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	All analyses were conducted using the R statistical computing environment (Version 4.2.1). All analyses used meta-analytic random effects models estimated using restricted maximum likelihood with the metafor package (Version 2.1.0). Standard errors and confidence intervals for all analyses were calculated using cluster-robust standard errors (CR2-type), clustering by study, using the clubSandwich package (Version 0.3.5).
Data analysis	All analyses were conducted using the R statistical computing environment (Version 4.2.1). All analyses used meta-analytic random effects models estimated using restricted maximum likelihood with the metafor package (Version 2.1.0). Standard errors and confidence intervals for all analyses were calculated using cluster-robust standard errors (CR2-type), clustering by study, using the clubSandwich package (Version 0.3.5).

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

Data for each of the individual studies can be found following the OSF links presented in Table S1 in the SI. Data for the overall analysis presented here can be found at https://osf.io/bnq5j/.

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	n/a, the data here is a meta-analysis and no effect sizes were reported broken down by sex or gender.
Reporting on race, ethnicity, or other socially relevant groupings	n/a
Population characteristics	This is a meta-analysis of studies. The complete population of studies is included.
Recruitment	Each study in this prospective meta-analysis was put forward for replication, and the confirmation and all replications are included in this meta-analysis.
Ethics oversight	The individual studies in this meta-analysis were all approved by the IRBs at University of California, Santa Barbara, Stanford University, University of Virginia, and University of California, Berkeley. This current study is a meta-analysis and does not involve human subjects and is exempt. The prediction survey of lay participants was found exempt by the Office for Research on Human Subjects at the University of California, Santa Barbara.

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	A prospective meta-analysis of quantitative effect sizes from new discoveries and their replications.
Research sample	The sample here are effect sizes from prospective meta-analysis of new discoveries and replications by the four labs. There is no publication bias in this sample as the full population of studies is used.
Sampling strategy	Each lab put forward a study for replication, and it was replicated by all labs. Each study was powered at N = 1,500 to be able to detect very small effect sizes. Based on a power analysis of the 13 self-confirmatory tests with statistically-significant results, the average replication power was 0.96 with a median approaching 1 and average power in replication studies of specific discoveries ranging from 0.62 to approaching 1.
Data collection	All labs studies effect sizes were calculated by them and verified by one of the teams. All data was then put into a .csv file that was used for data analysis.
Timing	Studies started 06/2016 and ended 07/2019, survey of participants occurred 12/2022
Data exclusions	No study put forward was excluded.
Non-participation	The survey of particpants was done on Prolific academic, non-participation is not possible to determine.
Randomization	Order of studies and replications were randomized in a latin square design.

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