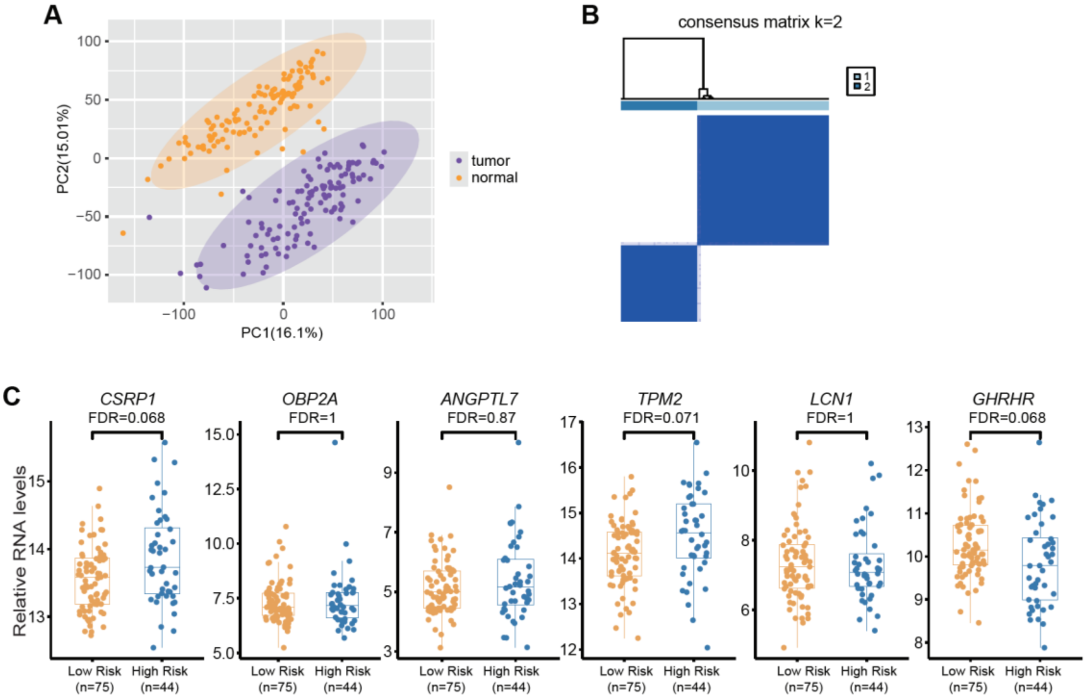
Supplementary figure 1 The identification of immune-related prognostic genes in ESCC

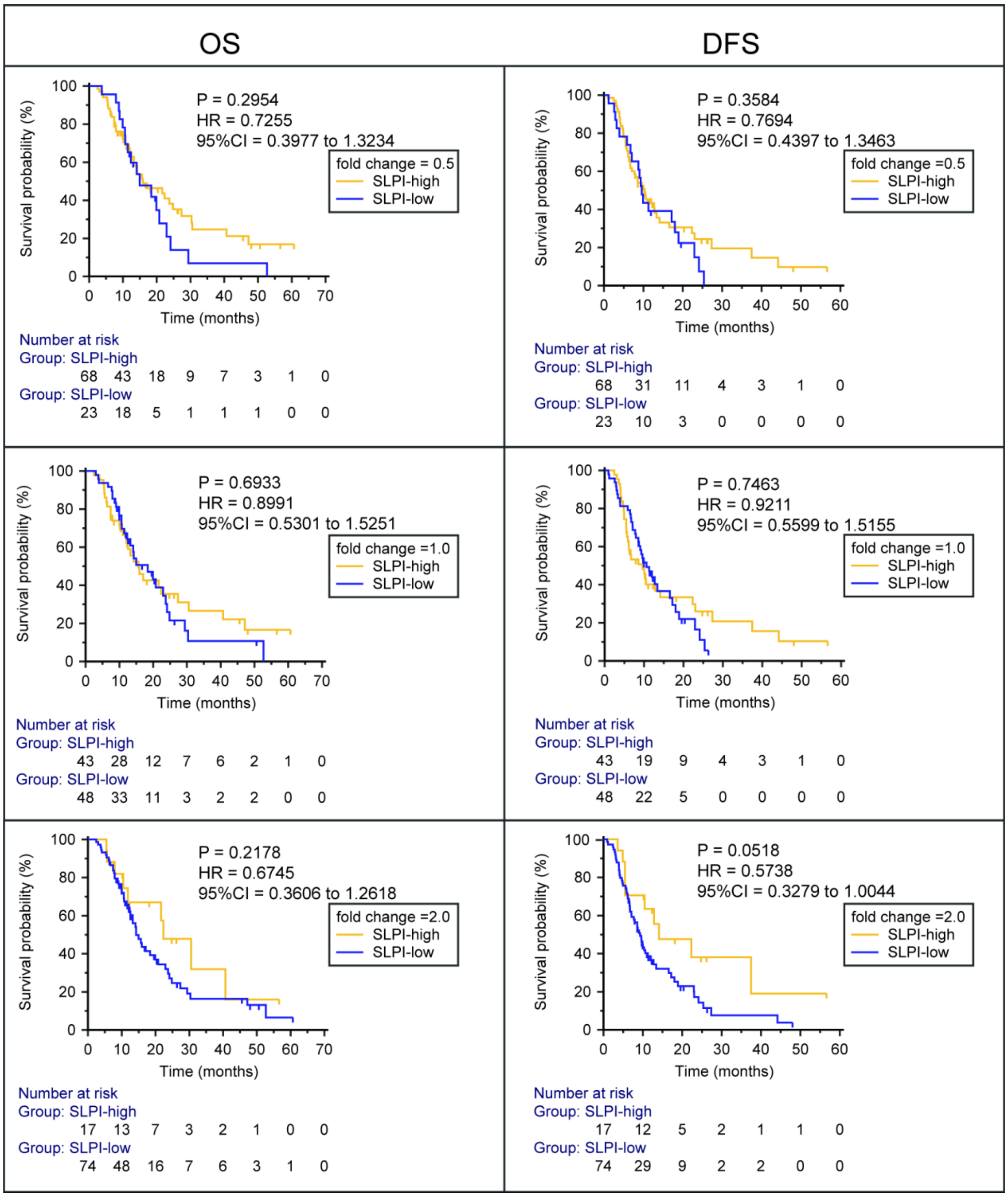
(A) PCA demonstrates significant transcriptomic differences between tumor and normal samples.

(B) Consensus matrix heatmap defining two subtypes (k = 2).

(C) Differential Expression of the remaining genes identified in Fig. 1C across High Risk and Low Risk clusters, analyzed using t-tests with p-values adjusted via the Benjamini-Yekutieli method.



Supplementary figure 2 Kaplan-Meier survival analysis was performed to evaluate the OS and PFS prognostic outcomes with the cut-off values of 0.5, 1.0, and 2.0.



Supplementary figure 3 Cell-cell communication between epithelial cells and other cell

populations, as inferred using CellChat, in patients with high or low SLPI expression levels.