***eLife’s* transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/" \t "_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: [editorial@elifesciences.org](mailto:editorial@elifesciences.org).

**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

**We did not perform a power analysis to decide sample size prior to the study. We included as many samples as possible given the availability of the frozen tissue samples and budget constraints of the project.**

**Information about the data collection can be found in “Materials and Methods”-“Sample Collection” subsection.**

**Replicates**

* 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)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

**RNA sequencing experiments were performed once per tissue sample. We generated sequencing libraries from four tissues of each individual mouse, regarded as biological replicates. We accounted for dependence among tissues of the same mouse throughout the analysis. This information can be found where relevant for each statistical method in the “Materials and Methods”. We did not include technical replicates. All data (raw and processed) have been deposited in the NCBI-GEO database with the accession code: GSE167665**

**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)
* 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.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

**Statistical methods are explained in detail in the “Materials and Methods”. Each method relevant to a statistical analysis is given in different subsections and/or sub-subsections so that each analysis pipeline can be followed easily. Values of N, centers, multiple testing correction, coefficient of variation, Spearman correlations etc. are presented throughout the “Results” and/or figure legends. If these data are unwieldy to be written in the main text, they are presented in “Source data” files.**

(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

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

**Grouping is not relevant to this study. We analysed age-related gene expression patterns in development and in ageing, and for each tissue, separately, or combined where relevant. Relevant information are presented in the “Results” and explained in the “Materials and Methods”. Randomization and masking are not relevant to this study.**

**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
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

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

**We included “source data” files for all figures and all figure supplements:**

**Figure1, Figure1-figure supplement 1-15,**

**Figure2, Figure2-figure supplement 1-20,**

**Figure3,**

**Figure4, Figure4-figure supplement 1-2,**

**Figure5, Figure5-figure supplement 1-6**

**All the analysis can be reproduced with the publicly available code provided in “Code Availability” section (https://github.com/hmtzg/geneexp\_mouse).**