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Last updated by author(s): Feb 17, 2026

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	All tasks were programmed in Python 2.7 using PsychoPy (Peirce, 2007) and in-house scripts.
Data analysis	All analyses were programmed in Python 3.7. We used the following Python packages: MNE-Python (version 0.23.4), HEDFpy (version 0.0.dev3), Autoreject (version 0.2.2), PyMC (version 2.3.8), HDDM (version 0.8.0). Bayesian tests were performed in JASP (version 0.95.0).

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 raw data (DOI: 10.21942/uva.31297489), figure source data (DOI: 10.21942/uva.31305934), and analysis scripts (DOI: 10.21942/uva.31305955) are freely available at FigShare.

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	We only included participants who self-reported their biological sex to be male. We did not ask for nor reported on gender,
Reporting on race, ethnicity, or other socially relevant groupings	We did not collect data on race, ethnicity, or other socially relevant variables.
Population characteristics	For this project, 30 healthy male participants (aged 18-30) were recruited from the online research environment of the University of Amsterdam. Participants were not taking any psychotropic medication (other than then study medication) at the time of the study and had no life-time history of neurological or psychiatric disorders.
Recruitment	Participants were recruited from the online research platform of the University of Amsterdam. Only male (biological sex) participants were included in the study. All participants underwent extensive screening, consisting of physiological measures (BMI, heart rate, and blood pressure), an electrocardiogram (ECG) and a psychiatric questionnaire to assess mental health. Participants were only included in the study following approval of the screening data by our study-associated physician.
Ethics oversight	This study was approved by the Medical Ethical Committee of the Amsterdam University Medical Centre and the local ethics committee of the University of Amsterdam.

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

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	The study used a within-subject, randomized, double-blind crossover design. The data were all quantitative.
Research sample	28 healthy male participants, aged 18-30. Participants were recruited from the participation platform of the University of Amsterdam, but not all participants were students.
Sampling strategy	See study description for the sampling strategy. The sample size was not formally calculated for this study, but based on sample sizes of pharmacological studies with similar behavioral tasks.
Data collection	Recorded data include binary behavioral responses made on a keyboard, continuous pupil size measurements (using an EyeLink 1000, SR Research), and EEG recordings (512Hz, 64-channel BioSemi, Biosemi B.V. Amsterdam). There were no other people in the room with the participant during testing. The researcher was blind to the pharmacological condition, but was aware of the hypotheses being tested.
Timing	Data collection started in June 2019 and ended February 2021. During the beginning of the COVID pandemic, the study was placed on hold for 5 months.
Data exclusions	We excluded all trials in which 1) participants did not respond to the task, 2) participants responded during stimulus presentation, 3) participants blinked during stimulus presentation or the response-window.
Non-participation	Two participants dropped out after having completed the first experimental session, for reasons unrelated to the study. We did not replace these participants.
Randomization	Drug order was randomized across participants

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.