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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 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	Zen software for confocal images, Excel, Living image software (Perkin Elmer) for IVIS images, BD FACSDiva Software for flow cytometry.
Data analysis	All statistical analyses were performed on Graphpad Prism (version 8). All flow-cytometry data were analysed on FlowJo (version 10). Confocal imgaing data were analysed on Zen software or Image J.

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 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

The main data supporting the results in this study are available within the paper and its Supplementary Information. The raw and analysed datasets generated during the study are too large to be publicly shared, yet they are available for research purposes from the corresponding authors on reasonable request.

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	Sample sizes were determined according to pilot studies and on the basis of previous experimental experience.
Data exclusions	No data were excluded.
Replication	The experiments were repeated, and the experimental findings were reproducible.
Randomization	All samples and organisms were randomly allocated into experimental groups.
Blinding	No formal blinding was used for the animal studies.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used

The following primary antibodies were used for flow cytometry.
1) Anti-mouse CD45 (Biolegend, Cat no: 103116, Clone: 30-F11)
2) Anti-mouse CD3 (Biolegend, Cat no: 100218, Clone: 17A2)
3) Anti-mouse CD4 (Biolegend, Cat no: 100421, Clone: GK1.5)
4) Anti-mouse CD8a (Biolegend, Cat no: 100711, Clone: 53-6.7)
5) Anti-mouse NKp46 (Biolegend, Cat no: 137606, Clone: 29A1.4)
6) Anti-mouse CD11c (Biolegend, Cat no: 117307, Clone: N418)
7) Anti-mouse/human Granzyme B (Biolegend, Cat no: 372208, Clone: QA16A02)
8) Anti-mouse IFN-γ (Biolegend, Cat no: 505849, Clone: XMG1.2)
9) Anti-mouse IFN-γ (Biolegend, Cat no: 505806, Clone: 492 XMG1.2)
10) Anti-mouse CD86 (Biolegend, Cat no: 105011, Clone: GL-1)
11) Anti-mouse CD16/32 (Biolegend, Cat no: 101302, Clone: 93)
12) Anti-mouse CD62L (Biolegend, Cat no: 104432, Clone: MEL-14)
13) Anti-mouse CD44 (BD Biosciences, Cat no: 560568, Clone: IM7)

The following primary antibodies were used for attachment to nanoparticles.
1) Anti-mouse CD54 (Biolegend, Cat no: 116102, Clone: YN1/1.7.4)
2) Anti-human CD54 (Biolegend, Cat no: 353102, Clone: HA58)

The following kit was used for ELISA or cytokine beads assay.
1) Mouse IP-10 ELISA kit (Invitrogen, Cat no: BMS6018)
2) LEGENplex Mouse Inflammation Panel with Filter Plate (Biolegend, Cat no: 740150)

Validation

All antibodies were verified by the supplier, and each lot was quality-tested.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Human lung microvascular endothelial cells (HLMVEC, adult) were purchased from Sigma-Aldrich. The 4T1 mammary carcinoma cell line expressing luciferase (4T1-Fluc-Neo) and the B16F10 cell line expressing luciferase (B16F10-Fluc-Puro) were purchased from Imanis Life Siences.
Authentication	HLMVEC was authenticated by the vendor. 4T1-Fluc-Neo and B16F10-Fluc-Puro were authenticated by CLEAR PCR panels from Charles River Laboratory.
Mycoplasma contamination	All cell lines were tested for mycoplasma contamination. No mycoplasma contamination was found.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Female Balb/c mice (50–56 days of age), and female and male C57/BL6 mice (50–56 days of age) were purchased from Charles River Laboratory.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	All animal experiments were performed according to the approved protocols by the Institutional Animal Care and Use Committee (IACUC) of the Faculty of Arts and Sciences (FAS), Harvard University, Cambridge.

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	The tissue was first made to single-cell suspensions using the tissue homogenization kit from Miltenyl Biotec, and single cells were resuspended in flow staining buffer for further processing.
Instrument	BD LSR II
Software	BD FACSDiva Software was used to collect data. All gating was done using FLowJo (version 10)
Cell population abundance	No sorting was performed.
Gating strategy	Cells were first gated on FSC/SSC. Singlet cells were then gated using FSC-H and FSC-A. Further gating was conducted on singlet cells. Positive and negative population gating were performed on the basis of FMO (Fluorescence Minus One).

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