

Genome-Wide Methylation Landscape Identifies Drivers of Early Carcinogenesis

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Published 2026-06-04

ABSTRACT

Aberrant DNA methylation is an early hallmark of malignant transformation. We profiled the genome-wide methylation landscape of 480 pre-malignant and tumour specimens across six tissue types, identifying 1,284 differentially methylated regions that separate pre-malignant from invasive disease. Hypermethylation of developmental transcription-factor loci emerged as the earliest detectable event, preceding copy-number change in 71% of cases. These findings position methylation profiling as a candidate substrate for early-detection assays.

KEYWORDS

DNA methylation, carcinogenesis, epigenomics, early detection

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