***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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Exact sample sizes can be found in the figure legends, and the raw data is located in Supplementary File 2. Our sample sizes were large so no explicit power analysis was used.

**Replicates**

* 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
* If you encountered any outliers, you should describe how these were handled
* Criteria for exclusion/inclusion of data should be clearly stated
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* Each full experiment was repeated on at least two independent occasions
* Biological replicates represent samples derived from distinct groups of animals, not multiple measurements of a sample from the same group of animals
* Raw values for all data collected and displayed in this manuscript are available in Supplementary File 2
* No data points were excluded from our analysis
* No high-throughput sequence data was generated in this study

**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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* For each experiment, statistical tests and exact *p*-values are indicated in figure legends
* Also, all statistical tests and *p*-values are displayed in Supplementary File 1
* Raw data is presented in figures, and raw values for all data collected and displayed in this manuscript are available in Supplementary File 2
* All *p*-values are listed in figure legends and in Supplementary File 1, not only the p-values that are less than 0.05

(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.)

**Group allocation**

* 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
* Indicate if masking was used during group allocation, data collection and/or data analysis

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* Age-matched animals were separated into different treatment groups (*e.g*. diet) randomly
* Masking was used in body size experiments during data collection and data analysis to prevent bias

**Additional data files (“source data”)**

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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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The source data for all the data presented in the paper is present in Supplementary File 2.

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