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* You should state whether an appropriate sample size was computed when the study was being designed
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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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This information can be found in the material and methods section, chapter “Statistics and sample size estimation”, as well as in the respective figure legends. The raw and processed sequencing data are available from the Gene Expression Omnibus database (https://www.ncbi.nlm.nih.gov/geo) under accession GSE143618. This dataset is accessible for editors and reviewers at https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE143618 upon entering the following private access token: ybyfiaqqrlmrvoh. The GEO submission will be made publicly available upon publication of the manuscript.

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* 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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The raw and processed sequencing data are available from the Gene Expression Omnibus database (https://www.ncbi.nlm.nih.gov/geo) under accession GSE143618. Analyzed RNA-seq data are provided as Supplemental Data File 1-4. The R-script for analyzing RNA-seq data is provided as Supplemental Data File 5. Raw data for lifespan and stress-resistance experiments, which were used to compute graphs and statistics, are included as Figure 1-source data 1.