



**Figure S3. Related to Figure 3.**

(a, b) GSEA was performed to analyze the enrichment of identified genes (HSPA8, KRT14, KLF9, KRT19, PTGDS, and ADM) in specific categories.

(b) Heatmap depicting the correlation coefficients (Cor) between the expression of genes (PTGDS, KRT19, KRT14, KLF9, HSPA8, ADM) and various immune cell subsets (DC, B cell, Monocyte, Macrophage, NK, Neutrophil, CD4\_Naive, CD4\_Memory, CD8\_Naive, Gamma delta, CD4\_Tfh, Th1, Treg, Th17, Th2, CD8\_Memory). Color intensity represents the correlation strength (red for positive correlation, blue for negative correlation), and asterisks (\*) indicate statistical significance with  $p < 0.05$ . Calculate the correlation through the Spearman method.

(c)