***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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The figure legends contain the number of biological replicates and statistical tests applied. Sample (replicate) numbers for each experiment were predetermined based on prior experience of the low level of data variance observed for experiments of this type and as standardly performed for this field.

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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
* 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)

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The figure legends contain the number of replicates in each experiment. At least three biological replicates were used whenever possible. All experiments were performed at least twice using different cultures and performed on different dates. Technical replication (multiple measurements on the same biological sample) was performed in triplicate for reverse-transcription PCR. No outliers were removed. High-throughput sequence data are publically available and their locations are described in the manuscript.

**Statistical reporting**

* Statistical analysis methods should be described and justified
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* 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.)

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

The source data are provided and are linked to each main figure, table, and figure supplement. Source data for RNAseq and tBLASTx analyses are publically available and their locations are described in the “data accession numbers” section of the manuscript.