

Integrating Genome-wide Chip-Chip & Chip-Seq Studies Profiling Histone Modifications

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Histones are a family of eukaryotic nuclear proteins that organize DNA strands into nucleosomes by forming molecular complexes around which the DNA winds. Nucleosomes, the basic unit of packing, comprise of an octamer of histone molecules, which consists of an H3–H4 tetramer and two H2A–H2B dimers. The development of massively parallel fast short reads of DNA sequences is a promising technique to profile histone modifications at a genome-wide scale. The goal of this project is to integrate histone post translational modifications data from disparate studies to obtain a global picture of histone modifications in mammalian cells. We collected data from ChIP-seq experiments to view globally the epigenetic landscape of the cell. We obtained data from 20 different ChIP-seq experiments profiling histone modifications in embryonic stem cells. Seven of these experiments were profiling single methylations, while 13 were profiling tri-methylations. We first extracted the genes that contained the height peaks in their proximity, and then compared the lists of genes extracted from each experiment to themselves as well as to libraries of gene lists from prior biological knowledge.