***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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* 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 descriptions of all experiments are complete, including general methods in Methods and particular details in Figure legend captions. The meanings of biological and technical replicates are defined in Methods. All of the data obtained are summarized in 4 different source files, pertaining to Figs. 2-5. No outliers were excluded. We also provide a supplementary file containing results and analyses from ribosome profiling. Sequencing data from this study have been submitted to the NCBI Gene Expression Omnibus (GEO; <http://www.ncbi.nlm.nih.gov/geo/>) under a pending accession number.

**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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The statistical significance testing is described in Methods and in Figure legends. The figures/captions clearly indicate where P values were <0.05. All quantitative data obtained are listed in the source files, with P values from the statistical testing indicated for every measurement of mutant versus wild-type samples.

(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:

We provide 4 different source files, pertaining to Figs. 2-5 and their corresponding figure supplements, and a supplementary file containing results and analyses from ribosome profiling.