***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
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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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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
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* 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)
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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.)

**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
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* 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).