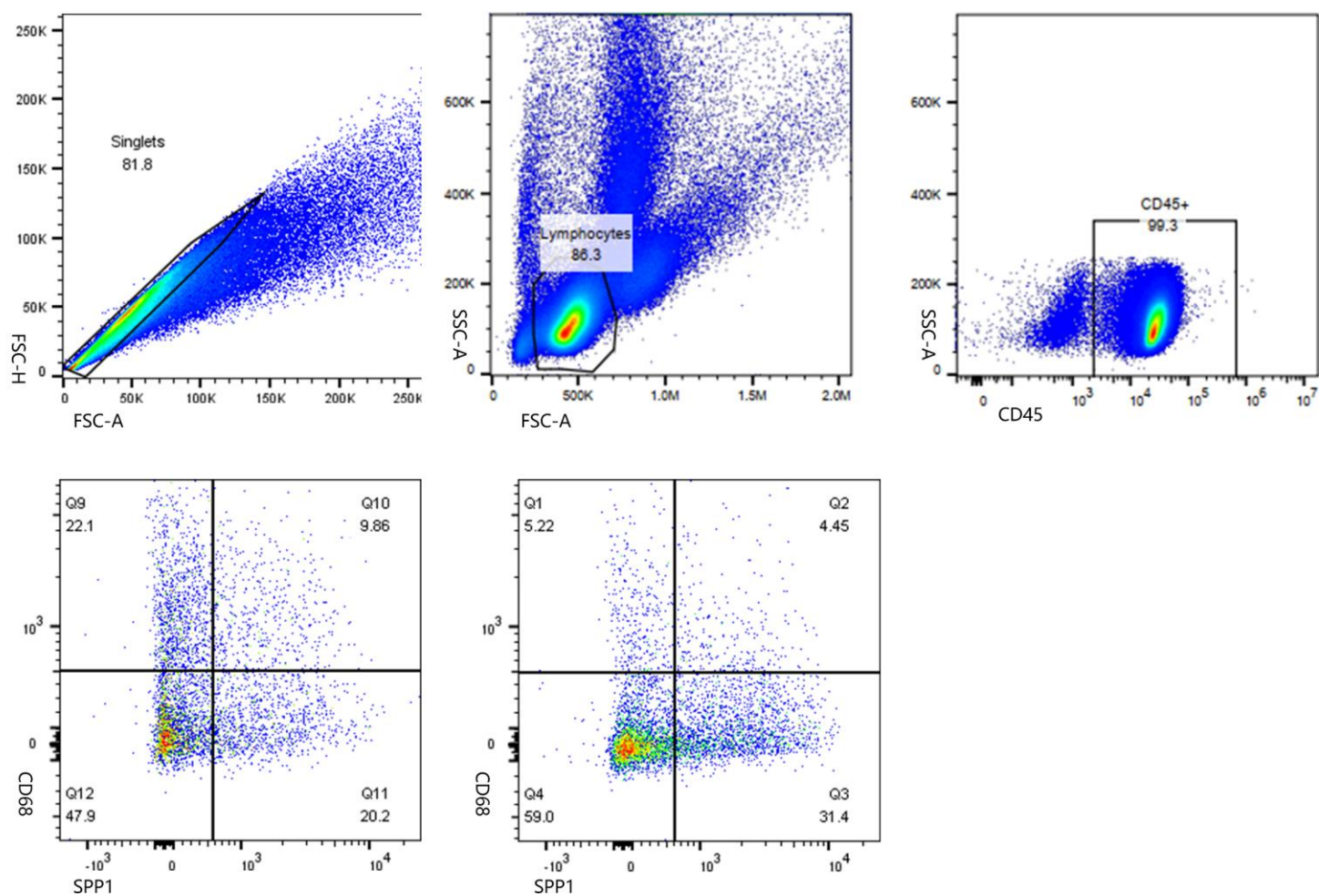
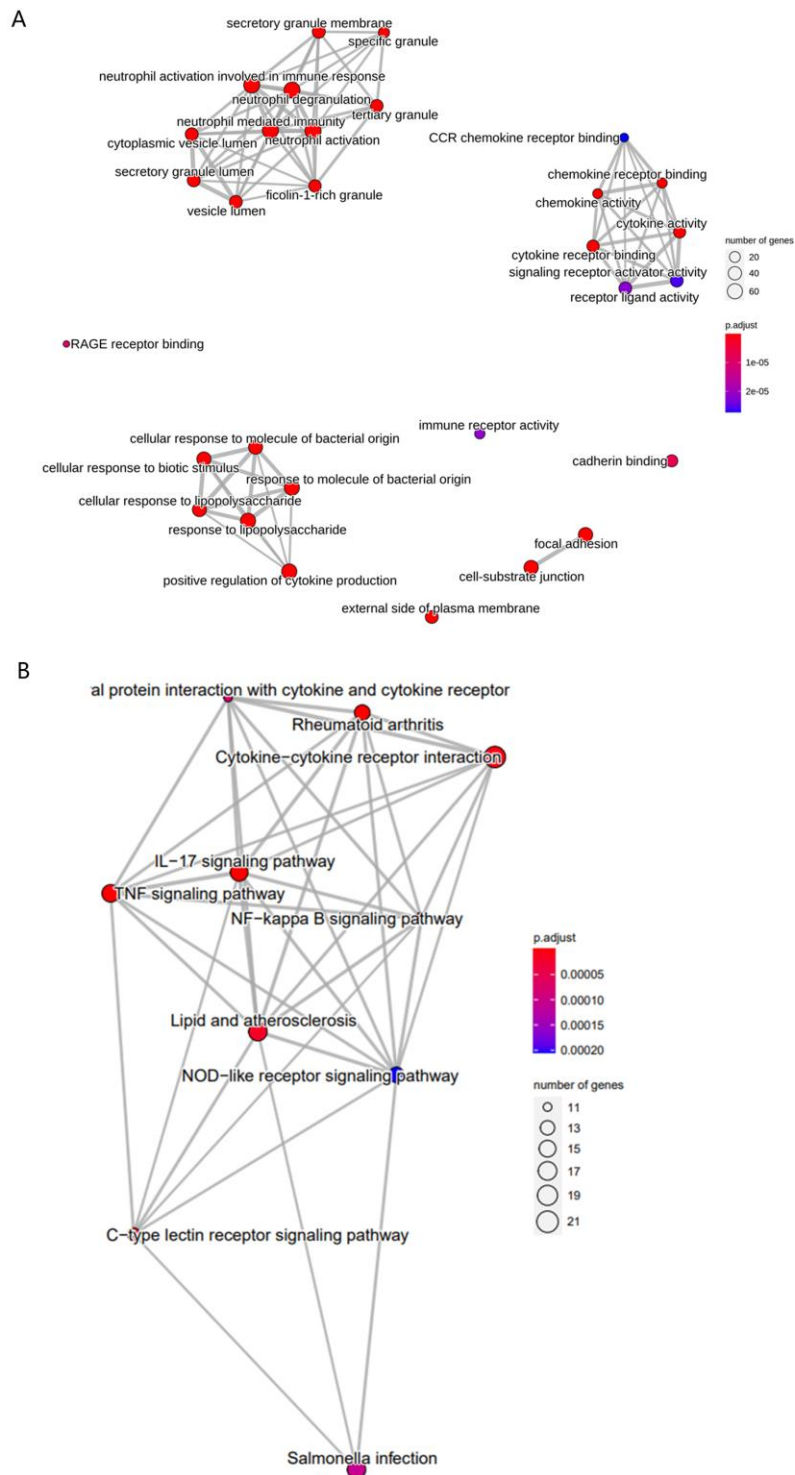
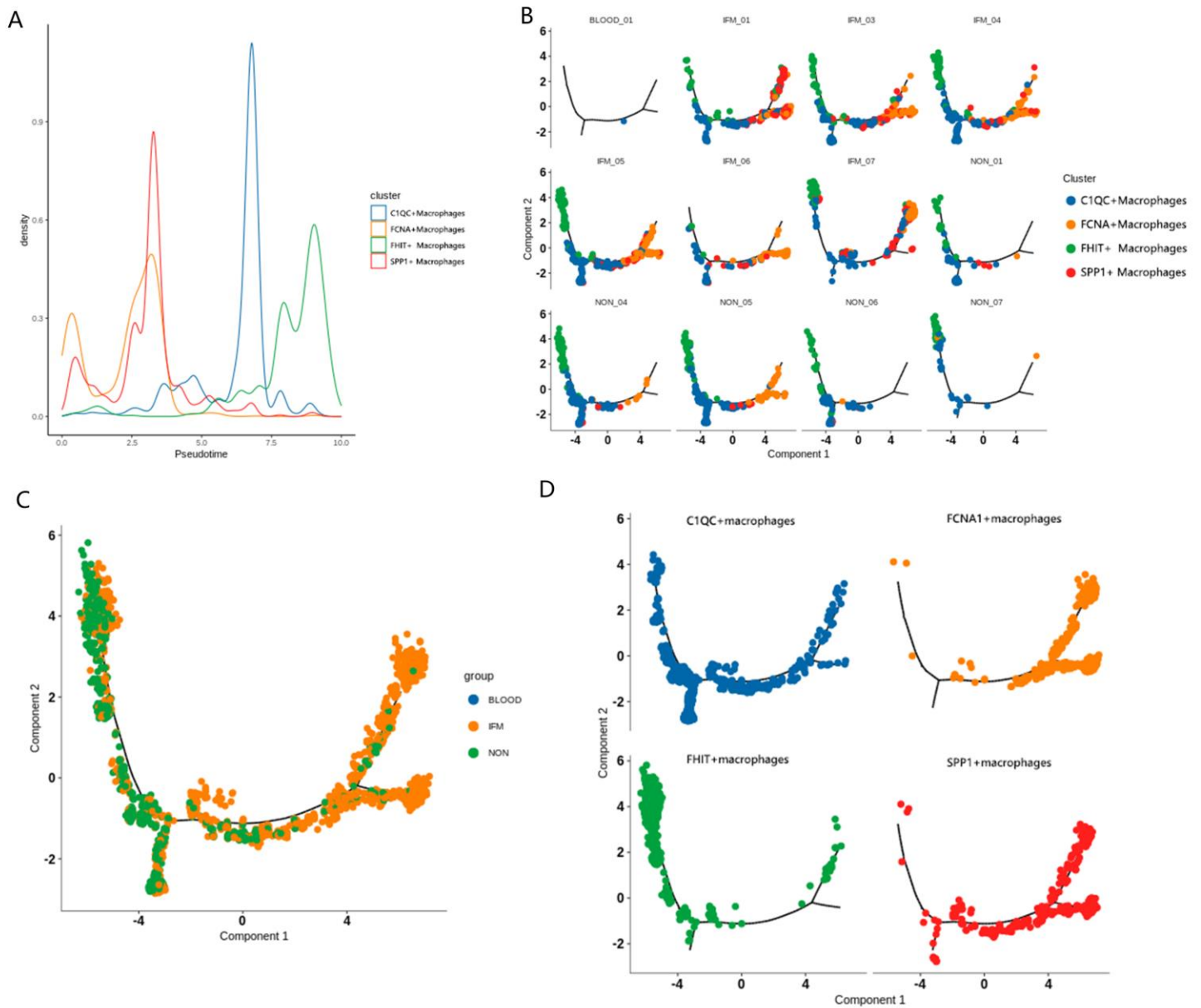




Supplementary figure 1: Representative gating strategy of SPP1+macrophages in UC patients.

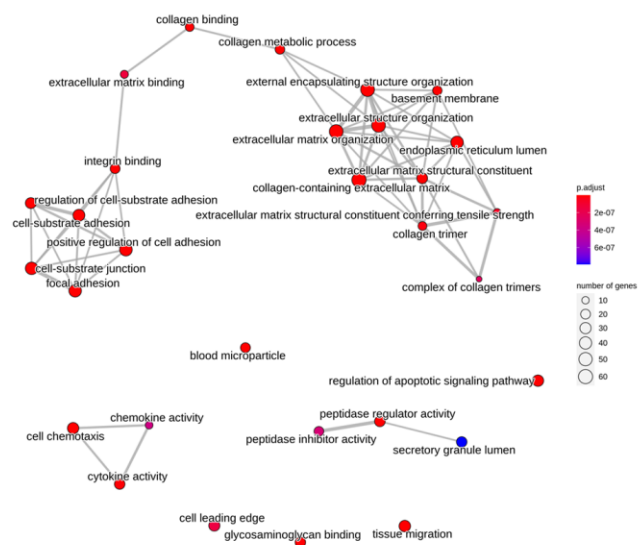


Supplementary figure 2: (A-B) Network diagram based on gene pathway and similarity according to GO (A) and KEGG (B) enrichment analyses for macrophages.

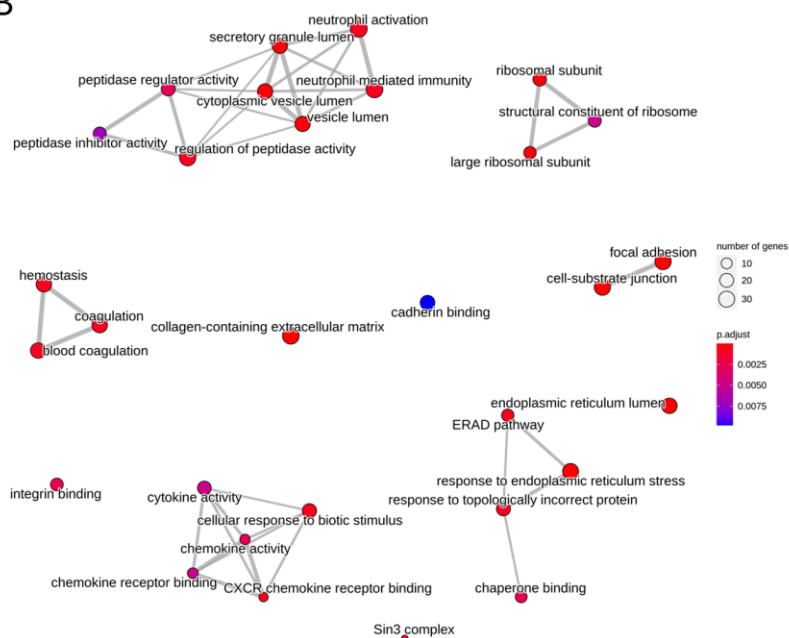


Supplementary figure 3: (A) Monocle2 was used to analyze the density distributions of different cell types over time. (B) Distribution of each sample in the pseudo-time trajectory, where different colors represent the cell types in each sample. (C) Distribution of different sample types in the pseudo-time trajectory. (D) Pseudo-time analysis colored by cell type.

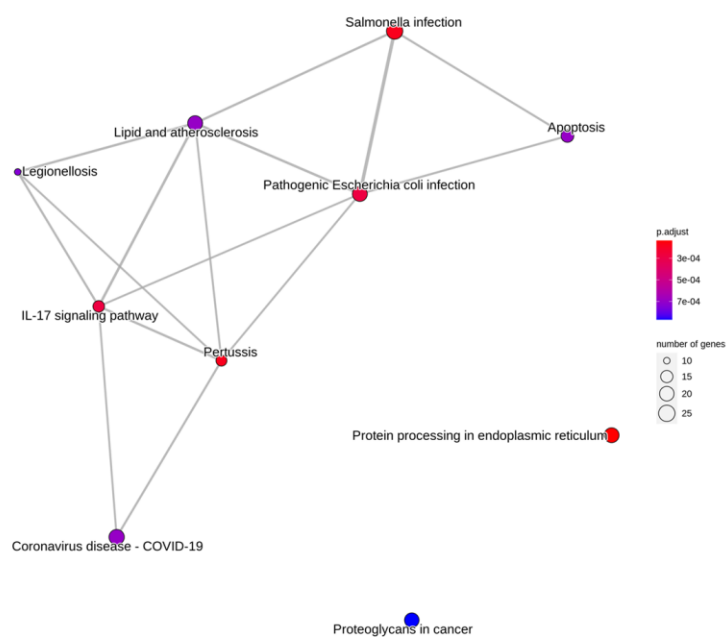
A



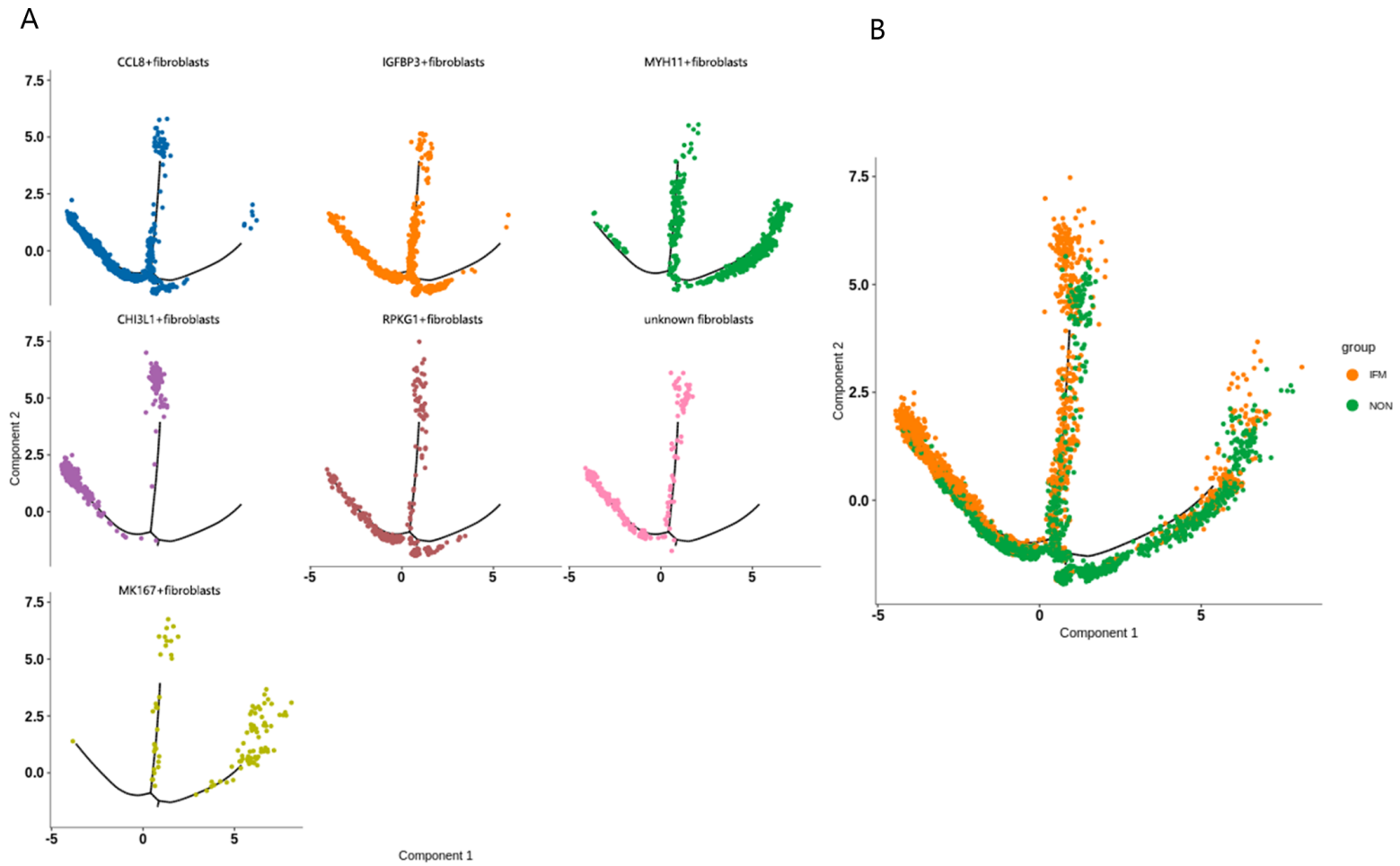
B



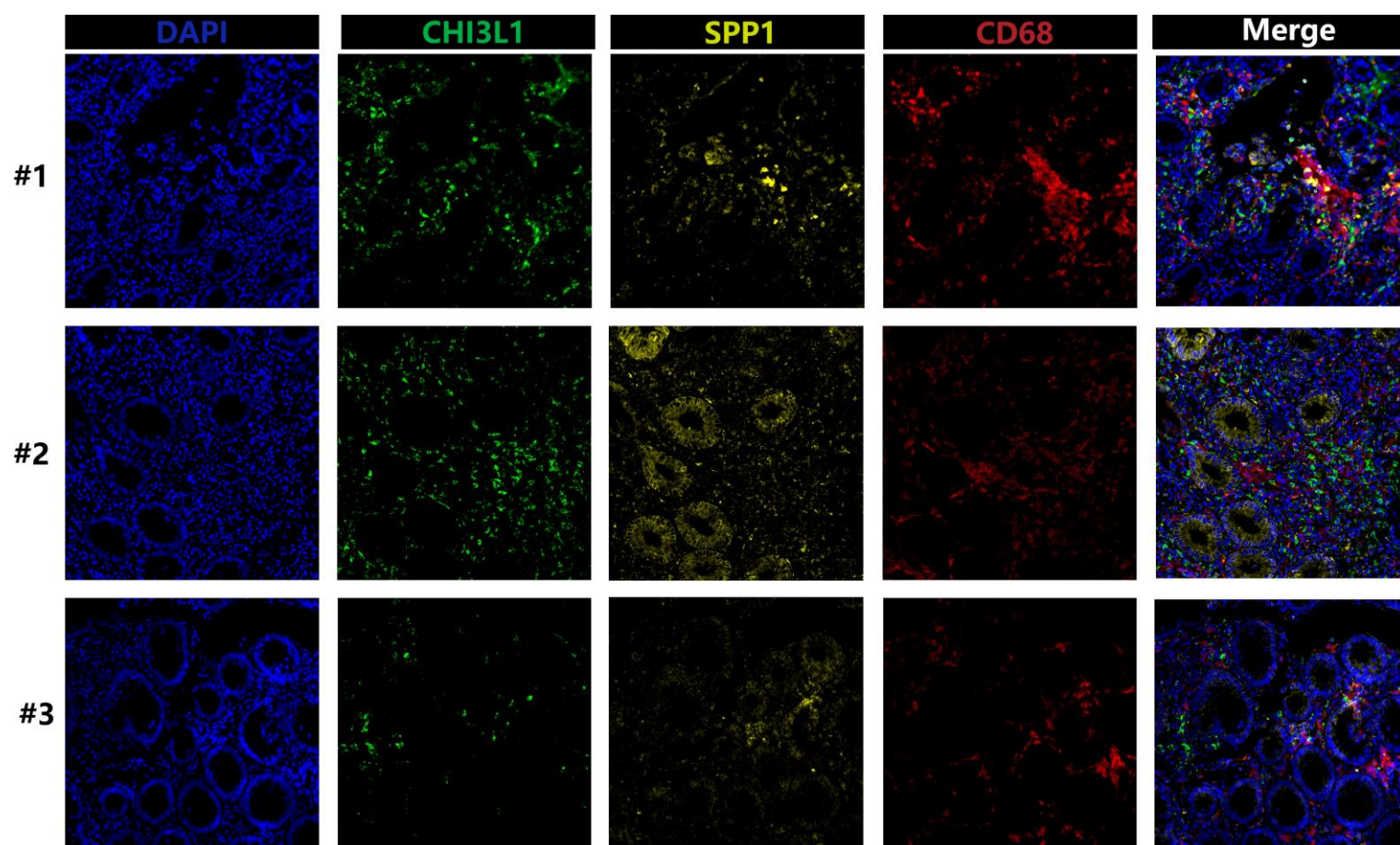
C



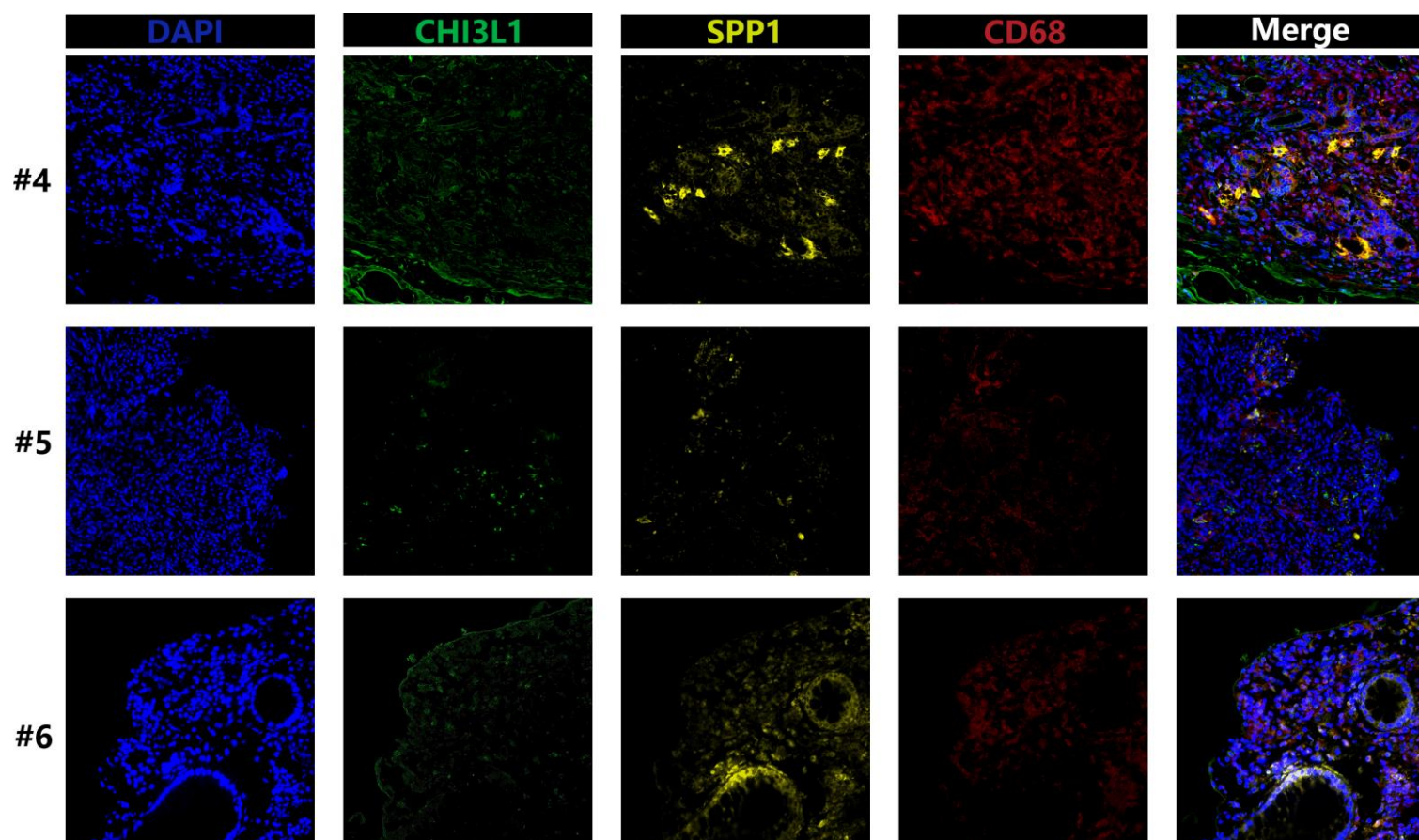
Supplementary figure 4: (A) Network diagram based on gene pathway and similarity in GO (B) enrichment analysis for Fibroblasts. (B-C) Network diagram based on gene pathway and similarity according to the GO (B) and KEGG (C) enrichment analyses in CHI3L1+fibroblasts.



Supplementary figure 5: (A)Pseudo-time series analysis colored by cell type. **(B)** Distribution of different sample types in the pseudo-time series trajectory.



Supplementary figure 6: Representative IF images of human UC tissues (20x). DAPI (blue), CHI3L1 (green), SPP1 (yellow), and CD68 (red) are shown in individual and merged channels. The experiment was performed in s3 independent patients.



Supplementary figure 7: Representative IF images of human UC-CRC tissues (20x). DAPI (blue), CHI3L1 (green), SPP1 (yellow), and CD68 (red) are shown in individual and merged channels. The experiment was performed in 3 independent patients.