***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 power analysis were employed to prepare statistical samples. For assays used in this study, technical and biological replicates are the primary concern.*

**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:

*-The number of replicates was reported in the figure legends and in the Materials and Methods. Each experiment was performed at least three times.*

*-The definition of biological and technical replicates can be found in the Materials and Methods section (Page 15, lines 394-397 of the current manuscript).*

*-The exclusion of outliers was not required for this study.*

**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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*-Precision and dispersion measures (standard deviation) were used in this study. The details can be found in the Materials and Methods section:*

*Page 17 lines 477-480*

*Page 19 lines 539-541*

*Page 20 lines 581-583*

*And in figure legends of Figure 6 and Figure6-figure supplement 2*

*-The name and functions of software used in this study were reported in the Materials and Methods section.*

(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 special method for group allocation was used.*

*-For each replicate, experimental and control groups were imaged, processed, and analyzed together. A detailed description of the processing and analysis was reported in the Materials and Methods section.*

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

*-No special datasets (deep sequencing or X-ray crystallography data) or codes have been generated for this study.*

*-All source data for all figures (BLItz traces and their replicates, uncropped gels etc…) have been uploaded to eLife.*