***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

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

**Sample size estimation:** Details are available in the Materials and Methods section, and in the related figures and figure legends. This has also been reported in the attached ARRIVE guideline checklist.

**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)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

All experiments represented in the study were repeated as mentioned in the Materials and Methods section and figure legends.

RNA-seq data has been deposited to the Gene Expression Omnibus (GSE127896). The information will be found under “Data Availability” 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)
* 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 have been represented in all the figures and explained in the figure legends. The modes of data representation, statistical tests, p-values, degrees of freedom have been clearly elaborated in respective figures, figure legends, and materials and methods section. This has also been reported in the attached ARRIVE guideline checklist.

(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
* Indicate if masking was used during group allocation, data collection and/or data analysis

Details are in the Materials and Methods section, in the “Sample Preparation” subsection.

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* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
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Please indicate the figures or tables for which source data files have been provided:

RNA-seq data has been deposited to the Gene Expression Omnibus (GSE127896). Parts of the processed data are shown in Figure6, Figure 6 – figure supplement 2, Figure 6 – figure supplement 3, Figure 6 – Source Data 1 and Figure 6 – Source Data 2.