



Single-Cell RNA Sequencing Reveals Cellular Heterogeneity and Differentiation Dynamics in Lung Adenocarcinoma Microenvironment

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ABSTRACT Lung adenocarcinoma contains diverse malignant, immune, and stromal cell populations that may influence tumour progression and therapeutic response. This study aimed to characterise cellular composition, transcriptional heterogeneity, and differentiation-related patterns in the lung adenocarcinoma microenvironment. The researchers performed an integrative single-cell RNA sequencing analysis using quality control, normalisation, principal component analysis, dimensionality reduction, clustering, cell annotation, marker gene identification, and pseudotemporal trajectory inference. Twelve major cell populations were identified, spanning immune, stromal, endothelial, epithelial, epithelial-like, tuft-like, and proliferating compartments. Principal component analysis suggested that cellular heterogeneity was mainly associated with epithelial-immune differences, extracellular matrix features, T-cell activation, and proliferation-related programs. Pseudotemporal analysis suggested branched cellular-state trajectories consistent with potential differentiation- or activation-related transitions. Marker genes, including *Sftpc*, *Sftpa1*, *Sftpb*, *Cxcl15*, *Mgp*, and *Sle34a2*, helped define distinct cell populations. These findings provide a single-cell transcriptomic overview of cellular diversity and possible differentiation dynamics in lung adenocarcinoma.