

Reporting Summary

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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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☐	☒ 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 <i>d</i> , Pearson's <i>r</i>), 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	No new data were collected for the present secondary meta-analysis. MRI and behavioural data acquisition software varied across the original contributing studies. The individual contributing studies are listed in Supplementary Table S1.
Data analysis	Code can be found on: https://github.com/MaurizioSicorello/NIDER_project . Analyses were performed using Matlab (v2023b), CanlabCore (v2024), MRICroGL (v.1.2.20220720), and R (v4.3.2). R packages used: psych (v2.6.5), lubridate (v1.9.3), forcats (v1.0.0), purrr (v1.0.2), tibble (v3.2.1), tidyverse (v2.0.0), progressr (v0.16.0), future.apply (v1.20.0), future (v1.67.0), scales (v1.3.0), tidyr (v1.3.1), readr (v2.1.5), Hmisc (v5.1-3), corpcor (v1.6.10), clusterGeneration (v1.3.8), corrplot (v0.92), RSpectra (v0.16-1), HiClimR (v2.2.1), poolr (v1.1-1), ggplot2 (v3.5.1), metaBMA (v0.6.9), Rcpp (v1.0.12), eulerr (v7.0.2), WebPower (v0.9.4), PearsonDS (v1.3.1), lavaan (v0.6-19), lme4 (v1.1-35.1), MASS (v7.3-60), metafor (v4.6-0), numDeriv (v2016.8-1.1), Matrix (v1.6-1.1), meta (v7.0-0), metadat (v1.2-0), dplyr (v1.1.4), stringr (v1.5.1), readxl (v1.4.3), here (v1.0.1), renv (v1.0.4)

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 40 primary task-fMRI datasets contributing to the consortium are listed individually in Supplementary Table S1. Participant-level data were not centrally collected. Study-level summary statistics and group-level statistical images used for the meta-analyses are available at https://github.com/MaurizioSicorello/NIDER_project. The systematic literature search used PubMed (<https://pubmed.ncbi.nlm.nih.gov/>), Web of Science (<https://www.webofscience.com/>) and PsycINFO (<https://www.apa.org/pubs/databases/psycinfo>). Neurosynth (<https://neurosynth.org/>) was used for automated meta-analytic decoding. Publicly available validation images were obtained from NeuroVault (<https://neurovault.org/>); permanent image identifiers are provided in the studyInfo_neurovault.xlsx file in the GitHub repository.

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

Participant sex and/or gender information was extracted from the demographic information provided by contributing study teams where available and is reported at the study level in Table S1. The present study was a secondary meta-analytic consortium analysis of previously collected, de-identified task-fMRI datasets. Sex/gender was not a primary variable in the study design, and the original studies varied in how this information was assessed and reported. We therefore did not conduct sex- or gender-stratified analyses. Low between-study heterogeneity indicates that results do not vary considerably along study characteristics.

Reporting on race, ethnicity, or other socially relevant groupings

Race, ethnicity, and other socially relevant groupings were not used as variables in the present analyses. The study combined secondary, de-identified datasets from multiple international research groups. Because race and ethnicity are socially constructed and context-dependent categories that are assessed differently across countries, institutions, and original studies, we did not aggregate or analyze them as comparable predictors or covariates. No conclusions are drawn about race-, ethnicity-, or socially defined subgroup differences. As for sex and gender, low between-study heterogeneity indicates that results do not vary considerably along study characteristics, but, notably, all samples were European or U.S. American, limiting generalizability.

Population characteristics

The analysis included adult, healthy/non-clinical participants from previously conducted task-fMRI studies of cognitive reappraisal. Eligible studies measured task-based fMRI during a cognitive reappraisal task using negative stimuli, included a view-without-regulation control condition, and assessed a trait-like questionnaire measure of cognitive reappraisal. The healthy-sample inclusion criterion was used to avoid excessive heterogeneity in disorder presentation and medication status. Across the consortium, 40 datasets from 32 contributing research teams were included, comprising up to 2,175 participants. Study-level characteristics are reported in Table S1.

Recruitment

No new participants were recruited for the present study. The study was based exclusively on secondary, de-identified data from previously conducted task-fMRI studies. Contributing research groups were identified in two ways: first, through a systematic literature search followed by direct contact with corresponding authors by e-mail or ResearchGate; and second, through advertisements distributed via academic society mailing lists. The systematic search identified 64 eligible studies, whose authors were contacted; additional relevant studies from the authors' libraries were also considered. In total, 32 research teams contributed 40 datasets. Potential recruitment and self-selection biases therefore primarily reflect the original source studies and the inclusion criteria of the present consortium analysis, particularly the restriction to healthy/non-clinical adult participants and to studies using cognitive reappraisal tasks with negative stimuli.

Ethics oversight

The present study was a secondary analysis of de-identified data from previously approved studies. No new participants were recruited, no new data were collected, and no identifiable participant information was accessed. Ethical oversight for the original data collection was provided by the respective institutional ethics committees or review boards at the contributing sites; accordingly, no separate ethics approval was obtained for the present secondary analysis.

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	No prospective sample-size calculation was performed for the present secondary consortium analysis. Sample size was determined by the number of eligible task-fMRI datasets contributed by participating research groups. In total, 40 datasets from 32 research teams were included, comprising up to 2,175 participants. This sample size provided high statistical power to detect small between-person associations and allowed confidence intervals and Bayes factors to quantify evidence for null effects.
Data exclusions	Data exclusions were based on predefined eligibility and quality-control criteria. Studies were eligible if they included healthy adult participants, task-based fMRI during cognitive reappraisal of negative stimuli, a view-without-regulation control condition, and a trait-like questionnaire measure of reappraisal. At the image level, two statistical maps were excluded from whole-brain analyses because of insufficient brain coverage. For trial-level variance-decomposition analyses, outlying trial-level observations and participants were excluded using a three-times-interquartile-range criterion to stabilize variance estimates.
Replication	The study tested reproducibility by aggregating evidence across 40 independent datasets and by assessing between-study heterogeneity. Robustness was further evaluated using jackknife analyses in which meta-analyses were repeated while leaving out one study at a time. Bayesian evidence, confidence intervals, power analyses, and heterogeneity estimates were used to evaluate the strength and reproducibility of both significant and null findings.
Randomization	The present study was a secondary analysis of previously collected task-fMRI datasets and did not allocate participants to experimental groups. Within the original cognitive reappraisal tasks, participants completed experimental conditions such as reappraise-negative and view-negative trials; condition ordering and stimulus presentation were determined by the protocols of the original studies. Randomization to participant groups was therefore not applicable to the present consortium analysis.
Blinding	Blinding was not applicable to the present secondary meta-analytic analysis because participants were not allocated to treatment or intervention groups. Contributing teams followed a standardized analysis protocol, and the primary analyses were based on predefined statistical contrasts and preregistered meta-analytic procedures. Quality-control procedures were applied to statistical images before aggregation.

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.

Magnetic resonance imaging

Experimental design

Design type	Task
Design specifications	Cognitive reappraisal task designs varied across contributing studies, including differences in stimulus type, timing, trial structure and task implementation. The individual contributing studies and their main study characteristics are listed in Supplementary Table S1.
Behavioral performance measures	Negative affective ratings were collected after each trial in the majority of studies (see Table S1).

Acquisition

Imaging type(s)	functional
Field strength	3T except for Berboth et al., who used 7T
Sequence & imaging parameters	Procedures and parameters were determined by the original contributing studies and varied across datasets. The individual contributing studies are listed in Supplementary Table S1.
Area of acquisition	Whole-brain
Diffusion MRI	☐ Used ☒ Not used

Preprocessing

Preprocessing software	SPM 6/8/12, FSL, AFNI
Normalization	Normalization procedures were performed by the original contributing studies and varied across datasets; no additional participant-level normalization was performed for the present meta-analysis. The individual contributing studies are listed in Supplementary Table S1, and group-level statistical images were resampled to a common $2 \times 2 \times 2$ mm ³ MNI space before meta-analysis.
Normalization template	MNI 152
Noise and artifact removal	Procedures and parameters were determined by the original contributing studies and varied across datasets. The individual contributing studies are listed in Supplementary Table S1.
Volume censoring	Procedures and parameters were determined by the original contributing studies and varied across datasets. The individual contributing studies are listed in Supplementary Table S1.

Statistical modeling & inference

Model type and settings	Mass-univariate image-based random and fixed effects meta-analyses. Use of previously published multivariate decoding models.
Effect(s) tested	Study-wise second-level correlational analyses were meta-analytically aggregated.
Specify type of analysis:	☐ Whole brain ☐ ROI-based ☒ Both
Anatomical location(s)	A priori regions of interest were defined in MNI space using standardized masks. The amygdala ROI was defined as the intersection of an anatomical amygdala mask from the SPM Anatomy Toolbox (v2.2b) and a functional emotion-generation network derived from a published emotion-regulation meta-analysis (see Methods and Ref. 2). The predefined networks of interest were derived from the same published meta-analysis. The ROI masks can be found in the github repository: https://github.com/MaurizioSicorello/NIDER_project/tree/main/data/masks
Statistic type for inference (See Eklund et al. 2016)	Voxel-wise
Correction	FDR

Models & analysis

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