***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
* 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:

For experiments in *C. elegans* requiring static imaging, we set the sample size *n*≥36 for each post-embryonic cell lineage based on a priori power analysis we conducted (Cohen 1992). For time-lapse experiments in *C. elegans,* we set the sample size *n*≥8 for each post-embryonic cell lineage, as these experiments were technically challenging and laborious. Following the same line of reasoning, in zebrafish, we set the sample size *n*≥50 for static imaging and *n*≥7 for time-lapse imaging experiments. See methods for more information about statistical analyses and reporting of statistical results.

**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)

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Each experiment was performed at least twice in order to achieve a sufficient sample size (see above). Biological replicates were performed on separate individuals of the same strain. Technical replicates were not performed. No outliers were encountered. For criteria regarding the exclusion/inclusion of animals analyzed in this study, see “Reporting of Statistical Results” in the methods.

**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:

See methods for detailed information about statistical analyses and reporting of statistical results. Sample sizes (*n*), statistical tests, and dispersion and precision methods are indicated in each figure legend. *p*-values are defined in each figure legend and exact *p*-values are located in Table S1.

(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:

DHB measurements upon palbociclib treatment in zebrafish embryos were performed blinded (see methods).

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

Raw data for graphs shown Figures 1-7 and Figures 1-7-Figure Supplements 1-7 are provided in 12 source data files accompanying this manuscript. In Supplementary File 1, a summary of all the *p*-values calculated in this study are presented. The code used to derive these values is available at GitHub (<https://github.com/abraham-kohrman/matus-dhb-stats>) and can be accessed through the “Statistical Analyses” section in the methods.