***eLife’s* transparent reporting form**

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* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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**Sample sizes were selected based on experience running similar assays and historical precedent, with n>3 biological replicates for most experiments. Individual data points are presented as ‘bubbles’ in bar graphs. In addition to the above, where applicable, this information can be found in either the figure legends or in the methods section. Outside of the omics datasets (proteomics, RNA-seq, metabolomics), all experiments were repeated at least twice.**

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

**RNA-seq data was deposited to NIH GEO (**[**https://www.ncbi.nlm.nih.gov/geo/**](https://www.ncbi.nlm.nih.gov/geo/)**) with the dataset identifier GSE189354; the mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE (**[**https://www.ebi.ac.uk/pride/**](https://www.ebi.ac.uk/pride/)**) partner repository with the dataset identifier PXD028632. Metabolomics data from Figure 1 and Figure 5—Figure Supplement 1A are included in Supplemental Table S5. Annotated raw blots are included for all Westerns as Source Data.**