Single-cell analyses and host genetics highlight the role of innate immune cells in COVID-19 severity

Atsushi Kumanogoh (Graduate School of Medicine, Osaka University/IFReC), Yukinori Okada (Graduate School of Medicine, Osaka University/IFReC/RIKEN/ Graduate School of Medicine, University of Tokyo) and the research group performed a single-cell analysis of 900,000 peripheral blood mononuclear cells (PBMCs) derived from 148 Japanese (73 COVID-19 patients and 75 healthy control) as well as an integrated analysis with host genome information.

They found that CD14+CD16++ monocytes, a rare cell type among monocytes, are involved in COVID-19 severity. Further, COVID-19 severity-associated genes identified by genome-wide association analysis (GWAS), such as IFNAR2, have specific function mainly in monocytes and dendritic cells. These findings are expected to lead to the development of new therapeutic strategy for various infectious diseases including COVID-19.

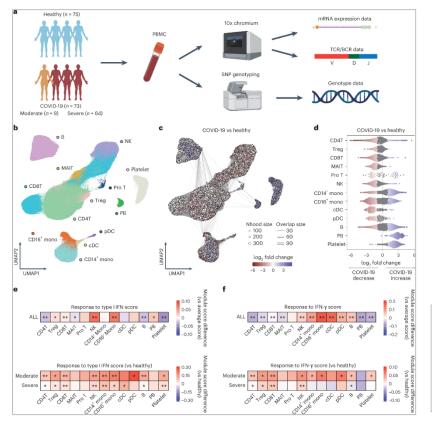


Figure: Study design and singlecell transcriptional analysis of PBMCs from COVID-19 patients and healthy controls.

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