***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:

Not applicable for this type of study

**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)

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Each experiment was performed in at least in triplicate. All replicates refer to biological repeats from independently performed experiments. No outliers were observed. In signaling assays based on overexpression, protein expression was confirmed before inclusion. N numbers for each independent experiment are explicitly stated in the corresponding figure legends (Figs. 1A, 5A-B, 7B and Supplemental Figs. 2, 3B, 8A-B).

**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 tests were selected for parametric data based on number of groups (2, students t-test; >2, ANOVA) and number of independent variables (one-way or two-way ANOVA). For ANOVA tests, post-hoc multiple comparisons analysis was performed to compare each group to the control. Mean and SEM were calculated for all statistical analysis, and p values are specified throughout. All statistical information is explicitly stated in the corresponding figure legends (Figures 1A, 5A-B, 7B; Figure 1-figure supplement 2; Figure 2-figure supplement 1B; Figure 5-figure supplement 2) and in Materials and Methods under ‘Quantification and Statistical Analysis.’

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

Uncropped Western blots uploaded as Supplementary file 1