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[Genomic mapping identifies cancer forerunners](#)

A genome-wide map of human bladder cancer has identified key genetic risk areas for the disease's development. The study, reported online this week in *Laboratory Investigation*, names six critical regions and offers new strategies for understanding the genetic changes underlying the progression of apparently normal tissue to cancer.

Bladder cancer is the sixth most common kind of cancer in the United States with 68,810 new cases and 14,100 deaths estimated in 2008

Like the majority of human cancers, bladder cancer arises from a number of spontaneous genetic changes that are challenging to pinpoint. These genetic changes are thought to be accompanied by microscopic changes in bladder tissue.

To identify factors that contribute to bladder cancer development, Bogdan Czerniak and colleagues mapped genome-wide changes across the entire surface of bladders containing cancer. They identified large regions of supposedly normal bladder tissue, containing expansions of cells with alterations in one or more of the six susceptible chromosomal regions. These 'forerunner genes' set the clock at an even earlier time point for the eventual development of cancer, which potentially includes environmental events that promote cancer.

This research provides important new insight into the earliest genetic origins of cancer, which could assist in the detection and prevention of bladder and other cancers.

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