, Fernández-Gallego N, et al. J Allergy Clin Immunol. 2020;145(1):199-214.e11.

Purified Rat Anti-Mouse CD16/CD32 BD Biosciences Cat# 553141, RRID: AB_39465 - Araujo-Jorge T, Rivera MT, el Bouhidi A, Daëron M, Carlier Y. Infect Immun. 1993;61(11):4925-4928.

BV786 Rat Anti-Mouse CD44 BD Biosciences Cat# 563736, RRID: AB_2738395 - Bendelac A. Curr Opin Immunol. 1995;7(3):367-374.

Alexa Fluor® 700 Rat Anti-Mouse Ly-6C BD Biosciences Cat# 561237, RRID: AB_10612017 - Jutila DB, Kurk S, Jutila MA. Immunol Lett. 1994;41(1):49-57.

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PE anti-mouse CD198 (CCR8) Antibody Biolegend Cat# 150312, RRID: AB_2617032 - Bhatt D, Kang B, Sawant D, et al. J Exp Med. 2021;218(6):e20201329.

PE anti-mouse CD185 (CXCR5) Antibody Biolegend Cat# 145504, RRID: AB_2561968 - Silva M, Kato Y, Melo MB, et al. Sci Immunol. 2021;6(66):eabf1152.

Brilliant Violet 421™ anti-mouse CD192 (CCR2) Antibody Biolegend Cat# 150605, RRID: AB_2571913 - Hou X, Chen G, Bracamonte-Baran W, et al. Cell Rep. 2019;28(1):172-189.e7.

Brilliant Violet 421™ anti-mouse Ki-67 Antibody Biolegend Cat# 652411, RRID: AB_2562663 - Piper CJM, Rosser EC, Oleinika K, et al. Cell Rep. 2019;29(7):1878-1892.e7.

Purified Hamster Anti-Mouse TCR $\gamma\delta$ BD Biosciences Cat# 553180, RRID: AB_394690 - Vicari AP, Mocci S, Openshaw P, O'Garra A, Zlotnik A. Eur J Immunol. 1996;26(7):1424-1429.

CD127 Monoclonal Antibody (A7R34), Brilliant Violet™ 650, eBioscience™ Thermo Fisher Scientific Cat# 416-1271-82, RRID: AB_2929104. Supplier validation: "Species reactivity, Reacts with: Mouse, applications suitable for: Flow cytometric analysis".

FITC anti-mouse/human CD11b Biolegend Cat# 101205, RRID: AB_312788 - Cho YK, Yoon YC, Im H, et al. Nat Commun. 2022;13(1):4084.

PerCP-Cy™5.5 anti-human CD45 Biolegend Cat# 304027, RRID: AB_1236444 - Kaczanowska S, Beury DW, Gopalan V, et al. Cell. 2021;184(8):2033-2052.e21.

PE/Cyanine7 anti-human HLA-DR Antibody Biolegend Cat# 361611, RRID: AB_2783278 - Ziegler A, Heinig J, Müller C, et al. Immunobiology. 1986;171(1-2):77-92.

APC anti-human HLA-DR Antibody Biolegend Cat# 307609, RRID: AB_314688 - Radtke AJ, Chu CJ, Yaniv Z, et al. Nat Protoc. 2022;17(2):378-401.

Goat Anti-Rabbit IgG H&L (Alexa Fluor® 488) Abcam Cat# ab150077, RRID: AB_2630356 - Fang Y, Zhang MC, He Y, et al. Signal Transduct Target Ther. 2023;8(1):381.

Goat Anti-Mouse IgG H&L (Alexa Fluor® 594) Abcam Cat# ab150116, RRID: AB_2650601 - Liu TT, Shi X, Hu HW, et al. Cell Death Dis. 2023;14(10):654.

Goat Anti-Rabbit IgG H&L (HRP) Abcam Cat# ab205718, RRID: AB_2819160 - Prieto-Ruiz F, Gómez-Gil E, Vicente-Soler J, et al. iScience. 2023;26(9):107611.

Anti-Histone H3 (citru line R2 + R8 + R17) antibody Abcam Cat# ab5103, RRID: AB_304752 - Qiao S, Sun QY, Zhou P, et al. 2022;13:1046778.

Anti-Myeloperoxidase antibody [EPR20257] Abcam Cat# ab208670, RRID: AB_2864724 - Chen Q, Yin H, Liu S, et al. J Immunother Cancer. 2022;10(12):e005798.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	A549 (Cat# CL-0016), MH-S (Cat# CL-0597), and RAW264.7 (Cat# CL-0190) cell lines were purchased from Punosai Life Science and Technology Co., Ltd
Authentication	All cell lines have been authenticated by short tandem repeat (STR) fingerprinting.
Mycoplasma contamination	The cells used were analysed to confirm the absence of mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No misidentified cell lines were used.

Palaeontology and Archaeology

Specimen provenance	<i>Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.</i>
Specimen deposition	<i>Indicate where the specimens have been deposited to permit free access by other researchers.</i>

Dating methods

If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight

Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.

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

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

Male wild-type (WT) C57BL/6 J mice, TrdcCreERT2 mice and Il7rflox/flox mice (C57BL/6 background) weighing between 23.0–25.0 g and aged 8–10 weeks, were obtained from Vital River Laboratory Animal Technology Co Ltd., Beijing, China. TrdcCreERT2 mice were mated with Il7rflox/flox mice to generate TrdcCreERT2 Il7rflox/flox mice. Kaede-transgenic (Kaede-Tg) mice (B6.Cg-Gt(ROSA)26Sor<tm1.1(CAG-kikGR) Kgwa>) were kindly provided by M. Tomura (Tokyo University). All mice were housed and maintained in specific pathogen-free conditions with a 12:12 light/dark schedule, controlled ambient temperature, and humidity, and were given free access to food and water.

Wild animals

No wild animals were used.

Reporting on sex

Male animals were used in this study.

Field-collected samples

The study did not involve samples collected from the field.

Ethics oversight

Ethical approval for all experiments was obtained from the committee of experimental animals of Tongji Medical College (Permission number: 3250) and followed the guidelines set by the National Institutes of Health Guide for the Care and Use of Laboratory Animals.

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

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration

Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.

Study protocol

Note where the full trial protocol can be accessed OR if not available, explain why.

Data collection

Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.

Outcomes

Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

- | No | Yes |
|--------------------------|---|
| ☐ | ☐ Public health |
| ☐ | ☐ National security |
| ☐ | ☐ Crops and/or livestock |
| ☐ | ☐ Ecosystems |
| ☐ | ☐ Any other significant area |

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☐	☐ Demonstrate how to render a vaccine ineffective
☐	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☐	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☐	☐ Increase transmissibility of a pathogen
☐	☐ Alter the host range of a pathogen
☐	☐ Enable evasion of diagnostic/detection modalities
☐	☐ Enable the weaponization of a biological agent or toxin
☐	☐ Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	The study did not involve in Plants.
Novel plant genotypes	The study did not involve in Plants.
Authentication	The study did not involve in Plants.

ChIP-seq

Data deposition

- ☒ Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- ☒ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links <i>May remain private before publication.</i>	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE266492
Files in database submission	GEO
Genome browser session (e.g. UCSC)	Pubmed

Methodology

Replicates	No replicate.
Sequencing depth	Range of 200–500 BPS libraries was enriched, quantified, and sequenced using a HiSeq 2500 sequencer (Illumina)
Antibodies	Lef1 (Cell Signaling Technology, Cat# 76010, RRID: AB_2799877)
Peak calling parameters	Peak calling was performed using MACS2 with the following parameters: log2FoldChange >= 0.5/p-value <= 0.05. Range of 200–500 BPS libraries was enriched, quantified, and sequenced.
Data quality	High
Software	Trimmomatic v0.39; FastQC v0.11.9; Bowtie2 v2.4.4; Samtools v1.13; Picard; MACS2 v2.1.4; Deeptools v3.5.1; R/ChIPseeker; IGV; R/DESeq2

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 spleen and mesenteric lymph nodes were carefully homogenized using the plunger of a 1 ml syringe, and cells were rinsed from the strainer with 5 ml of PBS. Cells from the spleen, mesenteric lymph nodes, and blood were then subjected to red blood cell lysis. The small intestine was meticulously cleaned, opened lengthwise, and washed with PBS before being cut into 1.0–1.5 cm segments. These segments were then incubated twice in 20 ml of HBSS with 10 mM HEPES, 8% FBS, 4 mM EDTA, and 0.5 mM dithiothreitol at 37°C with constant agitation for 15 minutes. After thoroughly remove any residual EDTA, the remaining pieces of the small intestine and lung were finely chopped and digested in RPMI-1640 medium containing fetal bovine serum, collagenase IV (0.1 mg/mL), and DNase I (0.1 mg/mL) at 37°C for 40 minutes. The digested tissues were converted into a single-cell suspension through vigorous shaking and filtration through a 40-µm cell strainer following the removal of red blood cells. 1×10^6 isolated cells were counted and resuspended in 100 µl 1% BSA in PBS blocked with 5 ng µl⁻¹ of anti-CD16/CD32 antibody for 5 min at 4 °C, and then stained with the appropriate antibodies. The following antibodies were used for extracellular staining: fixable viability dye, CD45 (0.5 ng µl⁻¹), CD3 (0.5 ng µl⁻¹), TCR γδ (2 ng µl⁻¹), CD44 (4 ng µl⁻¹), Ly6C (0.6 ng µl⁻¹), IL7R (2 ng µl⁻¹), CD8 (0.6 ng µl⁻¹), CD11C (2 ng µl⁻¹), F4/80 (2 ng µl⁻¹), CD206 (5 ng µl⁻¹), CD86 (5 ng µl⁻¹), CD11B (2 ng µl⁻¹), Ly6G (2 ng µl⁻¹), CCR8 (3 ng µl⁻¹), CCR2 (5 ng µl⁻¹) and CXCR5 (5 ng µl⁻¹). For intracellular staining, cells were first stained for surface markers as detailed above, fixed and permeabilized, then the following antibodies were used: IL-17A (4 ng µl⁻¹), IFN-γ (4 ng µl⁻¹), Ki67 (2 ng µl⁻¹) and Siglec-F (0.5 ng µl⁻¹).

Instrument

Samples were analyzed on a BD LSRFortessa X-20 cytometer (BD Biosciences,) or Beckman CytoFLEX cytometer (Beckman Coulter).

Software

Samples were analyzed on a BD LSRFortessa X-20 cytometer (BD Biosciences,) or Beckman CytoFLEX cytometer (Beckman Coulter).

Cell population abundance

All cell populations were distinct in all experiments.

Gating strategy

Voltage and cell populations were set by unstained samples and stained control samples. All cells obtained were first gated on SSC-A (record at least 400,000 cells) and SSC-H to obtain single cells. Samples from the same experiment were recorded under the same settings. The FCS files were exported and analysed by FlowJo v10.

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

Magnetic resonance imaging

Experimental design

Design type

Indicate task or resting state; event-related or block design.

Design specifications

Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.

Behavioral performance measures

State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).

Acquisition

Imaging type(s)

Specify: functional, structural, diffusion, perfusion.

Field strength

Specify in Tesla

Sequence & imaging parameters

Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.

Area of acquisition

State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.

Diffusion MRI

☐

Used

☐

Not used

Preprocessing

Preprocessing software

Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).

Normalization

If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.

Normalization template

Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.

Noise and artifact removal

Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).

Volume censoring

Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.

Statistical modeling & inference

Model type and settings

Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).

Effect(s) tested

Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

(See [Eklund et al. 2016](#))

Correction

Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).

Models & analysis

n/a | Involved in the study

- ☐ ☐ Functional and/or effective connectivity
☐ ☐ Graph analysis
☐ ☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

Graph analysis

Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).

Multivariate modeling and predictive analysis

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.