

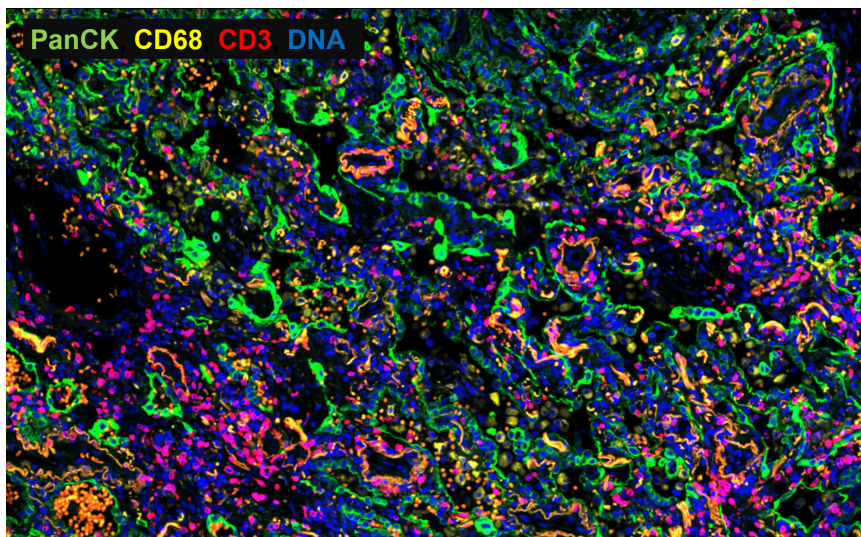
Lung COVID-19

Study Purpose

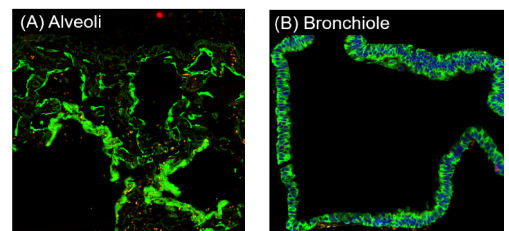
To understand viral pathogenesis and explore the pulmonary transcriptional landscape of COVID-19, normal lung tissue and lung tissue affected by COVID-19 were profiled using the GeoMx Human Whole Transcriptome Atlas. Regions of interest (ROIs) were selected in the alveoli and bronchiole areas of the lung, and differentially expressed genes between tissue affected by COVID-19 and non-infected control lung tissue were examined as potential biomarkers.

Study Summary

Sample Type	FFPE
Species	Human
AOI* Strategy	Geometric
Assay	Human Whole Transcriptome Atlas
Morphology Markers	Pan-Cytokeratin (PanCK), CD68, CD3, DNA
Targets Detected	11,006 targets
Application	Biomarker discovery

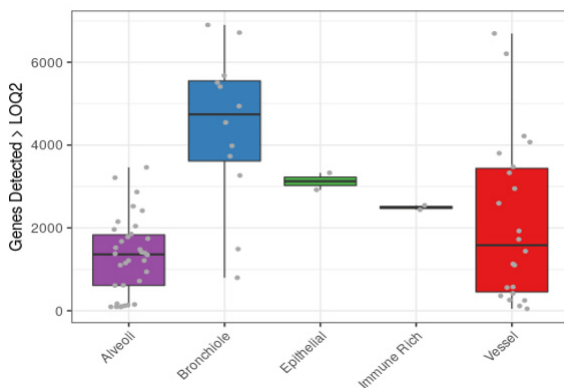


Segmentation Strategy



Legend

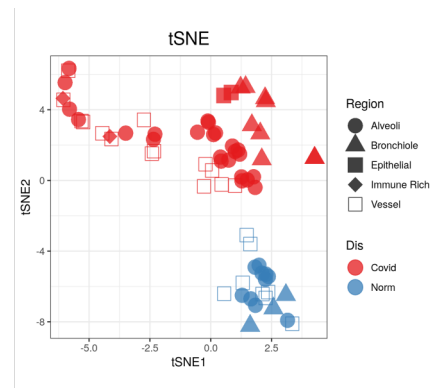
Both alveoli and bronchiole epithelial cells are stained positive for PanCK. ROIs were placed by freehand drawing on alveoli (A) and bronchiole (B) areas.



Legend

Left:
The number of targets detected above the background (LOQ2*) by AOI groups.

Right:
T-distributed stochastic neighbor embedding (tSNE) plot.



*AOI = Area of Illumination

Acknowledgement: We sincerely thank Dr. Arutha Kulasinghe from the University of Queensland for sharing these images.

Reference: <https://erj.ersjournals.com/content/early/2021/10/14/13993003.01881-2021.abstract>

For more information, please visit

<https://nanosttring.com/geomx-morphology-markers/>