

Epigenetic Reprogramming of the Tumour Microenvironment

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ABSTRACT

The tumour microenvironment is epigenetically remodelled during progression. We mapped methylation changes in stromal and immune compartments of breast tumours using sorted-population bisulfite sequencing. Cancer-associated fibroblasts acquired a distinct hypomethylated enhancer landscape driving chemokine secretion, while infiltrating T cells showed progressive methylation at effector loci consistent with exhaustion.

KEYWORDS

tumour microenvironment, epigenetic reprogramming, cancer-associated fibroblasts

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