SCIENCE MEETS LIFE

Emerging Technologies in Single Cell Research
19-20 November 2020
Leuven, Belgium

Discriminating Mild from Critical COVID-19 by Innate and Adaptive Immune Single-cell Profiling of Bronchoalveolar Lavages

Full article: Wauters E, Van Mol P, Garg A, et int, Neyts J, Wauters J, Qian J, Lambrechts D. Discriminating Mild from Critical COVID-19 by Innate and Adaptive Immune Single-cell Profiling of Bronchoalveolar Lavages. Cell Res. (accepted). Preprint at https://www.biorxiv.org/content/10.1101/2020.07.09.196519v1.

Pierre Van Mol

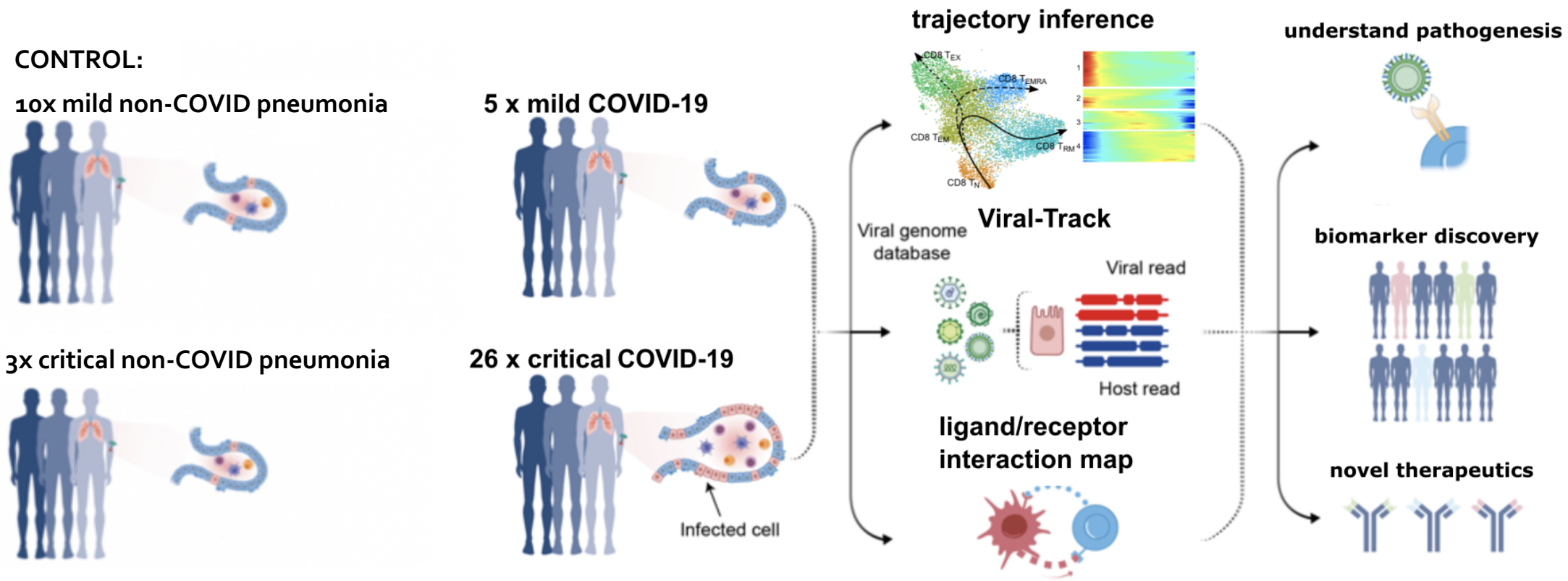
VIB - KU Leuven Laboratory of Translational Genetics

Department of Pneumology, University Hospitals Leuven

VIB

KU LEUVEN UZ LEUVEN

Methods

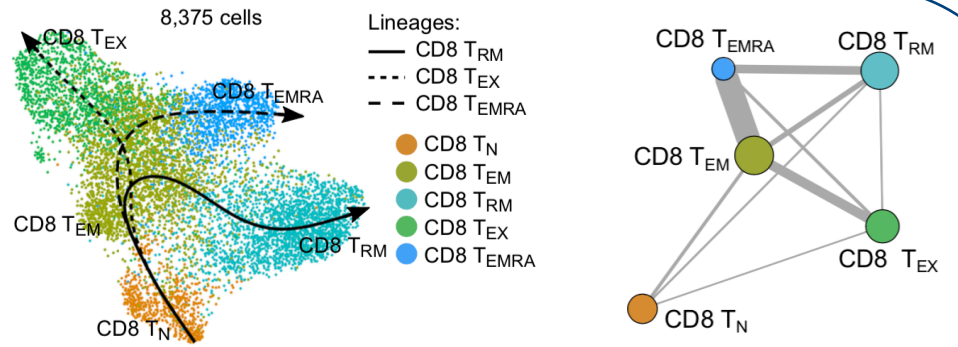


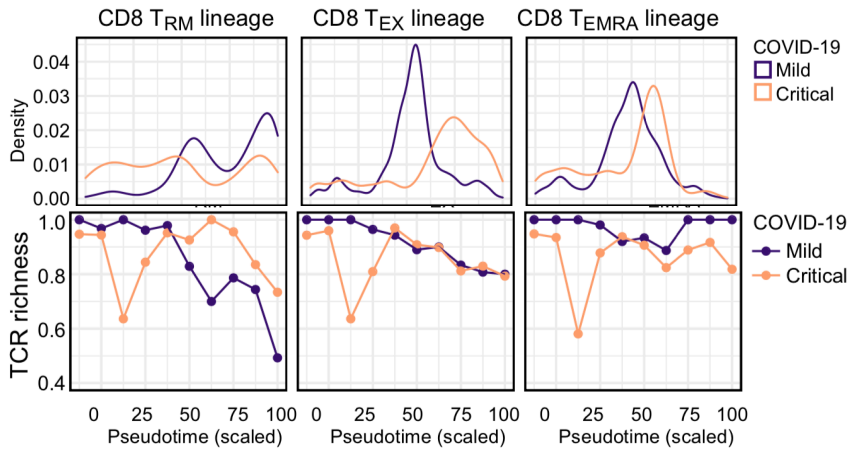
After quality control, scRNA-seq data was obtained of 65,166 prospectively collected cells which was analysed integratively with publicly available scRNA-seq data of 143,773 cells.

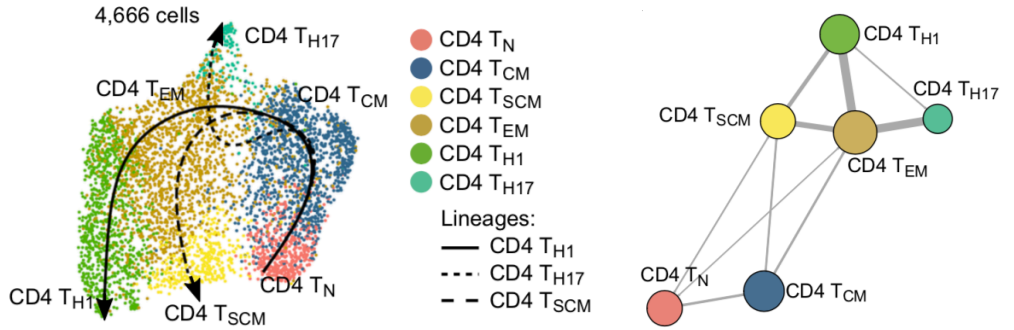
Figure adapted from: Weizmann Institute of Science

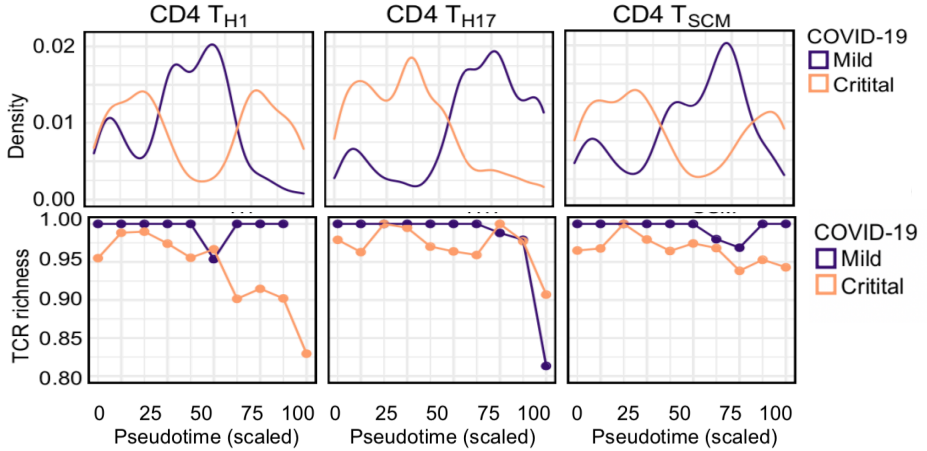
Datasets: Wauters, Cell Res (accepted), 2020 ; Liao, Nat Med, 2020 ; Lambrechts, Nat Med, 2018 ; Reyfman, Am J Respir Crit Care Med, 2019

Heterogeneity of the CD8+ (left) and CD4+ (right) T-cell response to SARS-CoV-2









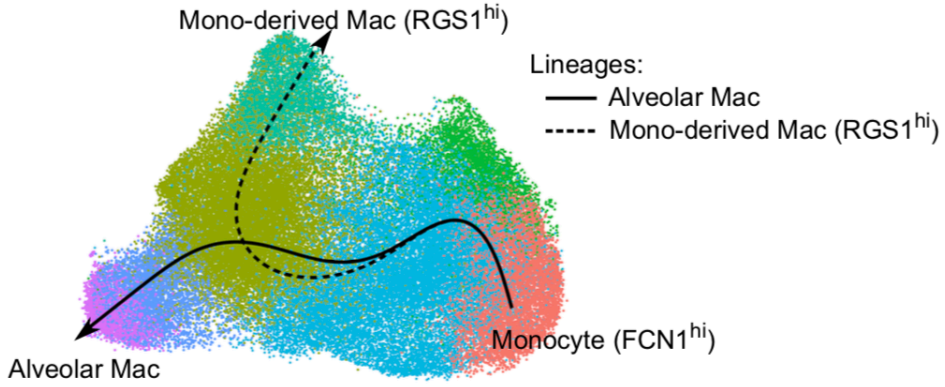
In mild COVID-19, CD8+ resident-memory and CD4+ T-helper-17 cells undergo active (presumably antigen-driven) expansion and are characterized by good effector functions, while in critical COVID-19 they remain more naïve.
Exhausted CD8+ and CD4+ T-helper-1-like cells are enriched halfway their trajectory in mild COVID-19 exhibiting good effector functions, while in critical COVID-19 they show evidence of inflammation-associated stress at the end of their trajectories.

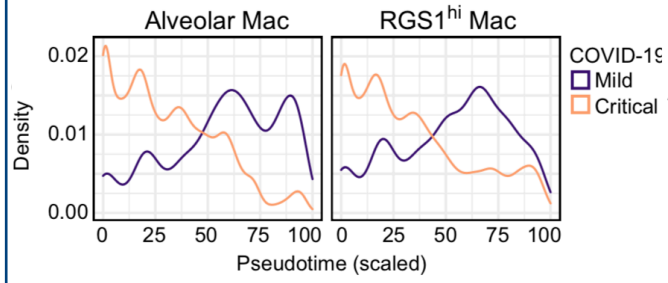
VIB

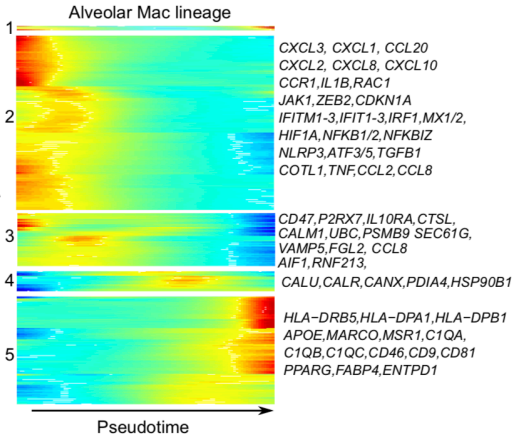
Wauters et al., Cell Res. (accepted), 2020

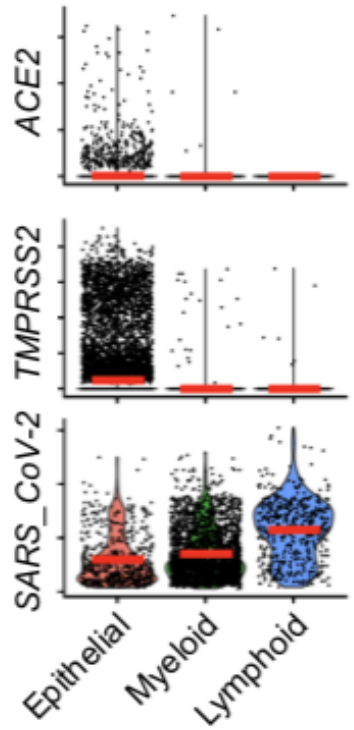
KU LEUVEN UZ LEUVEN

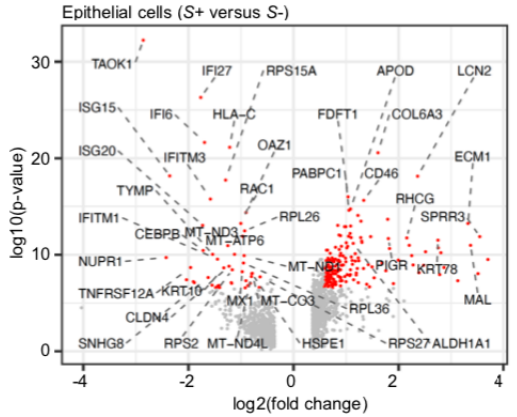
Heterogeneity of the innate immune response to SARS-CoV-2, related to disease severity (left) and viral entry or phagocytosis (right)

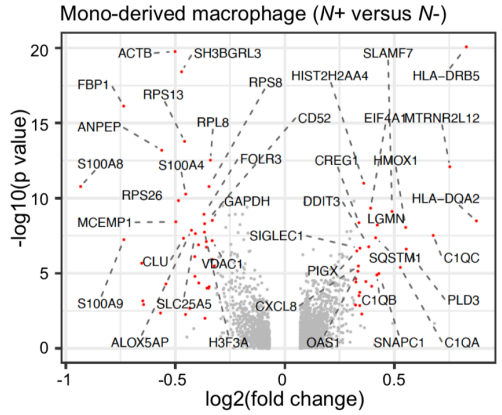












Monocyte-to-macrophage trajectories show chronic hyperinflammatory monocytes that are enriched in critical COVID-19, while alveolar macrophages, otherwise characterized by anti-inflammatory and antigen-presenting characteristics, are depleted.
Differential gene expression analysis reveals that (infected) S+-epithelial cells exhibit reduced expression of IFN-stimulated genes, an immune evasion mechanism. Phagocytising N+-macrophages show upregulation of IFN-induced and MHC II genes, suggesting an adequate first-line response to SARS-CoV-2.

VIB

Wauters et al., Cell Res. (accepted), 2020

KU LEUVEN UZ LEUVEN