nature portfolio

Corresponding author(s): Daoxin Ma

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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	The algorithm was operated with the R-package and the data were visualized with R package ggplot2. GSEA analysis was conducted using GSEA 4.1.0 software. Cells were analyzed using a Gallios flow cytometer (Beckman Coulter, USA) and the results were analyzed by Flowjo.
Data analysis	Illustrator CS6, flowjo 10.4.0, Graphpad prism 7 , Microsoft excel 2011 for Windows, Living Image v4.3.1, RNAseq analysis was performed with the following software HTSeq v0.5.3,Solexa pipeline v1.8, FastQC software 0.11.7, Hisat2 software, StringTie 1.3.3, R 3.4.1,

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 seq datasets have been deposited in the GEO database under the GSE285518 and GSE275283. The Proteomics data have been deposited in PRIDE database under the PXD059463. All data are included in the supplementary information or available in this Article. The raw numbers for charts and graphs are available in the

Source Data file whenever possible.

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	This study did not involve sex or gender-based analysis. And sex was not considered in this study design.
Reporting on race, ethnicity, or other socially relevant groupings	This information has not been collected.
Population characteristics	37 lung cancer samples collected from surgical patients were fixed with formalin and embedded with paraffin and then examined. These tumors represented a range of stages from I to IV, ensuring a comprehensive disease spectrum. Detailed patient information, including age, sex, smoking history, pathological classification, and tumor stage, has been provided in the supplementary data.
Recruitment	The informed consent was obtained from patients who received a lung cancer operation at Qilu Hospital. The surgical resection or biopsy specimens were then subjected to experiments. There is no potential self-selection bias.
Ethics oversight	The study was conducted according to the principles of the Declaration of Helsinki and approved by the Human Research Ethics Committee of Qilu Hospital of Shandong University with the ethic number of KYLL-202311-045.

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	Group size was based on previous experience. For example, Experiments were performed in biological triplicates n=3 unless otherwise noted. And sample size of at least 5 mice in each group was widely accepted in life science experiment to support the consistency of the data and conclusion.
Data exclusions	No data was excluded. When tumors reach >300 mm^2, the mice were euthanized in accordance with the guidelines of the Institutional Animal Care and Use Committee of Shandong University.
Replication	All attempts at replication were successful, and standard deviations were within expected ranges. Unless otherwise noted, each experiment was repeated three or more times.
Randomization	After tumor injection when tumor size reached about 40mm^2, all mice were allocated randomly for each group. And within animal controls were performed wherever possible. And the possible confounders 'experimenter' and 'day of experiment' were equally matched between groups. For experiments other than mice studies, randomization is irrelevant to our study, because different groups were defined by either different cell lines or different conditions.
Blinding	For all in vitro or vivo experiments whose data were generated by machine reading, blinding or not won't affect the results. For caliper measurement of tumor size, different people were involved in measuring even they were aware of group labeling which was conducted partially blinded.

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
☐	☒ 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

anti-CD8 antibodies (10 mg/kg, BE0004-1, BioXCell); PD-1 antibodies (10 mg/kg, CP162, BioXCell); IFNAR1 antibody (2.5 mg/kg, InVivoMAb, Clone: MAR1-5A3, BioXcell); anti-NAT10 (1:1000, Abcam, cat#ab194297), anti-Myc (1:1000, CST, cat#18583), anti-CDK2 (1:1000, CST, cat#2546), anti-DNMT1 (1:1000, CST, cat#5032), anti-RIG-I (1:1000, CST, cat#3743), anti-HA-tag (1:1000, CST, cat#3724), anti-Tubulin (1:1000, CST, cat#2146), anti-β-Actin (1:1000, CST, cat#4970); HRP-linked secondary antibodies (1:2000, CST, cat#7074); cell death dye (1:300, Invitrogen, eBioscienceTM Fixable Viability Dye eFluorTM 780, cat#2633409), CD45.2 (1:100, BioLegend, cat#109814), CD8a (1:100, BioLegend, cat#B373965), CD11c (1:100, Invitrogen, cat#2400633), and IA/IE (1:100, BioLegend, cat#107608); IFN-γ (1:100, Invitrogen, cat#2481435); Granzyme B (1:100, BioLegend, cat#515406); anti-NAT10 (1:250, Abcam, cat#ab182744), anti-CD8a (1:250, Abcam, cat#ab237709); anti-PD-L1 (1:250, Abcam, cat#ab213524); Primary antibodies against CD8a (1:100, Abcam, cat#ab217344); J2 antibody [1:250 dilution, 4 mg/ml, English and Scientific Consulting Kft (SCICONS), cat#10010200]; anti-mouse CD3 Antibody (Biolegend, cat#100238); 0.5 μg/ml anti-mouse CD28 Antibody (Biolegend, cat#102112); Dye eFluor™ 670 in CD4+ T (Biolegend, cat#100428, 1:100); CD8+ T (Biolegend, cat#100708, 1:100); CD3 Antibody (Biolegend, cat#100238) and 0.5 μg/ml anti-mouse CD28 Antibody (Biolegend, cat#102112) for T-cell proliferation assay. cell death dye (1:300, Invitrogen, eBioscienceTM Fixable Viability Dye eFluorTM 780, cat#2633409), CD45.2 (1:100, BioLegend, cat#109814), CD8a (1:100, BioLegend, cat#B373965), CD11c (1:100, Invitrogen, cat#2400633), and IA/IE (1:100, BioLegend, cat#107608) ; CD25(1:100, Invitrogen, cat#2151388),LY6G (1:100, Tonbo, cat#SKU 65-1276-U100),IA/IE (1:100, Biolegend, cat#107608) for Flow cytometry analysis.

Validation

All antibodies used in this study were validated by manufacturers for that specific application. Relevant validating results can be found in the website of each manufacturer.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

MCA205 fbrosarcoma cell line (SCC173) was purchased from Millipore Sigma. Human embryonic kidney 293T cell line (CRL-3216), A549 human lung adenocarcinoma (CCL-185) and TC-1 lung epithelial tumor cell line (CRL-2785) were purchased from American Type culture collection (ATCC).

Authentication

All cell lines used were authenticated vis STR profiling.

Mycoplasma contamination

All cell lines were routinely tested for mycoplasma contamination and found negative

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	C57BL/6J background mice and athymic nude BALB/c mice (nude/nude), female, 6–8 weeks. All mice used in this study were age-matched littermates.
Wild animals	The study didn't involve wile animals.
Reporting on sex	Sex was not considered in the study design and analysis because previous studies and our preliminary data did not indicate significant sex-based differences in the tumor models used.
Field-collected samples	The study didn't involve samples collected from the field.
Ethics oversight	Female C57BL/6N background mice and BALB/c athymic nude mice (nude/nude), aged 6-8 weeks, were purchased from Vital River Laboratory Animal Technology Co., Ltd. (Beijing, China; license number SCXK [Jing] 2021-0011). All animal experiments were approved by the Institutional Animal Care and Use Committee of Qilu Hospital of Shandong University (DWLL-2024-176).

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	Mice were sacrificed at appropriate time, and the tumors were collected and separated into single cells. Briefly, tumors were excised and minced. Then Liberase TL Research Grade 10 (2 μg/mL, Roche, cat#05401020001) and DNase I (Roche, cat#10104159001) was used for the digestion. After being filtered with strainer, the cell suspensions were stimulated with brefeldin A (BFA, PeproTech, 10 mg/mL), phorbol myristate acetate (PMA, PeproTech, 100 μg/mL) and ionomycin (PeproTech, 1mg/mL) at 37℃for 4 h.
Instrument	Beckman Coulter, USA
Software	Collection: FACS analysis: Flowjo 10.4.0
Cell population abundance	Purity of post-sort fractions is regularly measured by flow for cD8+ and purity was >95%
Gating strategy	Starting cells were gated on alinear fsc/S$C plot, and then negative population in viability stain lower than 10^3 was selected aslive cells for the following gating which was shown in all flow figures, Positive/negative populations were determined by FMO controls

☒ 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.