

An Epigenomic View of Cell Differentiation and Development

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Epigenetic mechanisms have been proposed to play crucial roles in mammalian development, but their precise functions are only partially understood. To investigate epigenetic regulation of cell fate determination, we have previously differentiated human embryonic stem cells into mesendoderm, neural progenitor cells, trophoblast-like cells, and mesenchymal stem cells, and systematically characterized DNA methylation, chromatin modifications, and the transcriptome in each lineage. Such epigenome maps provide a general framework for deciphering transcription regulation during hESC differentiation. Interestingly, we have found unusually large genomic loci that are devoid of DNA methylation, or DNA methylation valleys (DMVs). Promoters with DMVs are strongly enriched for developmental genes and genes encoding for transcription factors. Here, I will discuss the regulation of DNA methylation including DMVs in the mammalian genomes, as well as their possible roles in transcription.