

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	Data of Spatial Transcriptomic was collected using 10x Genomics Visium. RNA-seq data of isolated tumor-associated macrophages was collected using illumina NovaSeq X Plus. mRNA expression data of patients were retrieved from TCGA and GEO databases.
Data analysis	Statistical analysis: GraphPad Prism 9.0, R programming environment (version 4.2.2) Flow cytometry analysis software: FlowJo v10 Spatial Transcriptomics analysis software: Space Ranger (v2.1.0), Seurat (v4.0.5), SCTransform (v0.3.3) RNAseq analysis software: Fastp (v0.23.4), Star (v2.7.10a), Featurecount (v2.0.1), DESeq2(v1.4.5), Pheatmap (v1.0.8)

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](#)

Spatial transcriptomic data that support the findings of this study have been deposited in the Genome Sequence Archive in National Genomics Data Center, Beijing Institute of Genomics, Chinese Academy of Sciences, under accession number HRA010548 (<https://ngdc.cncb.ac.cn/gsa-human>). RNA-seq data of isolated tumor-associated macrophages from LLC tumor tissue has been deposited on Zenodo with an identifier of <https://doi.org/10.5281/zenodo.15605493>.

The human lung cancer data were derived from the TCGA Research Network: <http://cancergenome.nih.gov/>. The datasets derived from Gene Expression Omnibus that support the findings of this study are available in GSE24551, GSE14814, GSE86166, GSE72968, GSE157009, GSE58812, GSE57495, GSE85916, GSE16446, GSE157010 and GSE157011.

All other data supporting the findings of this study are available from the corresponding author on reasonable request

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	Human NSCLC tissue samples were included for analysis in this study irrespective of their sex and gender.
Reporting on race, ethnicity, or other socially relevant groupings	All of the enrolled patients were Chinese.
Population characteristics	Demographic characteristics of the human specimens utilized in this investigation were neither collected nor pertinent to the study objectives.
Recruitment	Non-small cell lung cancer tumor tissues were obtained from the Department of Oncology, Xinqiao Hospital, Third Military Medical University (XQ cohort), and Department of Oncology, Tongji Hospital, Huazhong University of Science and Technology (TJ cohort 1 and TJ cohort 2).
Ethics oversight	The protocols of this study were approved by the Institutional Review Boards of Tongji Hospital (Huazhong University of Science and Technology), Xinqiao Hospital (Third Military Medical University), and Shanghai Pulmonary Hospital (Tongji University School of Medicine). Informed consent was obtained from all participants.

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	No statistical methods were used to predetermine sample size. The numbers of samples used is sufficient to result in statistically significant differences under standard power calculations.
Data exclusions	None.
Replication	Experiments in the article were reliably reproduced, replication were described in the section of Statistics and reproducibility.
Randomization	For animal experiments, mice with similar age, gender and weight were randomly allocated to treatment groups.
Blinding	Investigators remained unblinded to experimental groups throughout the study, as all reported outcomes were derived from objective measurements that precluded potential observer bias.

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

Flow cytometry antibodies used in this study:

eBioscience Fixable Viability (#65-0865-14, eBioscience, 1:1000)
 anti-mouse CD45 (#103125, Biolegend, clone 30-F11, 1:100)
 anti-mouse CD3 (#100205, Biolegend, clone 17A2, 1:100)
 anti-mouse CD4 (#100433, Biolegend, clone GK1.5, 1:100)
 anti-mouse CD8 (#100721, Biolegend, clone 53-6.7, 1:100)
 anti-mouse NK1.1 (#156505, Biolegend, clone PK136, 1:100)
 anti-mouse CD11b (#101227, Biolegend, clone M1/70, 1:100)
 anti-mouse CD11c (#117320, Biolegend, clone N418, 1:100)
 anti-mouse F4/80 (#123123, Biolegend, clone BM8, 1:100)
 anti-mouse I-A/I-E (#107613, Biolegend, clone M5/114.152, 1:100)
 anti-mouse Gr-1 (#108407, Biolegend, clone RB6-8C5, 1:100)
 anti-Glut1 APC Antibody(#NB110-39113APC, Novus, 1:200)
 anti-mouse Arginase 1 (#17-3697-82, eBioscience, clone AlexF5, 1:100)
 anti-mouse IL-1 beta (Pro-form)(#25-7114-82, eBioscience, NJTEN3, 1:100)
 anti-mouse TGF-β1 (#141405, Biolegend, clone TW7-16B4, 1:100)
 anti-mouse IL-10 (#17-7101-82, eBioscience, clone JES5-16E3, 1:100)
 anti-mouse IFN-γ (#163511, Biolegend, clone XMG1.2, 1:100)
 anti-mouse TNF-α (#506307, Biolegend, clone MP6-XT22, 1:100)
 anti-mouse Granzyme B (#372217, Biolegend, clone GB11, 1:100)
 anti-mouse Perforin (#12-9392-82, eBioscience, clone eBioOMAK-D, 1:100)
 anti-mouse Ki-67 (#652403, Biolegend, clone 16A8, 1:100)
 anti mouse Anti-Active Caspase-3(#570332, BD, clone C92-605.rMAb (RUO), 1:100)

The antibodies used for Immunofluorescence and immunohistochemistry were listed:

Glut1 Monoclonal antibody (#73015, Cell Signaling Technology, 1:500)
 CD8α Monoclonal antibody (#70306, Cell Signaling Technology, 1:500)
 CD68 Monoclonal antibody (#76437, Cell Signaling Technology, 1:1500)
 CD8α Monoclonal antibody (#98941, Cell Signaling Technology, 1:100)

Antibodies used in vivo:

InVivoMAb anti-mouse CD8α (BE0061, clone 2.43, Bio X cell)
 InVivoMAb anti-mouse CD4 (BE0003-1, clone GK1.5, Bio X cell)
 InVivoMAb anti-mouse CSF1R(BE0213, AFS98, Bio X cell)
 InVivoMAb anti-mouse PD-L1(BE0101, clone 10F.9G2, Bio X Cell)

Validation

Representative flow cytometric data were validated as indicated in the figure legends. Antibodies are used to identify specific cell populations.

eBioscience Fixable Viability, <https://www.thermofisher.cn/order/catalog/product/cn/zh/65-0865-14>
 anti-mouse CD45, <https://www.biolegend.com/de-at/products/pacific-blue-anti-mouse-cd45-antibody-3102>
 anti-mouse CD3, <https://www.biolegend.com/en-gb/products/pe-anti-mouse-cd3-antibody-47>
 anti-mouse CD4, <https://www.biolegend.com/en-gb/products/percp-cyanine5-5-anti-mouse-cd4-antibody-4220>
 anti-mouse CD8, <https://www.biolegend.com/en-gb/products/pe-cyanine7-anti-mouse-cd8a-antibody-1906>
 anti-mouse NK1.1, <https://www.biolegend.com/en-gb/products/apc-anti-mouse-nk-11-antibody-19843>
 anti-mouse CD11b, <https://www.biolegend.com/de-de/products/percp-cyanine5-5-anti-mouse-human-cd11b-antibody-4257>
 anti-mouse CD11c, <https://www.biolegend.com/en-gb/products/alexa-fluor-700-anti-mouse-cd11c-antibody-3429>
 anti-mouse F4/80, <https://www.biolegend.com/en-gb/products/pacific-blue-anti-mouse-f4-80-antibody-4075>
 anti-mouse I-A/I-E, <https://www.biolegend.com/nl-be/products/apc-anti-mouse-i-a-i-e-antibody-2488>
 anti-mouse Gr-1, <https://www.biolegend.com/en-gb/products/pe-anti-mouse-ly-6g-ly-6c-gr-1-antibody-460>
 anti-mouse Glut1, https://www.novusbio.com/products/glut1-antibody_nb110-39113apc

anti-mouse Arginase 1, <https://www.thermofisher.cn/cn/zh/antibody/product/Arginase-1-Antibody-clone-A1exF5-Monoclonal/17-3697-82>
 anti-mouse IL-1 beta (Pro-form), <https://www.thermofisher.cn/cn/zh/antibody/product/IL-1-beta-Pro-form-Antibody-clone-NJTEN3-Monoclonal/25-7114-82>
 anti-mouse TGF- β 1, <https://www.biolegend.com/en-gb/products/apc-anti-mouse-lap-tgf-beta1-antibody-7310?GroupID=BLG9065>
 anti-mouse IL-10, <https://www.thermofisher.cn/cn/zh/antibody/product/IL-10-Antibody-clone-JES5-16E3-Monoclonal/17-7101-82>
 anti-mouse IFN- γ , <https://www.biolegend.com/en-gb/products/fitc-anti-mouse-ifn-gamma-antibody-24409>
 anti-mouse TNF- α , <https://www.biolegend.com/en-gb/products/apc-anti-mouse-tnf-alpha-antibody-975>
 anti-mouse Granzyme B, <https://www.biolegend.com/en-gb/sean-tuckers-tests/pacific-blue-anti-humanmouse-granzyme-b-recombinant-antibody-15596>
 anti-mouse Perforin, <https://www.thermofisher.cn/cn/zh/antibody/product/Perforin-Antibody-clone-eBioOMAK-D-Monoclonal/12-9392-82>
 anti-mouse Ki-67, <https://www.biolegend.com/en-gb/products/pe-anti-mouse-ki-67-antibody-8134>
 anti mouse Anti-Active Caspase-3, https://www.bdbiosciences.com/zh-cn/products/reagents/flow-cytometry-reagents/research-reagents/single-color-antibodies-ruo/alexa-fluor-647-rabbit-anti-active-caspase-3.570332?tab=product_details

The antibodies used for immunofluorescence and immunohistochemistry were listed:

Glut1 Monoclonal antibody, <https://www.cellsignal.cn/products/primary-antibodies/glut1-e4s6i-rabbit-mab/73015>
 CD8 α Monoclonal antibody, <https://www.cellsignal.com/products/primary-antibodies/cd8a-c8-144b-mouse-mab/70306>
 CD68 Monoclonal antibody, <https://www.cellsignal.com/products/primary-antibodies/cd68-d4b9c-xp-rabbit-mab/76437>
 CD8 α Monoclonal antibody, <https://www.cellsignal.com/products/primary-antibodies/cd8a-d4w2z-xp-rabbit-mab/98941>

Antibodies used in vivo:

InVivoMAb anti-mouse CD8 α , <https://bioxcell.com/invivomab-anti-mouse-cd8-alpha-be0061>
 InVivoMAb anti-mouse CD4, <https://bioxcell.com/invivomab-anti-mouse-cd4-be0003-1>
 InVivoMAb anti-mouse CSF1R, <https://bioxcell.com/invivomab-anti-mouse-csf1r-cd115-be0213>
 InVivoMAb anti-mouse PD-L1, <https://bioxcell.com/invivomab-anti-mouse-pd-l1-b7-h1-be0101>

Eukaryotic cell lines

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

Cell line source(s)	Colon adenocarcinoma MC38 (a gift from Dr. Liufu Deng, Shanghai Jiao Tong University), melanoma B16-F10 (ATCC CRL-6475), Lewis lung carcinoma LLC (ATCC CRL-1642), and TC-1 (BeNa Culture Collectin BNCC341334)
Authentication	All the cells lines used in this study were authenticated by short tandem repeat (STR) profiling prior to use.
Mycoplasma contamination	All the cells were routinely tested for mycoplasma contamination and the cells used in the study were tested negative.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in this study.

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	To generate myeloid-specific Slc2a1 knockout mice (Slc2a1cko), we crossed Slc2a1fl/fl mice with Lyz2Cre mice, both on a C57BL/6 background and obtained from Shanghai Model Organisms (Shanghai, China). Genotyping primers are listed in Supplementary Table 2. Wild-type C57BL/6J and BALB/c-nude mice were acquired from HFK Bioscience (Beijing, China). All experiments utilized 6- to 8-week-old mice. Mice were housed in specific pathogen-free (SPF) facilities at Third Military Medical University and under strictly controlled environmental conditions. The light/dark cycle was set at 12 hours each (lights on from 06:00 to 18:00). The ambient temperature was maintained at 23 $\pm$ 2°C with approximately 50% relative humidity. All animals had free access to food and water.
Wild animals	No wild animals were used in this study.
Reporting on sex	In this study, the mice were randomly assigned to different experimental groups and sex-matched littermate controls were followed.
Field-collected samples	This study did not involve samples collected from field.
Ethics oversight	All animal experiments were conducted in full compliance with the guidelines and under the approval of the Laboratory Animal Welfare and Ethics Committee of Third Military Medical University.

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

Plants

Seed stocks	Not applicable.
Novel plant genotypes	Not applicable.
Authentication	Not applicable.

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	Single-cell suspensions were prepared from tumor tissues by enzymatic digestion using 1 mg/mL collagenase I (Sigma) and 50 µg/mL DNase I (Roche). To assess T cell function, single-cell suspensions were stimulated for 5 hours with a Cell Activation Cocktail containing Brefeldin A (BioLegend; 1:250) prior to surface staining. Following surface marker staining, cells were fixed and permeabilized using the BD Fixation/Permeabilization Solution Kit for intracellular effector function cytokine detection, or the Foxp3/Transcription Factor Staining Buffer Set (eBioscience) for Ki-67 staining. Tumor-associated macrophages (CD11b+ GR1-F4/80+) were isolated from LLC tumors at day 20 post-inoculation using fluorescence-activated cell sorting.
Instrument	Data were obtained with a Gallios flow cytometer (BECKMAN COULTER)
Software	The results were analyzed with FlowJo v10 software (FlowJo LLC).
Cell population abundance	After antibody staining of single cells, FSC/SSC gating was used to determine pure live cell population to be analyzed.
Gating strategy	Cells were gated in an FSC/SSC plot to exclude debris in all acquired events. CD45+ cells were gated for analysis of immune cells.

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