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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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This information can be found in the material and methods section, chapter “Statistics and sample size estimation”.

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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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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
* 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.

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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. Single data points are shown in figures, where applicable. If sample sizes were larger than 3, superimposed box plots indicate the sample distribution. Exact p-values for lifespan and stress-resistance experiments are reported in Table 1. Exact p-values and false discovery rates for RNA-seq are reported in Supplemental Data File 1-4.

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

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.