***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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No explicit power analysis was performed *a priori*. Sample sizes used were determined to be similar to those deemed acceptable in the field.

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* You should report how often each experiment was performed
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Information for replicate information can be found in the following:

* Experiment replication can be found in each corresponding results sections.
* Data, including replication information is deposited at doi:10.17632/fd886tcx5y.1
* Outlier exclusion is detailed in the Methods section, Statistical Analysis sub-section
* RNASequencing data is deposited at GEO Accession number GSE122176, as detailed in the Methods section, Bioinformatics analyses sub-section

**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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(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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Randomization of animal collection is detailed in the corresponding Methods section and sub-sections.

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Additional data files for all the figures may be found at doi:10.17632/fd886tcx5y.1.