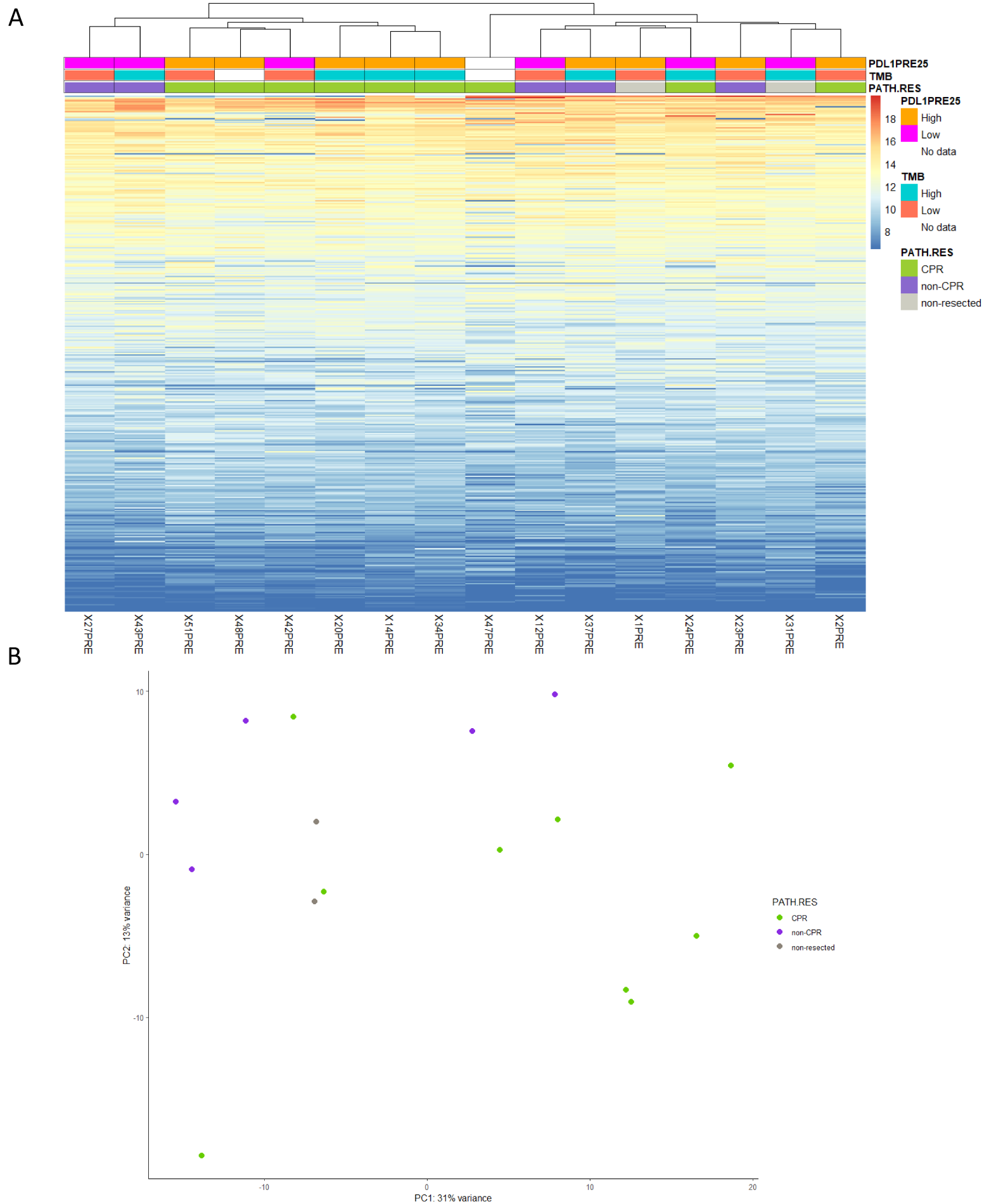
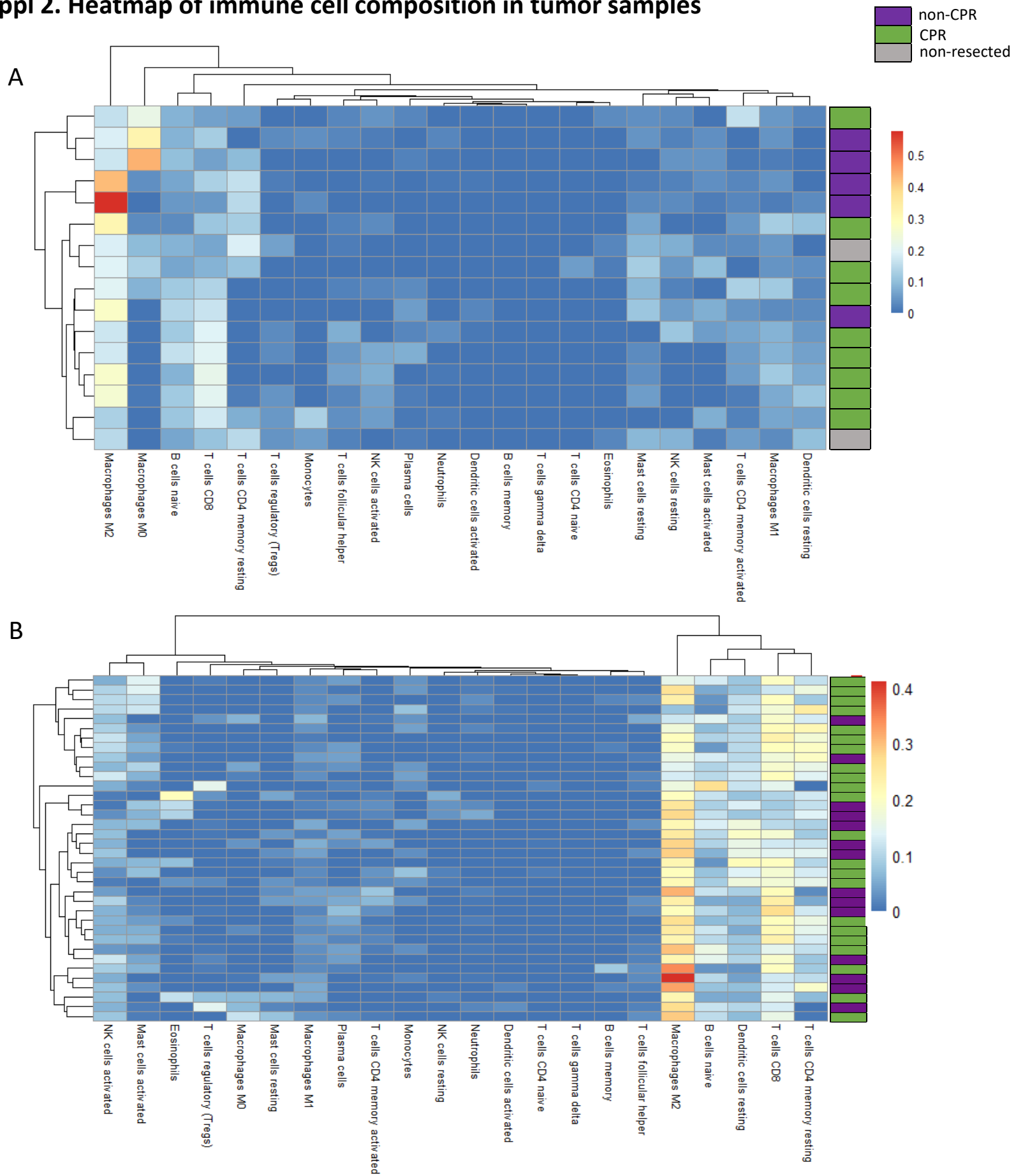


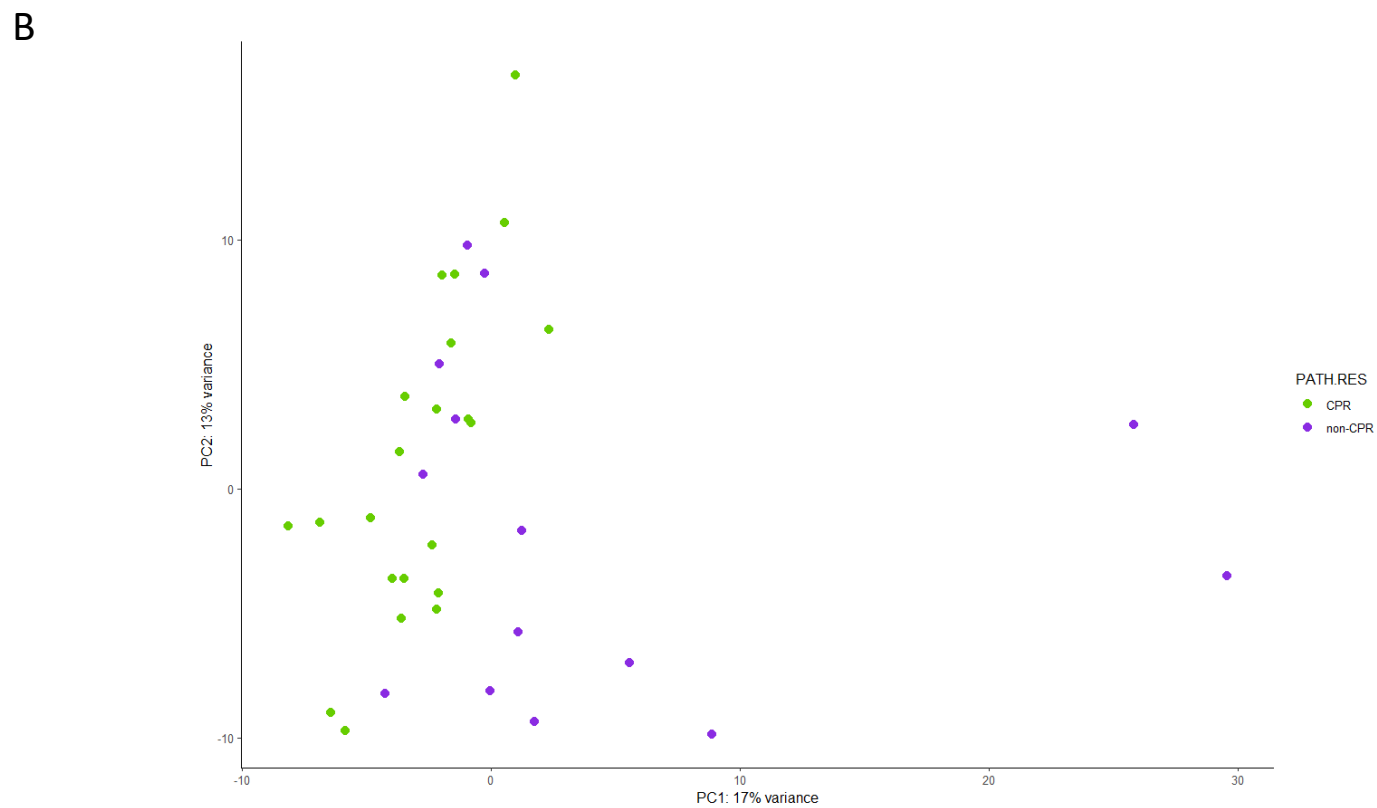
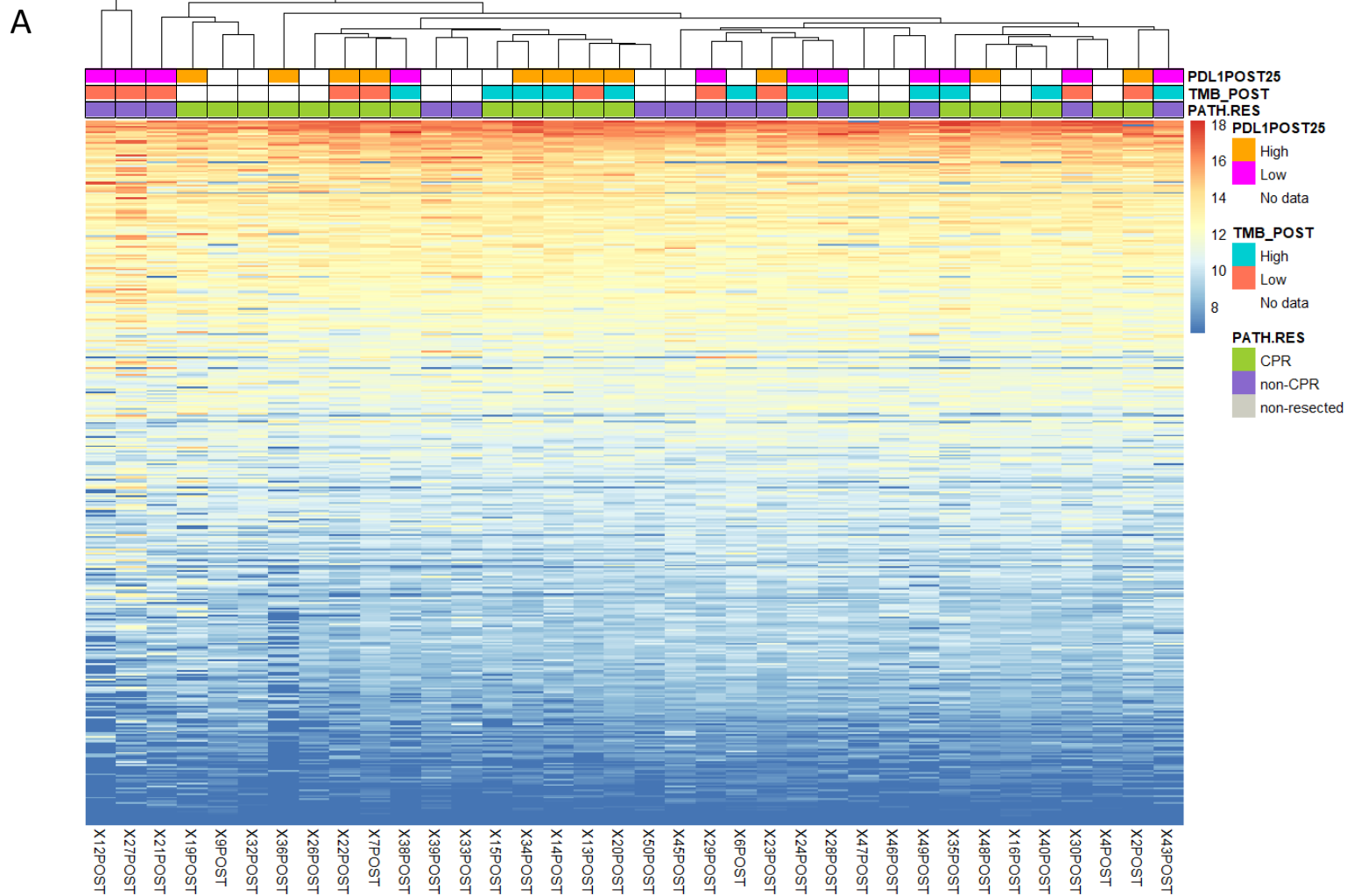
Suppl 1. Heatmap and PCA of pre-treatment tumor samples

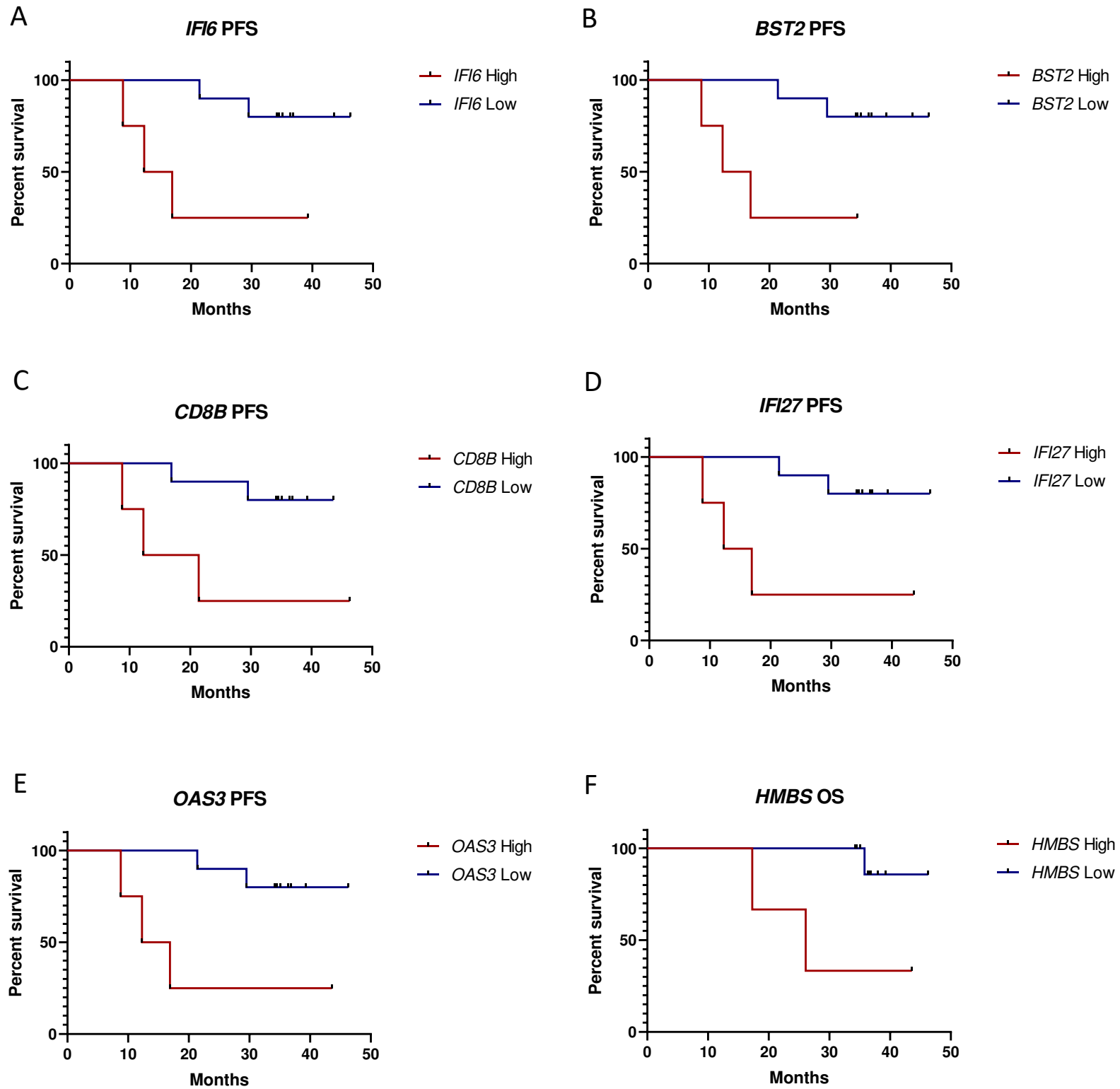


Suppl 2. Heatmap of immune cell composition in tumor samples

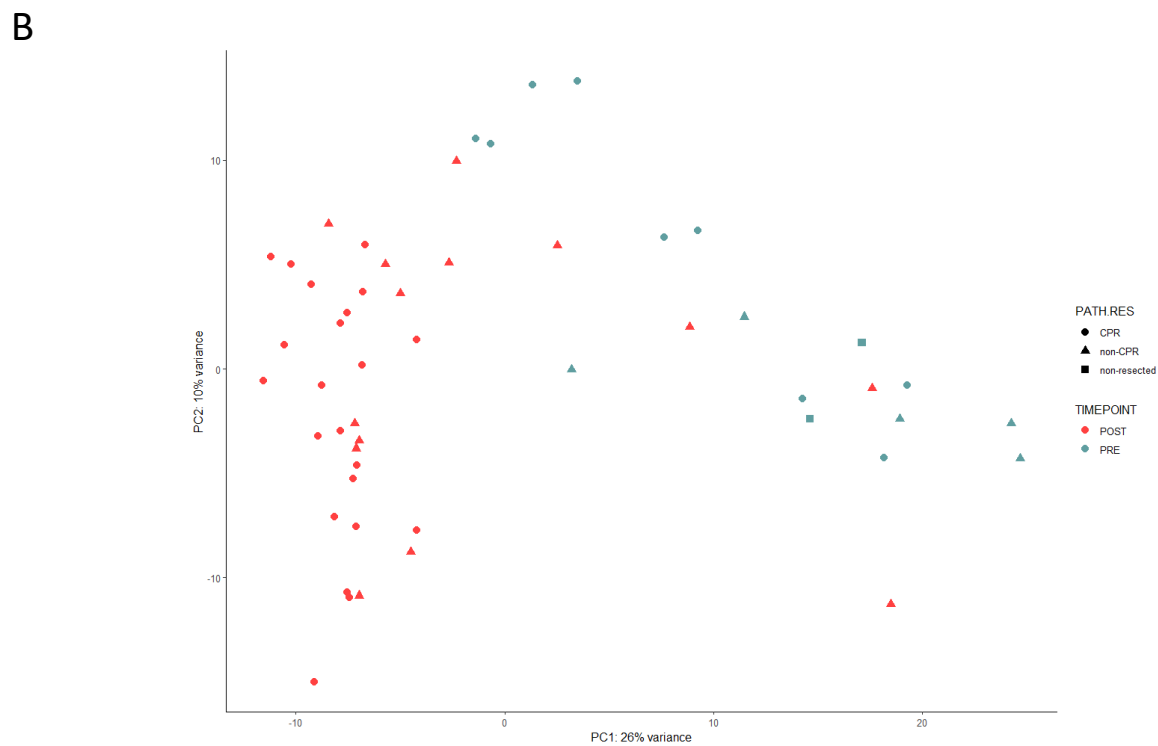
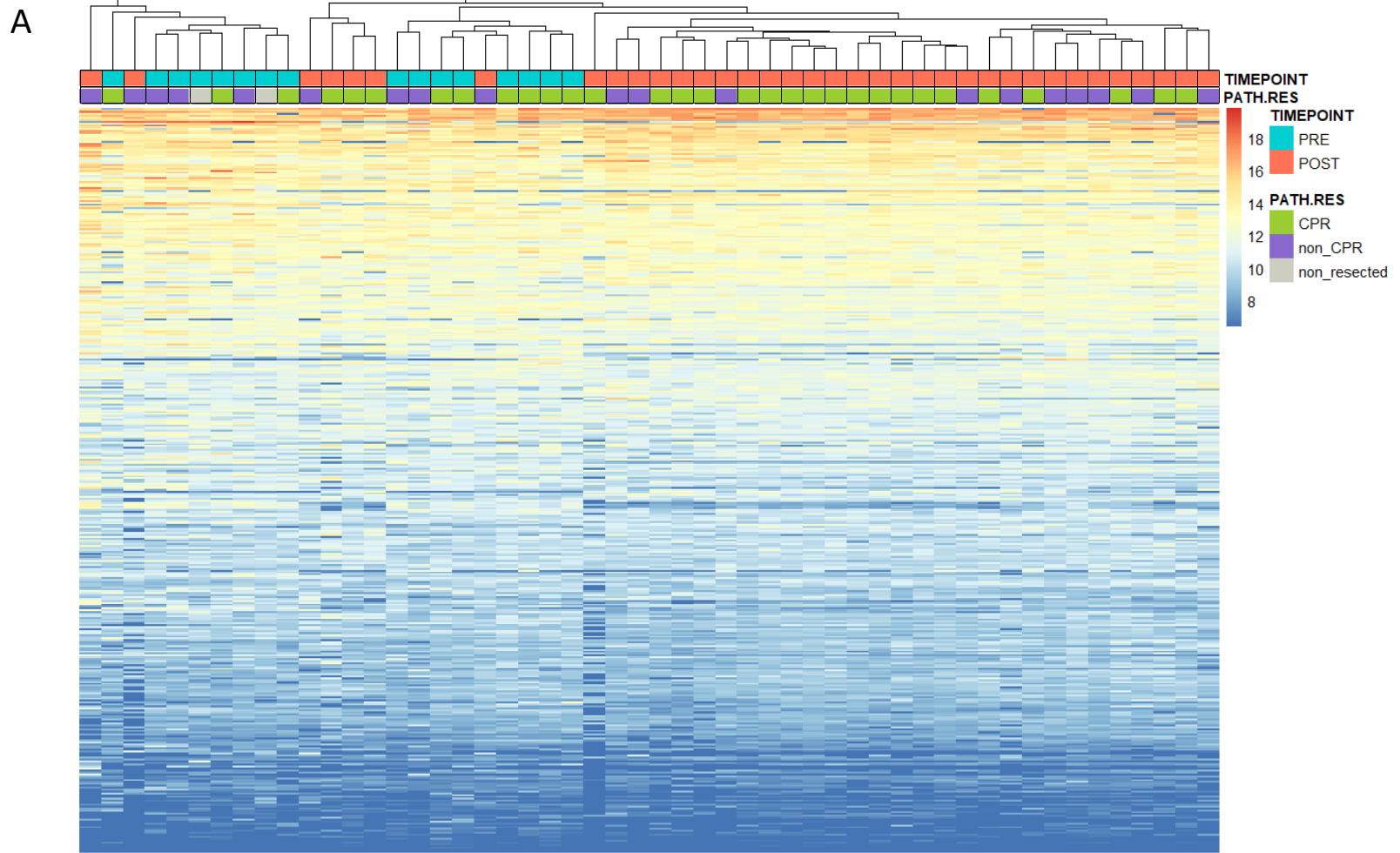


Suppl 3. Heatmap and PCA of post-treatment tumor samples



Suppl 4. Correlation of differential-expressed genes with PFS and OS

Suppl 5. Heatmap and PCA of pre- and post-treatment tumor samples



SUPPLEMENTARY FIGURE LEGENDS:

Supplementary figure 1. A. Heatmap clustered by the expression of the 395 immune-related genes in pre-treatment tumor samples (n=16). The row represents an individual gene and the column individual patient's tumor sample which have been grouped using unsupervised clustering with vsd normalization of data derived from the DESeq analysis. Pathological response, TMB and PD-L1 status of each tumor sample were plotted. **B.** PCA analysis of the RNA seq data of pre-treatment samples with the pathological status of each sample plotted.

Supplementary figure 2. A. Heatmap of immune cell composition in pre-treatment tumor samples (n=16) after deconvolution of RNA seq data with CIBERSORTx. **B.** Heatmap of immune cell composition in post-treatment tumor samples (n=36) after deconvolution of RNA seq data with CIBERSORTx. The row and column represent individual tumor samples and immune cell subtypes respectively, which have been grouped using unsupervised clustering. The pathological response of each sample was plotted.

Supplementary figure 3. A. Heatmap clustered by the expression of the 395 immune-related genes in post-treatment tumor samples (n=36). The row represents an individual gene and the column individual patient's tumor sample which have been grouped using unsupervised clustering with vsd normalization of data derived from the DESeq analysis. Pathological response, TMB and PD-L1 status of each tumor sample were plotted. **B.** PCA analysis of the RNA seq data of post-treatment samples with the pathological status of each sample plotted.

Supplementary figure 4. Kaplan-Meier plots of progression-free survival and overall survival for patients with high and low expression of DEGs in post-treatment samples of non-CPR tumors with disease progression or not. **A.** *IFI6* PFS (p=0.010). **B.** *BST2* PFS (p=0.010). **C.** *CD8B* PFS (p=0.019). **D.** *IFI27* PFS (p=0.010). **E.** *OAS3* PFS (p=0.010). **F.** *HMBS* OS (p=0.018). Red lines indicate high expression of the gene and blue lines indicate low expression.

Supplementary figure 5. A. Heatmap clustered by the expression of the 395 immune-related genes in pre-(n=14) and post-treatment tumor samples (n=36). The row represents an individual gene and the column individual patient's tumor sample which have been grouped using unsupervised clustering with vsd normalization of data derived from the DESeq analysis. The timepoint and pathological response of each tumor sample were plotted. **B.** PCA analysis of the RNA seq data of pre- and post-treatment samples with timepoint pathological status of each sample plotted.