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**Replicates**

* You should report how often each experiment was performed
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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, pleasse 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:

All the data and code used in this study is available on Github (https://github.com/Shechterlab/PRMTsRegulatePostTranscriptionalDI). Raw data for RNA seq and SKaTER seq is deposited under GEO (GSE163421). Accessions for publicly available RNA-seq data used in this study can be found in supplementary file 3. Raw data for chromatin-associated poly(A) LC-MS/MS is deposited under Chorus (1729).