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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	BDFACS DIVA v(.0.1
Data analysis	FlowJo v10.4.2, Prism v6 and v7, Clustal at www.ebi.ac.uk/Tools/msa/clustalo/, Exom sequencing analysis: Trimmomatic v0.33, Bowtie2, GATK's HaplotypeCaller v3.5, SnpEff v4.1l, Bedtools v2.27

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 reported exom sequencing dataset was uploaded to ENA (Study:PRJEB30681) and can be downloaded from www.ebi.ac.uk/ena/data/view/PRJEB30681

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	Most of our experiments are in vitro experiments using cell lines. Sample size was determined during experimental design, based on the measurements made (flow cytomerty, tumor mass measurments), our experience with data variation of each technique, literature and pilot experiments. A power calculation was not done.
Data exclusions	No data was excluded from the analysis.
Replication	If not stated otherwise, experiments were repeated at least 2 times. All attempts at replication were successfull.
Randomization	Mice were allocated to the experimental gorups at a random fasion.
Blinding	The analysis reported in figure 7fgh was performed in a double-blinded fashion. For other experiments, given appropriate handling and equal sample treatment and because data collection and analysis were performed by computer-based methods (e.g. flow cytometric analysis), we believe blinding was not necessary.

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	Fc block (CD16/CD32; 2.4G2; home-made). BioLegend: CD4-APC(GK1.5)#100412, CD4-PE(GK1.5)#100408, TCRβ-APC (H57-597)#109212, I-A-PE(M5/114.15.2)#107608, CD11b-PE(M1/70)#101208, IL-4-PeCy7(11B11)#504118, IFNg-APC(XMG1.2)#505810. eBioscience: CD3e-APC(2C11)#17-0031-83. BD Pharmingen Vbeta TCR Screening Panel #557004.
Validation	Antibodies were tested using appropriate FMO controls for flow cytometry. All antibodies had validation statement provided on the website of the manufacturer.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Modifications of the BALB/c-derived 16.2 T cell hybridoma, as well as other T cell lines and hybridomas were generated in our laboratory.
Authentication	Cells were not authenticated other than by flow cytometry staining for CD3e, TCR, CD4 and I-A.
Mycoplasma contamination	Cells were not tested for mycoplasma 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	C57Bl/6J Mice, females, 6-8 weeks old were used.

Wild animals	none
Field-collected samples	none
Ethics oversight	All animal experiments were approved by the local animal ethics committee (Kantonales Veterinärsamt Zürich, licenses ZH061/17), and performed according to local guidelines (TschV, Zurich) and the Swiss animal protection law (TschG).

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	Single cell suspenssions were done by standard tissue culture procedures.
Instrument	BD FACSAria III, BD LSRFortessa
Software	FlowJo v10.4.2
Cell population abundance	Post-sort cell populations were >95% pure, as determined by re-analysis.
Gating strategy	Gates were set according to FMO or unstained/untreated controls.

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