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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), life science research (see the BioSharing Information Resource), or the ARRIVE guidelines 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.

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:

Sample sizes were not computed in advance.

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:

In situ hybridisation image analysis was done for 16, 17, 18 and 18 biological replicates of wild-type and heterozygous, and mutant zebrafish. No data were excluded. (Methods/Whole-mount *in situ* hybridisation, Figure 6O).

Quantitative real-time PCR was performed in 3 biological replicates of 7 larvae per genotype (Methods/Quantitative PCR analysis of gene epression, Figure 6P). Each sample was repeated three times – technical replicates. Excluded points failed to produce a CT value.

Optical Projection Tomography analysis was done for 12, 10 and 8 biological replicates of wild-type, heterozygous and mutant zebrafish, respectively. Each zebrafish in this sample is a biological replicate. No data were excluded. (Methods/Optical Projection Tomography, Figure 7-figure supplement 1, Figure 7B-G).

Geometric Morphometric Analysis was done for 24, 20 and 16 biological replicates of wild-type, heterozygous and mutant zebrafish jaw joints, respectively. Each zebrafish jaw joint in this sample is a biological replicate. No data were excluded. (Methods/ Geometric Morphometric Analysis, Figure 7A).

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 analysis methods are described in: Methods/ Whole-mount *in situ* hybridisation Methods/ Quantitative PCR analysis of gene expression Methods/ Geometric Morphometric Analysis For all statistical tests that were computed, we reported the specific test that was used; the sample size; and the exact p-values. Mean values and standard deviations were derived based on all biological and technical replicates of a given sample.

(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:

Samples were allocated into experimental groups based on genotypes (wild-type, heterozygous mutant, homozygous mutant) and age.

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:

Figure 2-figure supplement 2-Source Data 1, Figure 3-Source Data 1, Figure 6O-Source Data 1, Figure 6P-Source Data 2, Figure 7A-Source Data 1, Fi.gure 7A-Source Data 2 containing numerical data for generating figures are provided.