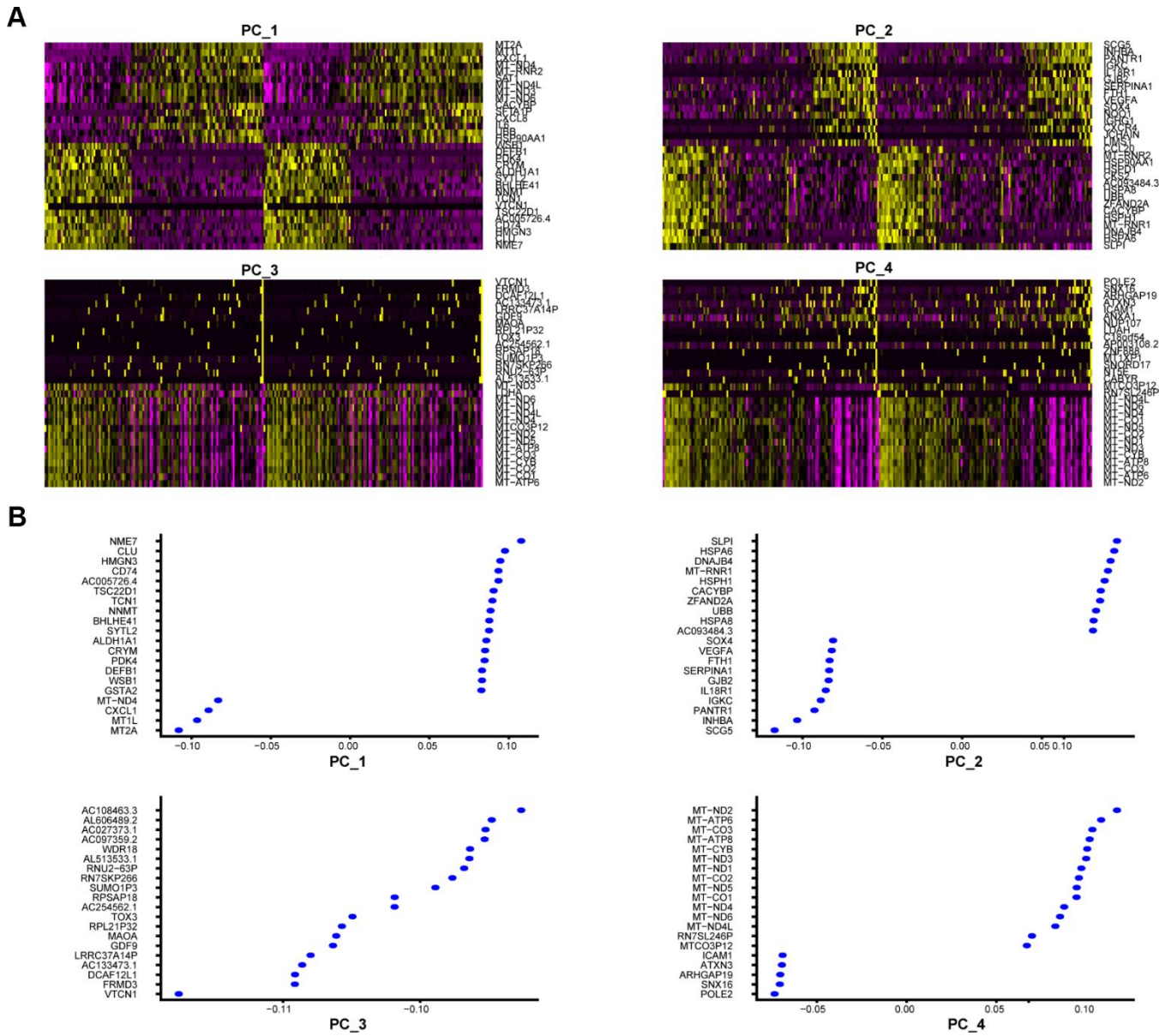
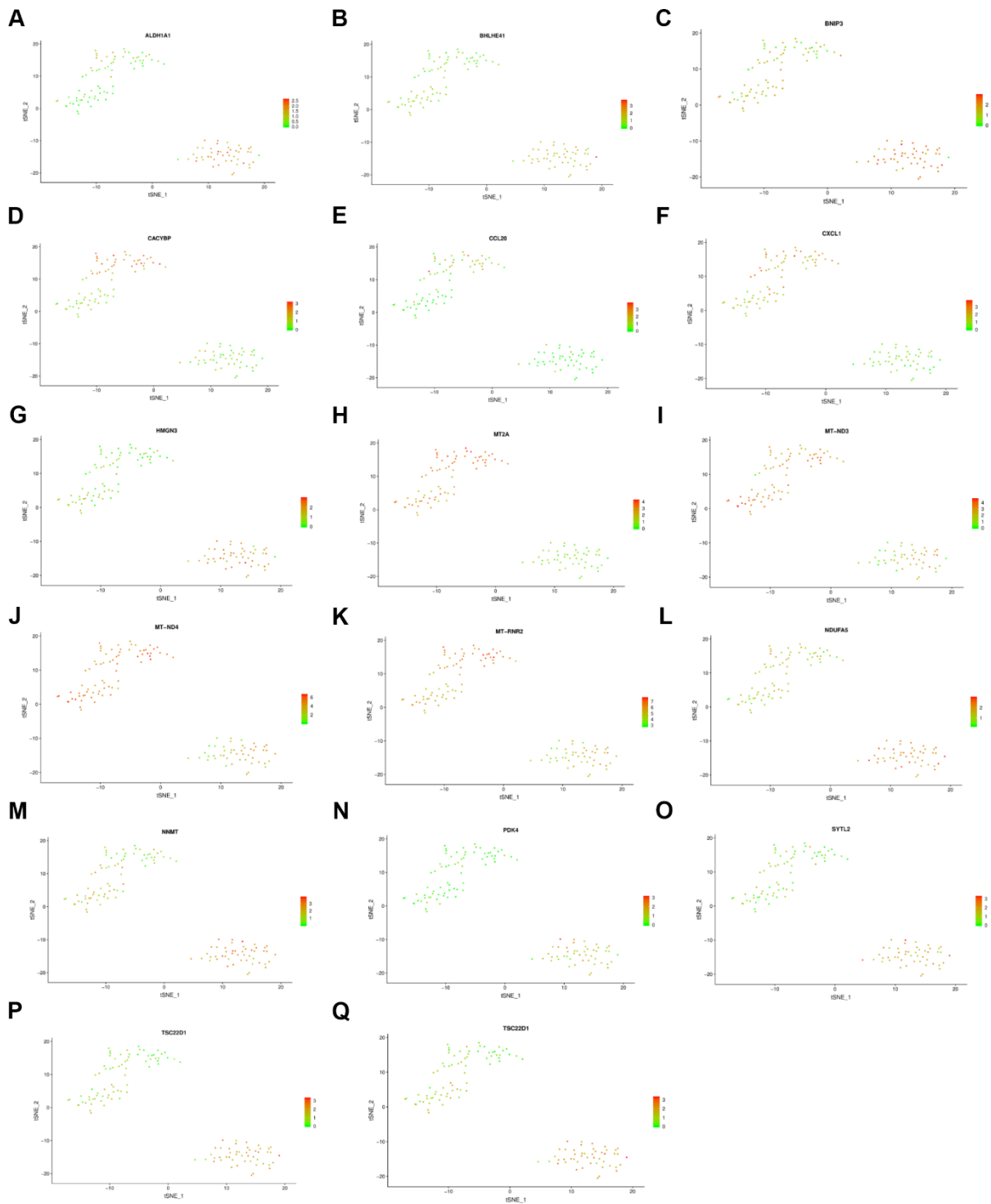


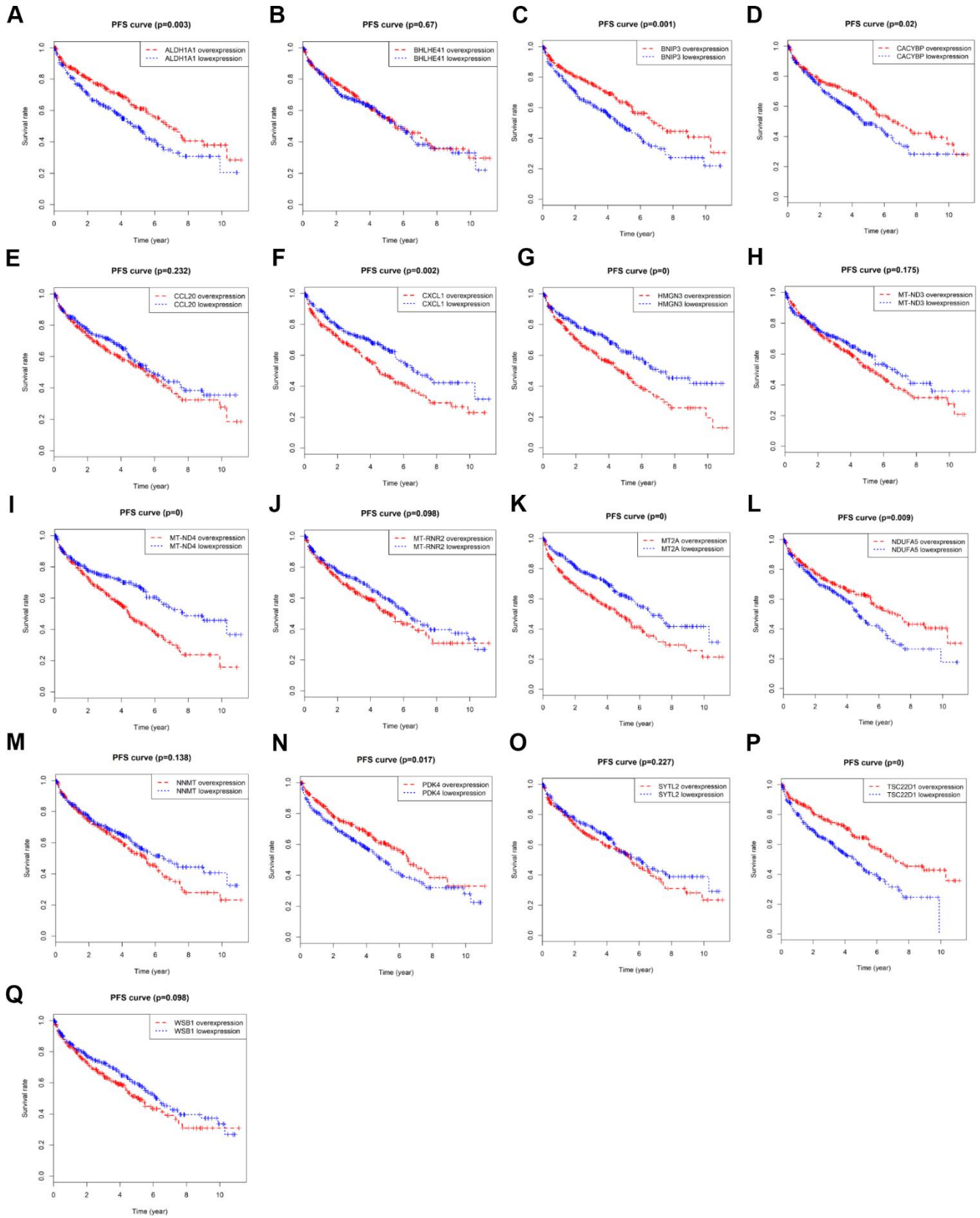
SUPPLEMENTARY FIGURES



Supplementary Figure 1. The top 4 components from PCA procedure were shown and we exhibited the correlated genes in each component. (A) Cluster analysis across each component. The colors ranging from purple to golden yellow represent the expression levels of correlated genes from low to high. (B) Correlation analysis of top relative genes in each component.



Supplementary Figure 2. The differential expression levels of 17 hub metastasis-associated genes in two clusters from the scRNA-seq.



Supplementary Figure 3. Survival analysis of the 17 hub metastasis-associated genes in total TCGA-KIRC cohort, where we observed that most of them correlate with PFS in ccRCC.