



eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](#)), life science research (see the [BioSharing Information Resource](#)), or the [ARRIVE guidelines](#) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

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 explicit power analysis was used, as all of our experiments were population-based assays with millions of yeast cells. Technical replicate size for qPCR assays (3) was determined empirically as the number of replicates required to get reproducible results.

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:

For each experiment in the paper, at least one biological replicate was performed. The plotted qPCR data was determined as the mean of three PCR (technical) replicates as stated in the methods.

**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.

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:

For all qPCR data, the mean is represented by the height of the bar and error bars represent the standard deviation from three independent experiments, as stated in the methods. For Figure 4C, the inhibition ratio was calculated from three independent experiments. Again, the mean is represented by the height of the bar and error bars represent the standard deviation, as stated in the figure legend. For Figure 6E, the mean is represented by the height of the bar and error bars represent the standard deviation from three independent experiments. All raw data for the qPCRs and the bar graphs in Figure 4C and Figure 6E is provided in the source data files, as well as the mean and standard deviations. P-values were not calculated for the qPCR data because they would be misleading due to the precision of qPCR measurements. The small differences observed between samples were often statistically significant despite not being biologically significant. Instead, we focused on the size of the observed differences in our experiments, which we discuss in the text.

(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

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:

For all experiments in the paper, treated and untreated samples both *in vitro* and *in vivo* were handled and analyzed simultaneously (for example, Figure 3, Figure 4, Figure 5, Figure 6).

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



- Include code used for data analysis (e.g., R, MatLab)
- Avoid stating that data files are “available upon request”

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

Figure 1B-1C
Figure 4B-4C
Figure 5A-5D
Figure 5-Figure supplement 2
Figure 6E
Figure 6-Figure Supplement 3