

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

Data analysis

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](#)

All data supporting the findings of this study are included in the Source Data file and Supplementary Information. The RNA sequencing data have been deposited in the NCBI Sequence Read Archive (SRA) under accession number PRJNA1330898 [<https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1330898>].

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

All the human research participants in this study were male.

Reporting on race, ethnicity, or other socially relevant groupings

All human research participants were Chinese.

Population characteristics

The clinical samples used for biological analysis were all from patients of Renji Hospital Affiliated to Shanghai Jiao Tong University School of Medicine with informed consent after approval by the ethical committees.

Recruitment

We collected postoperative sample tissues from patients diagnosed with prostate cancer.

Ethics oversight

Ethical committees of Renji Hospital Affiliated to Shanghai Jiao Tong University School of Medicine (approval KY2022-136A)

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

Sample sizes were predetermined from pilot experiments and/or experiments that have been done in the past, to obtain statistically significant data.

Data exclusions

No data were excluded.

Replication

The experiments were repeated at least once. Studies that were repeated are noted in the figure captions, and include all studies that demonstrate the primary principles reported in the manuscript. All experimental findings were reliably reproduced.

Randomization

All samples and organisms were randomly allocated into experimental groups.

Blinding

We did not perform blinding for in vivo measurement, as blinding was considered not to affect the measurement result. Other analyses were performed without informing the investigators with the group allocation.

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

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. All antibodies were diluted as the supplier suggested.

1) Anti-mouse CD45, Biolegend, cat. no. 103108, Clone: 30-F11, Dilution: 1:200;

- 2) Anti-mouse CD3, Biolegend, cat. no. 100204, Clone: 17A2, Dilution: 1:500;
- 3) Anti-mouse CD4, Biolegend, cat. no. 100412, Clone: GK1.5, Dilution: 1:200;
- 4) Anti-mouse CD8, Biolegend, cat. no. 140408, Clone: 53-5.8, Dilution: 1:200;
- 5) Anti-mouse IFN- γ , Biolegend, cat. no. 505806, Clone: XMG1.2, Dilution: 1:500;
- 6) Anti-mouse CD80, Biolegend, cat. no. 104707, Clone: 16-10A1, Dilution: 1:100;
- 7) Anti-mouse CD86, Biolegend, cat. no. 105011, Clone: GL-1, Dilution: 1:200;
- 8) Anti-mouse CD11c, Biolegend, cat. no. 117310, Clone: N418, Dilution: 1:200;
- 9) Anti-mouse CD62L, Biolegend, cat. no. 104405, Clone: MEL-14, Dilution: 1:200;
- 10) Anti-mouse CD44, Biolegend, cat. no. 103024, Clone: IM7, Dilution: 1:100;
- 11) Anti-mouse H-2Kb/H-2Db, Biolegend, cat. no. 114616, Clone: 28-8-6, Dilution: 1:100;
- 12) Anti-mouse I-A/I-E, Biolegend, cat. no. 107614, Clone: M5/114.15.2, Dilution: 1:100;
- 13) Anti-mouse H-2Kb bound to SIINFEKL, Biolegend, cat. no. 141604, Clone: 25-D1.16, Dilution: 1:100;
- 14) Anti-mouse XCR1, Biolegend, cat. no. 148204, Clone: ZET, Dilution: 1:100;
- 15) Anti-mouse PDCA-1, Biolegend, cat. no. 127025, Clone: 927, Dilution: 1:100;
- 16) Anti-mouse Ly-6C, Biolegend, cat. no. 128017, Clone: HK1.4, Dilution: 1:100;
- 17) Anti-mouse CD11b, Biolegend, cat. no. 101206, Clone: M1/70, Dilution: 1:100;
- 18) Anti-mouse T-Select H-2Kb OVA Tetramer-SIINFEKL, MBL, cat. no. TS-5001-1C, Dilution: 1:10;

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

- 1) Anti-mouse CD4, BioXCell, cat. no. BE0003-1, Clone: GK1.5;
- 2) Anti-mouse CD8 α , BioXCell, cat. no. BE0061, Clone: 2.43.

For western blot analysis, the following primary antibodies were used:

- 1) Rabbit anti-PAP (Abcam, ab109004, 1:1000)
- 2) Rabbit anti-PSMA (Abcam, ab133579, 1:50000)
- 3) Rabbit anti-PSCA (Proteintech, Cat No. 17171-1, 1:500)
- 4) Rabbit anti-GM130 (Thermo Fisher, MA5-35107, 1:1000)
- 5) Rabbit anti-CD63 (Abcam, ab315108, 1:1000)
- 6) Rabbit anti-CD9 (Abcam, ab307085, 1:1000)
- 7) Rabbit anti-Flotillin-1 (Abcam, ab133497, 1:10000)
- 8) Goat anti-rabbit IgG (Abcam, ab6721, 1:2000)
- 9) Rabbit anti-ApoA-I (MCE, HY-P81137, 1:1000)
- 9) Rabbit anti-Calnexin (Abcam, ab22595, 1:1000)

Validation

All primary antibodies were purchased from the vendors listed above and have been validated by the manufacturers for the indicated applications. Many of these antibodies have also been widely used and validated in previous studies, as referenced in the literature.

Eukaryotic cell lines

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

Cell line source(s)

The RM-1-luc prostate-cancer cell line, B16 melanoma cell line and the 4T1-luc breast-cancer cell line were generously donated by Liang Dong at Renji Hospital Affiliated to Shanghai Jiao Tong University School of Medicine.

Authentication

None of the cell lines were authenticated.

Mycoplasma contamination

The cell lines were tested for mycoplasma contamination, and no mycoplasma contamination was found.

Commonly misidentified lines (See [ICLAC](#) register)

No commonly misidentified cell lines were used.

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

6-8 weeks old male C57BL/6 and female BALB/c mice were obtained from Shanghai Lingchang Biotechnology Co., Ltd.

Wild animals

The study did not involve wild animals

Reporting on sex

Female and male mice were used in this study.

Field-collected samples

The study did not involve samples collected from the field.

Ethics oversight

All experiments were performed in accordance with the animal protocol approved by the Animal Care and Welfare Committee at Shanghai Jiao Tong University.

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

Plants

Seed stocks	Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.
Novel plant genotypes	Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.
Authentication	Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.

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	Peripheral blood was collected by cardiac puncture before harvesting other tissues. Tumors or spleens collected from mice were digested into single-cell suspensions. Cells were then stained with fluorescencelabelled antibodies following the manufacturer's instructions.
Instrument	LSRFortessa instrument (BD Biosciences).
Software	FBD CellQuest™ Pro Software (BD Biosciences, version 5.2) and FlowJo software package (version 10.0.7; TreeStar, USA, 2014).
Cell population abundance	No sorting was performed.
Gating strategy	Cells was first gated on FSC/SSC. Singlet cells were usually gated using FSC-H and FSC-A. Surface antigen gating was performed on the live cell population.

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