



## ***eLife's* transparent reporting form**

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. If you have any questions, please contact us: [editorial@elifesciences.org](mailto: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., page numbers or figure legends), or explain why this information doesn't apply to your submission:

The same-size in individual assays is listed below:

- Gene knockdown: Two individual shRNAs were used to downregulate one gene (Line 1-3, page 7).
- Cell lines with different genetic background: At least 4 different cell lines with different genetic background were used in cell proliferation response (Line 3-5, page 7).
- Proliferation assays: 3 assays were used to confirm cells response to gene downregulation (Line 3-7, page 7).
- Rescue experiment: The rescue experiment by each gene was performed in two different cell lines (Line 7-11, Page 7).
- CRISPR-Cas9 KO: At least 2 different KO clones for each genetic engineering were generated and tested (Table 1, page 29).
- ChIP-MS study: Conducted in two different cell lines (Line 23-24, page 9).
- Molecular mechanism study: It was tested in at least two cell lines (Line 24 on page 10 to line 1 on page 11).
- In vivo xenograft study: Each experiment data point had six mice (Fig 1G, page 32).

## 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., page numbers or figure legends), or explain why this information doesn't apply to your submission:

The cell assays including cell proliferation, Western Blotting, PCR etc all had at least three biological replications in addition to the technical replication in each individual experiment. In ChIP-MS or ChIP-seq study, three biological replication samples were combined and subjected to machine detection.

The ChIP-seq GEO accession number can be found on Page 19.

### 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., page numbers or figure legends), or explain why this information doesn't apply to your

The information can be found in the 'Statistical Analysis' paragraph in the 'Method' part (Line 4-9 on Page 18).

submission:

(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 page numbers in the manuscript.)

### 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:

The data included in this manuscript are valid and authentic, and the source data of all the Figures and Tables can be provided later. The original data of ChIP-MS and ChIP-seq are included in Supplementary table 1, 3, and 4.