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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	Flow cytometry (Stratedigm, model:S1000) was used to collect infectivity data by sorting GFP-, RFP-, or BFP-expressed cells. Illumina HiSeq 2500 was used to generate RNA-seq data. qRT-PCR data were generated by ABI 7500 fast real-time PCR machine. Luciferase reporter, ELISA, and cell viability data were measured by FLUOstar OPTIMA (BMG labtech).
Data analysis	FlowJo 10.0.6 was used to analyze FACS data; Graphpad prism 7 was used to perform statistical analysis; Tophat (v2.0.10) was used to map the RNA-seq reads; Cufflinks/Cuffdiff (v2.1.1) was used to calculate the gene expression value; fastqc (v0.11.2) and fastq_screen (v0.4.4) were used to check the quality of RNA-seq reads; fastq-mcf (ea-utils/1.1.2-806) was used to trim quality of reads; picard-tools (v1.127) was used to mark the duplicates; featureCounts was used to count the reads; edgeR was used to distinguish the differential gene expression; Ingenuity Pathway Analysis tool was used to perform pathway analysis; various R packages was used to plot the pathway enrichment.

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

All figures associated raw data of graphs and western blot gels were deposited in Source data and in Supplementary figure.
All data or materials associated this study are available from authors upon reasonable request.
RNA-seq data have been deposited to NCBI GEO. Accession number is XXX

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	Although no statistical methods were used to predetermined sample size in vitro and in vivo analyses, we conducted preliminary experiments to estimate variances in each assay and determined sufficient sample size. The biological sample size is presented in the figure or stated in the figure legends section.
Data exclusions	No data were excluded from the analyses.
Replication	All attempts at replication were successful. The experiments number has been clearly stated in the figure legends.
Randomization	No randomization was used in this study. For in vitro experiments, indicated genotype cells were transduced with indicated lenti-virus, transfected with indicated plasmids, or treated with indicated drugs. For in vivo mice experiments, mice were grouped according to the genotype.
Blinding	For in vitro experiments, no blinding was done. For clinical score analysis, survival mice were evaluated blindly to reach clinical score.

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

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

We have listed indicated antibodies information used in this study as follows.

Antibody Name;	Purpose;	Source;	Manufacturer;	Cat. No.;	Clone No.;	Lot No.;	WB Dilution
1. Flag;	WB;	HRP;	Sigma;	A8592;	M2;	SLBD9930;	1:10000
2. Actin;	WB;	Rabbit;	Sigma;	A2066;	N/A;	103M4826V;	1:5000
3. HA;	WB;	Mouse;	Covance;	MMS-101P;	16B12;	D14FF01308;	1:5000
4. GFP;	WB;	Rabbit;	Clontech;	632592;	N/A;	1404005;	1:5000
5. pIκBα;	WB;	Rabbit;	Cell Signaling	; #2859;	14D4;	14;	1:2500
6. IκBα;	WB;	Mouse;	Cell Signaling;	#4814;	L35A5;	10;	1:5000
7. NIK;	WB;	Rabbit;	Cell Signaling;	#4994;	N/A;	4;	1:1250
8. SIX1;	WB/Ch-IP;	Rabbit;	Cell Signaling;	#12891;	D4A8K;	1;	1:2500
9. RelA;	WB;	Rabbit;	Cell Signaling;	#8242;	D14E12;	8;	1:5000
10. RelA;	Ch-IP;	Rabbit;	Santa Cruz;	sc-372X;	C-20;	E0916;	N/A

11. pRelA;	WB;	Rabbit;	Cell Signaling;	#3033;	93H1;	16;	1:5000	
12. RelB;	WB;	Rabbit;	Santa Cruz;	sc-226X;	C-19;	L2915;	1:2500	
13. p100/52;	WB;	Mouse;	Santa Cruz;		sc-7386;	C-5;	H1913;	1:500
14. H3;	WB;	Rabbit;	Abcam;	ab1791;	N/A;	GR293197-1;	1:5000	
15. PARP;	WB;	Rabbit;	Cell Signaling;	#9542;	N/A;	14;	1:5000	
16. Cleaved Casp 3;	WB;	Rabbit;	Cell Signaling;		#9664;	5A1E;	20;	1:1000
17. TAK1;	WB;	Rabbit;	Cell Signaling;	#4505;	N/A;	7;	1:5000	
18. TAK1;	WB;	Mouse;	R&D;	MAB5307;	#491840;	CBLE0214061;	1:5000	
19. cIAP1;	WB;	Goat;	R&D;	AF8181;	N/A;	KHS0414051;	1:1000	
20. SIX2;	WB;	Rabbit;	Proteintech;		11562-1-AP;	N/A;	N/A;	1:1000
21. CD40;	WB;	Rabbit;	Abcam;	ab13545;	N/A;	GR159102-4;	1:5000	
22. Pol II;	Ch-IP;	Mouse;	Active motif;		39097;	4H8;	10618019;	N/A
23. IgG;	Ch-IP;	Rabbit;	Millipore;	12-370	; N/A;	2972424;	N/A	

Validation

All primary antibodies were used in this study are commercial (please see details above). Most antibodies were validated by knocking out indicated gene.
1. Flag, product citation is 640 from the manufacturer's website: https://www.sigmaaldrich.com/catalog/product/sigma/a8592?lang=en&region=US
2. Actin, Species (amoeba, chicken, wide range, vertebrates, slime mold, human); Application (IF, IHC(p), WB). Product citation is 1846 from the manufacturer's website: https://www.sigmaaldrich.com/catalog/product/sigma/a2066?lang=en&region=US
3. HA, Application (WB-Quality tested, IF, IP-Validated, Purification-Reported in literature). Product citation is 102 from the manufacturer's website: https://www.biolegend.com/en-us/products/purified-anti-ha-11-epitope-tag-antibody-11374
4. GFP, Application (WB, IP, Ch-IP seq etc.). Information is from the manufacturer's website: https://www.labome.com/product/Takara-Bio-Clontech/632592.html
5. pIκBα, Species (Human, Mouse, Rat, Monkey), Application (WB, IP). Product citation is 416 from the manufacturer's website: https://www.cellsignal.com/products/primary-antibodies/phospho-ikba-ser32-14d4-rabbit-mab/2859
6. IκBα, Species (Human, Mouse, Rat, Monkey, Bovine, Pig), Application (WB, IP etc.). Product citation is 338 from the manufacturer's website: https://www.cellsignal.com/products/primary-antibodies/ikba-l35a5-mouse-mab-amino-terminal-antigen/4814
7. NIK, Species (Human, Mouse), Application (WB). Product citation is 59 from the manufacturer's website: https://www.cellsignal.com/products/primary-antibodies/nik-antibody/4994
8. SIX1, Species (Human, Mouse, Rat, Monkey), Application (WB, IP, etc.). Product citation is 2 from the manufacturer's website: https://www.cellsignal.com/products/primary-antibodies/six1-d4a8k-rabbit-mab/12891
9. RelA, Species (Human, Mouse, Rat, Hamster, Monkey, Dog), Application (WB, IP, Ch-IP etc.). Product citation is 739 from the manufacturer's website: https://www.cellsignal.com/products/primary-antibodies/nf-kb-p65-d14e12-xp-rabbit-mab/8242
10. RelA, Species (mouse, rat and human), Application (WB, IP, etc.). Product citation is 1057 from the manufacturer's website:https://www.scbt.com/scbt/product/nfkappab-p65-antibody-c-20
11. pRelA, Species (Human, Mouse, Rat, Hamster, Monkey, Pig), Application (WB, IP, etc.). Product citation is 964 from the manufacturer's website: https://www.cellsignal.com/products/primary-antibodies/phospho-nf-kb-p65-ser536-93h1-rabbit-mab/3033
12. RelB, Species (mouse, rat and human), Application (WB, IP, etc.). Product citation is 283 from the manufacturer's website: https://www.scbt.com/scbt/product/relb-antibody-c-19?requestFrom=search
13. p100/52, Species (mouse, rat and human), Application (WB, IP, etc.). Product citation is 123 from the manufacturer's website: https://www.scbt.com/scbt/product/nfkappab-p52-antibody-c-5?requestFrom=search
14. H3, Species (Mouse, Rat, Chicken, Dog, Human etc.), Application (WB, IP, Ch-IP etc.). Product citation is 2428 from the manufacturer's website: https://www.abcam.com/histone-h3-antibody-nuclear-loading-control-and-chip-grade-ab1791.html
15. PARP, Species (Human, Mouse, Rat, Monkey), Application (WB). Product citation is 1581 from the manufacturer's website: https://www.cellsignal.com/products/primary-antibodies/parp-antibody/9542
16. Cleaved Casp 3, Species (Human, Mouse, Rat, Monkey), Application (WB, IP, etc.). Product citation is 1504 from the manufacturer's website:
17. TAK1, Species (Human, Mouse, Rat, Monkey, Bovine), Application (WB). Product citation is 72 from the manufacturer's website: https://www.cellsignal.com/products/primary-antibodies/tak1-antibody/4505
18. TAK1, Species (Human), Application (WB). Product citation is 1 from the manufacturer's website: https://www.rndsystems.com/products/human-tak1-antibody-491840_mab5307
19. cIAP1, Species (Human), Application (WB). Product citation is 33 from the manufacturer's website: https://www.rndsystems.com/products/human-ciap-1-hiap-2-antibody_af8181
20. SIX2, Species (human, mouse, rat, American alligator, pig), Application (WB, IP, etc.). Product citation is 121 from the manufacturer's website:
21. CD40, Species (Human, Mouse, Rat, etc.), Application (WB, IHC-P). Product citation is 5 from the manufacturer's website: https://www.abcam.com/cd40-antibody-ab13545.html
22. Pol II, Species (Human, Mouse, Rat, etc.), Application (WB, Ch-IP, Ch-IP Seq). Product citation is 29 from the manufacturer's website: https://www.activemotif.com/catalog/details/39097/rna-pol-ii-antibody-mab
23. IgG, Application (WB, IP). http://www.emdmillipore.com/US/en/product/Normal-Rabbit-IgG,MM_NF-12-370

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

SV40-immortalized STAT1-/- fibroblasts provided by Dr. Jean-Laurent Casanova (Rockefeller University); HCT116 and U-2 OS were obtained from ATCC; HEK293A provided by Jack Dixon (University of California, San Diego); HEK293T provided by Paul Bieniasz (Aaron Diamond AIDS Research Center); NSCLC cell lines H1155, H1792, and H2087 provided by Dr. John Minna (UT Southwestern Medical Center)

Authentication	Common cell lines were identified by their morphology. Specific cell lines used in this study were authenticated by PCR or mutational status
Mycoplasma contamination	All cell lines were tested and negative for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell line

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	SIX1 transgene mice are FVB genetic background. CAG-rtTA3 mice are C57BL/6 background. rtTA3-SIX1 mice and their littermate controls (rtTA3) were obtained by intercrossing SIX1 mice with CAG-rtTA3 mice. 6-7 weeks old mice were given doxycycline water for 10 days prior to LPS administration experiments. Nik-/- mice are C57BL/6 background. 6-week-old mice were used for experiment. Both males and females were used for experiments.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	All animal experiments were performed according to the protocol that approved by UT Southwestern Medical Center IACUC.

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, 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.

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.*

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	We seeded indicated cells in the 24-well-plate. Cells were then transduced with indicated lentivirus and then challenged with the GFP-expressing bacterial or viral pathogens. Cells were then detached by 37°C warmed Accumax (Sigma), followed by centrifugation at 800×g for 2 minutes. Cells were then fixed by suspending in PBS/1% PFA at 4°C for at least 30 minutes. Cells were then stored in PBS/3% FBS.
Instrument	Stratedigm, model:S1000
Software	Flowjo 10.0.6
Cell population abundance	We analyzed 30,000 single cells which are live
Gating strategy	For most part of analysis, we gated the live cells, single cells population from live cells, and then gated the RFP positive cells. Finally, we gated the GFP positive units from the RFP positive population. For Extended Data Fig. 1h and 4b, we performed extra one step (BFP positive cells from RFP positive population) before we gated the GFP positive cells. For, Extended Data Fig. 1e, we only performed GFP positive analysis in single cells.

☐ 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.