***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

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Sample sizes were not computed in advance.

**Replicates**

* 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
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
* 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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The bar graphs in Figure 1C-D, 2A-E, S2E-F, and Appendix 1-Table 3- 4 show mean values and the error bars represent standard deviations. In addition, the mean values and standard deviations for three biological experiments. In Appendix 1-Figure4B, the data pooled from 10 biological experiments.

**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.

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As described above, mean values and standard deviations were derived
based on all biological and technical replicates of a given sample.

In the “materials and methods” section, figure and figure legend we describe the number of replicates, Statistical analysis methods and the criteria used to exclude samples, if applicable.

The bar graphs in Figure 1C-D, 2A-E, 4B, 4D, S2A-B, S2E-F and Appendix 1-Table 3-4 show mean values and the error bars represent standard deviations; Figure 3A-B, 4C, 4E, Appendix 1-Figure 2C-D, Appendix 1-Figure 3C-D, Appendix 1-Figure 4B and Appendix 1-Figure 5 show median value.

For P value, we displayed P value for 2A-E, 3A-B, 4B-E, Appendix 1-Figure 4B, and Appendix 1-Figure 5 in the figure; we also described P Value for Appendix 1-Figure 2A-F and Appendix 1-Figure 3 A-D in the legend.

(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.)

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* 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
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**Additional data files (“source data”)**

* 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
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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All available data is reported in the manuscript