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Single-cell analysis reveals shared and distinct immune response and metabolism between SARS-CoV-2 and HIV-1 infections

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SARS-CoV-2 and HIV-1 are RNA viruses that have killed millions of people worldwide. Understanding the similarities and differences between these two viral infections is critical for developing effective vaccines and therapies, particularly for 38 million HIV-1$^+$ patients who are vulnerable to SARS-CoV-2 co-infection. Here, we utilized single-cell transcriptomics to perform a systematic comparison of 115,000 single PBMCs from 7 COVID-19 and 9 HIV-1$^+$ patients in an integrated immune atlas, in which 27 different cell types were identified using an accurate consensus single-cell annotation method. While immune cells in COVID-19 and HIV-1$^+$ patients share a similar hallmark of inflammation and IFN-I signaling, COVID-19 patients exhibit stronger plasmablast responses and more diverse antibody repertoires, broader IFN-I-mediated cellular functions, elevated Rho GTPase and mTOR pathway activities, and downregulated mitophagy. Our results elucidate similar and distinct transcriptional signatures associated with COVID-19 and HIV that reveal insights into fundamental disease biology and potential therapeutic targets.