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Titel des Beitrags:
Genomic profiling of hormone-naïve lymph node metastases in patients with prostate cancer.

Abstract:
The progression of organ-confined prostate cancer to metastatic cancer is inevitably fatal. Consequently, identification of structural changes in the genome and associated transcriptional responses that drive this progression is critical to understanding the disease process and the development of biomarkers and therapeutic targets. In this study, whole genome copy number changes in genomes of hormone-naïve lymph node metastases were profiled using array comparative genomic hybridization, and matched primaries were included for a subset. Matched primaries and lymph node metastases showed very similar copy number profiles that are distinct from primary tumors that fail to metastasize.

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