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	As stated in the Research Transparency Statement in our submitted paper, all data are available at https://researchbox.org/see_one_private_public.php?b=s88kXars9RnaulBnYKR11GEuBJX53kdSCzFwbbBJDgA
Data analysis	All code and descriptions of code are available at https://researchbox.org/see_one_private_public.php?b=s88kXars9RnaulBnYKR11GEuBJX53kdSCzFwbbBJDgA

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

Our pre-registrations, materials, and code can be found at https://researchbox.org/see_one_private_public.php?b=s88kXars9RnaulBnYKR11GEuBJX53kdSCzFwbbBJDgA

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	To consider the effects of gender, we sent emails employing three male and three female sender names. At the start of the project, we had also intended to evaluate the effect of email recipient gender by inferring gender from email addresses. However, after observing lower-than-expected delivery rates and a large proportion of email addresses with no interpretable gender markers, we collapsed our data across recipient genders. We discuss these issues in more detail in Appendix 5 of the paper.
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable to our study design.
Population characteristics	See the study description in the "Behavioural & Social Sciences Study Design" section below.
Recruitment	See the study description in the "Behavioural & Social Sciences Study Design" section below.
Ethics oversight	Harvard University IRB approved the study protocol.

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	In partnership with Mail2Ru, a prominent citizen-led grassroots initiative, we conducted two pre-registered field experiments on the effectiveness of citizen-to-citizen email communication. For Study 1, a large-scale "mega-study," we invited behavioral science experts to design theoretically informed persuasive messages encouraging Russians to watch an uncensored video about Russia's invasion of Ukraine. Approximately 260,000 email recipients were randomly assigned to one of eleven treatments or two control conditions. Study 2 successfully replicated the effects of our top-performing intervention six months later, confirming its robustness.
Research sample	Our research sample consisted of Russian email recipients.
Sampling strategy	Email recipients were chosen at random from Mail2Ru's database of over 350,000,000 Russian email addresses scraped from publicly available sources to enable global volunteers to send messages to Russian recipients.
Data collection	We hosted the video on a private YouTube channel and created unique links associated with each treatment in order to track the clicks associated with each experimental condition using YouTube analytics. To preserve participants' anonymity, we collected data only at the aggregate level of each experimental arm, not at an individual level that could link email addresses to clicking behavior.
Timing	Study 1 was conducted between July 16 and August 26, 2023. Study 2 was conducted between February 16 and February 18, 2024.
Data exclusions	No data were excluded from our analyses.
Non-participation	Non-participation rates are not applicable to our research design.
Randomization	Assignment of email addresses to treatment arm was randomized.

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.