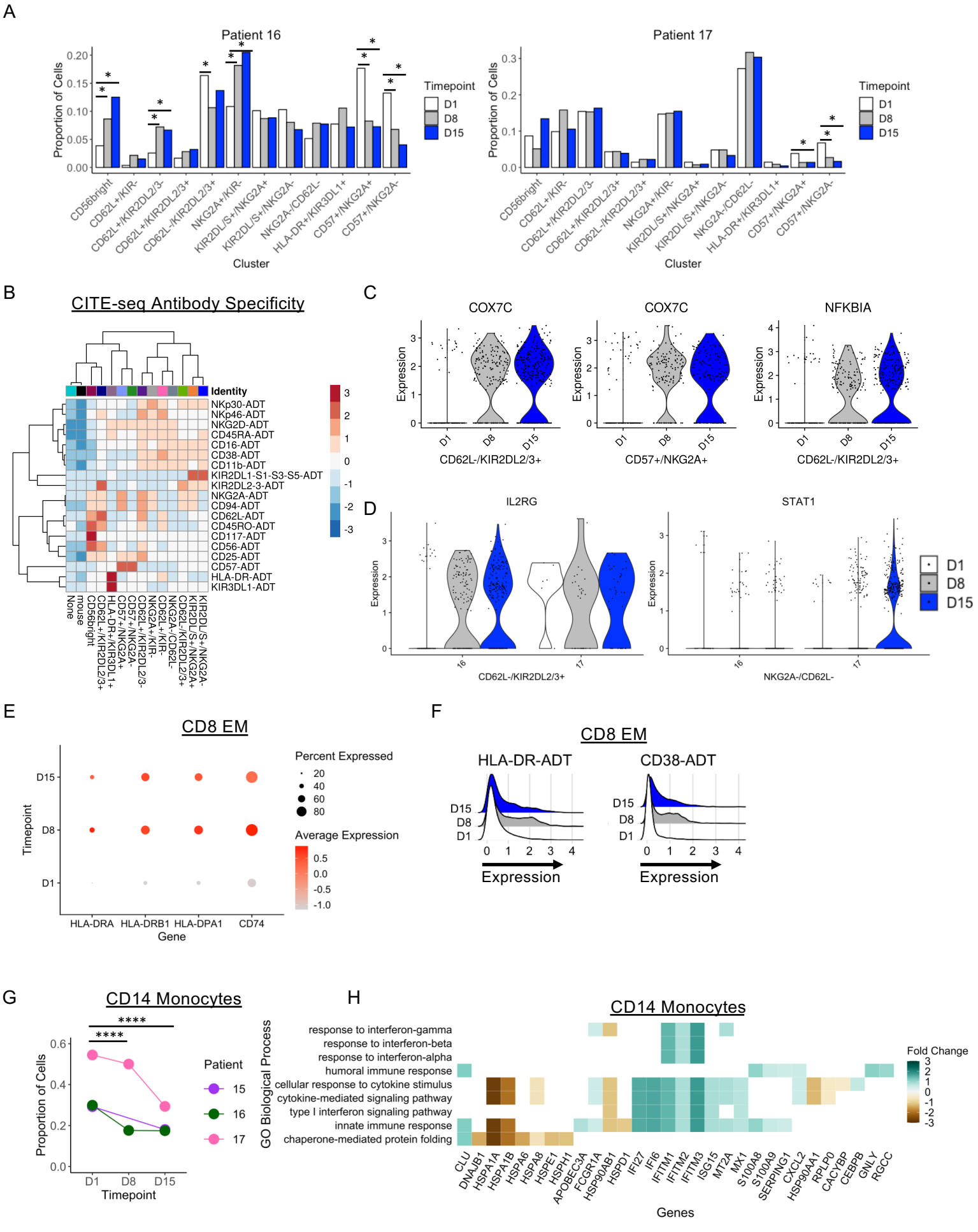
Supplemental Figure 4.



Supplemental Figure 4. CITE-seq identifies differential modulation of PBMC subsets.

A) Proportion of each NK cluster in each patient at each timepoint- D1 (white), D8 (grey), and D15 (blue). Two-sided Fishers' Exact test and Holm's multiple comparisons p-value adjustment. KIR- clusters are negative for KIR2DL2/3, KIR3DL1, and KIR2DL1/S1/S3/S5. * Denotes significant changes. B) Heatmap depicting relative expression of CITE-seq antibodies in CiteFuse clustered NK cells compared to spiked-in mouse negative control cells. Average expression for each group is scaled by rows. C) Violin plots of select significantly changed genes in NK clusters split by timepoint, and D) genes driven by one donor. Donor is labeled on X-axis. White= Day 1, Grey = Day 8, Blue = Day 15. E) Expression of significantly changed MHC Class II related genes in in CD8 EM T-cells between Day 1 and Day 15. The size of the dot corresponds to the percent of cells expressing the gene, and the color corresponds to the scaled expression of each gene. F) Ridge Plot of HLA-DR and CD38 protein expression in CD8 EM T-cells. G) Line graphs of the proportion of CD14 Monocytes in each patient at each timepoint. Each patient is connected by a line. Two-sided fisher's Exact test with Holm's multiple comparisons p-value adjustment. H) Select enriched GO Biological Processes in CD14+ Monocytes between D15 and D1. Colored boxes depict average $\log_2$ fold change of the genes in the BP gene set. White boxes correspond to genes not included in the GO BP gene set. Wilcoxon Rank-Sum test for all DEGs with an adjusted p-value of < 0.05 and fold change of ≥ 0.5 absolute $\log_2$ fold change. Enriched GO terms of < 0.05 and q-value threshold of 0.05. n=2-3 patients for all, 2 independent experiments.