***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
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Sample size was determined by reproducibility of experiments and similar to other papers in the same field. We have provided number of replicate for all experiments throughout the manuscript in figure legends or Materials and Methods.

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* You should report how often each experiment was performed
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The replicates information is written at the end of each of the Figure legends or Materials and Methods.

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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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All graphs or ratio for quantification were generated using Graphpad Prism software or Microsoft Excel. For graphs in Figure 1C, mean was calculated from average of two biological replicates and standard deviation of the mean was calculated. For graphs in Figure 5E, mean was calculated from average of fluorescence intensities from each cells and standard deviation of the mean was calculated. To analyze the significance between two samples, student t-test was used to derive P-value. Detailed information can be found in each of the Figure legends or Materials and Methods.

(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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Samples were allocated into experimental groups based on genetic and molecular manipulations.

**Additional data files (“source data”)**

* 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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* Include model definition files including the full list of parameters used
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* Avoid stating that data files are “available upon request”

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

Source data files were provided for Figure 1D, Figure 2A-F, Figure 3A-D, Figure 4A-C, Figure 4 – Figure supplement 1 A-B, Figure 5A-D and Figure 5 – Figure supplement 1 A-D.