***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:

No explicit power analysis was used. The sample size was chosen based on common practice in the field for each specific experiment and based on the uniformity of the readout within and between experiments.

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* You should report how often each experiment was performed
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* 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
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All the information about the number of experiments and the number of measurements can be found in the corresponding figure legends of all plots shown in the figures.

**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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Statistical analysis methods and tests are described where relevant; raw data are presented as dot plots for small numbers of measurements.

(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.)

**Group allocation**

* 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

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No explicit randomization method was used as no clinical experiments were performed but the different experimental groups were subjected to the same conditions, e.g same culture conditions were analyzed at the same time. No masking was applied.

**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
* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* 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:

The images of uncropped Western blots assembled into figures, with the relevant bands clearly labeled, are included directly in the article file to facilitate peer review (the last two pages of the manuscript file).

The configuration file for Cytosim, the software used for simulations, is included as Supplemental File 1.

All numerical data and all raw Western blot data are included as Source Data, as indicated below.Figure 1 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel B, G and I.

Figure 2 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel J.

Figure 3 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel B and D.

Figure 4 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel C and F.

Figure 4 - source data 2

Full raw unedited Western blots shown in panel D.

Figure 5 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel C and F.

Figure 6 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel G.

Figure 7 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel D.

Figure 8 - source data 1

An Excel sheet with numerical data of the quantifications shown in panel E, F, K and L.

Figure 1 - figure supplement 1 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel B and F.

Figure 1 - figure supplement 2 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel B and D.

Figure 2 - figure supplement 1 - source data 1

Full raw unedited Western blots shown in panel A and B.

Figure 2 - figure supplement 2 - source data 1

Full raw unedited Western blots shown in panel F and K.

Figure 2 - figure supplement 3 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel D.

Figure 2 - figure supplement 4 - source data 1

Full raw unedited Western blots shown in panel B.

Figure 2 - figure supplement 5 - source data 1

Full raw unedited Western blots shown in panel B.

Figure 5 - figure supplement 1 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel E.

Figure 6 - figure supplement 1 - source data 1

An Excel sheet with numerical data on the quantifications shown in panel E.

Figure 7 - figure supplement 3 - source data 1

Full raw unedited Western blots shown in panel F and G.

Figure 8 – figure supplement 1 source data 1

An Excel sheet with numerical data of the shown quantifications