***eLife’s* transparent reporting form**

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* 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

For all the experiments showed in the manuscript we have used at least biological triplicates, and where possible (depending on the availability of the biological material) we have increased the sample size to more than 3.

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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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* 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)
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This information can be found in the figure legends and in the “Statistical analysis” paragraph.

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

Figure1

Figure1-figure supplement 1

Figure2

Figure2-figure supplement 1

Figure3

Figure3-figure supplement 1

Figure4

Figure4-figure supplement 1