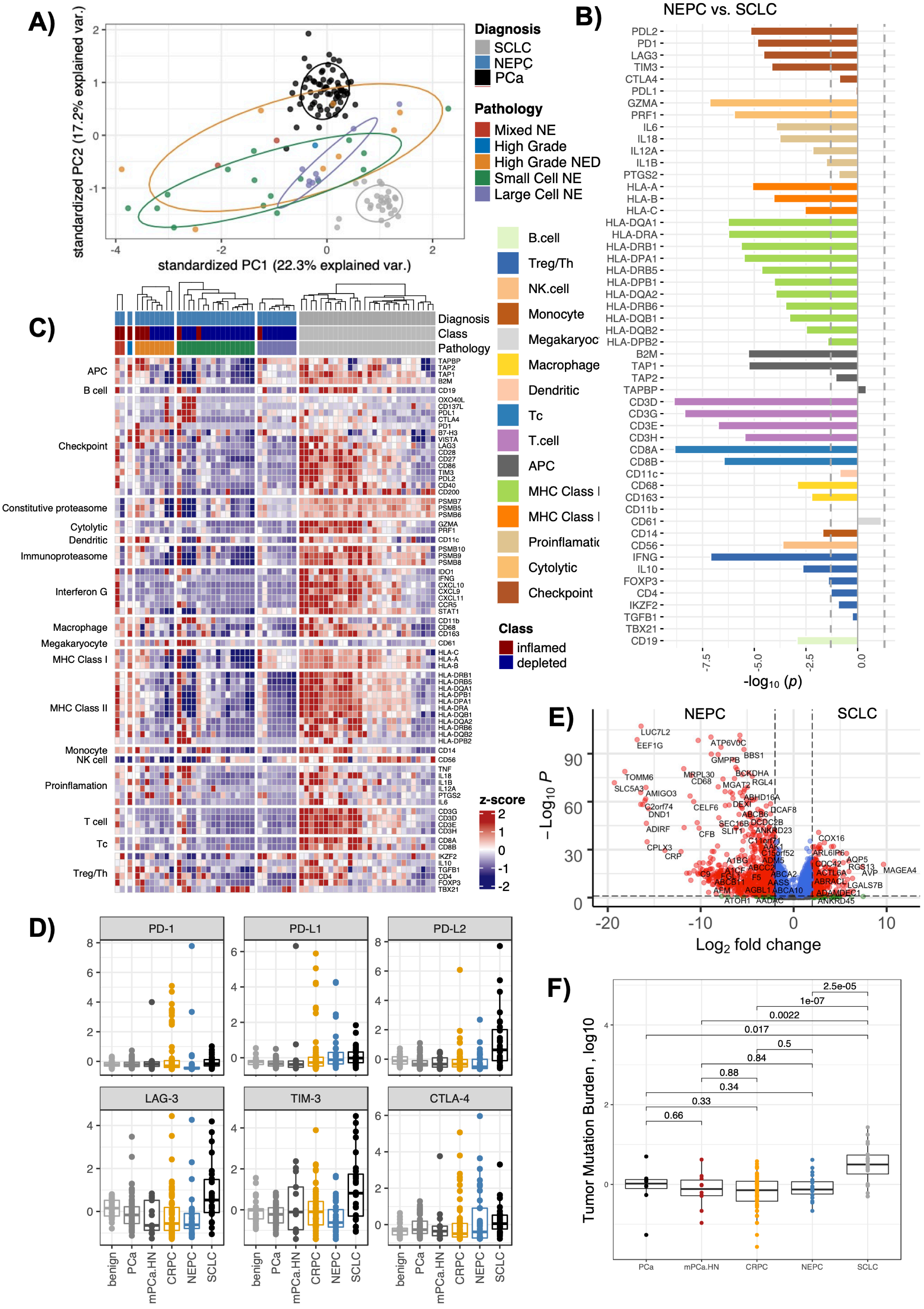
Supple Figure S5



Suppl Figure 5. Comparative analysis between NEPC and SCLC. A) Principal component analysis plot for the gene expression profiles grouped by NEPC histopathology classifications, PCa and SCLC tumors, B) Barplot showing the p-values for the differences in the median expression of immune related genes between the SCLC and the NEPC tumors. The p-values are reported on a -log10 scale on the x-axis and the direction of the bars is determined by the sign of the difference in medians of NEPC from SCLC. The values above the dashed line are considered statistically significant. This is a companion plot to the heatmap shown in Figure 4B, C) Heatmap showing expression of marker genes for immune cell types and immune checkpoint among the NEPC and SCLC tumors segregated by cancer diagnosis and different histology subtypes of NEPCs tumors D) Boxplots showing the expression levels of the immune checkpoint genes among all diagnoses in the prostate cancer cohort and the SCLC cohort, E) Volcano plot for the genes differentially expressed between the SCLC and the NEPC tumors. The red dots denote genes with absolute log fold change values > 2 and adjusted p-value < 0.1. F) Boxplots showing differences between the median tumor mutation burden among SCLC and all prostate cancers in the cohort. p values reported are from the Wilcoxon signed-rank test,