***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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Sample size for each experiment is consistent with previous studies. This information is discussed in the text, figure legends, and methods.

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* You should report how often each experiment was performed
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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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Number of samples used for each assay is specified within the figures and/or in the figure legends. Sequencing data generated for this study have been submitted to the NCBI Gene Expression Omnibus (GEO; http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE123173.

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* 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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Raw data is provided in the Supplementary figures and tables accompanying the manuscript. P-values are provided in the text, figures, figure legends, and supplementary tables. Statistical methods applied to all data are described in the text, methods, and figure legends.

(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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Source data has been provided in supplementary figures and tables. Both raw and processed sequencing data have been submitted to the NCBI Gene Expression Omnibus (GEO).