***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
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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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Experiments were performed using budding yeast cells and do not involve clinical research. Therefore, this information does not apply to our submission.

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* 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
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* 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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Experiments for Figures 1B, 2A, 2D, 3B, 4A, 4B, 4C, 4D, 4E, 4F, 5B, S2A, and S3 included 3 independent biological repeats. These repeats included distinct strains with the same genotypes. This information can be found in the indicated figure legends within the submission. 3 technical repeats performed for flow cytometry data shown in Figure 1E and S2B.

**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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For protein quantification analysis, averages of band intensities were calculated from 3 independent biological repeats in Figures 1C, 2B, 2E, 3C, 4A, 4B, 4C, 4D, 4E, 4F, 5B, S2A, and S3. SEM were used for error bars. Unpaired student t-test analysis were performed in Figures 1C, 2B, 2E, 3C, and 5B. Exact p-values and n-values can be found in each respective figure legends.

(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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Experiments are not part of clinical research. Therefore, this information does not apply to our submission.

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* 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:

Source data for blots have been provided for Figures 1B, 1D, 2A, 2D, 3B, 3D, 4A, 4B, 4C, 4D, 4E, 4F, 5A, S1, S2A, and S3. Source data for protein quantification analysis for Figures 1C, 1E, 1H, 2B, 2E, 3C, 3E, 4A, 4B, 4C, 4D, 4E, 4F, 5B, S2A, and S3. Prism was used for data analysis.