nature portfolio

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Last updated by author(s): Oct 17, 2025

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	MEG data were collected using Acq Version 6.2.0-el8_9.x86_64-20240409-X by CTF-MEG-Neuroinnovations Ltd., Vancouver, Canada. Eye-Tracking Data were collected using the same software and using an Eyelink System by SR Research Ltd., Mississauga, Canada.
Data analysis	For data analysis we used Matlab (version 2022b) and the fieldtrip toolbox (Oostenveld et al. 2011).

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 datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

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	see submitted manuscript for details on the recruited sample
Reporting on race, ethnicity, or other socially relevant groupings	see submitted manuscript for details on the recruited sample
Population characteristics	see submitted manuscript for details on the recruited sample
Recruitment	Participants were recruited at the University Clinic of Münster, Germany.
Ethics oversight	Participants gave written informed consent in line with the declaration of Helsinki prior to the experiment and the study was approved by the ethics committee of the University of Münster (#2015-263-f-S).

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 analyses at hand were explorative. The sample size was therefore chosen from experience of similar MEG studies.
Data exclusions	Participants were excluded from the study, if they reported a history of psychotic disorders in themselves or in first degree relatives, since eye movement data might be impacted. Participants were excluded from the study if they had non-removable metal parts in their body, that would impact the collection of MRI or MEG data. Participants were excluded from analysis if the data quality did not allow a proper data analysis. This was due to technically caused (squid) jumps in the data.
Replication	Authors provided complete information on experimental procedure.
Randomization	Our study design did not require group allocation.
Blinding	Our sutdy design did not require group allocation.

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

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.*

Magnetic resonance imaging

Experimental design

Design type	only structural MRI was collected with no task (i.e. resting state)
Design specifications	no experiment was conducted in the MRI
Behavioral performance measures	no experiment was conducted in the MRI

Acquisition

Imaging type(s)	T1-weighted, structural
Field strength	3 T
Sequence & imaging parameters	Using a 3 T Siemens Magnetom Skyra scanner (Siemens, Erlangen, Germany; 64-channel head coil), structural T1 images were acquired (1 x 1 x 1 mm resolution; 192 x 256 x 256 mm FoV; 3D MP-RAGE sequence, TR = 2300ms,TE=3.6ms,TI=1100ms,FA=8°).
Area of acquisition	A whole brain scan was used

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	Matlab (version 2022b) and Fieldtrip toolbox (Oostenveld et al. 2011) calling SPM toolbox.
Normalization	non-linear transformation implemented in Fieldtrip toolbox (SPM)
Normalization template	MNI-based source grid for MEG-analyis distributed with Fieldtrip toolbox
Noise and artifact removal	No noise and artifact removal
Volume censoring	No Volume censoring

Statistical modeling & inference

Model type and settings	no statistics were computed using MRI data
Effect(s) tested	no statistics were computed using MRI data

Specify type of analysis: ☐ Whole brain ☒ ROI-based ☐ Both

Anatomical location(s)	We used the reduced Human Connectome Project atlas (HCP atlas) with 230 cortical parcels. Glasser et al. 2016, Tait et al. 2021
Statistic type for inference (See Eklund et al. 2016)	no statistics were computed using MRI data
Correction	no statistics were computed using MRI data

Models & analysis

n/a	Involved in the study
☒	☐ Functional and/or effective connectivity
☒	☐ Graph analysis
☒	☐ Multivariate modeling or predictive analysis