eLIFE
1st Floor
24 Hills Road
Cambridge CB2 1JP, UK
P 01223 855340
W elifesciences.org
T @elife

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:

This information can be found within statistical analyses in Methods section. All details related to the sample sizes are detailed in the Figure legends. For *in vitro* experiments, the sample size was chosen based on common practice and previous experience. The sample size was not determined based on power calculations. However, we consistently achieved at least three biological replicates for all *in vitro* experiments. For *in vivo* experiments, an estimate was made for the number of mice required based on our previous experience with tumor xenografts. The sample size was not determined based on power calculations because there was no previous data available on the expected size effects in response to induction of CBS expression in this system.

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:

The information of the number of replicates performed for each experiment is indicated in the figure legends. All data was obtained from biological replicates.
For the metabolomics GC-MS analysis, one sample in the myrAKT1-shCtrl group was excluded due to a technical issue during the sample processing. This information has been stated in the figure 3 legend.
For RNAseq data, FastQ raw data and processed files are available in the public depository NCBI GEO under accession number GSE200479.
https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE200479

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:

The statistical methods and their justification have been described in the Material and Methods section. The specific statistical tests used, the N per experimental group, Mean, SEM, P value, etc. are specified in the legends of the Figures.

(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:

For the *in vivo* xenograft study, a statement about randomization has been included in the Material and Methods section, "When tumors reached an average volume of 100mm3 calculated by $V = (W^2 \times L)/2$, mice were randomized into two groups".

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 1B, 2A, 2C, 2F, 4C, 4D, 4F, 6F, 7A, 7C, 7E, 7H; Figure 1-figure supplement 1B, Figure 2-figure supplement 1A, 1D and 1E; Figure 3-figure supplement 1B; Figure 4-figure supplement 1A; Figure 5-figure supplement 1A and Figure 6-figure supplement 1D.