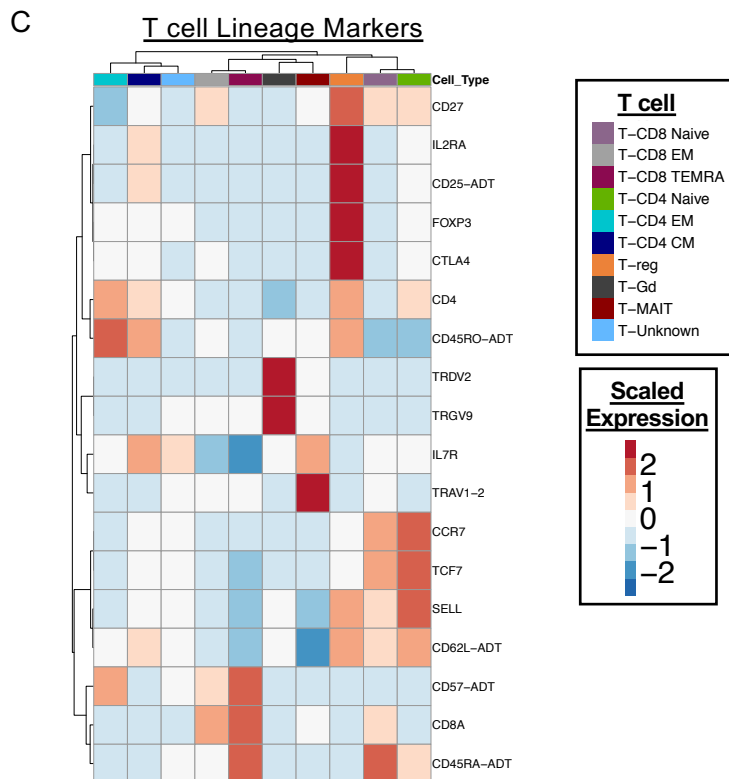
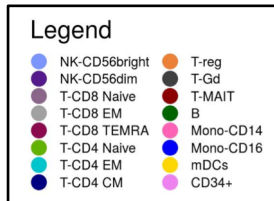
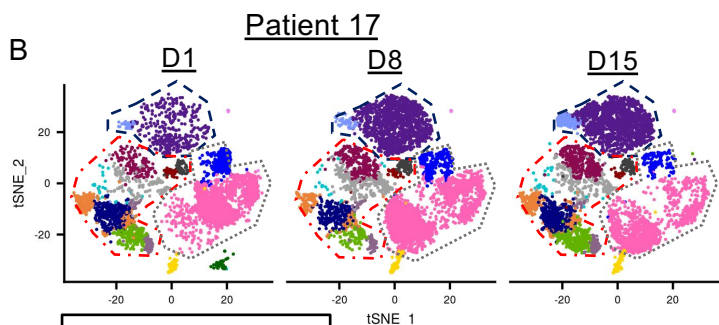
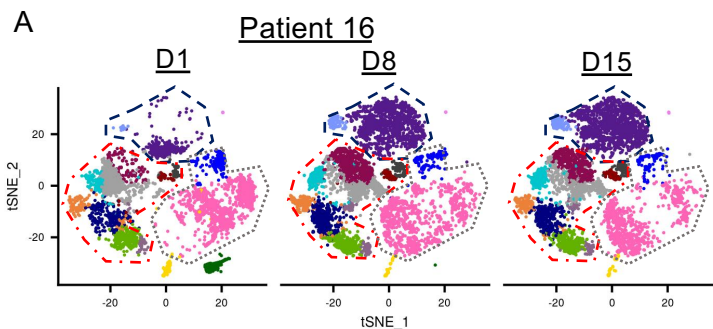
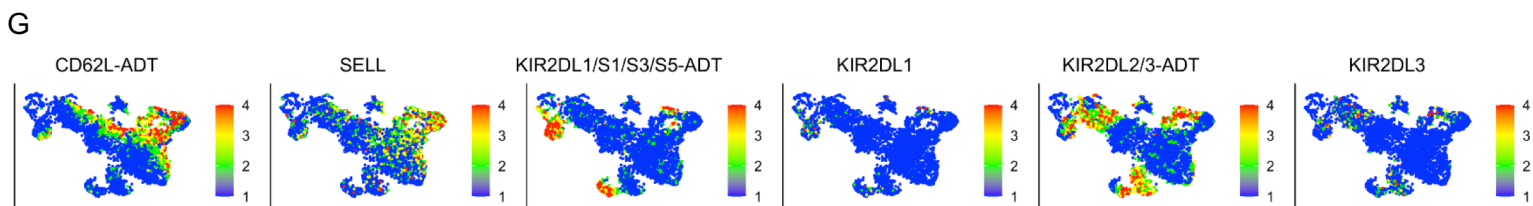
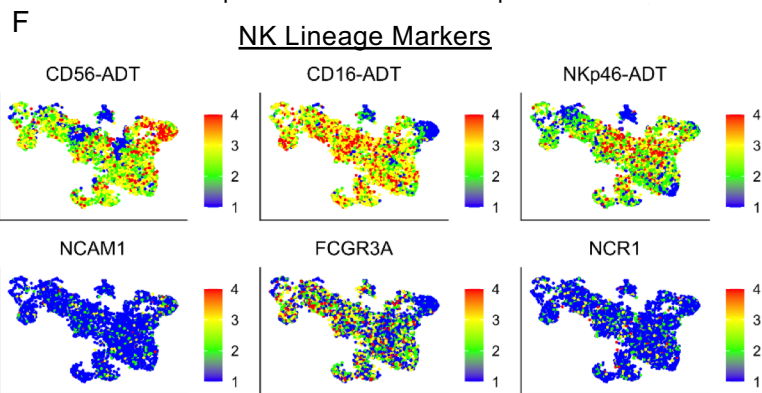
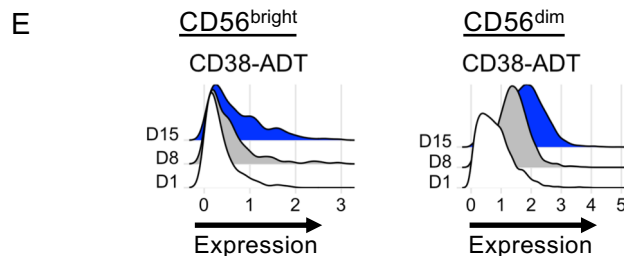
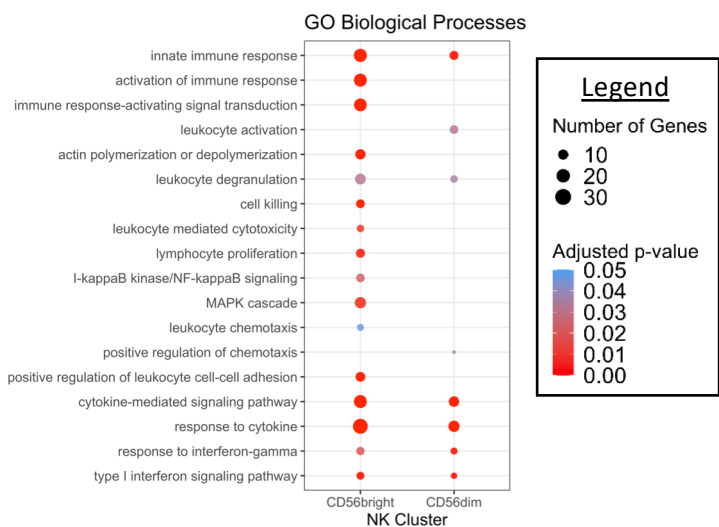


Supplemental Figure 3.



D CD56^{bright} vs. CD56^{dim} Enriched Gene Ontology



Supplemental Figure 3. CITE-seq reveals N-803 and rituximab mediated activation of peripheral blood NK cells. A-B) *t*SNE visualization of PBMC transcriptomes colored by immune cell type in patient 027-016(16) A), and 027-017(17) B) before (D1) and after one (D8) or two doses (D15) of N-803 plus rituximab split by patient. Dashed lines depict major immune cell lineages: NK (navy), T cells (red), Monocytes (grey). C) Heatmap of markers used to define T cell lineages. Expression is scaled by row. ADT denotes antibodies to cell surface proteins. D) Dot Plot depicting select significantly enriched Gene Ontology (GO) Biological Process in CD56^{bright} and CD56^{dim} NK cell following N-803 plus rituximab treatment at D15 compared to pre-treatment (D1). The size of each individual dot corresponds to the number of genes significantly changes in the GO term, and the color corresponds to the adjusted p-value. No dot means the GO term was not enriched. E) Ridge Plot of CD38 protein expression in CD56^{bright} and CD56^{dim} NK cells by time. F) Feature Plots depicting protein (ADT) and RNA expression of key NK lineage markers. G) Feature Plots of additional NK and RNA markers that define NK clusters. All feature plots expression is min. cutoff = q02, max.cutoff = q98. 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 $p < 0.05$ and q-value threshold of 0.05. n=2-3 patients for all, 2 independent experiments.