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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.

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	FACS Diva v8.0 was used for flow cytometry data collection.
Data analysis	FlowJo v10 was used for analysis of flow cytometry data. GraphPad Prism v7.0 and v8.0 was used for statistical analysis.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. 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

The data that support the findings of this study are available within the paper and its supplementary information files. Additional data are available from the authors upon reasonable request.

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

Life sciences study design

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

Sample size	We calculate sample size in our studies by using a power analysis and appropriate statistical test in G*Power 3.1 software. Previous animal studies, or small pilot studies when necessary, served as the basis for calculations of expected averages and deviations used to calculate power, for which we set experiment studies to a value of 0.8. This typically results in an experimental group size to be n = 4–7, depending on the experiment. Sample size is explicitly stated for each experimental group for individual experiments in figure captions and data descriptions.
Data exclusions	No data were excluded.
Replication	All in vitro experiments were successfully repeated at least once. in vivo tumor experiments and immunophenotyping experiments were successfully repeated 2-3 times.
Randomization	The treatment groups were filled by randomly selecting from a pool of animals of comparable tumor volume at the beginning of all in vivo experiments.
Blinding	Investigators were not blinded to treatment groups.

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used	Anti-mouse antibodies used for flow cytometry (clone, dilution, supplier, cat#) anti-B220 BUV496 (RA3-6B2, 1:400, BD, 564662), anti-CD4 BV510 (RM4-5, 1:400, BioLegend, 100553), anti-CD8a PE-TexasRed (53-6.7, 1:400, BioLegend, 100761), anti-NKp46 BV605 (29A1.4, 1:200, BD, 137619), anti-Gr-1 PE (RB6-8C5, 1:400, Tonbo, 50-5931) anti-CD11b BV510 (M1/70, 1:400, BD, 562950), anti-F4/80 PE-eFluor610 (BM8, 1:400, eBioscience, 61-4801-82) anti-SIRPa PerCP-Cy5.5 (P84, 1:200, BioLegend, 144010), anti-MHC Class II (I-A/I-E) redFluor710 (M5/114.15.2, 1:800, Tonbo, 80-5321-U100), anti-CD3e PE-Cy7 (145-2C11, 1:400, Tonbo, 60-0031-U100), anti-TCRb BV711 (H57-597, 1:400, BD, 563135), anti-CTLA4 PE (UC10-4B9, 1:400, eBioscience, 12-1522-82), anti-Foxp3 FITC (FJK-16s, 1:400, eBioscience, 11-5773-82), anti-Ki-67 AF700 (SolA15, 1:400, Thermo, 56-5698-82), anti-Granzyme-B APC (QA16A02, 1:400, Biolegend, 372204), anti-IL-17A eFluor450 (eBio17B7, 1: 400, eBioscience, 48-7177-82), anti-TNF-a APC (MP6-XT22, 1: 400, eBioscience, 17-7321-82), anti-IFN-g PE (XMG1.2, 1:400, Tonbo, 50-7311-U100), anti-CD47 FITC (miap301, 1:200, BioLegend, 127504)
Validation	Antibodies used in this study were validated by manufactures and used according to supplied instructions. In certain cases, antibodies were re-validated and appropriate dilutions were determined by titration on ex vivo naive and activated splenocytes.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	A20 murine lymphoma (ATCC: TIB 208), 4T1 mammary carcinoma (ATCC: CRL 2539), B16-F10 murine melanoma (ATCC: CRL6475)
Authentication	Cell lines purchased from ATCC were frozen at early passage, thus did not require additional authentication.
Mycoplasma contamination	All cell lines tested negative for mycoplsma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Animals and other organisms

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

Laboratory animals	4-8 week old BALB/c females or C57BL/6 females were purchased from Taconic Biosciences for in vivo experiments.
Wild animals	This study did not involve wild animals
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	All animal experiments were approved by the Institutional Animal Care and Use Committee (Columbia University, protocol AC-AAAN8002 and AC-AAAZ4470).

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

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	Lymphocytes were isolated from tumor tissue by mechanical homogenization of tumor tissue followed and digestion with collagenase A (1 mg/ml; Roche) and DNase I (0.5 µg/ml; Roche) in isolation buffer (RPMI 1640 supplemented with 5% FBS, 1% l-glutamine, 1% pen-strep and 10 mM Hepes) for 1 hour at 37°C. Cells were filtered through 100 µm cell strainers, washed in isolation buffer and stained. Dead cells were excluded by staining with Ghost Dye cell viability reagent.
Instrument	BD LSRFortessa, FACS Diva v8
Software	FlowJo v10
Cell population abundance	Depends upon treatment - clearly identifiable by conventional flow cytometric approaches following tumor digestion.
Gating strategy	Gating of isolated TILs was performed following exclusion of B220+ A20 tumor cells; followed by identification of TCRb+ CD3+ NK1.1– prior to gating for CD4+ and CD8+ subpopulations.

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