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Histone code or not? Combinatorial pattern analyses of histone modifications CHONGZHI ZANG, WEIQUN PENG, Department of Physics, The George Washington University, ZHIBIN WANG, DUSTIN E. SCHONES, ARTEM BARSKI, SURESH CUDDAPAH, KAIRONG CUI, TAE-YOUNG ROH, KEJI ZHAO, National Heart, Lung, and Blood Institute, National Institutes of Health, JEFFREY ROSENFELD, MICHAEL ZHANG, Cold Spring Harbor Laboratory — Eukaryotic genomes are organized into chromatin, the structure of which plays critical role in the program of gene expression. Chromatin structure and function is regulated by a myriad of posttranslational modifications on histone tails of the nucleosomes, the fundamental unit of chromatin. It remains unclear how different modifications interact. Based on high- resolution genomic maps of close to 40 histone methylations and acetylations in human T-cells obtained experimentally by ChIP- Seq technique, we investigated the combinatorial patterns of histone modifications at gene promoter regions. We found that a very limited number of patterns dominate. Modifications within a pattern are strongly correlated and each pattern is associated with a distinct gene expression distribution. Our results suggest that it is the patterns rather than the individual modifications that affect the downstream readout.

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