Analyzing aberrantly methylated extracellular matrix genes in colorectal adenocarcinoma

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Background.

- Examination of methylation patterns across the genome in large patient populations aids the identification of novel biomarkers.
- Through the modulation of proliferative signals and the facilitation of invasivity, extracellular matrix (ECM) proteins play a multifaceted role in tumor progression.

Aims.

This study investigates DNA methylation alterations in extracellular matrix (ECM)-related genes using a large-scale, genome-wide DNA methylation dataset.

Results I:

• All 20 ECM genes with regions over 0.91 AUC contained CpG islands in proximal promoter regions (both platforms).

Methylation by

regions







Scan the code to save the web address







Conclusions.

Aberrant promoter hypermethylation of extracellular matrix genes, particularly ITGA4 and COL25A1, is significantly associated with colorectal adenocarcinoma, expression reduced in gene suggesting their potential as epigenetic biomarkers.



Compare methylation of healthy and tumor tissues

www.epigenplot.com

Methods III: Statistics

filtered beta values

methylation of gene regions

filtered gene regions

ECM gene regions