
Supplementary information

Spatial single-cell profiling reveals macrophage niches in severe COVID-19 lungs

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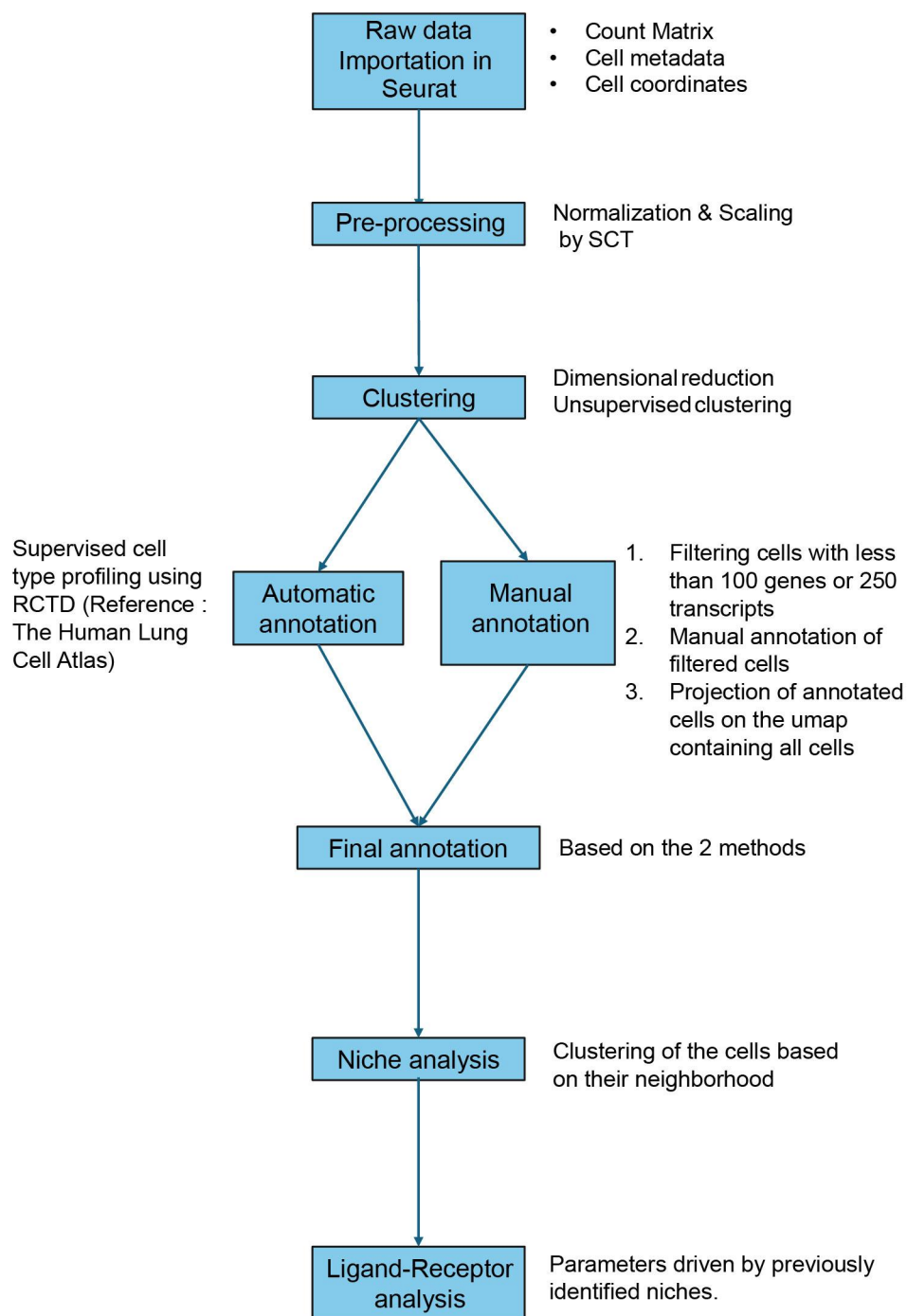


Figure S1. Overview of the bioinformatic analytic pipeline employed in this study. SCT = Single-Cell Transform; RCTD = robust cell type decomposition.

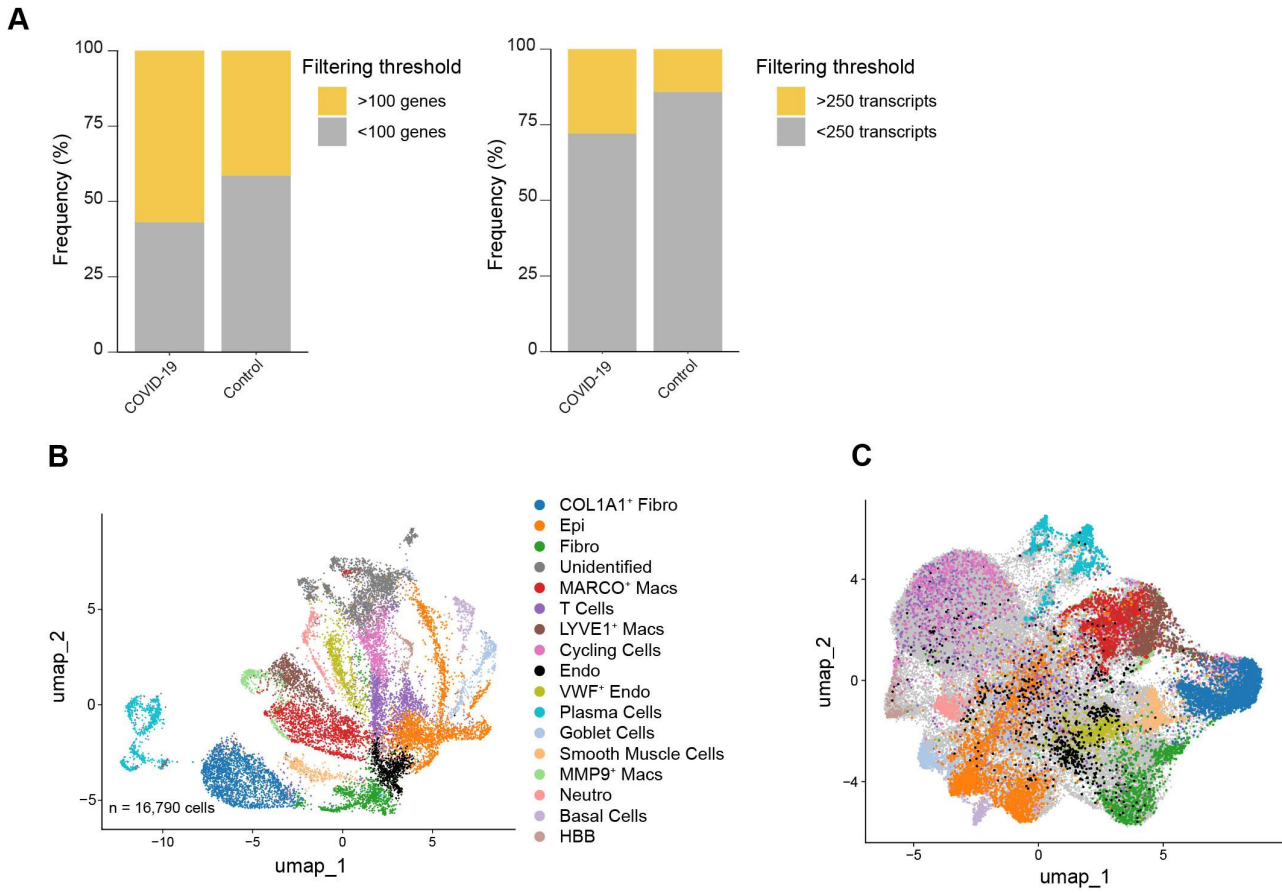


Figure S2. Analysis of filtered CosMx output. (A) Bar graphs showing the proportions of cells passing the threshold of 100 genes (left) and 250 transcripts (right); (B) UMAP plots of filtered CosMx output after cell annotation; (C) UMAP plot of global CosMx output where filtered annotated cells have been highlighted.

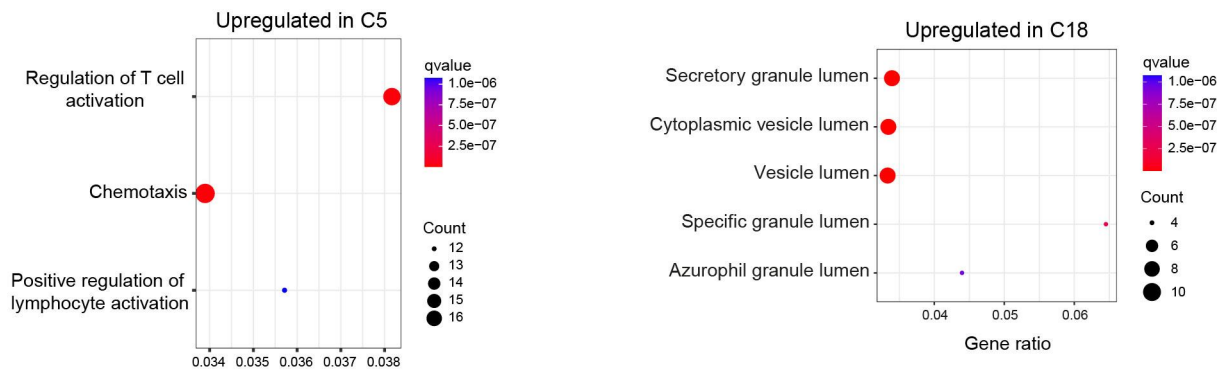


Figure S3. Gene ontology of DEGs in C5 et C18.

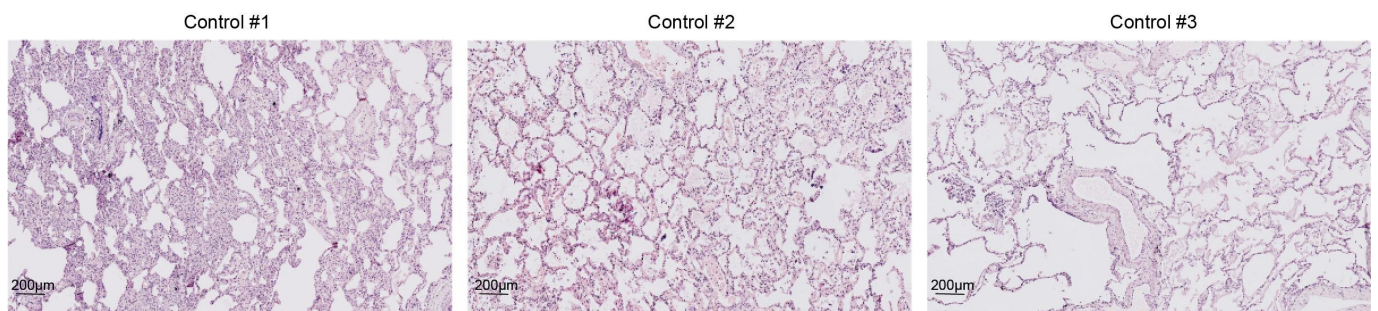


Figure S4. Pictures of H&E-stained lung sections from Control subjects. Scale bar = 200 μ m.

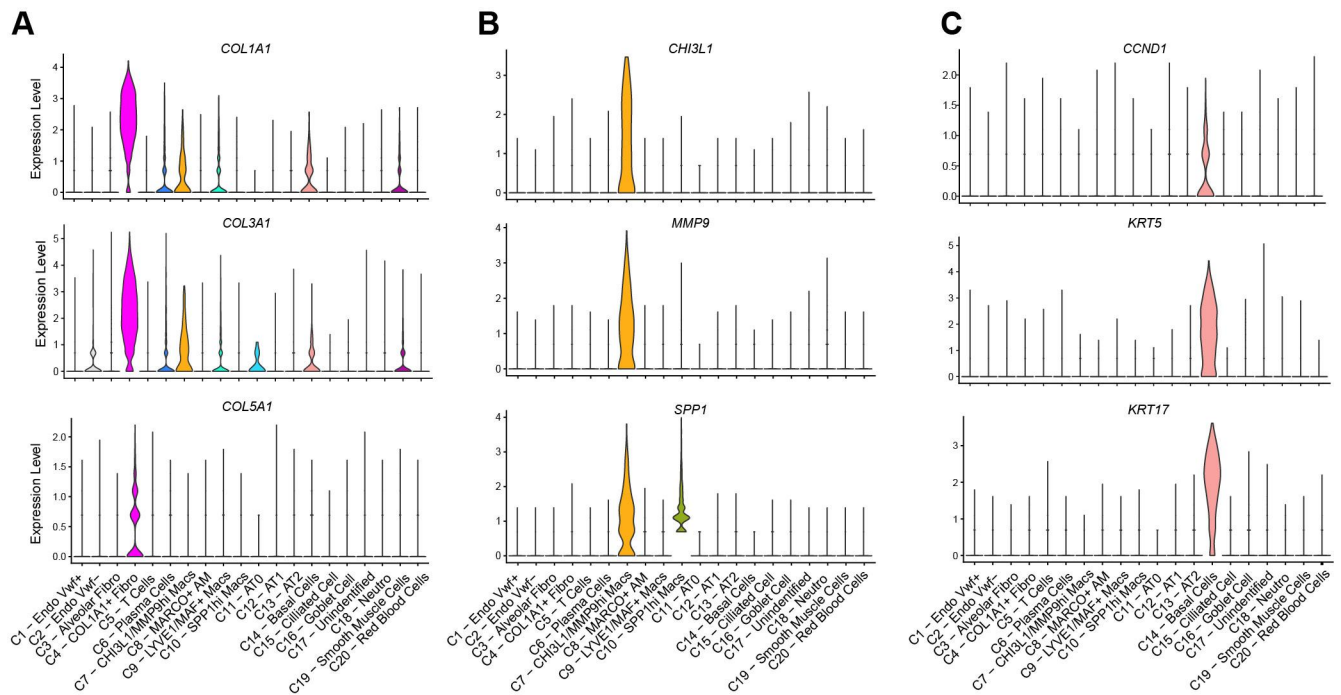


Figure S5. Annotation of cell populations. Feature plots exhibiting the expression level of genes related to ECM (A), pro-fibrotic macrophages (B) and basal cells (C).

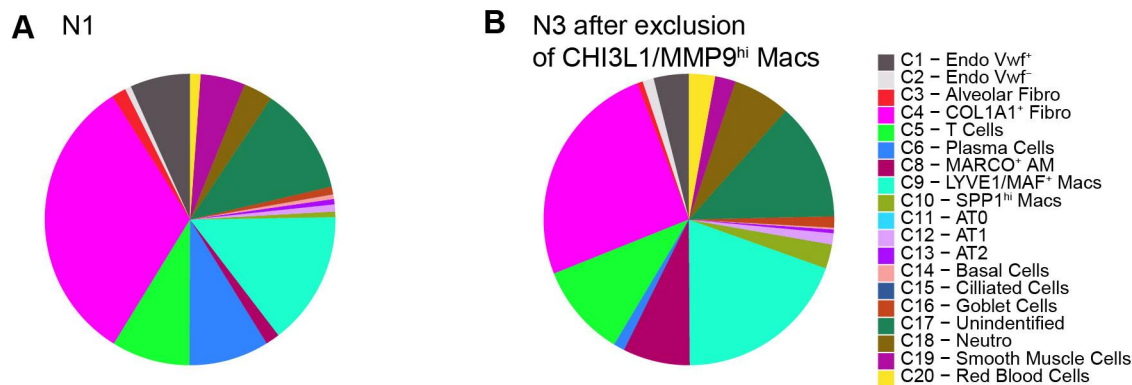


Figure S6. Cell proportions in fibrotic niches. (A) Pie chart displaying the cell proportion 21 of Niche 1; (B) Pie chart displaying the cell proportion of Niche 3 after exclusion of 22 CHI3L1/MMP9^{hi} Macs.

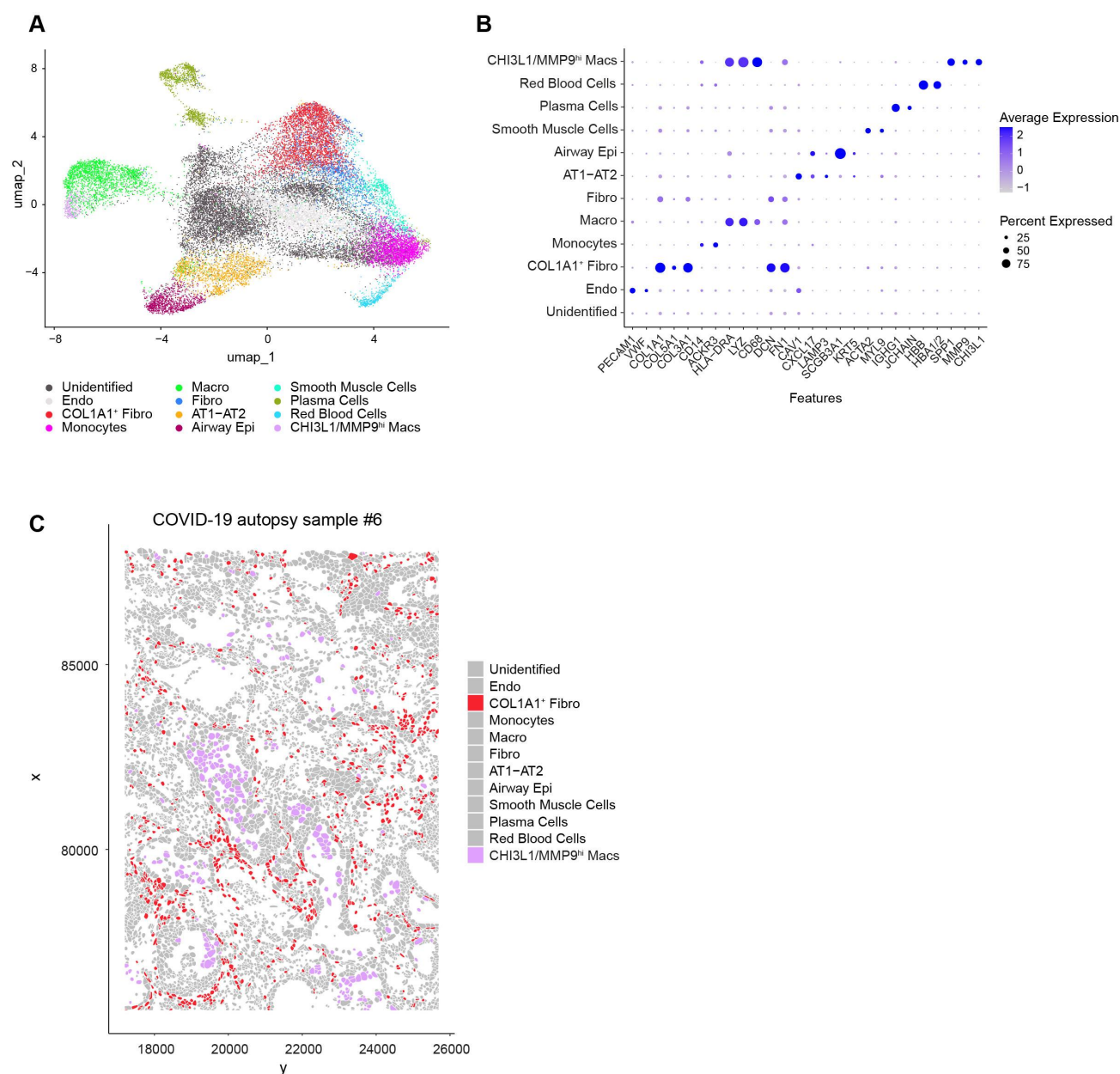


Figure S7. Validation of CHI3L1/MMP9^{hi} macrophage-COL1A1⁺ fibroblast proximity in an independent dataset. (A) UMAP representation of CosMx SMI data from an independent COVID-19 autopsy lung sample (sample #6), showing the annotated cell populations; (B) Dot plot showing the average expression and percentage of cells expressing the indicated cell type-specific markers across the annotated populations; (C) Spatial representation of cells across FOVs 90-96 from COVID-19 sample #6, 30 highlighting the spatial proximity between CHI3L1/MMP9^{hi} macrophages and COL1A1⁺ fibroblasts.