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## eLife's transparent reporting form

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## Sample-size estimation

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- 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

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Replicates  • You should report how often each experiment was performed
<ul> <li>You should include a definition of biological versus technical replication</li> <li>The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates</li> <li>If you encountered any outliers, you should describe how these were handled</li> <li>Criteria for exclusion/inclusion of data should be clearly stated</li> <li>High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)</li> </ul>
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## **Statistical reporting**

- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- 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.

Please outline where this information can be found within the submission (e.g., sections of
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(For large datasets, or papers with a very large number of statistical tests, you may upload
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Group allocation
<ul> <li>Indicate how samples were allocated into experimental groups (in the case of</li> </ul>
clinical studies, please specify allocation to treatment method); if randomization
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<ul> <li>Indicate if masking was used during group allocation, data collection and/or data</li> </ul>
analysis
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Additional data files ("source data")
<ul> <li>We encourage you to upload relevant additional data files, such as numerical data</li> </ul>
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<ul> <li>Where provided, these should be in the most useful format, and they can be</li> </ul>
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<ul> <li>Include model definition files including the full list of parameters used</li> </ul>
<ul> <li>Include code used for data analysis (e.g., R, MatLab)</li> </ul>
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Please indicate the figures or tables for which source data files have been provided: