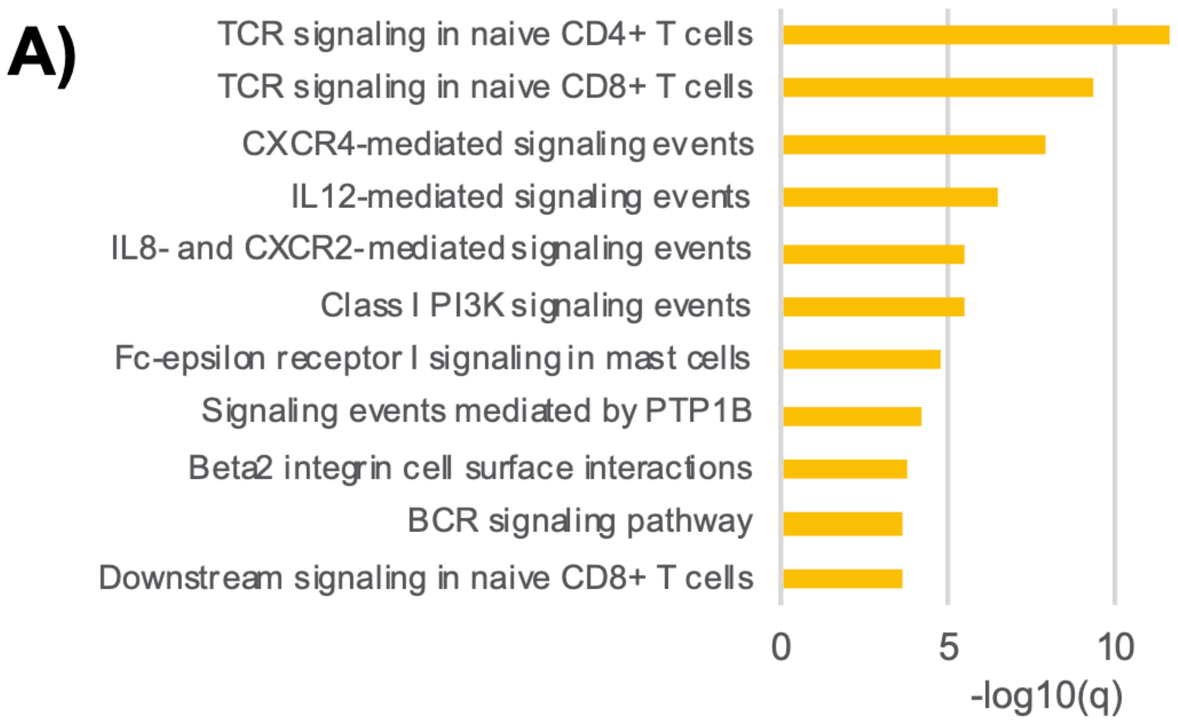
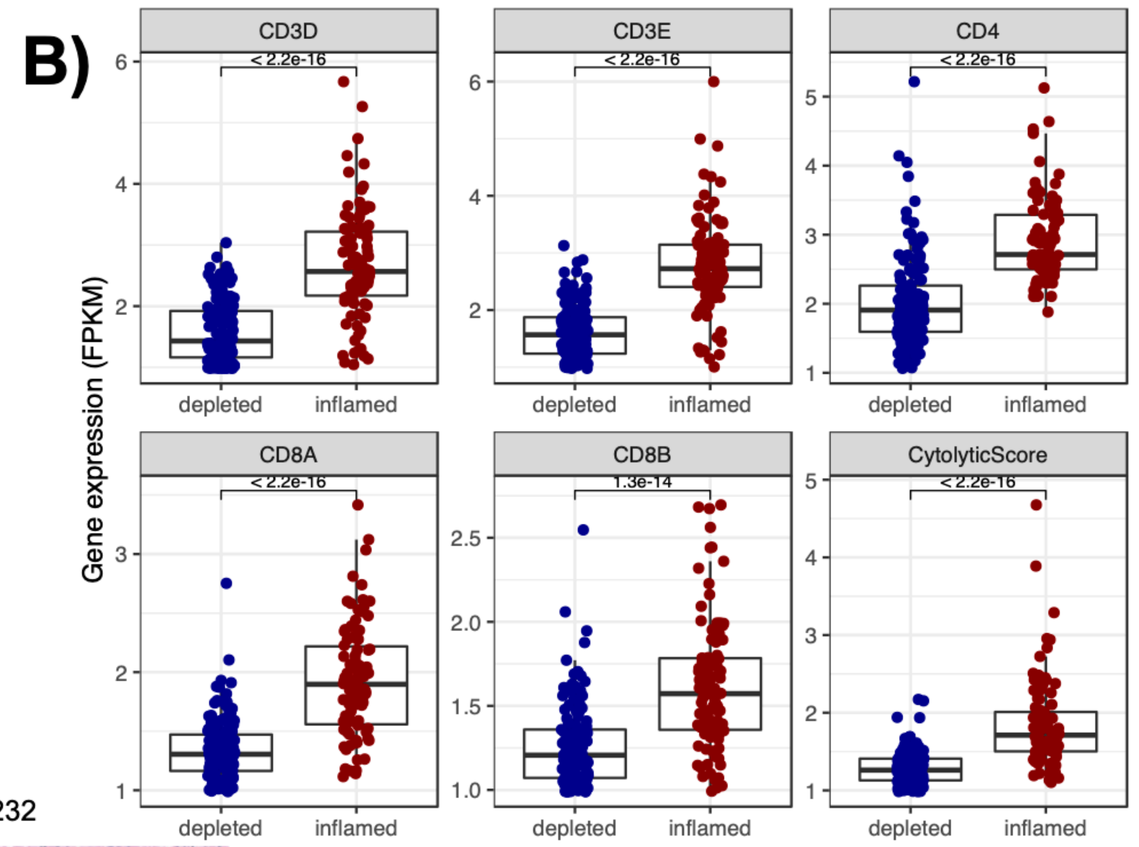
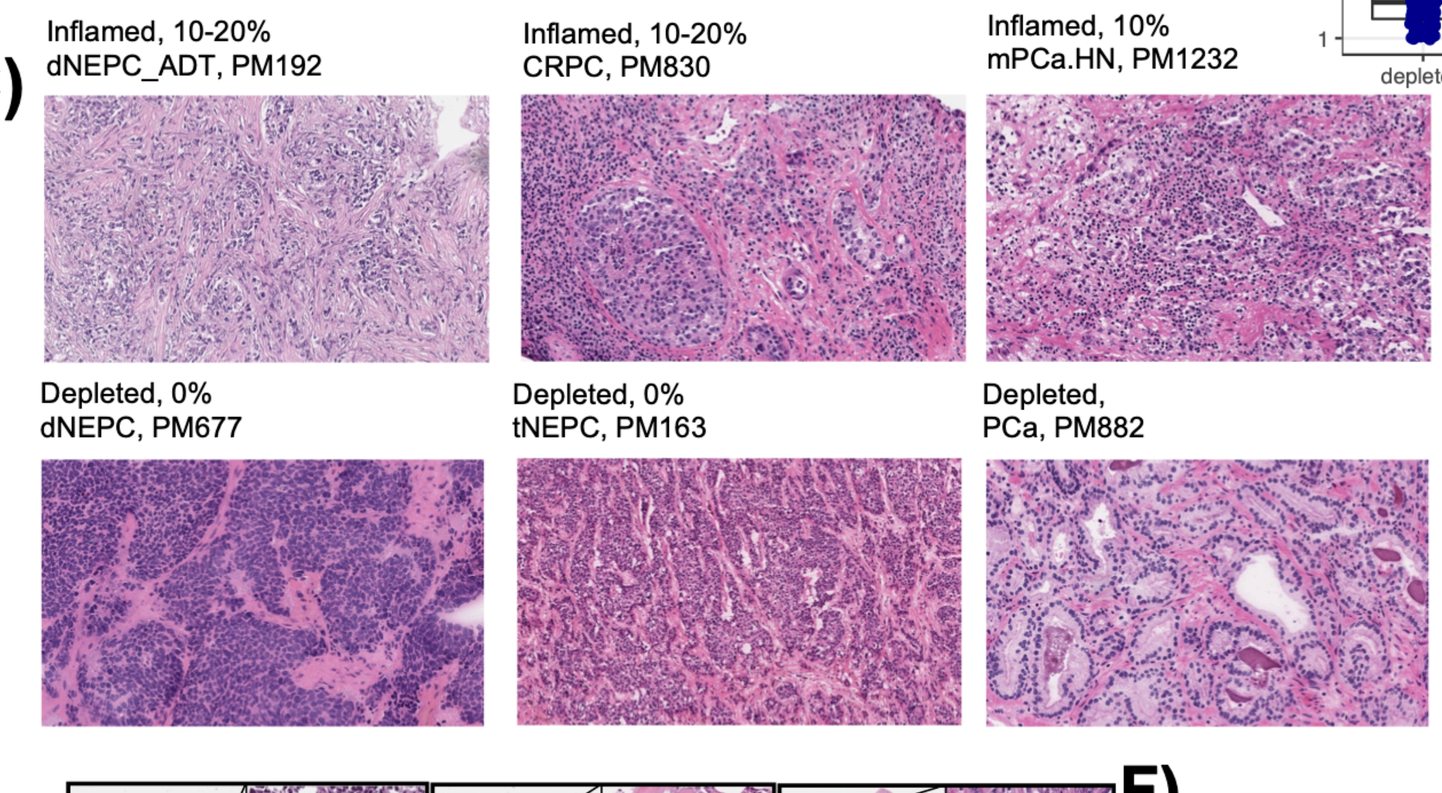
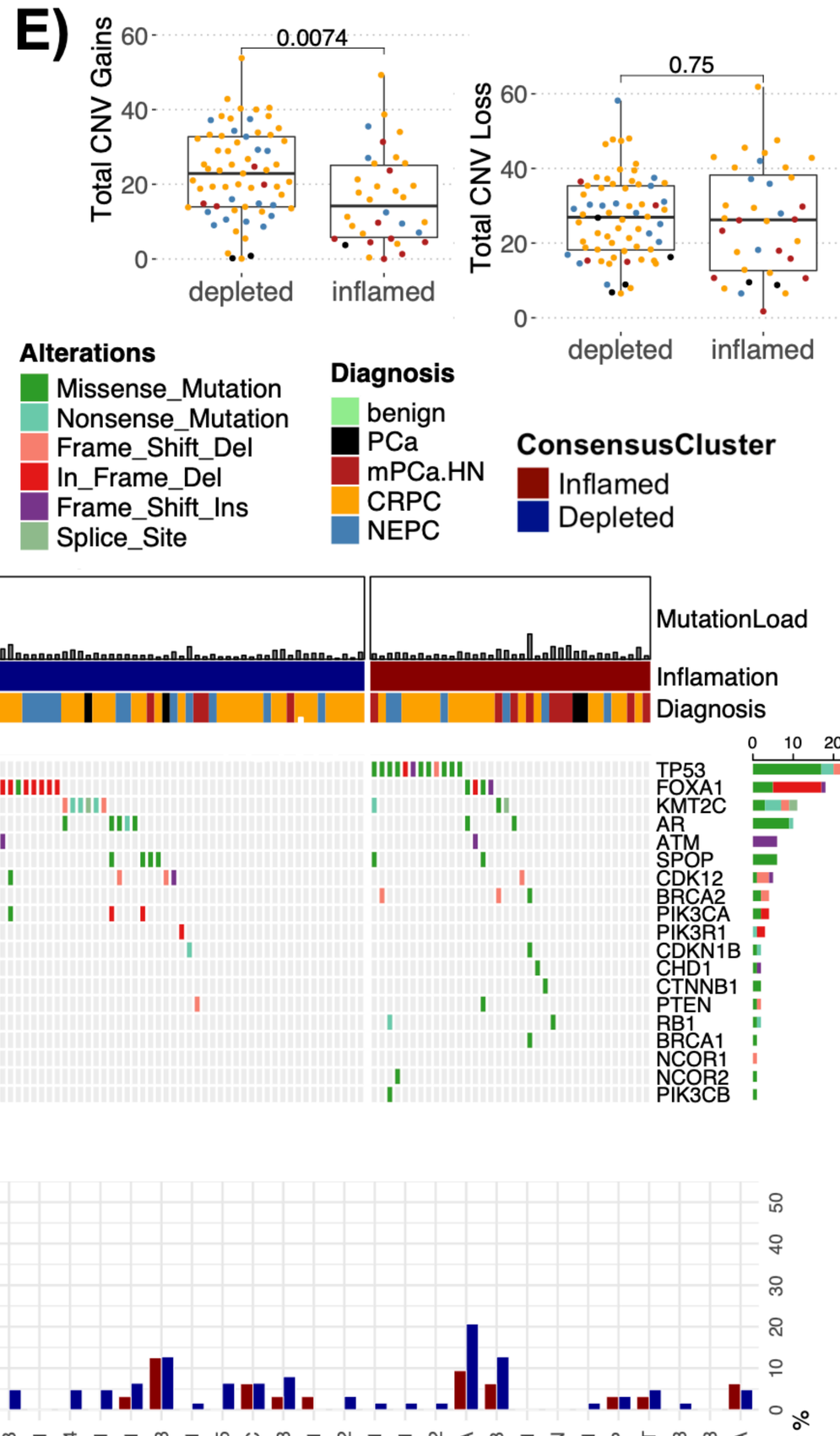
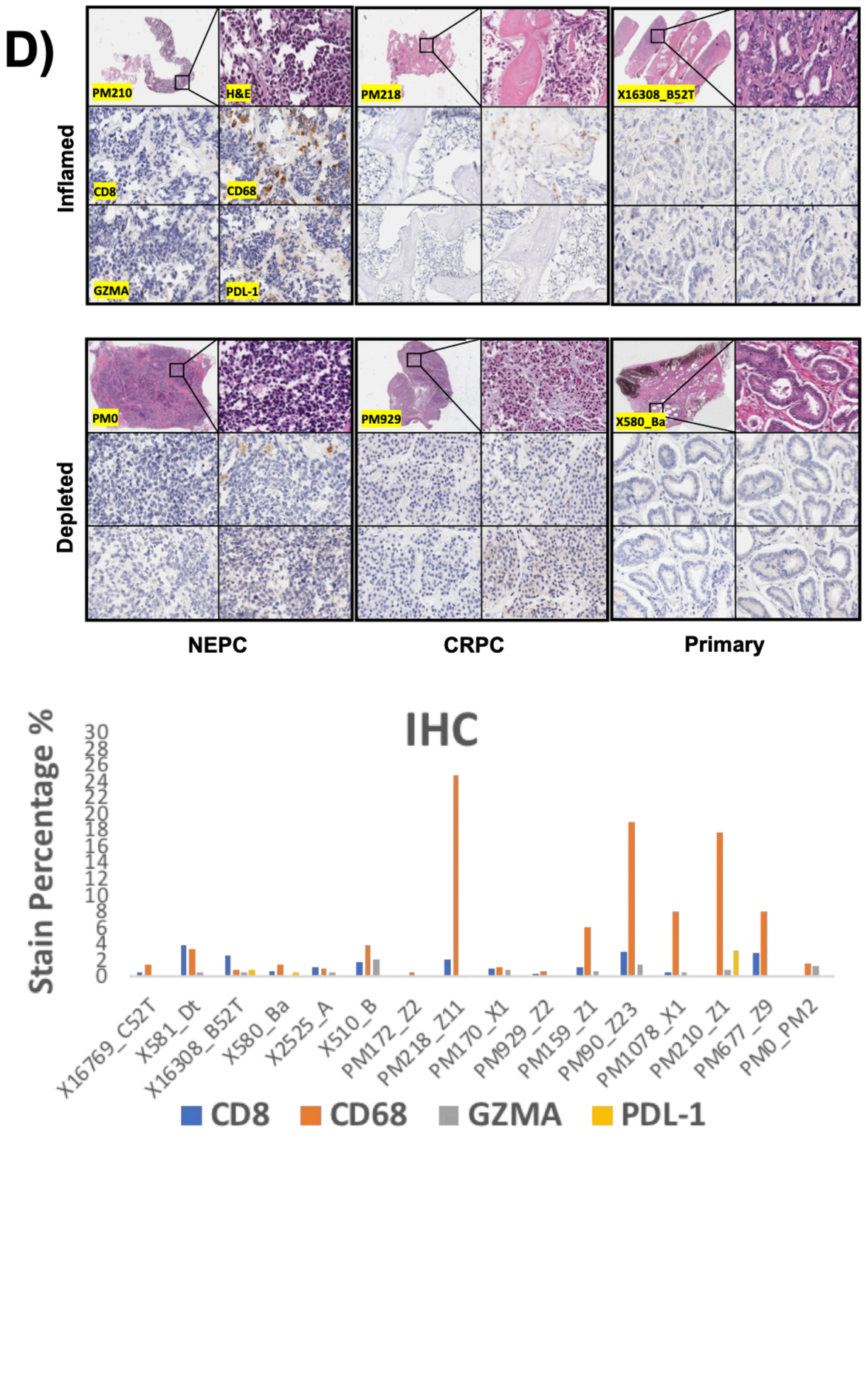
Suppl Figure S1











Suppl Figure 1. Classification of prostate tumors based on T-cell immune status. A) Top pathways associated with the 361 T-cell grouping signatures (Enrichr, NCI-Nature 2016 Pathways), B) Boxplots showing differences in the gene expression levels of key T-cell biomarkers between the inflamed and the depleted clusters. p values reported are from the Wilcoxon signed-rank test, C) Hematoxylin and eosin (H&E) stained histopathology for three tumors each for inflamed and depleted phenotypes. The slide shows the total leukocyte infiltration, also reported on top of each corresponding slide as percentage leukocytes quantified in that tissue. D) Representative IHC images (30X) of inflamed and depleted prostate cancer samples stained with immune markers (CD8, CD68, Granzyme A and PDL-1) (Top Panel). Barplot showing %IHC stain for each immune marker tested by sample (bottom panel. E) Boxplots to show differences between the median total copy number variation (CNV) gains only (left panel) and losses only (right panel) obtained from the two T-cell immune clusters. p values reported are from the Wilcoxon signed-rank test, F) Oncoprint plot showing the non-silent and truncating mutations in known prostate driver genes segregated by T-cell groups. G) Barplot showing the frequency of cases with the copy number gains/amplifications (left panel) or losses/deletions (right panel) in the T-cell inflamed (red) versus depleted (blue) groups for 31 genes. Asterisk next to a gene denotes p-values significant at < 0.05 in a Fisher's exact test for that gene.