**eLife’s transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](https://www.equator-network.org)), life science research (see the [BioSharing Information Resource](https://www.biosharing.org)), or the [ARRIVE guidelines](https:// ARRIVEguidance.org) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

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**Sample-size estimation**

- You should state whether an appropriate sample size was computed when the study was being designed
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- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Statistical information including sample sizes and replicate definitions is included in the figure legends and methods.

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- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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This information is provided in legends, text and methods; wherever possible, biological replicates were carried out.
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• Statistical analysis methods should be described and justified
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• For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d))
• Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

Group allocation

• Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
• Indicate if masking was used during group allocation, data collection and/or data analysis

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• We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
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• Include model definition files including the full list of parameters used
• Include code used for data analysis (e.g., R, MatLab)
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Please indicate the figures or tables for which source data files have been provided:

The code is available as described in the Methods by link: https://bitbucket.org/dmorgens/castle. Additional tables show sequences used and full data obtained after analysis.