

Cancer epigenomics: DNA methylomes and histone-modification maps

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An altered pattern of epigenetic modifications is central to many common human diseases, including cancer. Many studies have explored the mosaic patterns of DNA methylation and histone modification in cancer cells on a gene-by-gene basis; among their results has been the seminal finding of transcriptional silencing of tumour-suppressor genes by CpG-island-promoter hypermethylation. However, recent technological advances are now allowing cancer epigenetics to be studied genome-wide — an approach that has already begun to provide both biological insight and new avenues for translational research. It is time to 'upgrade' cancer epigenetics research and put together an ambitious plan to tackle the many unanswered questions in this field using epigenomics approaches.

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