

Figure legends for Supplementary Figures

Supplementary Figure 1: Disease association analysis. Shown is a heat map. The red color indicates common associations between differently expressed genes in a gene list and other diseases. Red color intensity is a surrogate for the strength of the association. Differently expressed genes between prostate tumors from African-Americans (AA, n = 33) and tumors from European-Americans (EA, n = 36) were analyzed for their relationship with other diseases using the genetic association database (20). The same analysis was conducted for the contrast of tumor (n = 69) versus non-tumor (n = 20) and the contrast of high (n = 51) versus low (n = 18) Gleason sum score. Gleason sum score was dichotomized into high (having a sum score of 7–9) and low (having a sum score of 5–6).

Supplementary Figure 2: BioCarta pathways that are uniquely enriched for differently expressed genes comparing prostate tumors from African-Americans (AA, n = 33) with tumors from European-Americans (EA, n = 36). For comparison, we also show the contrast of tumor (n = 69) versus non-tumor (n = 20) and the contrast of high (n = 51) versus low (n = 18) Gleason sum score. Gleason sum score was dichotomized into high (having a sum score of 7–9) and low (having a sum score of 5–6). The results of our analysis are displayed by a heat map with the red color indicating an enrichment of differently expressed genes in a BioCarta pathway.

Supplementary Figure 3: GOBP terms that are uniquely enriched for differently expressed genes comparing prostate tumors from African-Americans (AA, n = 33) with tumors from European-Americans (EA, n = 36). The same GOBP terms were also evaluated for the differently expressed genes in the surrounding non-tumor (“normal”) tissue comparing African-American patients (n = 7) with European-American patients (n = 11). The results of our analysis are displayed by a heat map with the red color indicating an enrichment of differently expressed genes in a GOBP term.