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Room 1360, Genetics/Biotechnology Center, 425 Henry Mall

Discerning Genome Wide Methylation Profiles via Optical Mapping

Abstract:

DNA methylation plays a critical role in development, cancer progression and aging. Alterations of genome-wide methylation profiles modulate affect gene regulation, which ultimately contributes to the determination of cell fate. A new approach for the discernment of genome wide methylation profiles using methylation sensitive restriction enzymes and rapid analysis of single molecules will be presented. Since the majority of type II restriction enzymes will not cleave if the cognate sequence is methylated, omissions in restriction mapping data can be attributed to methylation and tabulated on a whole-genome basis. Results for the *E.coli* genome, as well as data from *Arabidopsis* and preliminary results for human will be presented.
