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Report

Gene expression correlates of clinical prostate cancer behavior

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Abstract

Prostate tumors are among the most heterogeneous of cancers, both histologically and clinically. Microarray expression analysis was used to determine whether global biological differences underlie common pathological features of prostate cancer and to identify genes that might anticipate the clinical behavior of this disease. While no expression correlates of age, serum prostate specific antigen (PSA), and measures of local invasion were found, a set of genes was identified that strongly correlated with the state of tumor differentiation as measured by Gleason score. Moreover, a model using gene expression data alone accurately predicted patient outcome following prostatectomy. These results support the notion that the clinical behavior of prostate cancer is linked to underlying gene expression differences that are detectable at the time of diagnosis.



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