nature portfolio

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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 *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	CytExpert software v. 2.3(Beckman), Image Studio software v. 5.2(Li-Cor Biosciences), ImageScope software v. 12.3.2 (Leica), Fotric 224s (FOTRIC), FV10-ASW v. 4.0 software (Olympus), Living Image software v.4.5 (PerkinElmer), LightField software v. 6.4 (Princeton Instruments).
Data analysis	Softwares used for analysis include GraphPad Prism v. 7.0 (GraphPad Software), FlowJo v. 10 (TreeStar), Living image software (PerkinElmer), Aperio ImageScope v. 12.3.2 (Leica), Image-Pro Plus v. 6.0 (Media Cybernetics), LightField software v. 6.4 (Princeton Instruments), Excel 2016 (Microsoft), Image Studio software v. 5.2 (Li-Cor Biosciences), CaseViewer v. 2.4 (3DHISTECH), Gaussian 16, Revision A.03.

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 scRNA-seq data generated in this study have been deposited in the NCBI Gene Expression Omnibus (GEO) database under accession code GSE268619 (https://

www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE268619). The authors declare that all the data supporting the findings of this manuscript are available within the manuscript and Supplementary Information files. All data are available from the corresponding author upon request. Processed feature barcode matrices for all scRNAseq data are available through the Gene Expression Omnibus with accession number GSE268619.

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Although no sample size calculation was performed, sample sizes for the in vivo experiments are similar to those generally employed and accepted in the field (Nat Nanotechnol 14(1):89-97 (2019); Nat Biotechnol 37(11):1322-1331 (2019) and were sufficient to support our conclusions with statistical significance. Sample sizes for the in vitro experiments are also based on previous work (Nat Commun 4;12(1):6371 (2021)).
Data exclusions	All results obtained in this study were successfully replicated. No data were excluded from the analyses. Except animal experiments, we have performed the experiments shown in our manuscript more than twice. Exact numbers of biologically independent repetitions are stated in the manuscript.
Replication	We excluded the mice that failed the model establishment. The experimental mice were grouped by random numbers table. We used female mice because mammary cancers occur primarily in females.
Randomization	We excluded the mice that failed the model establishment. The experimental mice were grouped by random numbers table. We used female mice because mammary cancers occur primarily in females.
Blinding	Investigators were not blinded during carrying out the experiment, but blinded during the allocation, sample collection, and data analysis. In vivo experiments were performed unblinded due to the requirements and regulations of the Institutional Animal Care and Use Committee (IACUC) guidelines of Wuhan University. Bioluminescence imaging were conducted by an independent operator, who was unaware of the treatment conditions.

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).*
Research sample	*State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.*
Sampling strategy	*Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a*

	rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.
Data collection	*Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.*
Timing	*Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.*
Data exclusions	*If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Non-participation	*State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.*
Randomization	*If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.*

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	*Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested, hierarchical), nature and number of experimental units and replicates.*
Research sample	*Describe the research sample (e.g. a group of tagged Passer domesticus, all Stenocereus thurberi within Organ Pipe Cactus National Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.*
Sampling strategy	*Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.*
Data collection	*Describe the data collection procedure, including who recorded the data and how.*
Timing and spatial scale	*Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken*
Data exclusions	*If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.*
Reproducibility	*Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.*
Randomization	*Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.*
Blinding	*Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.*

Did the study involve field work? ☐ Yes ☒ No

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
[ ]	[x] Antibodies
[ ]	[x] Eukaryotic cell lines
[x]	[ ] Palaeontology and archaeology
[ ]	[x] Animals and other organisms
[x]	[ ] Clinical data
[x]	[ ] Dual use research of concern
[x]	[ ] Plants

Methods

n/a	Involved in the study
[x]	[ ] ChIP-seq
[ ]	[x] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used

The following primary antibodies were used for blocking. They are listed as antigen first, followed by supplier and clone/ catalog number as applicable.
1) anti-mouse PD-1 (aPD-1), 200 μg per mouse, Bioxcell, Clone RMP1-14, Cat BE0146;
2) anti-mouse CTLA-4 (aCTLA-4), 200 μg per mouse, Bioxcell, Clone 9H10, Cat BE0131.
The following antibodies were used for immunohistochemistry (IHC) and immunofluorescence. They are listed as antigen first, followed by supplier, catalog number as applicable.
1) anti-HMGB1 1:100 , Abcam, Cat ab18256;
2) anti-Ki67, 1:400, Abcam, Cat ab15580;
3) anti-Cleaved Caspase-3, 1:1000, Cell Signaling Technology, Cat 9664;
4) anti-Calreticulin, 1:300, Abcam, Cat ab92516;
5) anti-CD4, 1:200, Cell Signaling Technology, Cat 25229;
6) anti-CD19, 1:400, Cell Signaling Technology, Cat 90176;
7) anti-F4/80, 1:300, Cell Signaling Technology, Cat 70076;
8) Purified anti-mouse/human PNAd Antibody, 1:400, Biolegend, Clone MECA-79, Cat 120801;
9) anti-CD11c, 1:600, Cell Signaling Technology, Cat 97585;
10) anti-CD3e, 1:400, Cell Signaling Technology, Cat 78588;
11) anti-CXCL13, 1:1000, Abcam, Cat ab199043;
12) anti-CD86, 1:400, Abcam, Cat 19589; 14) Goat anti-Rabbit IgG DyLight 488 , 1:200, abbkine, Cat A23220;
13) anti-Grp94, 1:200, Cell Signaling Technology, Cat 20292T;
14) anti-LAMP1, 1:100, Abcam, Cat ab208943;
15) anti-HSP60, 1:400, Cell Signaling Technology, Cat 12165S;
16) anti-PDL1, 1:200, Cell Signaling Technology, Cat 64988S;
17) Goat anti-Rabbit IgG DyLight 488 , 1:200, abbkine, Cat A23220;
18) anti-MHC Class II, 1:200, Abcam, Cat ab23990;
The following primary antibodies were used for flow cytometry. They are listed as antigen first, followed by supplier and clone/ catalog number as applicable.
1) Fixable Viability Dye, 1:1000, eBioscience, eFluor 506, Cat 65-0866-14
2) anti-mouse CD45, 1:500, eBioscience, APC-Cyanine7, Clone I3/2.3, Cat A15395;
3) anti-mouse CD3e, 1:500, eBioscience, FITC, Clone 145-2C11, Cat 11-0031-82;
4) anti-mouse CD4, 1:500, eBioscience, eFluor 450, Clone RM4-5, Cat 48-0042-82;
5) anti-mouse CD8a, 1:500, Biolegend, PerCP, Clone 5H10, Cat MCD0831;
6) anti-mouse CD11b, 1:500, Biolegend, FITC, Clone M1/70, Cat 101206;
7) anti-mouse CD11c, 1:500, eBioscience, FITC, Clone N418, Cat 11-0114-82;
8) anti-mouse CD80, 1:300, eBioscience, PE, Clone 16-10A1, Cat 12-0801-82;
9) anti-mouse CD86, 1:300, eBioscience, APC, Clone GL1, Cat 17-0862-82;
10) anti-mouse MHC-II, 1:300, Biolegend, Bv421, Clone M5/114.15.2, Cat 25-5321-82;
11) anti-mouse MHC-II, 1:300, eF450, Clone AF6-120.1, Cat 48-5320-82;
12) anti-mouse CD44, 1:500, eBioscience, PE, Clone IM7, Cat 12-0441-82;
13) anti-mouse CD62L, 1:200, eBioscience, APC, Clone MEL-14, Cat 17-0621-82;
14) anti-mouse Ly6C, 1:200, Biolegend, APC, Clone HK1.4, Cat 128016;
15) anti-mouse Ly6G, 1:200, Biolegend, PE, Clone 1A8, Cat 127607

Validation

No customized antibodies were used. Validation data of the antibodies purchased from commercial vendors are available on the manufactures' website and datasheets.
1) anti-mouse PD-1 (aPD-1), Bioxcell, Clone RMP1-14, Cat BE0146 https://bxcell.com/product/invivomab-anti-m-pd-1/
2) anti-mouse CTLA-4 (aCTLA-4), Bioxcell, Clone 9H10, Cat BE0131 https://bioxcell.com/invivomab-anti-mouse-ctla-4-cd152-be0131
3) anti-HMGB1 1:100 , Abcam, Cat ab anti-HMGB1 1:100 , Abcam, Cat ab18256 https://www.abcam.cn/products/primary-antibodies/hmgb1-antibody-ab18256.html
4) anti-Ki67, 1:400, Abcam, Cat ab15580 https://www.abcam.cn/products/primary-antibodies/ki67-antibody-ab15580.html
5) anti-Cleaved Caspase-3, 1:1000, Cell Signaling Technology, Cat 9664 https://www.cellsignal.cn/products/primary-antibodies/cleaved-caspase-3-asp175-5a1e-rabbit-mab/9664
6) anti-Calreticulin, 1:300, Abcam, Cat ab92516; 5) anti-Calreticulin https://www.abcam.cn/products/primary-antibodies/calreticulin-antibody-epr3924-er-marker-ab92516.html

7) anti-CD4, 1:200, Cell Signaling Technology, Cat 25229 https://www.cellsignal.cn/products/primary-antibodies/cd4-d7d2z-rabbit-mab/25229
8) anti-CD19, 1:400, Cell Signaling Technology, Cat 90176 https://www.cellsignal.cn/products/primary-antibodies/cd19-intracellular-domain-d4v4b-xp-rabbit-mab/90176
9) anti-F4/80, 1:300, Cell Signaling Technology, Cat 70076 https://www.cellsignal.cn/products/primary-antibodies/f4-80-d2s9r-xp-174-rabbit-mab/70076
10) Purified anti-mouse/human PNAd Antibody, 1:400, Biolegend, Clone MECA-79, Cat 120801 https://www.biolegend.com/en-us/products/purified-anti-mouse-human-pnad-antibody-2975
11) anti-CD11c, 1:600, Cell Signaling Technology, Cat 97585 https://www.cellsignal.cn/products/primary-antibodies/cd11c-d1v9y-rabbit-mab/97585
12) anti-CD3e, 1:400, Cell Signaling Technology, Cat 78588 https://www.cellsignal.cn/products/primary-antibodies/cd3e-e4t1b-xp-174-rabbit-mab/78588
13) anti-CXCL13, 1:1000, Abcam, Cat ab199043 https://www.abcam.cn/products/primary-antibodies/cxcl13-antibody-epr19259-147-ab199043.html
14) anti-CD86, 1:400, Cell Signaling Technology, Cat 19589 https://www.cellsignal.cn/products/primary-antibodies/cd86-e5w6h-rabbit-mab/19589
15) anti-Grp94, 1:200, Cell Signaling Technology, Cat 20292T https://www.cellsignal.cn/products/primary-antibodies/grp94-d6x2q-xp-rabbit-mab/20292
16) anti-LAMP1, 1:100, Abcam, Cat ab208943 https://www.abcam.cn/products/primary-antibodies/lamp1-antibody-epr21026-ab208943.html
17) anti-HSP60, 1:400, Cell Signaling Technology, Cat 12165S https://www.cellsignal.cn/products/primary-antibodies/hsp60-d6f1-xp-rabbit-mab/12165
18) anti-PDL1, 1:200, Cell Signaling Technology, Cat 64988S https://www.cellsignal.cn/products/primary-antibodies/pd-l1-d5v3b-rabbit-mab/64988
19) Goat anti-Rabbit IgG DyLight 488 , 1:200, abbkine, Cat A23220 https://www.abbkine.cn/product/a23220/
20) anti-MHC Class II, 1:200, Abcam, Cat ab23990 https://www.abcam.cn/products/primary-antibodies/mhc-class-ii-antibody-mrc-ox-6-ab23990.html
21) anti-mouse CD45, eBioscience, APC-Cyanine7, Clone I3/2.3, Cat A15395 https://www.thermofisher.cn/cn/zh/antibody/product/CD45-Antibody-clone-30-F11-Monoclonal/45-0451-82
22) anti-mouse CD3e, eBioscience, FITC, Clone 145-2C11, Cat 11-0031-82 https://www.thermofisher.cn/cn/zh/antibody/product/CD3e-Antibody-clone-145-2C11-Monoclonal/11-0031-82
23) anti-mouse CD4, eBioscience, eFluor 450, Clone RM4-5, Cat 48-0042-82 https://www.thermofisher.cn/cn/zh/antibody/product/CD4-Antibody-clone-RM4-5-Monoclonal/48-0042-82
24) anti-mouse CD8a, eBioscience, PerCP, Clone 5H10, Cat MCD0831 https://www.thermofisher.cn/cn/zh/antibody/product/CD8-alpha-Antibody-clone-5H10-Monoclonal/MCD0831
25) anti-mouse CD11b, Biolegend, FITC, Clone M1/70, Cat 101206 https://www.biolegend.com/en-us/products/fitc-anti-mouse-human-cd11b-antibody-347
26) anti-mouse CD11c, eBioscience, FITC, Clone N418, Cat 11-0114-82 https://www.thermofisher.cn/cn/zh/antibody/product/CD11c-Antibody-clone-N418-Monoclonal/11-0114-82
27) anti-mouse CD80, eBioscience, PE, Clone 16-10A1, Cat 12-0801-82 https://www.thermofisher.cn/cn/zh/antibody/product/CD80-B7-1-Antibody-clone-16-10A1-Monoclonal/12-0801-82
28) anti-mouse CD86, eBioscience, APC, Clone GL1, Cat 17-0862-82 https://www.thermofisher.cn/cn/zh/antibody/product/CD86-B7-2-Antibody-clone-GL1-Monoclonal/17-0862-82
29) anti-mouse MHC-II, 1:300, Biolegend, Bv421, Clone M5/114.15.2, Cat 25-5321-82;https://www.biolegend.com/en-us/products/brilliant-violet-421-anti-mouse-i-a-i-e-antibody-7147
30) anti-mouse MHC-II, 1:300, eF450, Clone AF6-120.1, Cat 48-5320-82; https://www.thermofisher.cn/cn/zh/antibody/product/MHC-Class-II-I-Ab-Antibody-clone-AF6-120-1-Monoclonal/48-5320-82
31) anti-mouse CD44, 1:500, eBioscience, PE, Clone IM7, Cat 12-0441-82; https://www.thermofisher.cn/cn/zh/antibody/product/CD44-Antibody-clone-IM7-Monoclonal/12-0441-82 ; https://www.thermofisher.cn/cn/zh/antibody/product/CD62L-L-Selectin-Antibody-clone-MEL-14-Monoclonal/17-0621-82
32) anti-mouse CD62L, 1:200, eBioscience, APC, Clone MEL-14, Cat 17-0621-82; https://www.thermofisher.cn/cn/zh/antibody/product/CD62L-L-Selectin-Antibody-clone-MEL-14-Monoclonal/17-0621-82
33) anti-mouse Ly6C, 1:200, Biolegend, APC, Clone HK1.4, Cat 128016; https://www.biolegend.com/en-us/products/apc-anti-mouse-ly-6c-antibody-6047
34) anti-mouse Ly6G, 1:200, Biolegend, PE, Clone 1A8, Cat 127607 https://www.biolegend.com/en-us/products/pe-anti-mouse-ly-6g-antibody-4777

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	The murine colon carcinoma cell line MC38 were purchased from the Shanghai Cell Bank of the Chinese Academy of Sciences. The murine squamous carcinoma cell line 4MOSC1 from Prof. J. Silvio Gutkind of the University of California San Diego via a material transfer agreement (SD2017-202). The 4MOSC1 cells were gifts from Prof.J.Silvio Gutkind at the University of California San Diego via a material transfer agreement (SD2017-202). The MC38 (CBP60825), MC38-Luc (CBP30169L), L929 (CCL-1) and RAW264.7 (TIB-71) cells were obtained from the American Type Culture Collection. The human oral keratinocyte (HOK) cell line was gifted by Shanghai Ninth People's Hospital, Shanghai Jiao Tong University.
Authentication	Each cell line used was morphologically confirmed according to the information provided by culture collections.

Mycoplasma contamination	All the cell lines presented in this study were tested for mycoplasma contamination and they were free of mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Palaeontology and Archaeology

Specimen provenance	*Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.*
Specimen deposition	*Indicate where the specimens have been deposited to permit free access by other researchers.*
Dating methods	*If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.*

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight	*Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.*

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

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	The female C57BL/6 mice (aged 6–8 weeks and weighing 18–20 g) were provided by the Experimental Animal Central of Wuhan University, sex was not considered in this study design.
Wild animals	The study did not involve wild animals.
Reporting on sex	All the mice used in this study were female, considering that fighting among male mice could affect the experimental results, especially in survival experiments, sex was considered in the study design.
Field-collected samples	The study did not involve samples collected from field.
Ethics oversight	Ethical approval for this study was granted by the Animal Ethics Committee of the School and Hospital of Stomatology of Wuhan University (approval number: S07920080I). All animal experimental procedures adhered to the Regulations for the Administration of Affairs Concerning Experimental Animals approved by the State Council of the People's Republic of China. The mice were housed under specific pathogen-free (SPF) conditions with a 12/12-h light/dark cycle, temperature of approximately 22 °C, and humidity of around 50%.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJEguidelines for publication of clinical research and a completedCONSORT checklist must be included with all submissions.

Clinical trial registration	N/A
Study protocol	N/A
Data collection	N/A
Outcomes	N/A

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☒	☐	Public health
☒	☐	National security
☒	☐	Crops and/or livestock
☒	☐	Ecosystems
☒	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☒	☐	Demonstrate how to render a vaccine ineffective
☒	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐	Increase transmissibility of a pathogen
☒	☐	Alter the host range of a pathogen
☒	☐	Enable evasion of diagnostic/detection modalities
☒	☐	Enable the weaponization of a biological agent or toxin
☒	☐	Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	*For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.*
Files in database submission	*Provide a list of all files available in the database submission.*
Genome browser session (e.g. UCSC)	*Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.*

Methodology

Replicates	*Describe the experimental replicates, specifying number, type and replicate agreement.*
Sequencing depth	*Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.*
Antibodies	*Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.*

Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*
Data quality	*Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.*
Software	*Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.*

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	For lymphocyte analysis, splenocytes and tumor-draining lymph nodes were collected from mice and made into cell suspensions by gentleMACS™ dissociator and digestive enzyme (Miltenyi Biotec) according to the manufacturer's instructions. Then, the samples were passed through 200-mesh nylon mesh filters to obtain single-cell suspensions. Live or dead cells were separated by Fixable Viability Dye (eBioscience, Dye eFluor 506). For all samples, cells were first stained with antibodies against surface antigens. In some experiments, cells were subsequently fixed, permeablized and stained for intracellular antigens.
Instrument	CytoFLEX flow cytometer (Beckman), MoFlo XDP cell sorter (Beckman)
Software	CytExpert v. 2.3 software (Beckman), FlowJo v. 10 (TreeStar)
Cell population abundance	The purity of the post-sorted cells was more than 95% as verified by flow cytometry.
Gating strategy	The gating strategy was shown in Supplementary Fig. 15-17. Generally, single cell gates based on SSC-H and SSC-A, and FSC-H and FSC-A were used to exclude non-singlets. A live/dead cell gate based on fixable viability dye was used to exclude dead cells.

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

Magnetic resonance imaging

Experimental design

Design type	*Indicate task or resting state; event-related or block design.*
Design specifications	*Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.*
Behavioral performance measures	*State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).*

Acquisition

Imaging type(s)	*Specify: functional, structural, diffusion, perfusion.*
Field strength	*Specify in Tesla*
Sequence & imaging parameters	*Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.*
Area of acquisition	*State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software — *Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).*

Normalization — *If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.*

Normalization template — *Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.*

Noise and artifact removal — *Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*

Volume censoring — *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

Statistical modeling & inference

Model type and settings — *Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).*

Effect(s) tested — *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference — *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*

(See Eklund et al. 2016)

Correction — *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity — *Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).*

Graph analysis — *Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).*

Multivariate modeling and predictive analysis — *Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.*