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All data in this manuscript was performed *in vitro* so experiment numbers are all reported as replicates. See next section.

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* Statistical analysis methods should be described and justified
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* 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.

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All statistical tests used to calculate p values are also provided in the figure legends. Quantifications are all reported as mean +/- SEM. Significance summary: p > 0.05 (ns), ∗p ≤ 0.05, ∗∗p ≤ 0.01, ∗∗∗p ≤ 0.001, and ∗∗∗∗p ≤ 0.0001. The program Prism 6 was used for generating graphs with associated statistical tests and p values.

(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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Bioinformatics packages used to analyze RNA, ATAC, and ChIP sequencing are reported in the supplement for each category of data as well as a table listing software names and references if available. Several references for sequencing techniques are also inserted into the appropriate portions of the main text of the manuscript.