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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:

Discussion regarding sample size for xenograft mouse experiments is included in the legend for Figure 1. The initial pilot experiments were performed with 5 mice for each condition for both the NIH 3T3 cell and SW 872 cell experiments. We then repeated the xenograft experiment with 10 mice for each group (EV, TAZ-CAMTA1, YAP-TFE3) for a total of 15 mice evaluated for each group when the two experiments are combined. This approximates the 16 mice/group calculated with the below power analysis.

Assuming use of a two sample t test, 16 mice are required to adequately power a study with a standard deviation of 100% (1.0), a true difference of the means of 1 in tumor size or metastasis using a significance threshold of less than 5% ($p<0.05$) and a fixed statistical power of 0.8.

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:

Discussion of how often each experiment was performed and description of biological replicates vs. technical replicates are included in the figure legends for Figures 1-8 and Figures S1-S8. Additional definition of biological replicates is included in the Statistics paragraph at the end of the Materials and Methods section. High-throughput sequence data has been uploaded onto GEO, and the GEO accession numbers are included in the manuscript in the Data and Code Availability section located before the references.

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:

Description of the statistical analysis methods are included in Figure Legends 1-8 and Figures S1-S8. Additional description of the statistical analysis methods are located in the Statistics paragraph in the Material and Methods section as well as other sub-sections of the Materials and Methods section. Raw data as individual data points are included in graphs throughout the manuscript. Exact p-values are reported throughout the manuscript.

(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:

Approximately equal numbers of male and female mice were used for the xenograft experiments and this is indicated in the Figure legend for Figure 1.

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:

Source files for RNA-Seq data, ChIP AME Motif Enrichment analysis, and merged ChIP-Seq/RNA-Seq data are provided in Tables S2-S5.