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Finding commonality between the pattern of histone modifications across normal and cancer cell types dictated by DNA sequence features

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Abstract

Introduction: Histone modification, a covalent post-translational modification of histone proteins, influences gene expression by altering chromatin structure giving rise to key characteristics to various cell types. While interaction of histone proteins with DNA is not known to be dependent on DNA sequence features, histone modifications are highly regulated in certain genomic regions. This specificity is required in normal cells to prevent genome instability, chromosome segregation defects and to maintain cellular homeostasis and is altered in cancer. Identifying [1] if specific sequence features are associated with certain histone modifications and [2] if these associations are consistently disrupted in transformed cells, will establish links between the genotype and epigenotype giving us valuable predictability about histone code. In this study, we have analyzed ChIP-seq data of different histone modifications in human across primary and immortalized cell lines from ENCODE database.

Experiments and key results findings: We have identified unique as well as common genomic regions that carry histone marks commonly in primary and immortal cell lines. Additionally, motif finding analysis indeed shows certain modifications are associated with crucial genes required for cell survival and function; some uniquely in transformed cell lines. The regions with consistently different histone marks are currently being studied to check whether they are associated with certain cytosine methylation profile too. Our results suggest a genotypic predisposition for epigenotype.

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