intracytoplasmic cilia up to 12 months post infection. There was no correlation with any ongoing nasal symptoms or symptoms of long COVID. In contrast, ciliogenesis was normal in the Omicron infected, vaccinated cohort, and no mislocalised basal bodies or intracytoplasmic cilia were seen. Defects in cilia function were present in both cohorts compared to pre-pandemic controls: reduced cilia beat frequency (FOLLOW p<0.01), reduced amplitude per second in both: (FOLLOW p<0.01, ULTRON p<0.01).

This ciliogenesis defect led us to explore FOXJ1 expression post-COVID: qRT-PCR showed a significant reduction of FOXJ1 mRNA levels 6 months (p<0.001) and 12 months (p=0.002) following pre-Omicron variant infections compared to healthy volunteers; however, there was a significant improvement between 6-months and 12-months.

Conclusion Cilia loss and defective ciliogenesis linked to reduced FOXJ1 expression persisted for a year following infection with early SARS-CoV-2 variants. No such defects were seen in vaccinated individuals infected with the Omicron variant despite some functional ciliary defects. This work illuminates novel long-term effects of viral infection on human epithelial function through altered expression of a key ciliary regulator gene.

**S84 SINGLE-CELL LANDSCAPE OF BRONCHOALVEOLAR CELLS IN INFLAMMATORY AND FIBROTIC POST-COVID RESIDUAL LUNG ABNORMALITIES**


**Background** Approximately 10% of patients hospitalised with COVID-19 have residual lung abnormalities (RLAs) at 12 months. In clinical practice, CT scan appearances are often used to guide management. Whether such radiological changes reliably reflect immunopathomechanisms, and can therefore inform the treatment approach, is unclear and an important clinical question.

**Methods** We compared the single cell transcriptomic and T cell receptor (TCR) profiles of bronchoalveolar lavage cells from patients with Post-COVID RLAs with either predominantly inflammatory or fibrotic radiological appearances.

**Results** We generated a dataset of 55,776 cells. CD4 central memory T cells (TCM) and CD8 effector memory T cells (TEM) were significantly increased in the inflammatory subphenotype. Both patient groups were transcriptionally similar and exhibited clonal expansion and high TCR clustering, without enrichment for SARS-CoV-2 reactive sequences.

**Conclusions** We describe the first comparison of purported radiological subphenotypes in patients with Post-COVID RLAs, which may actually represent different manifestations of the same disease. Antigen-specific immune responses to unidentified T cell targets, imply a breach of immune tolerance in the lung and a potential role for T-cell directed therapies in these patients, agonistic of radiological appearance.

Please refer to page A285 for declarations of interest related to this abstract.