Biomarkers are needed to address overtreatment that occurs for the majority of prostate cancer patients that would not die of the disease but receive radical treatment. A possible barrier to biomarker discovery may be the polyclonal/multifocal nature of prostate tumors as well as cell-type heterogeneity between patient samples. Tumor-adjacent stroma (tumor microenvironment) is less affected by genetic alteration and might therefore yield more consistent biomarkers in response to tumor aggressiveness. To this end we compared Affymetrix gene expression profiles in stroma near tumor and identified a set of 115 probe sets for which the expression levels were significantly correlated with time-to-relapse. We also compared patients that chemically relapsed shortly after prostatectomy (< 1 year), and patients that did not relapse in the first four years after prostatectomy. We identified 131 differentially expressed microarray probe sets between these two categories. 19 probe sets (15 genes) overlapped between the two gene lists with p < 0.0001. We developed a PAM-based classifier by training on samples containing stroma near tumor: 9 rapid relapse patient samples and 9 indolent patient samples. We then tested the classifier on 47 different samples, containing 90% or more stroma. The classifier predicted the risk status of patients with an average accuracy of 87%. This is the first general tumor microenvironment-based prognostic classifier. These results indicate that the prostate cancer microenvironment exhibits reproducible changes useful for predicting outcomes for patients.