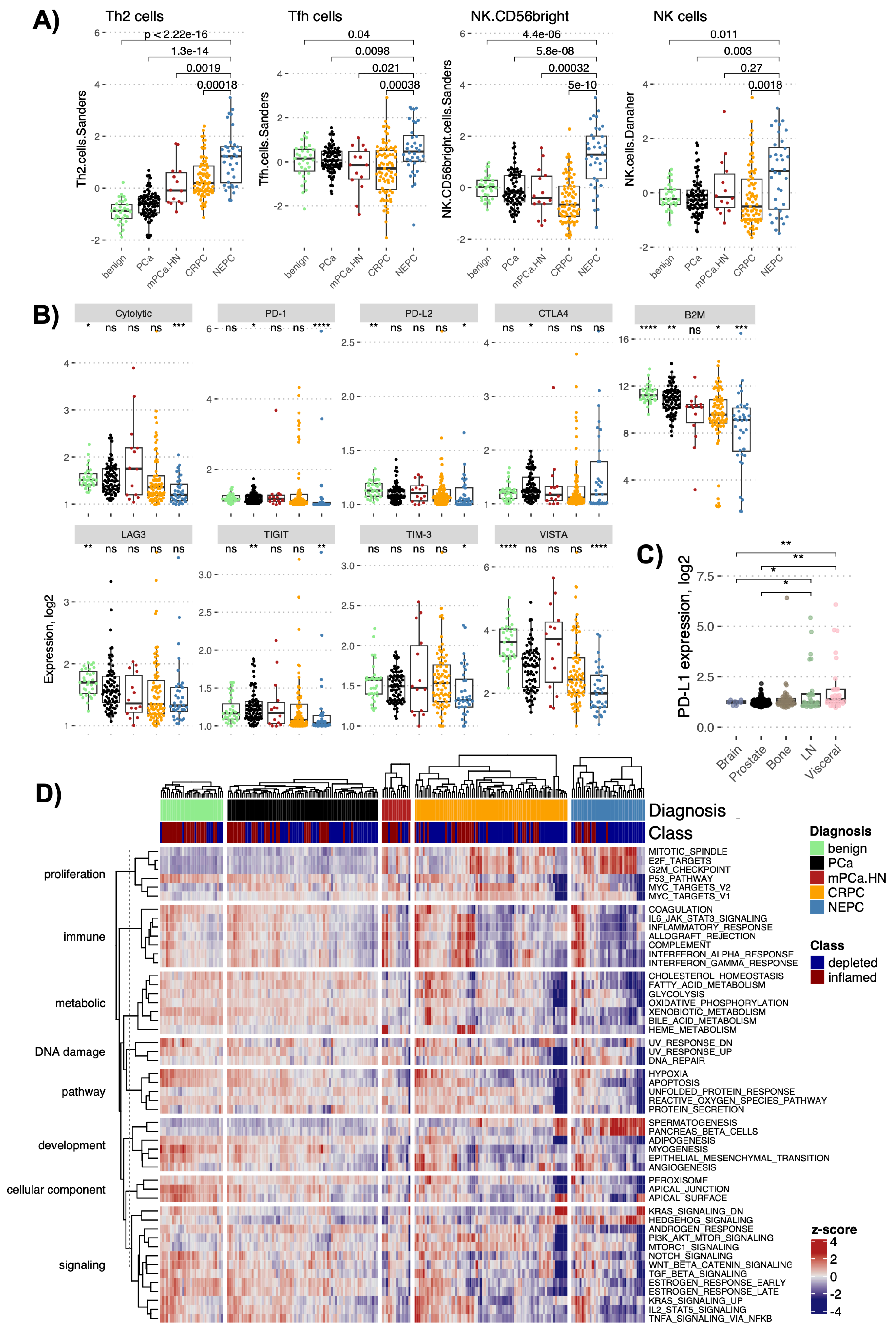
Suppl Figure S4



Suppl Figure 4. TME profile of distinct prostate cancer types in the cohort. A) Boxplots for the immune cell types that were significantly higher in NEPCs compared to other cancer diagnosis, B) Boxplots showing the expression levels of cytolytic score, and immune checkpoint genes. Asterisk denotes levels significantly different from all other cancer types compared ($p < 0.05$), while ns denotes not significant p-values from Wilcoxon signed-rank test, C) Boxplots showing expression levels of gene PD-L1 by tumor site. The plot does not show tumors with unknown sites. Asterisk denotes significant p-values from a t-test between each group ($p < 0.05$), non-significant p-values are not shown, D) Heatmap showing enrichment scores for 50 cancer hallmark pathways (MSigDB) quantified from ssGSEA analysis applied to GEPs. The enrichment score values are scaled by row and the plot is segregated column-wise by cancer diagnosis and grouped row-wise by broader biological categories for the hallmark pathways.