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	The raw data obtained from the image analysis reader were validated using the internal controls embedded in each test. The mean pixel intensity of the reaction was corrected for background noise, expressed as a value ranging between 0 and 130, and used without preprocessing in the analysis. Inconsistent or aberrant signal measures or antigen patterns were retested. Patients who withdrew from the study or who discontinued early were eliminated from the analysis. Validated data were incorporated into a Microsoft Excel 2016 database for further analysis.
Data analysis	Validated data were incorporated into a Microsoft Excel 2016 database for further analysis. A Visual Basic for Applications (VBA 7.1) User Defined Function from Microsoft Excel 2016 was programmed to calculate the DF50-value from the Dillution Factors (DF) and biomarker intensities. Linear Mixed Model analysis was performed with SAS 9.4 (SAS Institute Inc., Cary, NC, USA). The code is available is available in the "Supplementary Data and Software" file.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

All data associated generated with in this study are available in the main text or the provided in the "Supplementary Data and Software" zip file. The data underlying the results presented in this study are available upon request because they contain potentially sensitive personal information, which must be deidentified at the individual level. Interested researchers may contact the Drugs for Neglected Diseases initiative (DNDi), commissioner of this study, for data access requests via email at CTdata@dndi.org. Researchers may also request data by completing the form available at https://www.dndi.org/category/clinical-trials/. In this, they confirm that they will share data and results with DNDi and will publish any results open access.

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	Not reported as irrelevant to the study
Reporting on race, ethnicity, or other socially relevant groupings	The study was conducted in Bolivia with Bolivian participants
Population characteristics	The eligibility criteria can be found under the ClinicalTrials.gov ID NCT03378661. The Screening criteria are the following: Signed, written informed consent form Age >18 to <50 years Weight >50 kg to <80 kg Diagnosis of T. cruzi infection by: Conventional serology (a minimum of two positive tests [Conventional ELISA, Recombinant Elisa and/or Indirect Immunofluorescence (IIF)]) Ability to comply with all protocol specified tests and visits and have a permanent address Patients must be residents of areas free of vectorial transmission (Triatoma infestans). For this protocol, it will be accepted the status of Vectorial Transmission Interruption or Consolidation as per the definition of PAHO/WHO, or the Local Health Program. No signs and/or symptoms of the chronic cardiac and/or digestive form of CD No acute or chronic health conditions, that in the opinion of the PI, may interfere with the efficacy and/or safety evaluation of the trial drug (such as acute infections, history of HIV infection, liver and renal disease requiring treatment) No formal contraindication to BZN (according to the Summary of Product Characteristics) and E1224 (according to the Investigator's Brochure) Note: The contraindications described for Benznidazole and E1224 are essentially hypersensitivity to the active ingredient or any excipient. In the case of hepatic or renal impairment or blood dyscrasia, the medication should only be administered under strict medical supervision. During all the treatment period, the blood count will be monitored, with special attention to leucocytes. Subjects will be indicated about the need of no alcohol intake. No history of hypersensitivity, allergic, or serious adverse reactions to any of the "azoles" compound, and/or its components No history of CD treatment with BZN or NFX at any time in the past No history of systemic treatment with itraconazole, ketoconazole, posaconazole, isavuconazole, or allopurinol in the past No history of alcohol abuse or any other drug addiction (as specified in the Study Manual of Operations) No condition that prevents patient from taking oral medication No concomitant or anticipated use of drugs that are either sensitive CYP3A4 substrates and/or extensively metabolized by CYP3A4 with a narrow therapeutic range (as per Appendix 2) No medical history of Familial Short QT syndrome or concomitant therapy with medications that can shorten the QT interval (as per Appendix 2) No family history of sudden death No family history of sudden infant death syndrome The Inclusion Criteria are the following: Following the screening period, patients must meet ALL of the following inclusion criteria to be eligible for randomization: Confirmed diagnosis of T. cruzi infection by: Serial qualitative PCR (three samples collected over a single day, at least one of which must be positive) AND Conventional serology (a minimum of two positive tests must be positive [Conventional ELISA, Recombinant Elisa and/or IIF) Women in reproductive age must have a negative serum pregnancy test at screening, must not be breastfeeding, and must use a double barrier method of contraception to avoid pregnancy throughout a clinical trial and for 3 months after completion of the trial, in such a manner that the risk of pregnancy is minimized especially during exposure to treatment. Women who are using oral, implanted, or injectable contraceptive hormones or mechanical products such as an intrauterine device with a hormonal component are required to use an additional barrier method of contraception for the time period specified.

Normal EKG (PR ≤200 msec, QRS <120 msec, and QTc ≥350 msec and ≤450 msec interval durations in males and QTc ≤470 msec in women) at screening.
The Exclusion Criteria are the following:
The presence of any of the following will exclude a patient from trial randomization:

Signs and/or symptoms of chronic cardiac and/or digestive form of CD
History of cardiomyopathy, heart failure, or ventricular arrhythmia.
History of digestive surgery or mega syndromes.
Any other acute or chronic health conditions that, in the opinion of the PI, may interfere with the efficacy and/or safety evaluation of the trial drug (such as acute infections, history of HIV infection, diabetes, uncontrolled systolic/diastolic blood pressure, liver, and renal disease requiring medical treatment).
Laboratory test values considered clinically significant or out of the allowable range at selection period as follows:
Total WBC must be within the normal range, with an acceptable margin of +/- 5% (3,800 - 10,500/mm3).
Platelets must be within the normal range up to 550,000/mm3
Total bilirubin must be within the normal range
Transaminases (ALT and AST) must be within the normal range, with an acceptable margin of 25% above the upper limit of normality (ULN), <1.25 x ULN.
Creatinine must be within an acceptable margin of 10% above the ULN, <1.10 x ULN.
Alkaline phosphatase must be within the normal range up to Grade 1 CTCAE (< 2.5 x ULN)
GGT must be within the normal range up to 2x ULN.
Fasting glucose must be within the normal range
Electrolytes (Ca, Mg, K) must be within the normal range
If the results of the blood tests (hematology and biochemistry) are out of the ranges defined above, but within the limits of CTCAE (version 4.03) Grade 1, and the laboratory finding is considered as non-clinically significant, a new sample can be collected for a retest. Only one retest will be allowed within the screening period.
If the result of retest is within the margins defined above, the Investigator will review the parameter(s) together with all other medical information available (medical history, clinical examinations, vital signs, etc.) and upon his/her medical judgment will decide if the patient is eligible or not for trial randomization.
Any condition that prevents the patient from taking oral medication
Patients with history of allergy (serious or not), allergic skin rash, asthma, intolerance, sensitivity or photosensitivity to any drug
Patients with any contra-indication (known hypersensitivity) to any nitroimidazoles, e.g. metronidazole.
Any concomitant use of allopurinol, antimicrobial, or anti-parasitic agents.
Any planned surgery likely to interfere with the trial conduction and/or treatment evaluation
Unlikely to co-operate with the trial
Any previous participation in any clinical trial for Chagas Disease treatment evaluation
Participation in another trial at the same time or within 3 months prior to selection (according to local regulations)

The Screening Criteria are the following

Recruitment

The recruitment took place in 3 outpatient units in Bolivia.

Ethics oversight

The trial was done in accordance with the Declaration of Helsinki and Good Clinical Practice guidelines after approval from the applicable ethics committees. The trial protocol can be accessed on the Drugs for Neglected Diseases initiative (DNDi) website.

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 method used to determine sample size is described in the article: Torrico, F. et al. New regimens of benznidazole monotherapy and in combination with fosravuconazole for treatment of Chagas disease (BENDITA): a phase 2, double-blind, randomised trial. The Lancet Infectious Diseases 21, 1129–1140 (2021).
Adults aged 18–50 years with chronic indeterminate Chagas disease, confirmed by serological testing and positive qualitative PCR results, were randomly assigned (1:1:1:1:1:1:1:1) to one of seven treatment groups using a balanced block randomisation scheme with an interactive response system.

Data exclusions

Nine patients were excluded from the study because they either discontinued the study or the withdrew their consent.

Replication	Each well of the Multi-cruzi assay contains a replicate of each of the 15 T. cruzi antigens. Moreover, each well has embeded positive controls in quadruplicate.
Randomization	Participants were enrolled by principal investigators and their teams at each site and were randomly assigned (1:1:1:1:1:1:1) by a statistician to one of seven treatment groups using a balanced block randomisation scheme with an interactive response system and randomisation list generated in SAS version 9.3. Using the interactive response system, each participant was assigned an identification code corresponding to a study treatment group.
Blinding	Participants, investigators, and sponsor staff were masked to treatment allocation and the randomisation list.

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 & 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	Horseradish Peroxidase-conjugated goat anti-human IgG antibodies (SouthernBiotech, Ref 2040-05)
Validation	https://www.clinisciences.com/en/other-products-186/goat-anti-human-igg-hrp-20002637.html

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: *For laboratory animals, report species, strain and age OR state that the study did not involve laboratory animals.*

Wild animals: *Provide details on animals observed in or captured in the field; report species and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.*

Reporting on sex: *Indicate if findings apply to only one sex; describe whether sex was considered in study design, methods used for assigning sex. Provide data disaggregated for sex where this information has been collected in the source data as appropriate; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex-based analyses where performed, justify reasons for lack of sex-based analysis.*

Field-collected samples: *For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.*

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.

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJEguidelines for publication of clinical research and a completedCONSORT checklist must be included with all submissions.

Clinical trial registration: The clinical trial is registered with ClinicalTrials.gov, NCT03378661

Study protocol: The full trial protocol can be accessed on ClinicalTrials.gov, NCT03378661 and in the article Torrico, F. et al. New regimens of benznidazole monotherapy and in combination with fosravuconazole for treatment of Chagas disease (BENDITA): a phase 2, double-blind, randomised trial. The Lancet Infectious Diseases 21, 1129–1140 (2021).

Data collection: For the purpose of this article, data collection was done a posteriori, by testing serum samples at 6 and 12 months following the end of treatment.

Outcomes: The primary outcome is to evaluate the serological response of follow-up samples by Multi-cruzi testing using the dilution method.
This outcome was assessed using the Linear Mixed Method analysis.
The secondary outcome is to compare these results with the existing conventional and non-conventional serology tests.
This outcome was assessed using the receiver operating characteristic (ROC) analysis comparing the slopes of the treatment groups versus the slopes in the placebo group to identify the threshold for the slope. The obtained results were compared to those obtained with conventional and recombinant serology's 20% reduction in mean optical density.

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	*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

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.