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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:

We have annotated sample size within the figures themselves and in figure legends, the sample size (n) is denoted for each subfigure, whether it refers to number of zebrafish or number of tumors used to calculate statistical differences. Appropriate sample size was determined by our prior studies in the literature involving initiation of embryonal rhabdomyosarcoma tumors in zebrafish. The effect of expressing human *TP53* mutations was unknown prior to our *in vivo* experiments. We have stated the studies we used as references in our Materials and Methods section.

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:



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We have stated in our materials and methods subsections that each *in vitro* and *ex vivo* experiment was repeated at least 3 times (3 biological replicates), with at least 3 technical replicates used per *in vitro* experiment.



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:

All statistical analyses performed are outlined in the Materials and Methods subsections, as well as often in the text following the experimental results and respective p values. P values are reported both in text, in the figures themselves, and occasionally in figure legends.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, N s, 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:

Similar zebrafish strains/fish were used for breeding to obtain embryos used for microinjection experiments. Zebrafish embryos were injected within the first 45 mins post fertilization and when they are still at the one cell stage. Both control and experimental groups were done on the same day, from embryos from mating pairs from the same tanks for all microinjection experiments. Therefore, the selection of which embryos/larval fish were allocated into experimental groups was determined by which linearized DNA injection cocktail they received during microinjection. The DNA combinations used were prepared from the same stock solutions. The Materials and Methods subsection involving microinjections will have the information pertaining to fish used and the concentrations of the linearized DNA cocktails used in experiments.

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



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- 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:

No other source data files are to be included with this manuscript. All of the necessary figures, supplemental figures, and tables are included within the manuscript.