

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 Our codes are available here: <https://zenodo.org/records/17792605> and <https://osf.io/8wsqx/>

Data analysis *Provide a description of all commercial, open source and custom code used to analyse the data in this study, specifying the version used OR state that no software was used.*

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 publicly available data are available here: <https://zenodo.org/records/17792605> and <https://osf.io/8wsqx/>. See Readme for more details.

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
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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](https://www.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	This systematic and large-scale reproduction effort tests the reproducibility and robustness of economics and political science, contributing to a growing literature on research credibility and self-correction in science. We reproduced original analyses and conducted robustness checks of 110 articles recently published in leading economics and political science journals, all of which have mandatory data and code sharing policies. We found that over 85% of published claims were computationally reproducible. In robustness checks, our re-analyses led to 72% of statistically significant estimates to remain significant and in the same direction, and the median reproduced effect size is (nearly) the same as the originally published effect size (that is, 99% of the published effect size). Additionally, six independent research teams examined 12 pre-specified hypotheses about determinants of robustness. Research teams with more experience found lower levels of robustness, and robustness correlated with neither author characteristics nor data availability.
Research sample	110 articles. This is not a representative sample. Not all studies from our targeted journals have been reproduced or replicated. Our approach leads to an over-representation of studies using publicly available data. Another feature of our sample is that the targeted journals have a data availability policy and enforce it. This is in contrast to many top field journals in both economics and political science. Our sample should thus be viewed as very selected both in terms of impact and high data and code availability rates. In fact, approximately 45% of replication packages in our sample included raw data and complete cleaning code. An additional 13.5% provided partial cleaning code.
Sampling strategy	No sample size calculation. We explore the reasons why the 110 teams selected their paper. All teams answered the following question: "For what reasons did you select your specific paper to reproduce and/or replicate from the list of papers provided?" 12 options were offered, including Other (please specify). Options were not mutually exclusive, so any one team could provide multiple reasons for why they selected their paper. Extended Data Figure 2 summarizes the percentage of teams who selected each category. Of note 13.6% of teams were assigned a study (ie., did not choose which study to work on), so they did not answer this question. About 45% of teams report "Methods used", 36% of teams selected because of the journal of publication, about 25% due to the "Length of time to reproduce results" and about 19% due to the "Size of replication package". This is in line with our provided guidelines for choosing a study. If a large portion of reproducers select papers based on the assumption that their findings are questionable, it could skew reproducibility rates downward, as there's a tendency to pick studies more prone to revealing problematic outcomes. However, in this project, only a minimal fraction of teams indicated that they chose their paper because of ex ante beliefs that main results are (not) robust/replicable (3.6%). Few teams also selected papers based on statistical power/sample size and trust of original authors. We explore if our sample is representative of all subfields within economics. We compare JEL Codes of economic papers that we reproduced relative to those of a random sample of representative journal articles published in the top 100 journals in Economics (as ranked by https://ideas.repec.org/top/top.journals.simple.html). Our sample under-represents, among other fields, C-Mathematical and Quantitative Methods, G-Financial Economics and F-International Economics.
Data collection	N/A. We did not collect data. We reproduce published articles.
Timing	The articles were published between 2022 and 2023.
Data exclusions	No data excluded.

Non-participation

No participants.

Randomization

Not applicable as we did not randomize the studies we reproduced.

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, mosaicism, off-target gene editing) were examined.