nature portfolio

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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	LSR Fortessa (BD Biosciences; San Jose, CA, USA), Leica Stellaris 8 tau-STED Microscope (Leica Microsystems), Bio-Plex 200 Multiplex system, CFX384 Touch Real-Time PCR Detection System (Bio-Rad), Cytation 5 Multi-Mode Reader (BioTek), Illumina NextSeq 550
Data analysis	BD FACSDiva 8.0.1 software, FlowJo v10.7.2,Bio-Plex Manager 6.2, CFX Manager™ Software version 3.1, Gen 5 version 2.07, ImageJ software version 1.53m NIH, GraphPad Prism v9,LAS-X software,Yasara web, (STAR) program, version 2.5.1b.

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

Transcriptomic data generated during this study has been deposited with the NCBI Gene Expression Omnibus (GEO) database under: GSE268640 accession number.

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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	The sample size was sufficient based on power calculations and differences observed between groups giving statistically significant analysis, and based on reproducibility between experiments. Low observed variability between samples and differences observed using internal controls.
Data exclusions	No data were excluded
Replication	Most experiments were performed at least 2 times with at least 2 biological replicates each giving consistent and reproducible results. Experiments were performed using multiple different approaches that helped reach the same conclusions.
Randomization	Mice of matched age, sex and samples were randomly allocated to the experiments.
Blinding	Collection of samples was not blinded. However, samples were analyzed blinded and group allocation was performed afterwards.

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*

Sampling strategy	*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

All antibodies were purchase from the manufacturer
Anti-Ly6G BioXCell (catalog# BP0075-1, lot 695418J, clone 1A8, 100µg/mouse), IgG isotype (BioXCell catalog# BP0089, lot 716718O1, 100µg/mouse), Anti- FNAR1 (Leinco Technologies catalog#I-401, lot 1123L460, clone MAR1-5A3, 2mg/per mice), IgG Isotype (Leinco Technologues catalog# I-536, lot 0923L495,2mg/per mice), Anti-CD45-PE(Biolegend,catalog#103105, lot B299555, clone 30-F11, 0.5µl/staining),Anti-Podoplanin PE-DAZZLE594 (Biolegend, catalog#127419, lotB298016, clone 8.1.1, 0.5µl/staining), Anti-CD24-BUV395 (BD Biosciences catalog# 744471, lot 2091087, cloneM1/69, 1µl/staining) Anti-CD31-BV510 (BD Biosciences catalog#740114, lot 2091082, clone 390, 1.5µl/staining), Anti- CD326-BV711 (Biolegend, catalog# 118233, clone G8.8, 0.5µl/staining), Anti- MHC-II-BV605 (Biolegend, catalog# 107639, lot B321059, clone M5/114.15.2, 0.5µl/staining), or Anti- PDCA-1-APC(Biolegend, catalog#127016, lot B337341, clone 927, 1.5µl/staining), Anti- CD11b-AF700(Biolegend, catalog#101222, lot B336447, clone M1/70, 1µl/staining), Anti- Ly6G-BV780(Biolegend, catalog#127645, lot B313888, clone 1A8, 1µl/staining), Anti-CD11c Percp-Cy5.5(Biolegend, catalog#117328, lot B332774, 1.5µl/staining), Anti- Ly6C-FITC. (Biolegend, catalog# 128005, lot B368467, clone HK1.4, 1µl/staining), Fixable viability dye eFluor506 (Invitrogen, catalog# 64-0866-14, lot 2290921, Ghost dye-Red780 (TONBO bioscience catalog#13-0865-T100, 1:2000 each), Apotracker Green(Biolegend, catalog# 427402, lot B347919, 1µl/staining), Rabbit anti-HA antibody (Sigma catalog # H6908, 1:2000, lot 0000160996), anti-FLAG antibodies (Sigma, catalog # F7425,1:2000, lot 078M4886V), Mouse anti-Ubiquitin(P4D1) (Enzo, catalog# BML-PW0930-0100, lot X08546c, clone P4D1, 1:1000),Mouse anti-histidine (Sigma, catalog# H1029-2ML, lot 106M4768V, clone His-1, 1:1000), Rabbit anti-TRIM7 (Sigma prestige, catalog#HPA039213-100UL, lot 000003488 1:500), Rabbit anti-GM130 rabbit polyclonal antibody (Cell Signaling catalog# D6B1X, 1:100), Anti-Rabbit IgG-HRP from donkey (cytiva Amersham catalog# NA934-1ML, lot 17572641, 1:10000) Anti-Mouse IgG-HRP from sheep (cytiva Amersham catalog# NA931V, lot 18034332,1:10000)), Anti-caspase-6 Cleaved Asp12 (Invitrogen catalog# PA5119529, lot ZD4285697D, 1:1000). Anti-N SARS-CoV-2 (Sinobiology catalog# 40588-T62, 1:1000), Mouse anti-β-actin (Genetex, catalog# GTX629630, clone GT5512, 1:2000), Rabbit anti-β-actin (Abcam, catalog# ab8227, 1:1000). Anti-pAKT S473 (Cell Signaling catalog# 4058S, lot 30, 1:1000), Anti-pAKT T308 (Cell Signaling catalog# 13038S, 1:1000), Anti-AKT (Cell Signaling catalog# 2920S, lot 3, 1:1000), Anti-pIKKα/β S176/180 (Cell Signaling catalog# 2694S, lot 2, 1:1000), Anti-IKKB (Cell Signaling catalog# 8943S, lot 4, 1:1000), Anti-pPDK1 S241 (Cell Signaling catalog# 3061S, lot 11, 1:1000), Anti-PDK1 (Cell Signaling catalog# 3062S, lot 12, 1:1000). Mouse anti-M SARS (Invitrogen catalog#MA5-14772, lot X133515711, 1:1000), Rabbit anti-TRIM7 (Proteintech, catalog#26285-1-AP, lot 00041738 1:1000).Rabbit anti-M SARS-CoV-2

Validation

For flow cytometry antibodies from Biolgend or BD Bioscience and western blot antibodies from cell signaling Anti-pAKT S473, Anti-pAKT T308, Anti-AKT, Anti-pIKKα/β S176/180, Anti-IKKB, Anti-pPDK1 S241, Anti-PDK1 validation was performed by the company using cell lines.

Validations of HA, FLAG, His and anti β-actin antibodies was reporter previously in the following publications:
Adam Hage, Preeti Bharaj, Sarah van Tol, Maria I Giraldo, Maria Gonzalez-Orozco, Karl M Valerdi, Abbey N Warren, Leopoldo Aguilera-Aguirre, Xuping Xie, Steven G Widen, Hong M Moulton, Benhur Lee, Jeffrey R Johnson, Nevan J Krogan, Adolfo García-Sastre, Pei-Yong Shi, Alexander N Freiberg, Ricardo Rajsbaum. The RNA helicase DHX16 recognizes specific viral RNA to trigger RIG-I-dependent innate antiviral immunity.
Carlos A. Rodrıguez-Salazar, Sarah van Tol, Olivier Mailhot, Maria Gonzalez-Orozco, Gabriel T. Galdino, Abbey N. Warren, Natalia Teruel, Padmanava Behera, Kazi Sabrina Afreen, Lihong Zhang, Terry L. Juelich, Jennifer K. Smith, Maria
Ines Zylber, Alexander N. Freiberg, Rafael J. Najmanovich, Maria I. Giraldo,Ricardo Rajsbaum. Ebola virus VP35 interacts non-covalently with ubiquitin chains to promote viral replication.

Sarah van Tol, Birte Kalveram, Philipp A. Ilinykh, Adam Ronk, Kai Huang, Leopoldo Aguilera-Aguirre, Preeti Bharaj, Adam Hage, Colm Atkins, Maria I. Giraldo, Maki Wakamiya, Maria Gonzalez-Orozco, Abbey N. Warren, Alexander Bukreyev, Alexander N. Freiberg, Ricardo Rajsbaum. Ubiquitination of Ebola virus VP35 at lysine 309 regulates viral transcription and assembly.

Validation of antibodies used in vivo Anti-Ly6G BioXCell was validated in several publications among them:
Richard W. Davis IV, Emma Snyder, Joann Miller, Shirron Carter, Cassandra Houser, Astero Klampatsa, Steven M. Albelda, Keith A. Cengel, Theresa M. Busch. Luminol Chemiluminescence Reports Photodynamic Therapy-Generated Neutrophil Activity In Vivo and Serves as a Biomarker of Therapeutic Efficacy
Kelly D Moynihan, Cary F Opel, Gregory L Szeto, Alice Tzeng, Eric F Zhu, Jesse M Engreitz, Robert T Williams, Kavya Rakhra, Michael H

Zhang, Adrienne M Rothschilds, Sudha Kumari, Ryan L Kelly, Byron H Kwan, Wuhbet Abraham, Kevin Hu, Naveen K Mehta, Monique J Kauke, Heikyung Suh, Jennifer R Cochran, Douglas A Lauffenburger, K Dane Wittrup & Darrell J Irvine. Eradication of large established tumors in mice by combination immunotherapy that engages innate and adaptive immune responses.
Validation of Anti- FNAR1 Leinco Technologies
Jacob T. Beaver,Lisa K. Mills,Dominika Swieboda,Nadia Lelutiu,Edward S. Esser,Olivia Q. Antao,Eugenia Scountzou,Dahnide T. Williams,Nikolaos Papaioannou,Elizabeth Q. Littauer &Ioanna Skountzoua. Zika virus-induced neuro-ocular pathology in immunocompetent mice correlates with anti-ganglioside autoantibodies.
James Brett, Case Paul W. Rothlauf, Rita E. Chen, Natasha M. Kafai, Julie M. Fox, Brittany K. Smith, Swathi Shrihari, Broc T. McCune, Ian B. Harvey, Shamus P. Keeler, Louis-Marie Bloyet, Haiyan Zhao, Meisheng Ma, Lucas J. Adams, Emma S. Winkler, Michael J. Holtzman, Daved H. Fremont, Sean P.J. Whelan, Michael S. Diamond.
Replication-Competent Vesicular Stomatitis Virus Vaccine Vector Protects against SARS-CoV-2-Mediated Pathogenesis in Mice.

Mouse anti-M SARS was validated by the manufacturer using recombinant protein

Rabbit anti-M SARS-CoV-2 was validated for IP using lysates from infected cells with SARS-CoV-2

Rabbit anti-TRIM7 (Proteintech, was validated by the company using mouse heart tissues
N6-Methyladenosine modification of the TRIM7 positively regulates tumorigenesis and chemoresistance in osteosarcoma through ubiquitination of BRMS1
The E3 ligase TRIM7 suppresses the tumorigenesis of gastric cancer by targeting SLC7A11

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	HEK293T (CRL-11268) and A549 (CCL-185) cell lines were obtained from ATCC. Calu-3 2B4 cells were kindly provided by Vineet D. Menachery (The University of Texas Medical Branch at Galveston), Vero E6 cells were kindly provided by Pei-Yong Shi (The University of Texas Medical Branch at Galveston). HEK293T-hACE2 cells were kindly provided by Benhur Lee (Mount Sinai). A549 TRIM7 KO cells were generated in previous work from out laboratory (Envelope protein ubiquitination drives entry and pathogenesis of Zika virus Maria I. Giraldo, Hongjie Xia, Leopoldo Aguilera-Aguirre, Adam Hage, Sarah van Tol,,Chao Shan, Xuping Xie, Gail L. Sturdevant, Shelly J. Robertson, Kristin L. McNally, Kimberly Meade-White, Sasha R. Azar, Shannan L. Rossi, Wendy Maury, Michael Woodson, Holly Ramage, Jeffrey R. Johnson, Nevan J. Krogan, Marc C. Morais, Sonja M. Best, Pei-Yong Shi & Ricardo Rajsbaum)
Authentication	Cells were not further authenticated. TRIM7 CRISPR KO cell lines were corroborated using anti-TRIM7 antibody by immunoblot.
Mycoplasma contamination	Cell lines were tested negative for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	None of the cell lines used in this study are commonly misidentified lines

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	All animal experiments were carried out following Institutional Animal Care and Use Committee (IACUC) guidelines and have been approved by the IACUC either at University of Texas Medical Branch at Galveston protocol numbers: 2103023 and 1904044, or at Rutgers University PROTO202200007. Mice were maintained under specific pathogen-free conditions in the Animal Resource Center (ARC) facility at UTMB or Rutgers University with cycles of 12h/ dark and 12h/light, at a temperature of 18 to 23 Celsius and humidity of 40-60%. Animal experiments involving infectious viruses were performed under animal biosafety level 3 (ABSL-3) conditions at

	UTMB or Rutgers in accordance with institutional biosafety approvals. Our studies utilized: 20- to 25-week-old C57BL/6NJ WT mice males and females (The Jackson Laboratory) 20- to 25 week-old Trim7-/- mice male and female, 25-week-old C57BL/6J WT male mice (The Jackson Laboratory).
Wild animals	The study did not involve wild animals
Reporting on sex	In this work both male and female mice were involved in most experiments. However due to a stronger phenotype observed in male mice some experiments were only performed in males, whenever specific sex was used is indicated in the figure legends.
Field-collected samples	The study did not involve field-collected samples.
Ethics oversight	IACUC of the University of Texas Medical Branch at Galveston and Rutgers University

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	*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 — *Lungs isolated from infected mice were collected in RPMI 10% v/v FBS 1% v/v penicillin-streptomycin, lungs were rinsed with DPBS cut into small pieces and digested in digestion media containing collagenase D 0.7mg/ml and DNase I 30µg/ml in serum-free RPMI for 30 minutes in a humidified 5% CO2 incubator at 37℃. FBS was added to the digestion media to inactivate the enzymes. Lungs were then passed through 70µm cell strainer to obtain single-cell suspension. Red blood cells were lysed using RBC lysing buffer Hybri-Max (Sigma), cells were counted and 1x106 cells were stained.*

Instrument	*LSR II Fortessa*
Software	*Acquisition software BD FACSDiva 8.0.1, and analysis software FlowJo v10.7.2,*
Cell population abundance	*No sorting of specific populations was performed in this study*
Gating strategy	*Supplementary figure 3 shows the gating strategy. Briefly the gating was performed by FSC-A vs FSC-H to select single events, then cell was gated by FSC-A vs SSC-A, follow by gating using the viability dye Fixable viability dye eFluor506 or Ghost dye-Red780, live cells was selected for following gating, first CD45-PE + or CD45-PE - population were selected for CD45+ following gating was performed by gating out PDCA-1+, negative cells were then gated by CD11b-AF710 vs CD11c-percp-c5.5 expression, CD11b+ cells were then gated by Ly6C expression (monocytes), intermediate or negative Ly6C population was then gated for Ly6G expression, cells expression high levels of Ly6G were considered neutrophils. The PDCA-1-APC + population was then gated for CD11b expression and cells expression PDCA-1 and negative for CD11b expression were considered pDCs. The CD45-PE negative populations were then gated for CD31-BV510 expression, cells expression CD31 were then gated for expression of epithelial cell markers Podoplanin- PE-DAZZLE594 vs CD24-BUV395. Podoplanin + cells are considered alveolar type 1, and CD24+ cells are considered ciliated cells, the negative fraction was then gated by for EpCAM-BV711 vs MHC-II-BV605 expression, cells positive for both markers were considered alveolar type 2 cells.* *For selection of cells in apoptosis the gating was performed by FSC-A vs FSC-H to select single events, then cell was gated by FSC-A vs SSC-A, follow by gating using the viability dye Ghost dye-Red780, live cells was selected CD45 PE and Apotracker FITC*

☒ 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.