***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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No statistical methods were explicitly used to pre-determine sample sizes. And the number of experiments used was chosen sufficiently large to reach statistical significance.

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* You should report how often each experiment was performed
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* We have indicated the number of replicates for each experiment with indicated samples numbers in the corresponding figure legends. All the replicates in the paper are biological and not technical replicates.
* RNA-seq data in this study have been deposited in Gene Expression Omnibus (GEO) under the accession number GSE154976.

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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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Data analysis are detailed in the “Statistical analysis” section of Materials and Methods. n, *P* values and statistical tests used are indicated in 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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