

Reporting Summary

Nature Research 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 Research policies, see [Authors & Referees](#) 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 FACS Diva software version 7(BD), ZEN Black Imaging Software (ZEISS)

Data analysis FlowJo v10.0.6 (Tree Star Inc.), GraphPad Prism v6.0e (GraphPad Software Inc.), Panoramic Viewer v1.15.4 (3DHISTECH), ImageJ, RStudio v1.2, R v3.5.3, R packages: matrixStats, Matrix.utils, mixtools, matrix, tglkmeans (<https://tanaylab.bitbucket.io/tglkmeans/>). Strategies for scRNAseq clustering, cell projection, and homology analyses are similar to previously described approaches (see methods), and scripts are available upon request.

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

Mouse scRNAseq, CITEseq, and bulk RNAseq (Fig. 1b-h; Extended Data Fig. 1a-g; Fig. 2a,b,e; Extended Data Fig. 2a,-c,i; Fig. 3h; Extended Data Fig. 3e,f Fig. 4f) data are available on GEO accession code GSE131957. All human processed gene expression data will be made available on GEO, and raw sequencing reads will be uploaded to dbGaP.

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. We followed standards in the field.
Data exclusions	For the single-cell RNAseq data, we excluded cells based on pre-established criteria for single-cells, excluded cells with low number of detected transcripts and high mitochondria content. Cell filtering for the human data is described in a manuscript currently in preparation as noted.
Replication	All mouse experiments were replicated in three or more individual cohorts.
Randomization	Mice were allocated to study groups randomly.
Blinding	Quantification of mouse tumor sizes was blinded by de-identifying samples.

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
☐	☒ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

Mouse:
 CD45
 Siglec F (clone E50-2440, BD Pharmingen)
 CD11c (clone N418, Invitrogen)
 CD24 (clone M1/69, Invitrogen)
 CD103 (clone 2E7, BioLegend)
 XCR1 (clone ZET, BioLegend)
 I-A/I-E (clone M5/114.15.2, eBioscience)
 CD11b (clone M1/70, eBioscience)
 CD40 (clone 1C10, ebioscience)
 PD-L1 (clone MIH5, Invitrogen)
 IL-12p40 (clone C17.8, eBioscience)
 IL-4Rα (clone I015F8, BioLegend)
 AXL (clone MAXL8DS, Invitrogen)
 FAS (clone SA367H8, BioLegend)
 CD47 (clone miap301, Invitrogen)
 CD107a (clone 1D4B, Biolegend)
 CD200 (clone OX90, eBioscience)
 CD70 (clone FR70, eBioscience)
 CD127 (clone A7R34, Biolegend)
 CD3 (clone 145-2C11, eBioscience)
 CD8 (clone 53-6.7)
 CD4 (clone GK1.5 ebioscience)
 Ki67 (clone 16A8, BioLegend)

TNF α (clone MP6-XT22, eBioscience)
 IFN γ (clone XMG1.2, eBioscience)
 CD25 (clone PC61.5, eBioscience)
 FOXP3 (clone FJK-16s, Invitrogen)

Mouse CITEseq: antibodies were ordered in purified format and conjugated in-house as described in the methods.

CD103 (clone 2E7, BioLegend)
 XCR1 (clone ZET, BioLegend)
 I-A/I-E (clone M5/114.15.2, eBioscience)
 CD11b (clone M1/70, eBioscience)
 CD11c (clone N418, Invitrogen)

Human CITEseq: BioLegend TotalSeq-A human antibodies

CD40 (clone 5C3)
 CD141 (clone M80)
 CD103 (clone Ber-ACT8)
 CD1c (clone L161)
 HLA-DR (clone L243)
 XCR1 (clone S15046E)
 PD-L2 (clone 24F.10C12)
 PD-L1 (clone 29E.2A3)
 CD86 (clone IT2.2)

Validation

Flow cytometry:

CD45: Flow cytometric analysis of CD45 expression on mouse splenocytes (website)
 SiglecF: Flow cytometric analysis of SiglecF expression on mouse bone marrow leukocytes (website)
 CD11c: Flow cytometric analysis of CD11c expression on mouse splenocytes (website)
 CD24: Flow cytometric analysis of CD24 expression in mouse splenocytes (website)
 CD103: Flow cytometric analysis of CD103 expression on mouse splenocytes (website)
 XCR1: Flow cytometric analysis of XCR1 expression on mouse splenocytes (website)
 I-A/I-E: Flow cytometric analysis of I-A/I-E expression on mouse splenocytes (website)
 CD11b: Flow cytometric analysis of CD11b expression on mouse bone marrow leukocytes (website)
 CD40: Flow cytometric analysis of CD40 expression on mouse splenocytes (website)
 PD-L1: Flow cytometric analysis of PD-L1 expression on mouse splenocytes (website)
 IL-12p40: Flow cytometric analysis of IL-12p40 expression in mouse thioglycollate-elicited peritoneal exudate cells, stimulated overnight with LPS and IFN γ in the presence of Brefeldin A. (website)
 IL-4R α : Flow cytometric analysis of IL-4R α expression on mouse splenocytes (website)
 AXL: Flow cytometric analysis of AXL expression on mouse bone marrow cells cultured in the presence of GM-CSF for 7 days (website)
 FAS: Flow cytometric analysis of FAS expression on mouse thymocytes (website)
 CD47: Flow cytometric analysis of CD47 expression on mouse splenocytes (website)
 CD107a: Flow cytometric analysis of thioglycollate-elicited mouse peritoneal macrophages (website)
 CD200: Flow cytometric analysis of CD200 expression on mouse splenocytes (website)
 CD70: Flow cytometric analysis of CD70 expression on LPS and Anti-Mouse/Rat CD40 stimulated mouse splenocytes (website)
 CD127: Flow cytometric analysis of mouse splenocytes (website)
 CD3 (clone 145-2C11, eBioscience)
 CD8: Flow cytometric analysis of mouse splenocytes (website)
 CD4: Flow cytometric analysis of CD4 expression on mouse splenocytes (website).
 Ki67: Flow cytometric analysis of Ki67 expression in Con A-stimulated (3 days), fixed and permeabilized mouse splenocytes (website)
 TNF α : Flow cytometric analysis of TNF α expression mouse splenocytes that were stimulated with ConA for 2 days, followed by mouse IL-2 recombinant protein and mouse IL-4 recombinant protein for 3 days, and restimulated with immobilized anti-mouse CD3 and soluble anti-mouse CD28 in the presence of Brefeldin A for 5 hours (website)
 IFN γ : Flow cytometric analysis of intracellular IFN γ expression in mouse splenocytes that had been treated with Cell Stimulation Cocktail (plus protein transport inhibitors) for 5 hours, fixed, and permeabilized. (website)
 CD25: Flow cytometric analysis of CD25 expression on mouse splenocytes stimulated for 2 days with anti-CD3, anti-CD28, and mouse IL-2 recombinant protein (website).
 FOXP3: Flow cytometric analysis of intracellular FOXP3 expression in mouse splenocytes (website).

Human:

CD40: Flow cytometric analysis of CD40 expression on human peripheral blood lymphocytes (website)
 CD141: Flow cytometric analysis of CD141 expression on human peripheral blood monocytes (website)
 CD103: Flow cytometric analysis of CD103 expression on PHA-stimulated (3 day) human peripheral blood lymphocytes (website)
 CD1c: Flow cytometric analysis of CD1c expression on human peripheral blood lymphocytes (website)
 HLA-DR: Flow cytometric analysis of HLA-DR expression on human peripheral lymphocytes (website)
 XCR1: Flow cytometric analysis of XCR1 expression on human peripheral blood cells (website)
 PD-L2: Flow cytometric analysis of PD-L2 expression on human monocyte-derived dendritic cells (website)
 PD-L1: Flow cytometric analysis of PD-L1 expression on PHA-stimulated (3 days) human peripheral blood lymphocytes (website)
 CD86: Flow cytometric analysis of CD86 expression on human peripheral blood monocytes (website)

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	KP cells were received from Tyler Jacks. OP9-DL1 cells were received from Boris Reizis.
Authentication	Cells were functionally authenticated: KP cells were injected intravenously into mice and lung tumor progression at different timepoints was followed. OP9-DL1 cells were used to differentiate dendritic cells from bone marrow. Dendritic cell markers were followed over time after culture with OP9-DL1 cells.
Mycoplasma contamination	All cell lines tested negative for mycoplasma.
Commonly misidentified lines (See ICLAC register)	<i>Name any commonly misidentified cell lines used in the study and provide a rationale for their use.</i>

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	C57/BL6 and B6D2F1/J male mice between 8 and 12 weeks of age were used.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve field-collected samples.
Ethics oversight	Ethical approval for mouse experiments was obtained by the IACUC at Mount Sinai Hospital.

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

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	Characteristics of the patients analyzed in this study are fully described in a separate manuscript in publication. Patients were undergoing resection with curative intent of early-stage non-small-cell lung cancer lesions.
Recruitment	Patients over the age of 45 years old were identified and recruited for the study by the surgeons performing the above procedure in collaboration with clinical research coordinators.
Ethics oversight	The study protocol was approved by the Mount Sinai IRB (study protocols HS# 10-00472 and HS#-00135)

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

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 suspension was generated from mouse lungs and lymph nodes. Both tissues were minced with scissors prior to digestion with Collagenase IV for 30min (lung) or 25min (lymph node). The cells were filtered and subjected to red blood cell lysis.
Instrument	BD LSRFortessa
Software	FACS Diva software version 7 (BD)
Cell population abundance	Purity of sorted populations was ~97% in all samples and was assessed by flow cytometry.
Gating strategy	gating for DC1: 1. Gate on fsc-a vs. ssc-a was set to include all cell populations, but excluding debris. 2. Gate on fsc-a vs. fsc-w was set to exclude doublets. 3. gate on ssc-a vs. ssc-w was set to exclude doublets. 4. gate on fsc-a vs. DAPI was set to exclude dead cells (DAPI+). 5. gate on CD45+ vs. fsc-a was set to exclude CD45- cells. 6. gate on Siglec-F vs. CD11c was set to exclude

Siglec-F+ cells. 7. gate on MHC-II+ and CD11c+ cells was set to include all DC subsets. 8. gate on CD24+ cells was set to exclude contaminating macrophages/monocytes. 9. gate on CD11b- CD103+ cells was set (DC1).

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