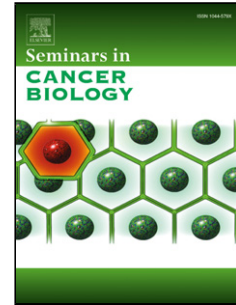


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Introduction: Epigenetics in cancer

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Thanks to the introduction of next-generation sequencing technologies, the genomic landscape of many cancer types have been rapidly unraveled in the last decade. These studies have discovered novel mechanisms behind tumor development, identified genetic markers linked to disease aggressiveness and therapy response as well as resulted in development of novel targeted therapy. In parallel, the recent technical advances in high-throughput sequencing and array-based technologies have also stimulated large-scale, systematic studies of the often complex epigenomic landscape in cancer. These efforts have highlighted deregulated transcriptional control at different levels, caused by aberrant DNA methylation,

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