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	No software was used for data collection
Data analysis	Bcftools 1.11; BWA 0.7 ; Samtools 1.11 ; Picard 2.25 ; FreeBayes 1.3.5 ; snpEff 5.0 ; R package poppr 2.0 ; ADMIXTURE 1.3 ; PLINK (v. 1.07) ; ChromoPainter 1.0; Ancestry_HMM 1.0; PopART 1.0; BEAST v1.10.4 ; Tracer v1.7.1; FigTree 1.4.4; PBScan 1.0; REHH 2.0 R package; iqtree2; karyoploteR 1.0 package

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

The 105 genomes sequenced in this study have been deposited in the ENA database under accession code BENIN01 (ERS13421591); BENIN02 (ERS13421592); BENIN04 (ERS13421593); BENIN05 (ERS13421594); BENIN03 (ERS13421595); BRAZIL01 (ERS13421596); CAMEROON01 (ERS13421597); DROC01 (ERS13421598);

FRANCE01(ERS13421599); FRANCE02 (ERS13421600); FRANCE03 (ERS13421601); FRANCE04 (ERS13421602); FRANCE05 (ERS13421603); FRANCE06 (ERS13421604); FRANCE07 (ERS13421605); FRANCE08 (ERS13421606); FRANCE09(ERS13421607); FRANCE10 (ERS13421608); FRANCE11 (ERS13421609); FRANCE12 (ERS13421610); FRANCE13 (ERS13421611); FRANCE14 (ERS13421612); FRANCE15 (ERS13421613); FRANCE16 (ERS13421614); FRANCE17(ERS13421615); FRANCE18 (ERS13421616); FRANCE19 (ERS13421617); FRANCE21 (ERS13421618); FRANCE22 (ERS13421619); FRANCE23 (ERS13421620); FRANCE24 (ERS13421621); FRANCE20 (ERS13421622);FRENCHGUIANA08 (ERS13421623); FRENCHGUIANA09 (ERS13421624); FRENCHGUIANA11 (ERS13421625); FRENCHGUIANA13 (ERS13421626); FRENCHGUIANA14 (ERS13421627); FRENCHGUIANA15 (ERS13421628); FRENCHGUIANA01(ERS13421629); FRENCHGUIANA02 (ERS13421630); FRENCHGUIANA05 (ERS13421631); FRENCHGUIANA06 (ERS13421632); FRENCHGUIANA03 (ERS13421633); FRENCHGUIANA04 (ERS13421634); FRENCHGUIANA10 (ERS13421635);FRENCHGUIANA07 (ERS13421636); GABON01 (ERS13421637); GABON03 (ERS13421638); GABON05 (ERS13421639); GABON07 (ERS13421640); GABON02 (ERS13421641); GABON04 (ERS13421642); GABON06 (ERS13421643);GUADELOUPE02 (ERS13421644); GUADELOUPE01 (ERS13421645); MARTINIQUE04 (ERS13421646); MARTINIQUE02 (ERS13421647); MARTINIQUE03 (ERS13421648); MARTINIQUE01 (ERS13421649); MARTINIQUE05 (ERS13421650);PORTUGAL01 (ERS13421651); PORTUGAL03 (ERS13421652); PORTUGAL05 (ERS13421653); PORTUGAL06 (ERS13421654); PORTUGAL07 (ERS13421655); PORTUGAL08 (ERS13421656); PORTUGAL02 (ERS13421657); PORTUGAL04(ERS13421658); PORTUGAL09 (ERS13421659); PORTUGAL10 (ERS13421660); SENEGAL05 (ERS13421661); SENEGAL10 (ERS13421662); SENEGAL22 (ERS13421663); SENEGAL25 (ERS13421664); SENEGAL04 (ERS13421665);SENEGAL14 (ERS13421666); SENEGAL23 (ERS13421667); SENEGAL01 (ERS13421668); SENEGAL02 (ERS13421669); SENEGAL03 (ERS13421670); SENEGAL06 (ERS13421671); SENEGAL07 (ERS13421672); SENEGAL08(ERS13421673); SENEGAL12 (ERS13421674); SENEGAL13 (ERS13421675); SENEGAL16 (ERS13421676); SENEGAL17 (ERS13421677); SENEGAL18 (ERS13421678); SENEGAL19 (ERS13421679); SENEGAL21 (ERS13421680);SENEGAL24 (ERS13421681); SENEGAL09 (ERS13421682); SENEGAL15 (ERS13421683); SENEGAL20 (ERS13421684); SENEGAL26 (ERS13421685); SENEGAL11 (ERS13421686); SERBIA01 (ERS13421687); SPAIN01(ERS13421688); TUNISIA01 (ERS13421689); TUNISIA03 (ERS13421690); TUNISIA02 (ERS13421691); TURKEY01 (ERS13421692); TURKEY02 (ERS13421693); UK01 (ERS13421694); USA01 (ERS13421695). RH2019 (ERR10079368); RH1989 (ERR10079367); PRU2019 (ERR10079366); PRU1989 (ERR10079365) were sequenced for datation purposes. RH-88 (GCA_013099955.1) and ME49 (GCA_000006565.2) were used as reference genomes in this study. The following publicly available sequence reads were also used in this study: BRAZIL02,TgCatBr01 (SRX099790); BRAZIL03,TgCatBr05 (SRX099804 SRX099805 SRX099795); BRAZIL04,TgCatBr09 (SRX099807 SRX099781 SRX099806); BRAZIL05,TgCatBr10 (SRX099791); BRAZIL06,TgCatBr15 (SRX099779); BRAZIL07,TgCatBr18 (SRX099794); BRAZIL08,TgCatBr25 (SRX160134); BRAZIL09,TgCatBr26 (SRX099780); BRAZIL10,TgCatBr3 (SRX160142); BRAZIL11,TgCatBr34 (SRX160051); BRAZIL12,TgCatBr44 (SRX160141); BRAZIL13,TgCatBr64 (SRX160743); BRAZIL14,TgCatBr72 (SRX160049); BRAZIL15,TgCkBr141 (SRX160124); CANADA01,COUG ; TgCgCa01 (SRX099803 SRX099786 SRX099802); CHINA01,PgCatPRC2 (SRX156168 SRX155517); COLOMBIA01,TgCtCo5 (SRX156192 SRX156164 SRX156155 SRX154747); COLOMBIA02,TgDgCo17 (SRX099787); COSTARICA1,TgCkCr01 (SRX160807); COSTARICA2,TgCkCr10 (SRX099784); COSTARICA3,TgRsCr01 (SRX160143); FRENCHGUIANA16,GUY-DOS (SRX099782); FRENCHGUIANA17,GUY-KOE (SRX099796); FRENCHGUIANA18,GUY-MAT (SRX099783); FRENCHGUIANA19,GUY-2003-MEL (SRX160131); FRENCHGUIANA20,GUY-2004-ABE (SRX160132); FRENCHGUIANA21,GUY009-AKO (SRX171132); FRENCHGUIANA22,GUY 021 - TOJ (SRX160041); FRENCHGUIANA24,RUB ; GUY-RUB (SRX055419 SRX055414 SRX099773 SRX055412); FRENCHGUIANA12,VAND ; GUY-VAND (SRX055413 SRX038726 SRX055418 SRX055416); FRENCHGUIANA23,GUY-JAG1 (SRX099776); GABON08,GAB3-2007-GAL-DOM2 (SRX160123); GABON09,GAB5-2007-GAL-DOM1 (SRX160069); GABON10,GAB1-2007-GAL-DOM10 (SRX159841 SRX159839); GABON11,GAB2-2007-GAL-DOM2 (SRX156037 SRX155963 SRX155534); GABON12,GAB3-2007-GAL-DOM9 (SRX160125); GABON13,GAB5-2007-GAL-DOM6 (SRX159842 SRX159840); GUYANA01,TgCkGy2 (SRX099785); PANAMA01,G662M (SRX160052); BOF,BOF ; BE-BOF (SRX099774); FOU,FOU ; BRE-FOU (SRX046277 SRX038725 SRX046278); LGE-CUV,LGE-CUV (SRX099775); MAS,MAS ; LPN-MAS (SRX057823 SRX038728 SRX038699); TgH20005,IPP-URB (SRX157499 SRX157465); TgH26044 (SRX160050); URUGUAY01,CASTELLS (SRX099789); USA12,ARI (SRX099777 SRX099800 SRX099801); USA11,B41 (SRX099774); USA13,RAY (SRX099793); USA03,GT1 (SRX156314); USA05,ME49 (SRX055421 SRX055417 SRX055410); USA04,M7741 (SRX159890 SRX159849); USA10,VEG (SRX156300); USA14,B73 (SRX159844 SRX159843); USA02,CAST ; US-CAST (SRX099788); USA06,P89 ; TgPgUs15 (SRX038693 SRX055420 SRX038727); USA07,ROD ; ROD-US (SRX160129 SRX160128); USA08,SOU (SRX160119); USA09,TgShUs28 (SRX160130).

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

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 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.*
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	*Describe how sample size was determined, detailing any statistical methods 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 exclusions	*Describe any 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.*
Replication	*Describe the measures taken to verify the reproducibility of the experimental findings. If all attempts at replication were successful, confirm this OR if there are any findings that were not replicated or cannot be reproduced, note this and describe why.*
Randomization	*Describe how samples/organisms/participants were allocated into experimental groups. If allocation was not random, describe how covariates were controlled OR if this is not relevant to your study, explain why.*
Blinding	*Describe whether the investigators were blinded to group allocation during data collection and/or analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.*

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	We analyse a set of 156 genomes and we provide estimates of T. gondii mutation rate and generation time. We elucidate how the evolution of T. gondii populations is intimately linked to the major events that have punctuated the recent history of cats.
Research sample	156 T. gondii whole genomes were analysed is in this study.
Sampling strategy	A world representative dataset of T. gondii genomes was constituted.
Data collection	T. gondii isolates provided by the French Biological Resource Centre (BRC) for Toxoplasma (http://www.toxocrb.com/)
Timing and spatial scale	Isolates came from all continents and were obtained between 1958 and 2019

Data exclusions	T. gondii genomes with unknown geographic origin & mixed infections were excluded
Reproducibility	This is not relevant to the population genetic analyses performed in this study.
Randomization	This case study does not involve experimental groups or require randomized treatment or measurement.
Blinding	This is not relevant to the population genetic analyses performed in this 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

Methods

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

Antibodies

Antibodies used	*Describe all antibodies used in the study; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Validation	*Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer's website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.*

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	*State the source of each cell line used and the sex of all primary cell lines and cells derived from human participants or vertebrate models.*
Authentication	*Describe the authentication procedures for each cell line used OR declare that none of the cell lines used were authenticated.*
Mycoplasma contamination	*Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination.*
Commonly misidentified lines (See ICLAC register)	*Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

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	Swiss mice ; two months ; mice were used for T. gondii strains multiplication before culture and were not used in new experiments
Wild animals	No wild animals were used in the study
Reporting on sex	female
Field-collected samples	No field collected samples were used in the study
Ethics oversight	Ethics Committee for Animal Experimentation n°033 validated by the French Ministry of National Education, Higher Education and Research (Registration numbers: APAFIS#14582-2018041010294175 v2).

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

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	*Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.*
Instrument	*Identify the instrument used for data collection, specifying make and model number.*

Software	*Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.*
Cell population abundance	*Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.*
Gating strategy	*Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.*

☐ 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.