***eLife’s* transparent reporting form**

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**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:

No explicit power analysis was carried out. Sample size and number of replicates were based on previous literature of similar studies. The minimum number of biological replicates required to reach statistical significance (p≤0.05) was used. When available, additional samples were included.

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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
* 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)

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The number of biological and technical replicates used in each analysis is indicated in figure legends, and detailed in the related source data files. The key steps of the data analysis, including filtering, are described in the legend of each figure, and detailed in the relevant section of Materials and Methods. All sequencing data associated with this manuscript have been deposited on the GEO database (identifier GSE141516).

**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.

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The details of the statistical analysis, including the tests, exact values of n, precision measures, and methods of multiple test correction used for each experiment are described either in the legend of each figure and/or in the relevant section of Materials and Methods. Exact p-values and individual data points are shown in 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

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* 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
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Please indicate the figures or tables for which source data files have been provided:

Source data files are provided for Figures 1-5.

Raw and processed data for ChIP-seq (Figures 5-8) are available on the GEO database (identifier GSE141516).

Codes used for analysis are available at github.com/MyersGroup/Zcwpw1 and archived at Zenodo (DOI: 10.5281/zenodo.3559759).