

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 (<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	This meta-analysis synthesized data extracted from existing datasets and research articles. We used Microsoft Excel (version 16.76) to input and organize data.
Data analysis	We used Microsoft Excel (version 16.76), R (R Core Team, 2020, version 4.2.2, 2022-10-31),metafor (Viechtbauer, 2010, 3.0-2, 2021-06-09) for data analyses.

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 data and scripts are available in the Open Science Framework (OSF: <https://osf.io/phu7w>).

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 reported gender information and results related to gender effect. We provided the source data containing gender information.
Reporting on race, ethnicity, or other socially relevant groupings	We reported continent/country/region from which the data were collected. Information on race, ethnicity and other socially relevant groupings were provided in each research article.
Population characteristics	We reported gender, age, continent/country/region from which the data were collected. We included studies that pre-screened participants based on history of psychiatric disorders.
Recruitment	This meta-analysis synthesized data extracted from existing datasets and research articles. Each article described how participants were recruited.
Ethics oversight	Ethical approval will not be required because this meta-analysis retrieved and synthesised existing data.

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	This meta-analysis examined lab-based techniques in modulating intrusive memories from lab-analogue trauma exposure. All data are quantitative experimental data, extracted from included research articles.
Research sample	This meta-analysis synthesized data extracted from existing datasets and research articles. Sample characteristics are provided in Table 1. Specific research samples for each study were described in the included research articles.
Sampling strategy	This meta-analysis synthesized data extracted from existing datasets and research articles. Sampling strategies were reported in the included research articles.
Data collection	This meta-analysis synthesized data extracted from existing datasets and research articles. The original data were recorded using computer-based tasks, pen-and-paper, mobile phones.
Timing	This meta-analysis started the first literature search and data input on Dec 15th, 2020, and was updated Dec 12th, 2023.
Data exclusions	This meta-analysis synthesized data extracted from existing datasets and research articles. Article inclusion and exclusion was provided in the Figure 3 PRISMA flowchart.
Non-participation	This meta-analysis synthesized data extracted from existing datasets and research articles. Information on non-participation was provided in the included research articles.
Randomization	This meta-analysis synthesized data extracted from existing datasets and research articles. Information on randomization was provided in the included research articles.

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

Methods

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

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.