

Supplementary Materials

Table S1: The number of cells in each subpopulation in different stage of LUAD. Table S2: The different expression genes in each subpopulation. Figure S1: The umap plot for integration with and/or without batch effect correction. Figure S2: IHC stain of IGHA1 and IGHG1 for three LUAD patients. Figure S3-S12: Multivariate analysis for S100P, SPP1, KLRB1, mean of CD79A and IGHA1, mean of CD79A and IGHG1, risk score in TCGA-LUAD, risk score in GSE72094, risk score in GSE31210, the proportion of S100P+ epithelial cells, and the proportion of S100P+ macrophages, respectively.