

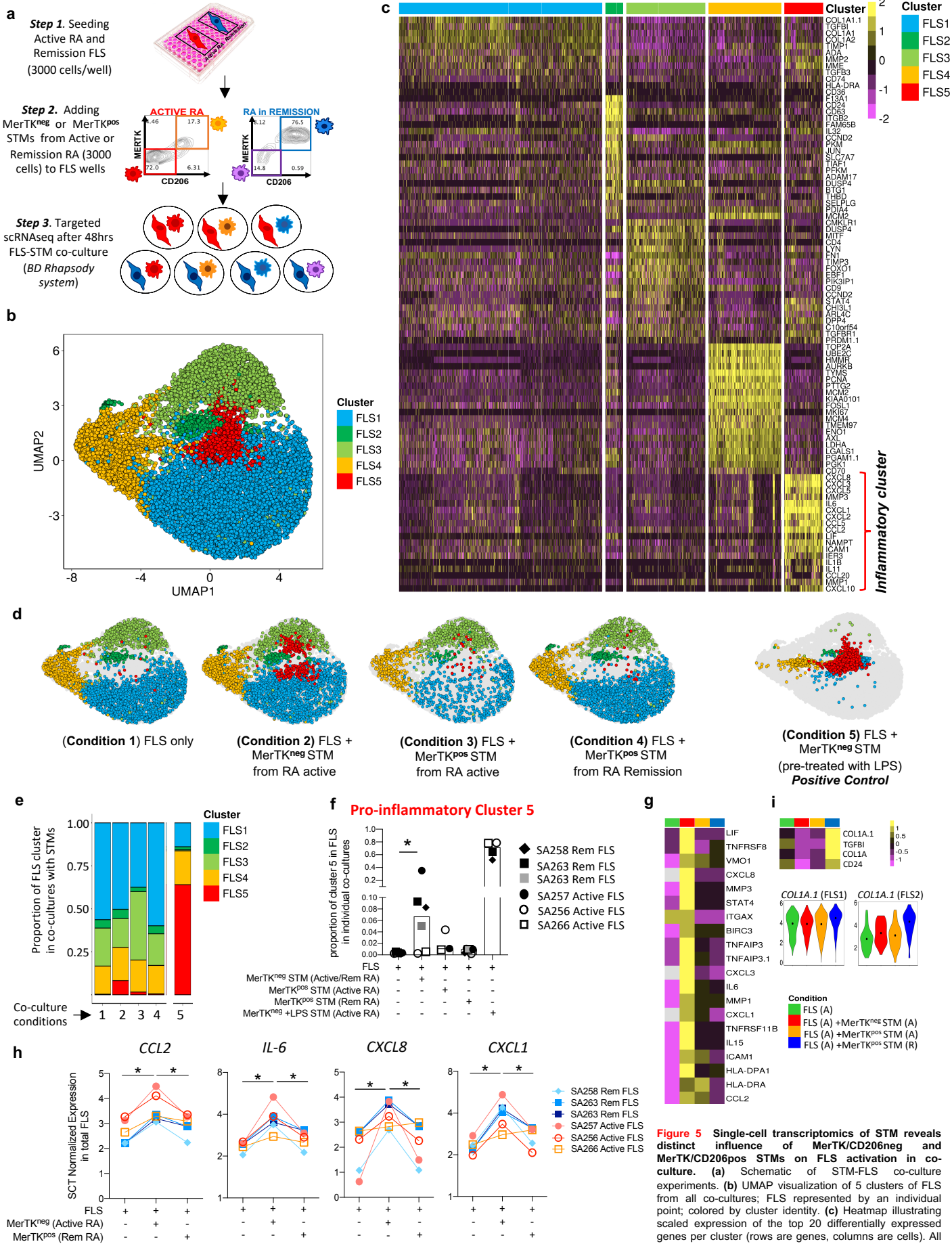


Figure 5 Single-cell transcriptomics of STM reveals distinct influence of MerTK/CD206^{neg} and MerTK/CD206^{pos} STMs on FLS activation in co-culture. (a) Schematic of STM-FLS co-culture experiments. (b) UMAP visualization of 5 clusters of FLS from all co-cultures; FLS represented by an individual point, colored by cluster identity. (c) Heatmap illustrating scaled expression of the top 20 differentially expressed genes per cluster (rows are genes, columns are cells). All genes are expressed in at least 40% of cells in each cluster. Average log-fold change ≥ 0.25 . (d) Split UMAP visualization demonstrating relative changes in the FLS phenotypes between distinct co-culture conditions. (e) Bar and (f) dot plots illustrating the change in FLS cluster distribution across conditions. *p<0.05 Mann-Whitney. Each symbol in f represents FLS from an individual patient (n=5) co-cultured with sorted MerTK^{neg} or MerTK^{pos} STMs from active RA (n=3) or remission RA (n=3). (g) Heatmap of scaled expression of the top differentially expressed genes in total FLS, induced by MerTK^{pos} STMs from RA in disease remission compared to MerTK^{neg} STMs from active RA. Rows are genes and columns show pseudo-bulk expression per condition. All genes are expressed in at least 60% of cells in that condition with an average log fold-change ≥ 0.25 , and p<0.05 corrected for multiple comparisons. Violin plots represent an expression of Col1a1 in collagen producing FLS cluster 1 and 2 induced by MerTK^{pos} STMs from RA in disease remission.