

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](#).

Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study.

For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

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	No Software Used.
Data analysis	FlowJo was used for flow cytometry analysis. GraphPad Prism was used to generate figures. Adobe Illustrator was used for figure layout.

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](#)

All data is represented within the manuscript. Raw data files from this manuscript are available upon request. The corresponding authors (JJT, JFEK) have repositories of antigens used for antigen tetramer construction which can be shared upon request. They are also willing to assist in construction of novel antigen tetramers, if contacted.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	N/A.
Population characteristics	N/A.
Recruitment	N/A.
Ethics oversight	Hamilton Integrated Research Ethics Board, Fred Hutchinson Cancer Center Institutional Review Board.

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

Life sciences study design

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

Sample size	Representative plots are shown as a sample for those following the protocol. n=5 mice were used in Figure 2 and Supplementary Figure 2, which
Data exclusions	No data was excluded.
Replication	In Figure 2 and Supplementary Figure 2, 5 mice were used to show reproducibility. Reproducibility for this technique is also verified through the
Randomization	N/A
Blinding	N/A

Behavioural & social sciences study design

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

Study description	
Research sample	
Sampling strategy	
Data collection	
Timing	
Data exclusions	
Non-participation	
Randomization	

Ecological, evolutionary & environmental sciences study design

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

Study description	
Research sample	
Sampling strategy	
Data collection	
Timing and spatial scale	

Data exclusions	
Reproducibility	
Randomization	
Blinding	

Did the study involve field work? Yes No

Field work, collection and transport

Field conditions	
Location	
Access & import/export	
Disturbance	

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		Methods	
n/a	Involved in the study	n/a	Involved in the study
<input checked="" type="radio"/>	Antibodies	<input type="radio"/>	ChIP-seq
<input type="radio"/>	Eukaryotic cell lines	<input checked="" type="radio"/>	Flow cytometry
<input type="radio"/>	Palaeontology and archaeology	<input type="radio"/>	MRI-based neuroimaging
<input checked="" type="radio"/>	Animals and other organisms		
<input type="radio"/>	Clinical data		
<input type="radio"/>	Dual use research of concern		

Antibodies

Antibodies used	All antibodies used are listed in Supplementary Tables, including catalogue numbers and dilutions.
Validation	All antibodies were validated by the manufacturer, and data can be found using the company and catalogue numbers provided in the

Eukaryotic cell lines

Policy information about [cell lines](#) and [Sex and Gender in Research](#)

Cell line source(s)	
Authentication	
Mycoplasma contamination	
Commonly misidentified lines (See ICLAC register)	

Palaeontology and Archaeology

Specimen provenance	
Specimen deposition	
Dating methods	

Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight	
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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	<input type="text" value="We provided the following statements:"/>
Wild animals	<input type="text" value="N/A"/>
Reporting on sex	<input type="text" value="N/A"/>
Field-collected samples	<input type="text" value="N/A"/>
Ethics oversight	<input type="text" value="McMaster University Animal Research Ethics Board, the University of Minnesota Institutional Animal Care and Use Committee, or with"/>

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 ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	<input type="text"/>
Study protocol	<input type="text"/>
Data collection	<input type="text"/>
Outcomes	<input type="text"/>

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 |
|-----------------------|---|
| <input type="radio"/> | <input checked="" type="radio"/> Public health |
| <input type="radio"/> | <input checked="" type="radio"/> National security |
| <input type="radio"/> | <input checked="" type="radio"/> Crops and/or livestock |
| <input type="radio"/> | <input checked="" type="radio"/> Ecosystems |
| <input type="radio"/> | <input checked="" type="radio"/> Any other significant area |

Experiments of concern

Does the work involve any of these experiments of concern:

- | No | Yes |
|-----------------------|--|
| <input type="radio"/> | <input checked="" type="radio"/> Demonstrate how to render a vaccine ineffective |
| <input type="radio"/> | <input checked="" type="radio"/> Confer resistance to therapeutically useful antibiotics or antiviral agents |
| <input type="radio"/> | <input checked="" type="radio"/> Enhance the virulence of a pathogen or render a nonpathogen virulent |
| <input type="radio"/> | <input checked="" type="radio"/> Increase transmissibility of a pathogen |
| <input type="radio"/> | <input checked="" type="radio"/> Alter the host range of a pathogen |
| <input type="radio"/> | <input checked="" type="radio"/> Enable evasion of diagnostic/detection modalities |
| <input type="radio"/> | <input checked="" type="radio"/> Enable the weaponization of a biological agent or toxin |
| <input type="radio"/> | <input checked="" type="radio"/> Any other potentially harmful combination of experiments and agents |

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

Files in database submission

Genome browser session
(e.g. [UCSC](#))

Methodology

Replicates

Sequencing depth

Antibodies

Peak calling parameters

Data quality

Software

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

Instrument

Software

Cell population abundance

Gating strategy

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

Design specifications

Behavioral performance measures

Acquisition

Imaging type(s)

Field strength

Sequence & imaging parameters

Area of acquisition

Diffusion MRI Used Not used

Preprocessing

Preprocessing software

Normalization

Normalization template

Noise and artifact removal

Volume censoring

Statistical modeling & inference

Model type and settings

Effect(s) tested

Specify type of analysis:

Whole brain ROI-based Both

Statistic type for inference
(See [Eklund et al. 2016](#))

Correction

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

Graph analysis

Multivariate modeling and predictive analysis



