

## Supplementary Figures

# Correlation of NTRK1 Downregulation with Low Levels of Tumor-Infiltrating Immune Cells and Poor Prognosis of Prostate Cancer Revealed by Gene Network Analysis

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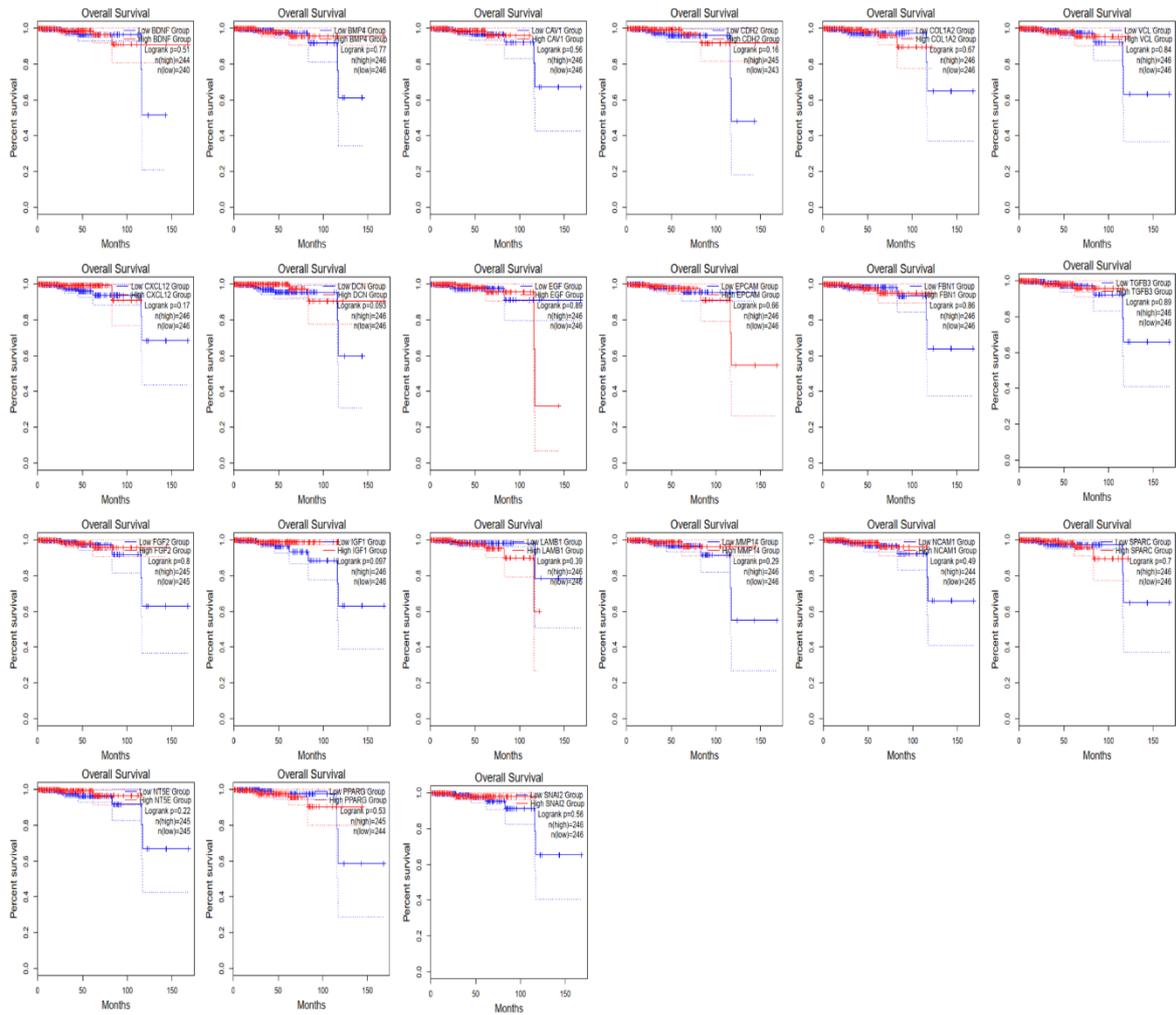
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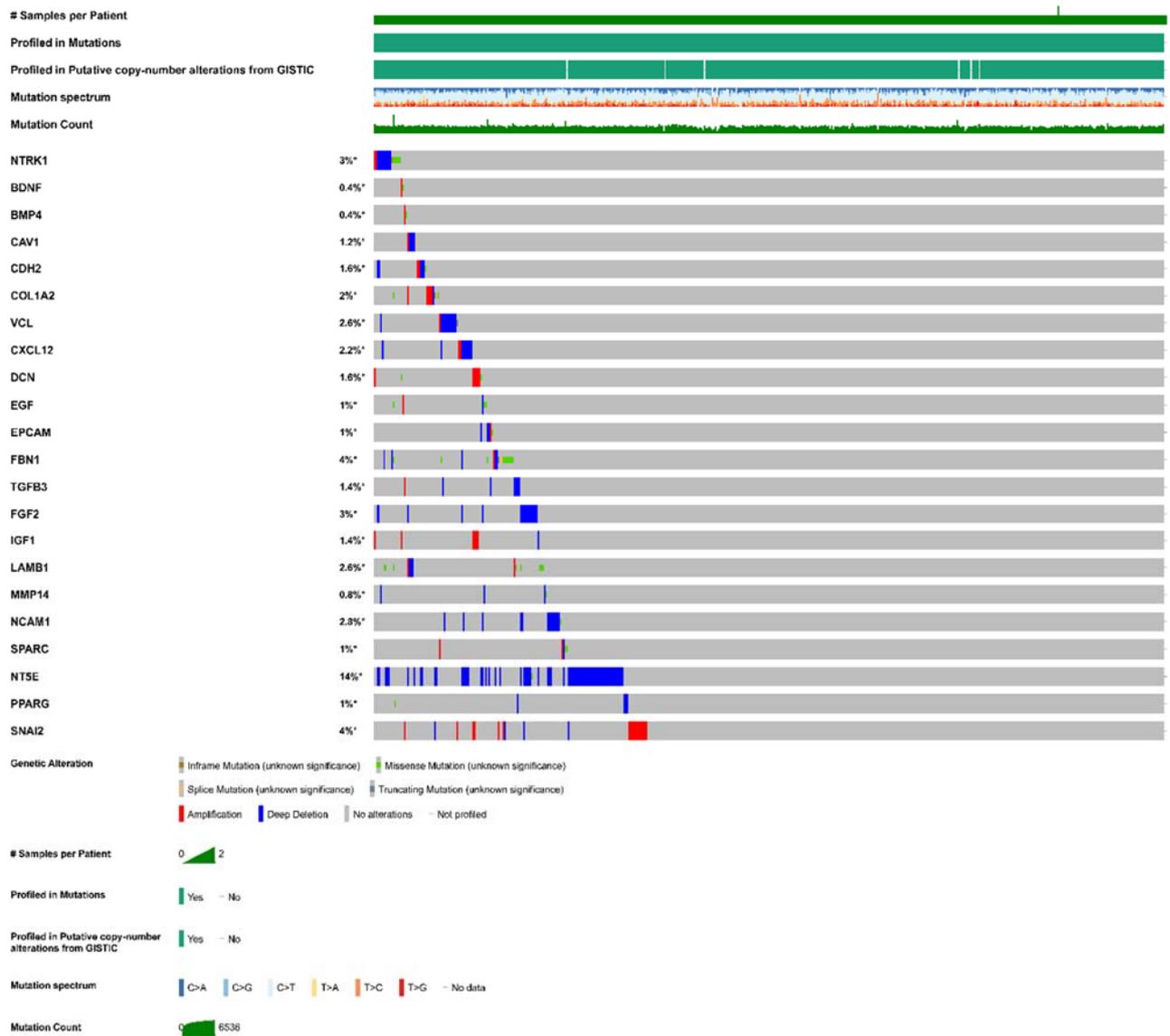
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**Figure S1.** OS analysis of PCa HUBs based on the GEPIA database determined by the KM curve. The expression of other 21 HUBs was not shown to significantly impact the prognosis of PCa in using KM estimates (their Log-rank  $p \geq 0.05$ ). HUBs, hub genes; PCa, prostate cancer; KM, kaplan-meier.



**Figure S2.** OncoPrint summarizes genomic alterations in 22 PCa HUBs across the TCGA-PRAD cohort comprising 501 patient samples. The bottom row represents frequency of genomic alterations in these HUBs with green, orange, grey, red, blue, and golden bars signifying missense, splice, truncating, amplification, deep deletion, and inframe mutations, respectively. First, second, third, fourth, and fifth rows depict the clinical annotation bars such as samples per patient, profiled in mutations, and putative copy-number alterations from GISTIC, mutation spectrum, and mutation count.