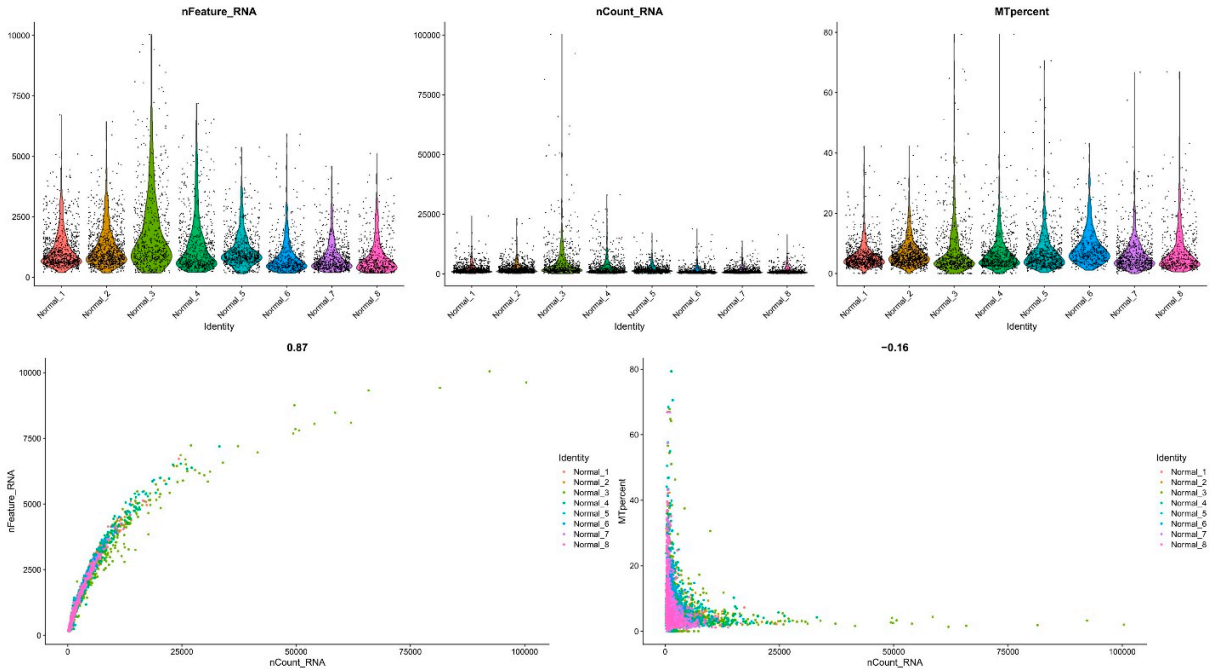
Single-Cell and Spatial Transcriptomics Reveal TXNIP and BIRC3 Contribute to Human Prostate Tumor Progression

Seyed Taleb Hosseini [1,2], Hossein Azizi [3,*] and Thomas Skutella [4,*]

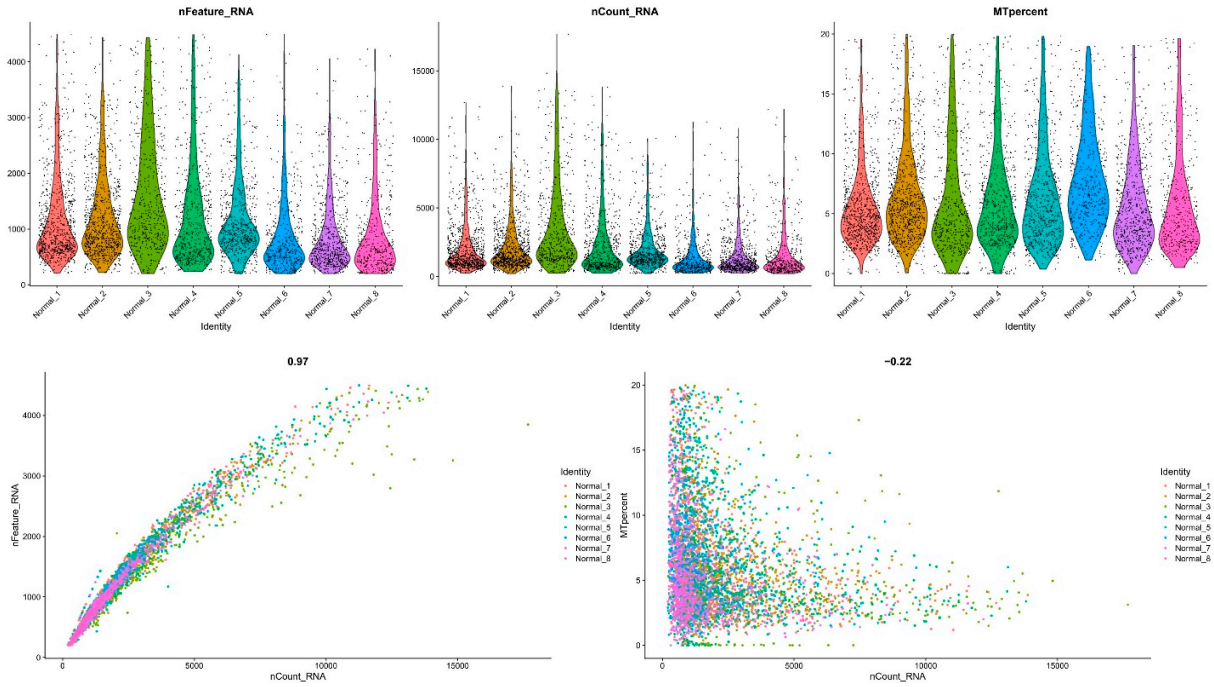
Supplementary Figures

Supplementary Figure S1. Quality control and principal component evaluation of scRNA-seq data from prostate cancer samples. (A) Quality control filtering of scRNA-seq data illustrating the removal of low-quality cells prior to downstream analysis. **(B)** Identification of the top 2,000 highly variable genes selected for dimensionality reduction and clustering analyses. **(C)** Principal component analysis (PCA) performed on highly variable genes using the RunPCA function to capture major sources of transcriptional variability across samples. **(D)** JackStrawPlot showing statistically significant principal components with low p-values and their associated variance contributions. **(E)** ElbowPlot depicting the variance explained by successive principal components and guiding the selection of an appropriate dimensionality cutoff. **(F)** Heatmap of the leading principal components highlighting genes with the highest contributions to each component, illustrating distinct transcriptional drivers across PCs. **(G)** Visualization of gene loadings across principal components using VizDimLoadings, supporting the identification of biologically informative PCs for downstream tSNE analysis.

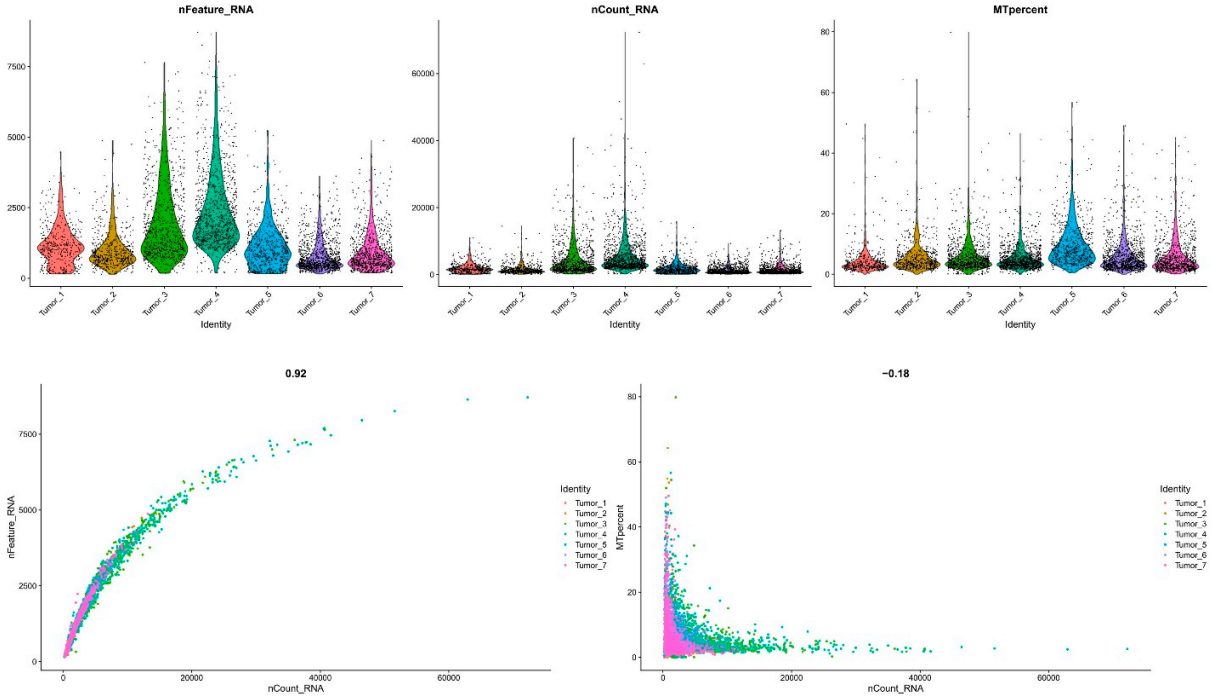
(A) Normal samples – Before Quality control



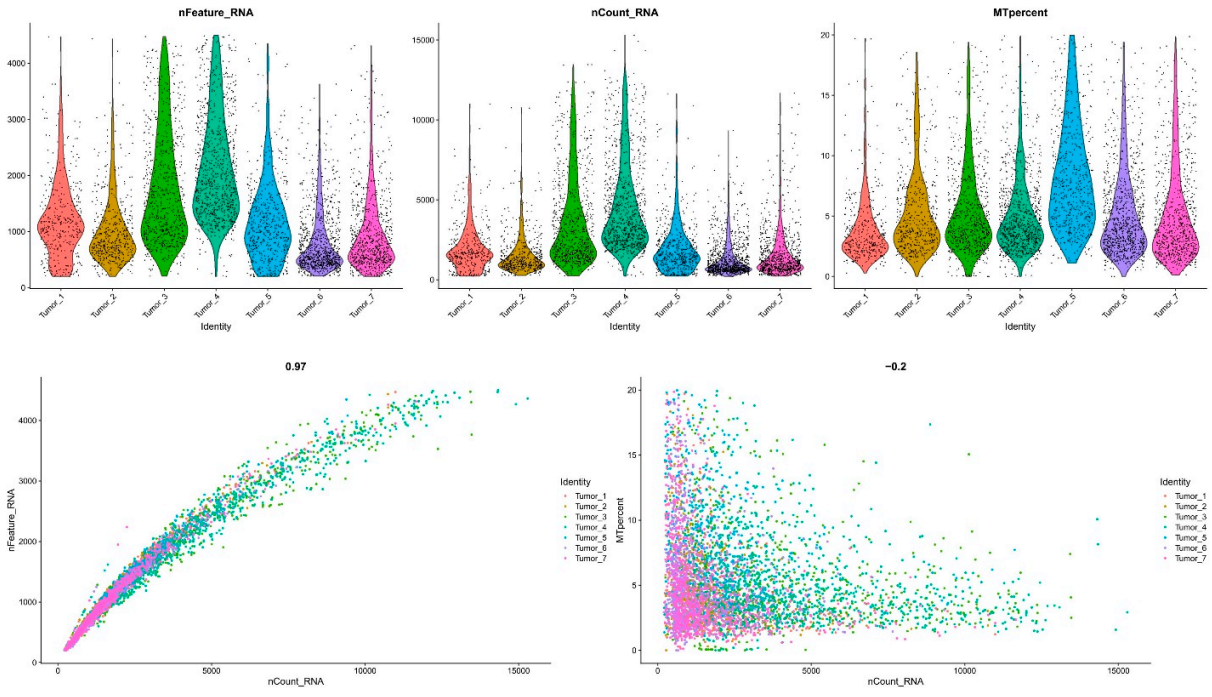
(A) Normal samples – After Quality control



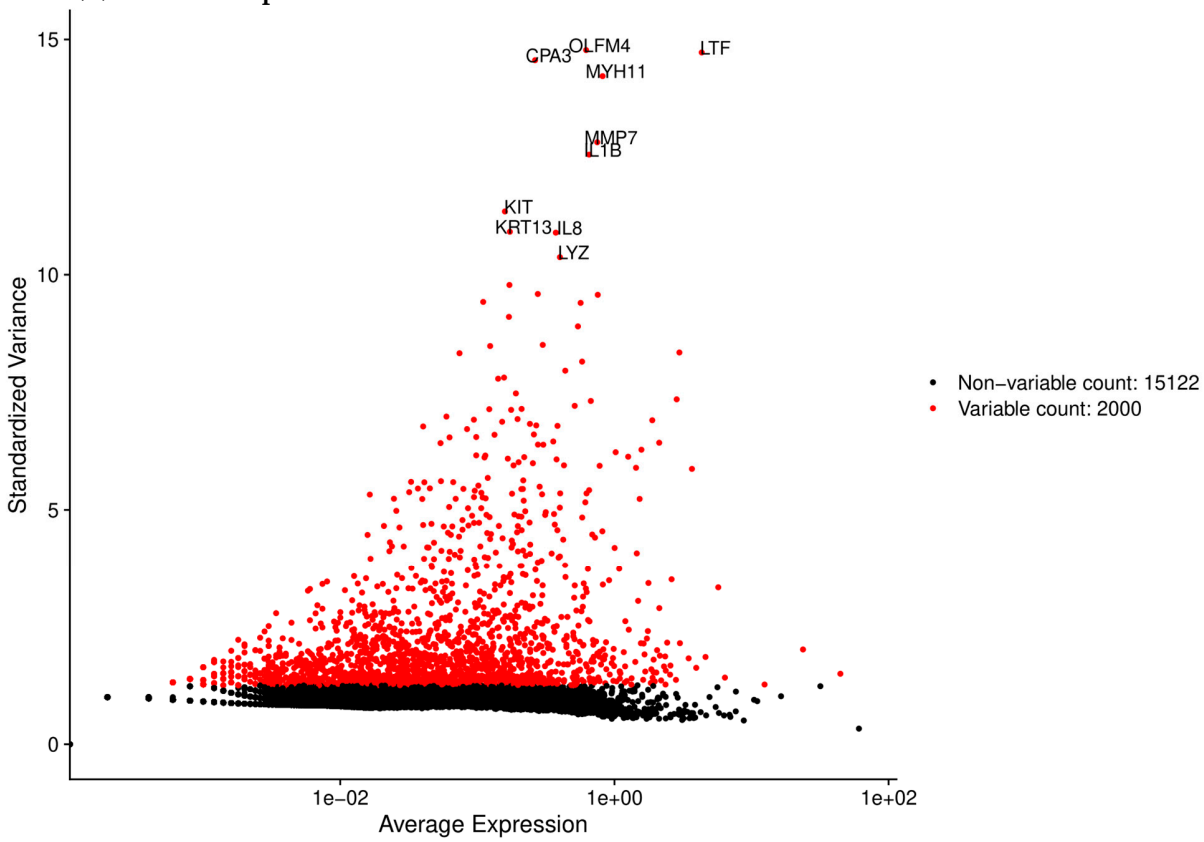
(A) Tumor samples – Before Quality control



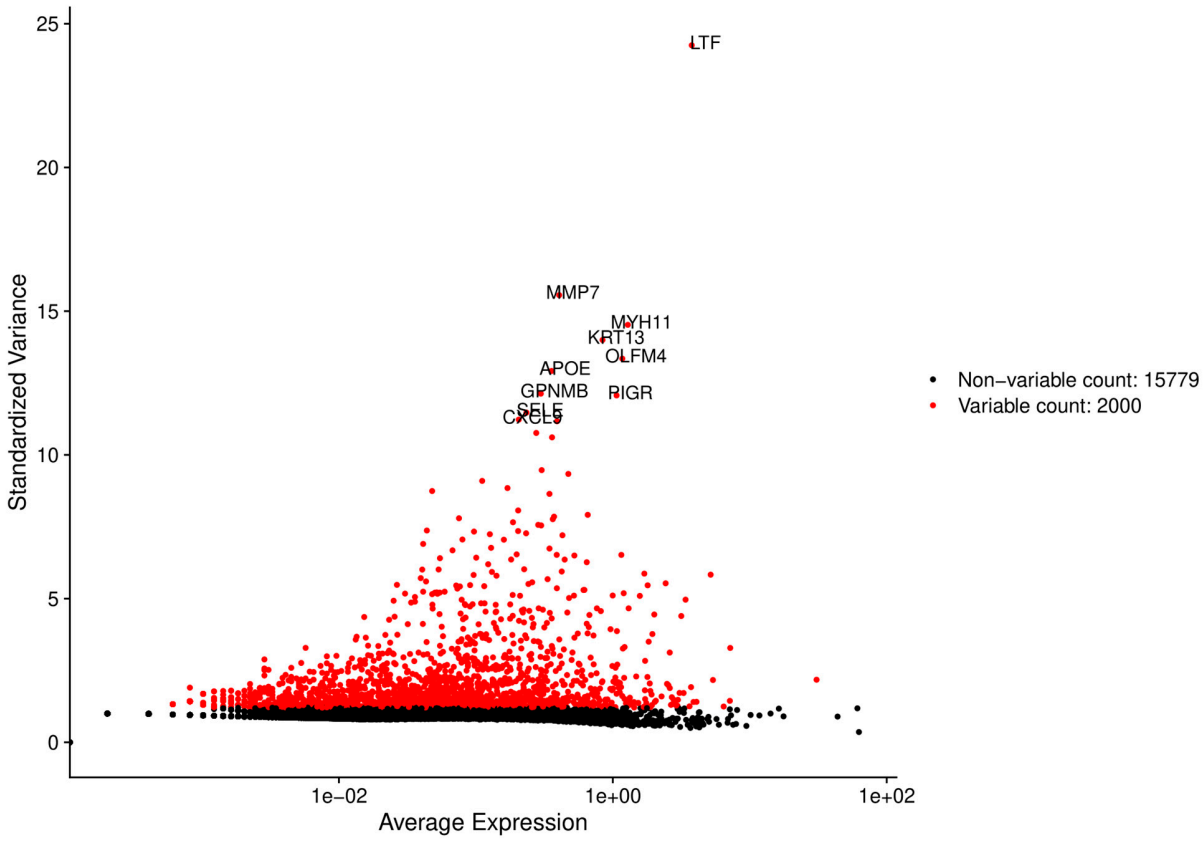
(A) Tumor samples – After Quality control



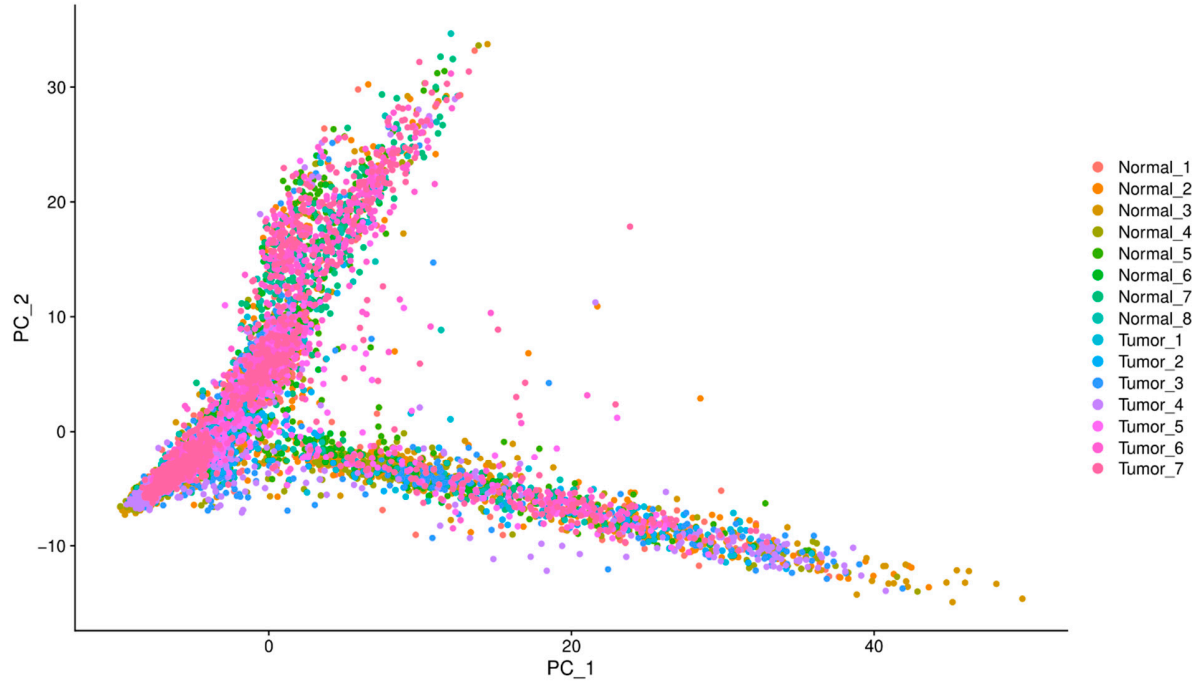
(B) Normal samples



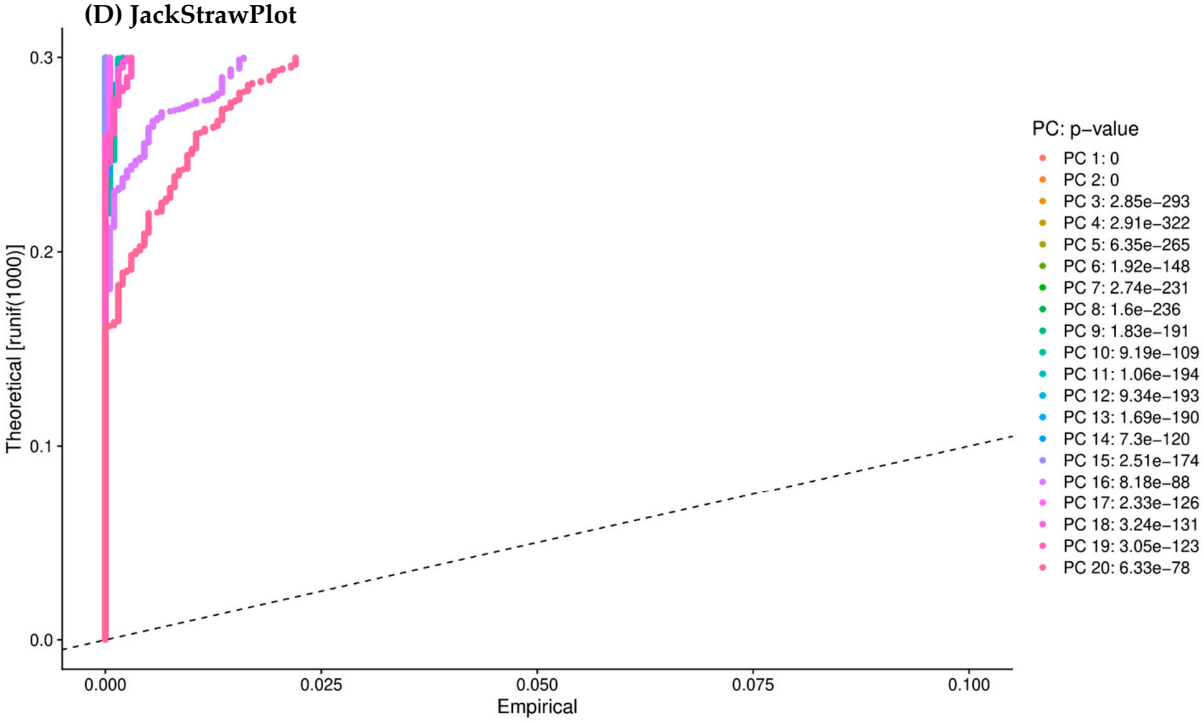
(B) Tumor samples



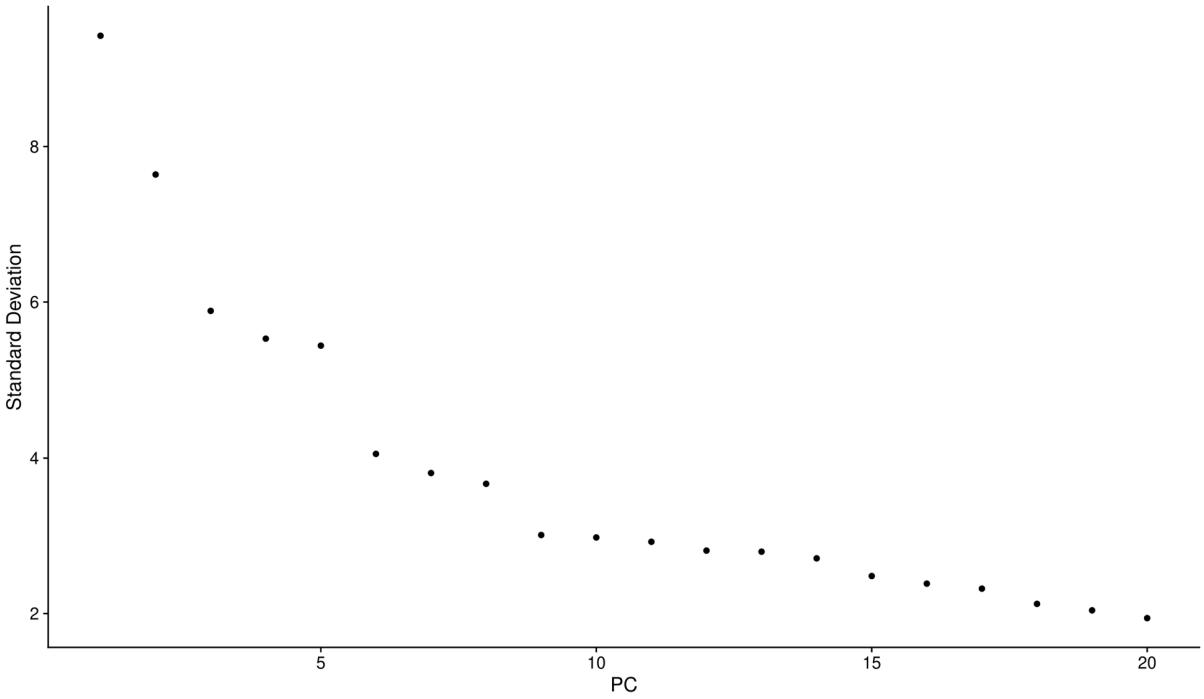
(C) Principal component analysis (PCA) - DimPlot



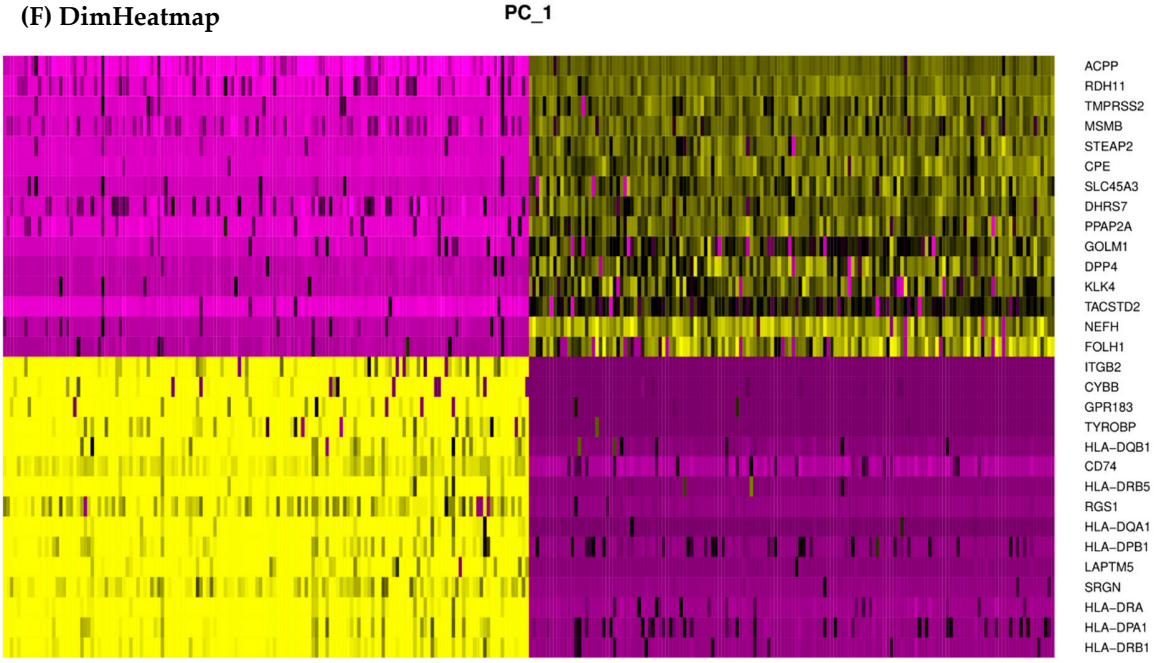
(D) JackStrawPlot



(E) ElbowPlot



(F) DimHeatmap



(G) VizDimLoadings

