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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:

Data regarding sample size statistical tests (and software) used for growth curve analyses have been provided in the Materials and Methods section as well as the figure legends for Figure 6. No explicit power analysis was used and we chose to pick 4 replicates per strain for the growth analyses shown in figure 6 based on feasibility of the experimental design and implementation of desired statistical tests. For all gels and blots shown in the text, the experiment was repeated a minimum of two times with one or two technical replicates to determine the experimental conditions for performing the final assays

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:

See above regarding replicates for experiments. The definition of biological versus technical replicates is provided in the materials and methods section. No outliers were removed for statistical analyses. Criteria for determining the points on the growth curve for determining the growth rate are clearly described in the materials and methods section. DNA sequencing data have been uploaded to the NCCBI sequencing reads archive (SRA) and can be accessed here: https://www.ncbi.nlm.nih.gov/Traces/study/?acc=PRJNA800036

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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:

Statistical analyses are only relevant for growth curves shown in figure 6. Statistical analyses methods are described in the materials and methods section. Raw data for for growth curves, including statistical tests used, exact value of N, and p-values, are presented in Supplementary table 2.

(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:

This information doesn't apply to our submission. No large scale 'omics analyses were performed. Strain identities were verified by PCR and sanger sequencing prior to analyses.

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:

Source data comprising of both (1) the original files of the full raw unedited gels or blots and; (2) figures with the uncropped gels or blots with the relevant bands clearly labeled are provided for Figures 1b, 2c, 3d, 4c, 5b as well as Supplementary Figures 4, 5, 6 and 7 are provided.

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