

Reporting Summary

Nature Research 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 Research 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	R and Rstudio for all statistical analyses (R Development Core Team. R: A Language and Environment for Statistical Computing (R Foundation for Statistical Computing, 2012)), RAYYAN software for abstract screening (Ouzzani, M., Hammady, H., Fedorowicz, Z. & Elmagarmid, A. Rayyan-a web and mobile app for systematic reviews. Syst Rev 5, 210, doi:10.1186/s13643-016-0384-4 (2016))
Data analysis	R and Rstudio for all statistical analyses (R Development Core Team. R: A Language and Environment for Statistical Computing (R Foundation for Statistical Computing, 2012)). All code is made available in OSF (https://osf.io/e34s9/).

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 Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

The datasets generated and analyzed during the current study are available at the OSF platform under the following identifier: <https://osf.io/e34s9/>.

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)

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	We present a meta-analysis on inbreeding avoidance in animals. Effect sizes were calculated based on standardized mean differences between kin and non-kin. Random effects for the species, effect size, study, and phylogenetic correlation are included in each model. Meta-analytic models were fitted on the full dataset and on increasingly smaller subsets of the dataset. Meta-regressions were fitted to test the effect of various moderators on the meta-analytic estimates. Publication bias was tested for using funnel plots, Egger's regression, and trim-and-fill methods.
Research sample	The effect sizes originate from experimental studies on inbreeding avoidance in diploid animals based on a literature survey.
Sampling strategy	A search of the literature identified research papers on inbreeding avoidance. Using a decision tree with inclusion and exclusion criteria a selection of these research papers was included in the meta-analysis.
Data collection	Research papers identified through a search of the literature were screened based on title and abstract by Raïssa de Boer and Regina Vega-Trejo. The full texts for these papers were then read by the same authors to determine whether they should be included in the meta-analysis.
Timing and spatial scale	Data collection started in April and May 2019 and was updated in October 2019. Thereafter the data was analysed and the manuscript written.
Data exclusions	Inclusion and exclusion criteria were established beforehand.
Reproducibility	The study is a meta-analysis, so no repeatability of experiments applies.
Randomization	The study is a meta-analysis, so no randomization of experimental groups applies.
Blinding	During selection of research papers a subset of papers were screened by both authors involved in the screening process, blind to each other's decision. The decisions of the authors were compared in order to determine the selection process and validate uniformity between authors.
Did the study involve field work?	☐ Yes ☒ No

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	We performed a meta-analysis of experimental studies on animals - therefore the current study does not directly involve experiments using animals.
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Wild animals	We performed a meta-analysis of experimental studies on animals - therefore the current study does not directly involve experiments using animals.
Field-collected samples	We performed a meta-analysis of experimental studies on animals - therefore the current study does not directly involve experiments using animals.
Ethics oversight	We performed a meta-analysis of experimental studies on animals - therefore the current study does not directly involve experiments using animals.

Note that full information on the approval of the study protocol must also be provided in the manuscript.