

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 |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> 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 NIS-Elements (Version 4.60), Attune NxT Flow Cytometer System, In vivo imaging system, Agilent 1220 Infinity system, Malvern Zetasizer Software version 7.11, i-control 2.0 system, FEI Tecnai T-12 Cryo TEM system

Data analysis All statistical analyses were performed on Graphpad Prism (version 8). All flow cytometry data were analyzed on FlowJo software package (Version 10.4). Living image software (Perkin Elmer, version 4.5) was used to analyse bioluminescent and fluorescent images.

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 authors declare that all the data supporting the findings of this study are available within the article, and the Supplementary Information and Source Data file.

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 | The sample size were determined by G-power analysis software correspondingly. |
| Data exclusions | No data were excluded. |
| Replication | Experiments were repeated at least three time unless otherwise stated in the respective figure legend. Experimental findings were reproducible. |
| Randomization | All samples and cells are randomly allocated to each group. Mice were randomly allocated to each treatment group. |
| Blinding | The investigator is not blinded for most of the in vitro experiments since the experimental design, execution, and data analysis are performed by the same person. For the in vivo experiments such as bioluminescence imaging, tumor size measurement and survival monitoring were conducted by independent operators, who were blinded to the group allocation during data collection and analysis. |

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 |
|-------------------------------------|---|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Antibodies |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern |

Methods

| n/a | Involved in the study |
|-------------------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Flow cytometry |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |

Antibodies

Antibodies used

The following primary antibodies were used for flow cytometry. They are listed as antigen first, followed by supplier, catalog number and clone/lot number as applicable.

- 1) Anti-mouse CD45, Biolegend, cat. no. 103108, Clone: 30-F11;
- 2) Anti-mouse CD11b, Biolegend, cat. no. 101227, Clone: M1/70;
- 3) Anti-mouse IFN γ , Biolegend, cat. no. 505806, Clone: XMG1.2;
- 4) Anti-mouse F4/80, Biolegend, cat. no. 123116, Clone: BM8;
- 5) Anti-mouse Granzyme B, Biolegend, cat. no. 372212, Clone: QA16A02;
- 6) Anti-mouse CD3, Biolegend, cat. no. 100236, Clone: 17A2;
- 7) Anti-mouse CD4, Biolegend, cat. no. 100406, Clone: GK1.5;
- 8) PE Anti-mouse CD8a, Biolegend, cat. no. 100708, Clone: 53-6.7;
- 9) Anti-mouse CD11b, Biolegend, cat. no. 101206, Clone: M1/70;

The following primary antibodies were used for ELISA. They are listed as antigen first, followed by supplier, catalog number and clone/lot number as applicable.

- 1) Anti-rat IgG, eBioscience, cat. no. 88-50490-22;
- 2) Anti-mouse TNF- α , Biolegend, cat. no. 430904;
- 3) Anti-mouse IFN gamma, Biolegend, cat. no. 430804;

The following antibodies were used for western blot. They are listed as antigen first, followed by supplier, catalog number and clone/lot number as applicable.

- 1) HRP Anti-beta Actin antibody [AC-15], Abcam, cat. no. ab49900;
- 2) Gasdermin D (E9S1X) Rabbit mAb, Cell Signaling Technology, cat. no. 39754S;
- 3) Cleaved Gasdermin D (Asp276) (E3E3P) Rabbit mAb, Cell Signaling Technology, cat. no. 10137S
- 4) Cleaved Caspase-1 (Asp296) (E2G2I) Rabbit mAb, Cell Signaling Technology, cat. no. 89332S
- 5) HMGB1 (D3E5) Rabbit mAb, Cell Signaling Technology, cat. no. 6893S
- 6) Anti-rabbit IgG, HRP-linked Antibody, Cell Signaling Technology, cat. no. 7074P2

Validation All antibodies are commercially available. Antibodies employed here in our manuscript were previously reported and routinely used for the application used. The validation and quality control are performed by the corresponding vendors.

Eukaryotic cell lines

Policy information about [cell lines](#)

| | |
|---|--|
| Cell line source(s) | The murine melanoma cell line B16F10 and murine breast cancer cell line 4T1 are from ATCC. The murine B16F10-luc and 4T1-luc are purchased from Imanis Life Sciences. ID-8-Luc cells are provided by Dr. Paula Hammond's lab at MIT. |
| Authentication | The cell lines were morphologically confirmed according to the information provided by ATCC and Imanis Life Sciences. |
| Mycoplasma contamination | All cell lines are tested for mycoplasma contamination. No mycoplasma contamination is 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 | Male and female C57BL/6 mice (6-8 weeks), and female Balb/c mice (6-8 weeks) were purchased from Jackson Lab. The animals were bred in the pathogen-free facility with a 12 h light/dark cycle at 20 ± 3 °C and humidity (40%-70%) and had ad libitum access to food and water. |
| Wild animals | The study did not involve wild animals. |
| Field-collected samples | The study did not involve samples collected from field. |
| Ethics oversight | The animal study protocol (M006373) was approved by the Institutional Animal Care and Use Committee at the University of Wisconsin-Madison. |

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

| | |
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| Sample preparation | For tissue sample, the tissue was first mechanically disrupted from mice and divided into small pieces and homogenized in cold staining buffer to form single cell suspensions in the presence of digestive enzyme. |
| Instrument | ThermoFisher Attune Flow Cytometer |
| Software | FlowJo software package (version 10.4; TreeStar, USA, 2014) |
| Cell population abundance | No sorting was performed. |
| Gating strategy | The gating strategies are displayed in the supplementary information. Briefly, preliminary FSC/SSC gates were utilized for debris exclusion and locating the position of lymphocytes. Immune cells were gated by FITC/APC/SSA to specify dendritic cells or T cells. Activated dendritic cells were gated by CD80-PE/CD86-APC and activated T cells were gated by CD3-APC/CD8-PE. |

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