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	Vevo 2100 high-frequency ultrasound system (VisualSonic, Toronto, ON, Canada), CFX96 Real Time PCR Detection System (BioRad), Odyssey system (Li-Cor Biosciences), automatic biochemical analyzer (Beckman-Coulter, USA), electron microscope (Hitachi, H-800, Tokyo, Japan), Leica Application Suite (Leica).
Data analysis	GraphPad Prism 8.0.2 (GraphPad Software, California, USA), Excel 2017 (Microsoft), FlowJo software (version 14.0.0), Image Studio Lite (Li-COR), ImageJ 1.52p (NIH, USA).

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 proteomics data was deposited at the iProx with a series number PXD031720.

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	Yes
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	The patients involved in this study were from Shanghai Changzheng Hospital and Shanghai Tenth People's Hospital between 2017 and 2021.
Recruitment	In an investigator-initiated trial (No. NCT03239015) with a primary aim for evaluating the efficacy of targeted precision therapy in patients with refractory tumors, the adverse drug reactions in cancer patients were monitored. After the first course of therapy, the patients were screened according to International Society of Cardio-Oncology (IC-OS) 2021 Consensus. A total of 6 patients diagnosed with myocarditis were included to this study for comparison of their blood GSDME concentrations at baseline and after aPD-1 therapy.
Ethics oversight	These studies were performed according to the declaration of Helsinki and approved by the Ethics Committee of Shanghai Changzheng Hospital (2017SL016) and Shanghai Tenth People's Hospital (2019-K-032). All participants provided written informed consent to take part in the study.

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	In animal study, sample size was determined based on published as well as our own prior studies. In this study, a total of 360 patients with tumor who underwent at least one course of aPD-1 therapy by anti-PD-1 antibody were monitored at the baseline and post the first course of therapy. After the first course of therapy, the patients were screened according to International Society of Cardio-Oncology (IC-OS) 2021 Consensus.
Data exclusions	In animal study, this study did not exclude data. In the human study, The exclusion criteria include special situation that patients were: (1) severe organ failure due to tumor growth; (2) with heart diseases such as myocardial infarction and heart failure before aPD-1 treatment; (3) with radiotherapy or other chemotherapy.
Replication	All experiments were repeated for three times with similar results.
Randomization	All mice were randomly assigned to different groups.
Blinding	All experiments were performed in a blinded way. All data were analyzed in a blinded way.

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

Field work, collection and transport

Field conditions	*Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).*
Location	*State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).*
Access & import/export	*Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).*
Disturbance	*Describe any disturbance caused by the study and how it was minimized.*

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

Immunoblotting: Primary antibodies against mouse GSDME (Abcam, ab215191, 1:1,000), GSDME-N (Abcam, ab222407, 1:1,000), GSDMD (Abcam, ab209845, 1:1,000), Caspase-1 (Abcam, ab207802,1:1,000), Caspase-11 (Abcam, ab180673, 1:1,000), Caspase-3 (Cell Signaling Technology, 9662, 1:2000), IL-18 (Abcam, ab71495, 1:1,000), IL-1β (Santa Cruz Biotechnology, sc-52012, 1:1,000), cGAS (Cell Signaling Technology, 31659S,1:1,000), STING (Cell Signaling Technology, 13647, 1:1,000), p-TBK1 (Bioss, bs-3440R, 1:1,000), total-TBK1 (t-TBK1, Bioss, bs-7497R, 1:1,000), p-IRF3 (Cell Signaling Technology, 29047,1:1,000), IRF3 (Cell Signaling Technology, 4302,1:1,000) and Tubulin (Proteintech, 66031-1-Ig, 1:5000) were used.

IHC and ICC: The following primary antibodies were used: anti-Myh-6 (Beyotime Biotechnology, AF7530,1:10-0), anti-CD68 (Proteintech, 25747-1-AP, 1:500), anti-GSDME-N (Abcam, ab222407, 1:500), anti-Ly6G (Abcam, ab238132, 1:500), anti-Caspase-3 (Cell Signaling Technology, 9662, 1:500) and anti-CD8 (Proteintech, 66868-1-Ig, 1:100).

Validation

All antibodies were purchased from commercial sources and were validated by the vendors.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

MC38 cells were obtained from the Cell Center of Chinese Academy of Medical Sciences.

Authentication

Cell lines were authenticated by STR.

Mycoplasma contamination

We confirmed that all cell lines tested negative for mycoplasma contamination.

Commonly misidentified lines
(See ICLAC register)

None

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 mice were bred and housed under specific pathogen free conditions in the central animal facility. All mice were housed at a temperature of 21°-23°C with relative humidity of 35%-65% and 12h light/dark cycle in individually ventilated cages with access to a standard chow diet.
Wild animals	This study did not use wild animals.
Reporting on sex	Yes. Only male mice were used in the present study.
Field-collected samples	This study did not use field-collected samples.
Ethics oversight	All operations in mice were approved by the Animal Care and Use Committee of Shanghai Tenth People's Hospital of Tongji University and compliant with the Guide for the Care and Use of Laboratory Animals published by the US National Institutes of Health (NIH Publication 8th edition, update 2011).

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	*Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.*
Study protocol	*Note where the full trial protocol can be accessed OR if not available, explain why.*
Data collection	*Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.*
Outcomes	*Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*

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

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, mosiacism, off-target gene editing) were examined.

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 cell extracting from heart, the mice were anesthetized and the hearts were harvested. After removing the aorta and epicardium adipose, the heart was cut into small pieces (1mm × 1mm × 1mm) and repeatedly washed in saline to remove blood cells. These cardiac pierces were digested in Hanks' Balanced Salt Solution (HBSS) with type II collagenase (0.08%, Worthington) and DNase I (10 mU/ml, Sigma) at 37°C for 40 min (shaking at 800 rpm). The cell-containing samples were passed with a cell strainer (70 um) to remove undigested tissue pieces. To completely digest the heart tissue, the above steps were repeated 3 times. The cell viability was greater than 98% using the trypan blue exclusion. For cell extracting from spleen, the spleen was isolated, placed in HBSS and gently minced with a scalpel repeatedly. Single cells suspensions were obtained by passing small pieces of spleen trough 70m cell strainers. The single cells suspensions were transferred to fresh tubes and centrifuged at 4°C and 300 g for 10 min. The pellet was re-suspended in 0.4 ml of RBC lysis buffer (eBiosciences) for 5 min at room temperature. Splenocytes were collected after centrifugation (10 min, 300 g) and then re-suspended.
Instrument	Pellets were analyzed using a CytoFLEX-S cytometer (Beckman).
Software	Data were analyzed with FlowJo software, version 14.0.0.
Cell population abundance	The number of immune cell used for CytoFLEX S is > 10^5.
Gating strategy	The following primary antibodies were used: Anti-CD45-PerCP/Cyanine5.5 (BioLegend, 103132, 1:500), Anti-CD3-FITC (BioLegend, 100204, 1:500), Anti-CD4-AF700 (BioLegend, 116022, 1:500), Anti-IFN-γ-BV650 (BioLegend, 505832, 1:500), Anti-IL-4-BV421 (BioLegend, 504119, 1:500), Anti-IL-17A-BV605 (BD Biosciences, 564169, 1:500), Anti-CD8a-APC/Cyanine7 (BioLegend, 100714, 1:500), Anti-CD62L-PE/Cyanine7 (BioLegend, 104418, 1:500), Anti-CD44-PE/Dazzle™ 594 (BioLegend, 103056, 1:500), Anti-TCR γ/δ-PE (BioLegend, 118108, 1:500), Anti-CD45-BV605 (BioLegend, 103139, 1:500), Anti-CD3-APC (BioLegend, 100236, 1:500), Anti-CD11B-BB515 (BD Biosciences, 564454, 1:500), Anti-LY6G-BV421 (BD Biosciences, 562737, 1:500), Anti-F4/80-APC-R700 (BD Biosciences, 565787, 1:500), Anti-CCR2-BV650 (BioLegend, 150613, 1:500), Anti-MHC-II-APC/Fire750 (BioLegend, 107651, 1:500), Anti-Ly6C-PE (BioLegend, 128007, 1:500), Anti-CD64-PE/Cyanine7 (BioLegend, 139314, 1:500), Anti-Nos2 (Cell signaling technology, 13120, 1:500), Anti-IFN-γ-FITC (BioLegend, 505806, 1:500), Anti-STING (Novus, NBP2-24683, 1:500), Anti-MPO-FITC (Thermo Fisher Scientific, 11-1299-42, 1:500), Anti-CXCR2-APC (BioLegend, 149312, 1:500), Anti-CD68-APC (BioLegend, 137008, 1:500), Anti-CD11B- APC/Fire750 (BioLegend, 101261, 1:500),Gating strategy was based on the fluorophore of primary antibodies.

☒ 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.*