

Fig. S3

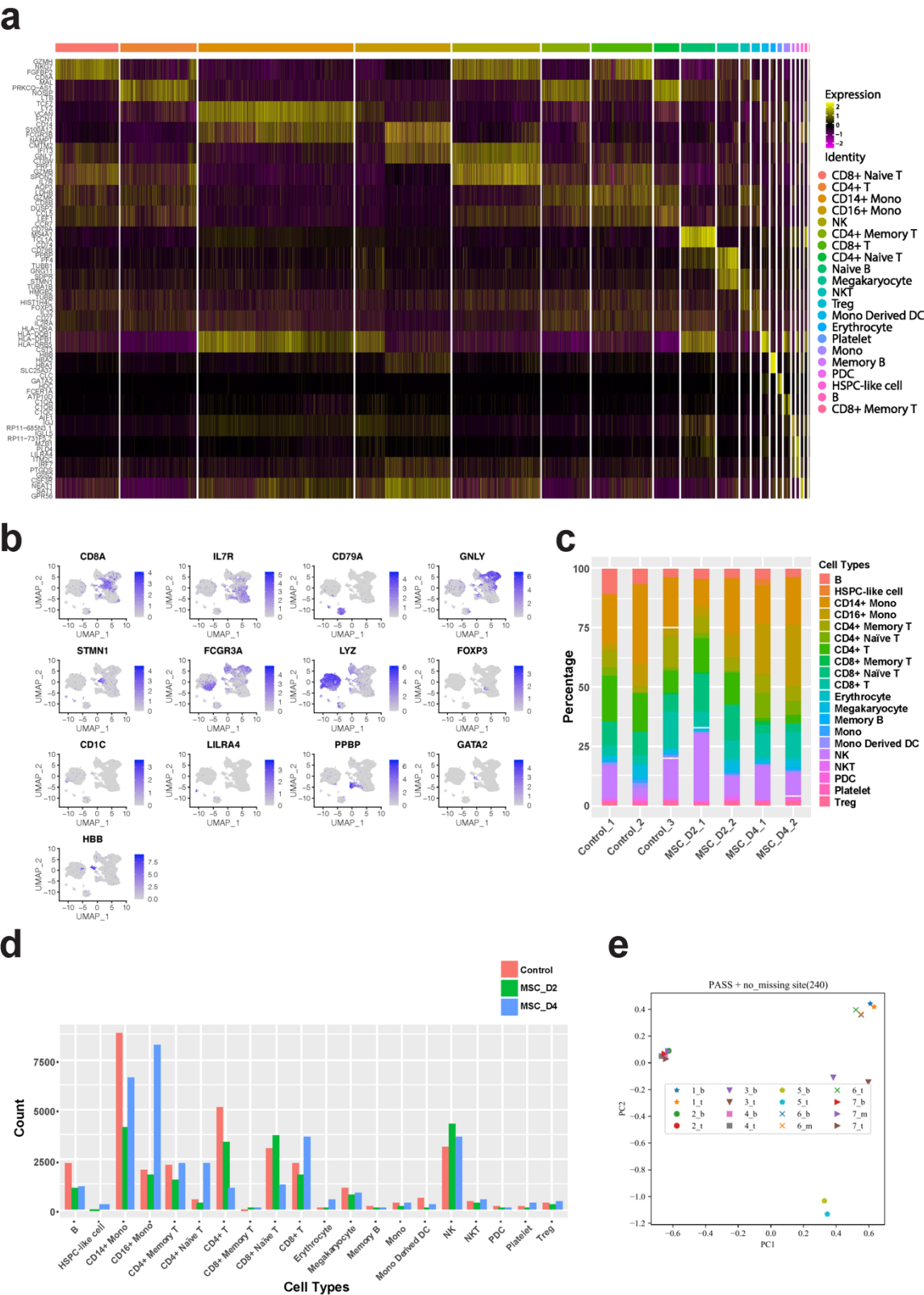


Fig. S3 Clustering Information for PBMCs from COVID-19 Patients. **a** Heatmaps for the top two most differentially expressed genes across 37 clusters. **b** UMAP projection of canonical markers of major cell types (n = 7). **c** The proportion of the major immune-cell types at a single sample. **d** Bar plot showing the counts of the major immune-cell types in samples among PBMCs from MSC-treated COVID-19 patients (MSC-D2 and MSC-D4) and MSC-untreated control samples. **e** Distribution of SNP principal components (PC) in CD4⁺ T cells, B cells, and HSPC-like cells in seven samples. The cell clusters are named X_Y, where X represents the sample number (1, 2,...,6,7), and Y represents the cell type (t: T cells, b: B cells). Sample 2 was acquired from a patient before treatment, samples 4 and 7 were from the same patient after MSC treatment, and sample 5 was collected from a healthy control. Although SNP loci of the day 2 post-MSC treatment sample (sample 3) belonging to the third patient on PC2 differed from the loci of the control sample (sample 1) and the day 4 post-MSC treatment sample (sample 6), on PC1, the three samples were consistent with regard to SNP status. The two groups of HSPC-like cells (6_m and 7_m) formed on day 4 post-MSC treatment in two patients were mainly grouped with other two clusters (6_t, 6_b, and 7_t, 7_b). UMAP, Uniform manifold approximation and projection for dimension reduction; control, MSC-untreated controls. Related to Fig. 2.