***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
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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For each technique, the number of replicates were decided based on the authors’ experience obtaining an accurate portrayal of data distribution.

**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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For experiments that featured multiple replicates, each replicate is displayed in the figure as an individual data point (i.e. Figure 1B, Figure 5A). Only Figure 5A (n=1-3) and Figure 5B (n=3) contained biological replicates. High-throughput sequencing data has been uploaded to SRA and the associated BioProject ID numbers are listed in the Acknowledgments.

**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)
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**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
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* 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
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* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Raw data summarized in Figure 2A, Figure 2B, and Figure 3A are detailed in Supplemental File 1.