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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☒	☐	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	No specific software was used for data collection.
Data analysis	Flow cytometry results were analyzed by FlowJo_V10(TreeStar). Graphs were prepared and analysized using Graphpad Prism(version 6.0).RT-PCR was analyzed using a LightCycler (Roche Diagnostics). Prepared libraries of RNA-seq were sequenced on an Illumina HiSeq 2000 sequencer and calculated and normalized in FPKM, and used for Gene Set Enrichment Analysis (GSEA, Broad Institute). For Bioinformatic analysis, raw sequence reads were first aligned to the mouse UniGene transcriptome with bowtie (v1.0.0) to estimate the insert fragment size and the standard deviations needed by TopHat2 to align the reads to the genome. Then, TopHat2 was used to align the reads to the reference mouse genome (GRCm38) with the aligning parameter-bowtie1 and Ensembl annotated transcripts (version 77) as a guide reference. Uniquely mapped reads were used to quantify gene expression, and differential gene expression evaluation was analyzed by Cuffdiff(a subpackage of Cufflinks(v2.1.1)) with Ensembl annotated genes (version 77). The abundance of transcripts (including mRNAs, pseudogenes, non-coding RNAs and other predicted RNAs) was calculated and normalized in FPKM as described above from the raw RNAseq data and used for Gene Set Enrichment Analysis (GSEA, Broad Institute).

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

All published non-commercial reagents can be made available upon request to the corresponding author. The RNA-seq data are available through GEO repository (Accession code: GSE106384)

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	For each individual experiments, the sample size was not predetermined before initial experiment. Normally 3 or up to 6 biological repeats were included based on experience or the sample availability. After the initial experiment, power analyses were performed to decide the final sample size.
Data exclusions	No data exclusions were taken for this manuscript.
Replication	Each experiment was repeated at least 2-3 times as described in Figure legends. Experimental findings were reliably reproduced between these experiments.
Randomization	Mice used in this experiment were randomly assigned to different groups. Patients were randomly selected according to the blood test results.
Blinding	N/A； Blood was taken from randomly selected patients based on availability and acceptance of consent. Grouping of patients was based on the routine clinical blood test and well accepted standard of anemia. The results of routine blood test, flow cytometry and EBV detection are all detected and reported by machine. No treatment had been given to the cancer patients prior to sample collection. There do not have any subjective bias and personal preference.

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 and 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

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☐	☒ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Unique biological materials

Policy information about availability of materials

Obtaining unique materials: *Describe any restrictions on the availability of unique materials OR confirm that all unique materials used are readily available from the authors or from standard commercial sources (and specify these sources).*

Antibodies

Antibodies used: Fluorophore- or biotin-conjugated antibodies specific for mouse cell-surface antigens and cytokines were as follows: anti-B220 (RA3-6B2, BioLegend), anti-CD4 (GK1.5, BioLegend), anti-CD8a (53-6.7, BioLegend), anti-CD11b (M1/70, BioLegend), anti-Gr1 (RB6-8C5, BioLegend), anti-CD25 (3C7, BioLegend), anti-Foxp3 (MF14, eBioscience), anti-TER119 (TER-119, BioLegend), anti-CD71 (R17 217.1.3, BioXCell for depletion; C2F2, BD biosciences for FACS analysis), anti-CD45 (I3/2.3, BioLegend), anti-CD90.1 (16-10A1, BioLegend), anti-Gzmb (GL1, BioLegend), anti-IFN-γ (XMG1.2, BioLegend), anti-CXCR5 (L138D7, BioLegend), anti-mouse/human CD44 (IM7, BioLegend), anti-human/mouse Bcl-6 (7D1, BioLegend), anti-T-bet (4B10, BioLegend), anti-mouse Ki-67 (16A8, BioLegend), anti-mouse TNF-α (MP6-XT22, BD).

For human studies, the following fluorophore- or biotin-conjugated antibodies specific for cell surface markers or cytokines were used: anti-CD3 (UCHT, BioLegend), anti-CD8 (PRA-T8, BioLegend), anti-CD45 (2D1, BioLegend), anti-CD71 (CY1G4, BioLegend), anti-CD235a (HI264, BioLegend). ROS production was measured by labelling with 2',7' –dichlorofluorescin diacetate using the ROS detection kit (S0033, Beyotime).

Validation: Validation available on the manufacturer's websites

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s): Lewis lung carcinoma cells (LLCs) and B16F10 melanoma cells (B16F10) were obtained from the American Type Culture Collection (ATCC).

Authentication: Lewis lung carcinoma cells (LLCs) and B16F10 melanoma cells (B16F10) were obtained from the American Type Culture Collection (ATCC). An aliquote of each cell lines were authenticated using ATCC DNA fingerprinting.

Mycoplasma contamination: Cell lines were routinely validated and they are free of mycoplasma contamination.

Commonly misidentified lines (See ICLAC register): No commonly misidentified cell lines were used.

Palaeontology

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).*

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.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	OT-1 transgenic C57BL/6J mice were obtained from Jackson Laboratories. P14 (CD90.1) TCR transgenic mice were obtained from Dr. Rafi Ahmed at Emory University. Both male and female mice,at 6-8 weeks old age, were included in each experiment.
Wild animals	The study did not involve wild animals
Field-collected samples	The study did not involve samples from the field

Human research participants

Policy information about studies involving human research participants

Population characteristics	Human research participant characteristics are listed in Supplemental Table 1-3. These included sex, age and stage of cancer patients. This information is provided for descriptive purposes. . We did not exclude patients based on their age or sex. In addition,we did not perform formal covariate analyses in this investigation.
Recruitment	According to our experiments and with the patient's consent, we divided inpatients (clearly diagnosed stage III-IV cancer patients) of Oncology Department of xinqiao hospital into different groups according to the blood test results. Patients in different groups are randomly selected into our experiments. At the same time, the healthy volunteers were randomly selected from Medical examination center. We do not have any potential self-delection bias or other biases.

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 analysis of cytokine production, splenocytes were first stimulated with the GP33 peptides (amino acid sequence: KAVYNFATC, 0.2 µg/ml) in the presence of brefeldin A for 5 hrs at 37 °C. Following surface staining, intracellular cytokine staining was performed with a Cytofix/Cytoperm Fixation/Permeabilization kit (554714, BD Biosciences) according to the manufacturer's instructions.To detect degranulation, splenocytes were stimulated for 5 hrs with the indicated peptide (0.2 µg/ml), in the presence of brefeldin A and anti-CD107a/b antibodies (1D4B,BD Biosciences). Samples were collected using a FACSCanto (BD Bioscience) and analyzed by FlowJo (TreeStar).
Instrument	Samples were collected using a FACSCanto (BD Bioscience), Cell sorting was performed on a FACSAriaII (BD Biosciences).
Software	Results were analyzed by FlowJo_V10(TreeStar).
Cell population abundance	The purity for all populations was >95%.
Gating strategy	Gating strategy: after excluding doublets or larger aggregates, DAPI-positive cells, which are likely membrane-permeable apoptotic cells, were excluded from further analysis. Next, very small events, likely nuclei or debris, were excluded. Positive and negative populations were defined by using fluorescence minus one controls, or staining cells purified from mice lacking the detected protein or appropriate positive and negative 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
(See Eklund et al. 2016)

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

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.