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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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Sample size estimation and power analysis is not applicable to this study, no biological samples were collected. We used n=3 technical replicates in all our experiments based on previous experiments in our laboratory. Information about replicates and statistics is found in figure legends.

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* 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
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* 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)

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Following previous experiments in our laboratory, we used n=3 technical replicates in all our experiments. Information about replicates is found in figure legends. All data were shown without excluding any outliers.

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* Statistical analysis methods should be described and justified
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* 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)
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(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.)

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Not applicable to our study

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* Include model definition files including the full list of parameters used
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Model simulation codes and raw experimental data are available on github: <https://github.com/dixitpd/FoldChange>