***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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This is described in the Materials and Methods.

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* You should report how often each experiment was performed
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* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* 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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For the lifespan assays and mating efficiency assays: The number of independent times each experiment was performed is listed in Supplemental Files 2 and 3. The criteria for censoring individuals from lifespan assays is described in the Materials and Methods.

RNA-seq data are available through NCBI SRA (PRJNA508378) and the output from differentially expression analysis is presented in a Figure 2—Source Data 1.

**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)
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The statistical tests used, N, and exact p-values are reported in the figure legends,

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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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For Figure 2 and Figure 2-supplemental figure 2: The RNA-seq read data are available on NCBI SRA (PRJNA508378). The DEseq2 differential expression and GO analysis outputs are included as excel datasheets. The code used to generate these data and figures is available online (<https://github.com/brunetlab/Booth_etal_2019.git>).

For Figure 4 and Figure 4-supplemental figure 1: These data are available in Figure 4—Source Data 1 and 2.

For Supplementary File 3: The raw values that make up this table are included as a source data file.