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A single-cell RNA-seq dataset of peripheral blood cells in long COVID patients on herbal therapy

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Long COVID is a condition defined by chronic, multisystemic symptoms that continue after resolution of SARS-CoV-2 infection. While several sources provide evidence indicating efficacy of herbal medicines in alleviating long COVID symptoms, the effectiveness and safety of such treatment remains poorly understood. In this study, we generated a single-cell RNA sequencing (scRNA-seq) dataset from peripheral blood cells of 26 participants in a clinical trial testing three commercially available herbal medications, targeting brain fog and fatigue in long COVID. The dataset comprises 276,761 quality control (QC)-passed cells with corresponding clinical metadata, providing a foundation for comparative analysis of immune cell populations across treatment groups. To investigate the differences in transcriptomic profiles of responders and non-responders, we conducted several bioinformatic analyses, including pseudo-bulk differential expression, pseudotime trajectory, and cell-cell interaction analyses. Our findings revealed enhanced antigen presentation by conventional dendritic cells and increased involvement of inflammatory monocytes in antiviral defense in individuals showing best response to herbal therapy. This dataset offers novel insights into the role of herbal medicines and may deepen our understanding of long COVID recovery.