

An integrated resource for genome-wide identification and analysis of human tissue-specific differentially methylated regions (tDMRs)

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Abstract

We report a novel resource (methylation profiles of DNA, or mPod) for human genome-wide tissue-specific DNA methylation profiles. mPod consists of three fully integrated parts, genome-wide DNA methylation reference profiles of 13 normal somatic tissues, placenta, sperm, and an immortalized cell line, a

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visualization tool that has been integrated with the Ensembl genome browser and a new algorithm for the analysis of immunoprecipitation-based DNA methylation profiles. We demonstrate the utility of our resource by identifying the first comprehensive genome-wide set of tissue-specific differentially methylated regions (tDMRs) that may play a role in cellular identity and the regulation of tissue-specific genome function. We also discuss the implications of our findings with respect to the regulatory potential of regions with varied CpG density, gene expression, transcription factor motifs, gene ontology, and correlation with other epigenetic marks such as histone modifications.

Footnotes

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[Supplemental material is available online at www.genome.org. The array data from this study have been submitted to ArrayExpress under accession no. E-TABM-445.]

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