***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

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The information on the sample-size is included in the “Statistics” sub-section of the material and methods.

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* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
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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)
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(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
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In animal studies, the mice were randomized before the experiment into experimental groups such that the average body weight of each group was similar. This information is included in the “Statistic” sub-section of the material and methods.

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* 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:

All the numerical data and the original western blot are available in the source data Excel files submitted with the manuscript. The raw proteomics data have been uploaded to a public server (Figshare).