Complement activation induces excessive T cell cytotoxicity in severe COVID-19

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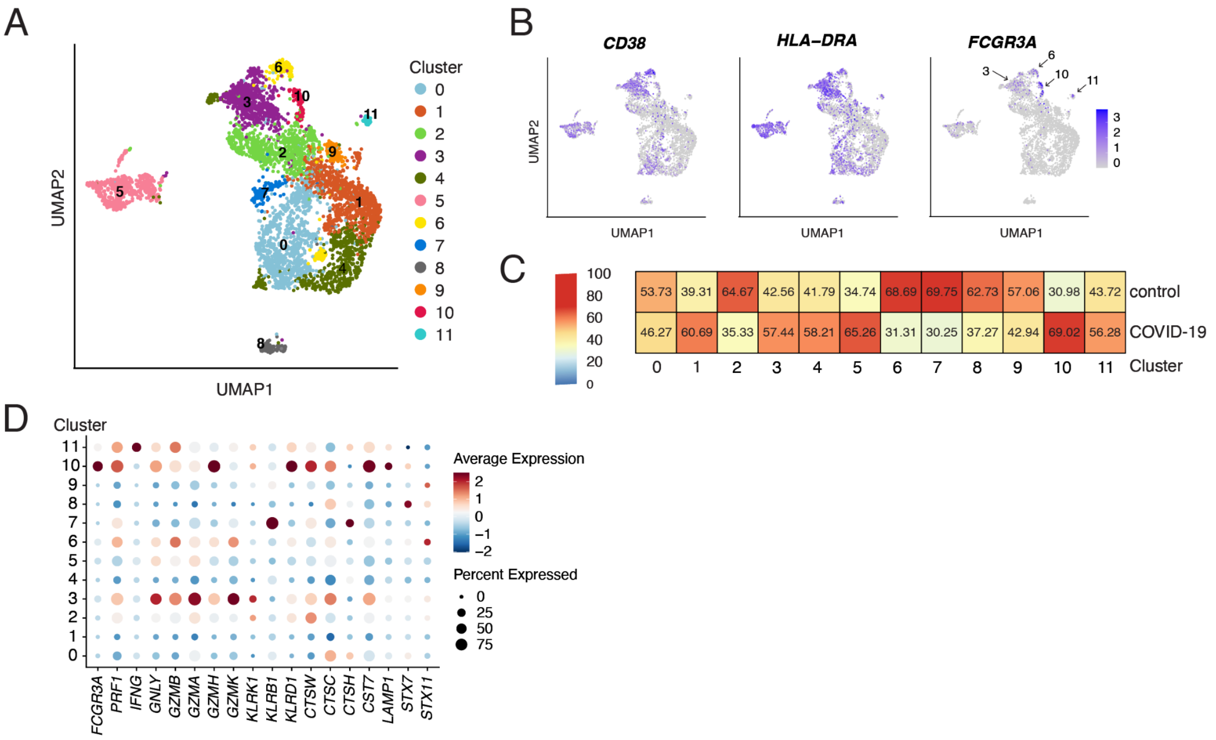
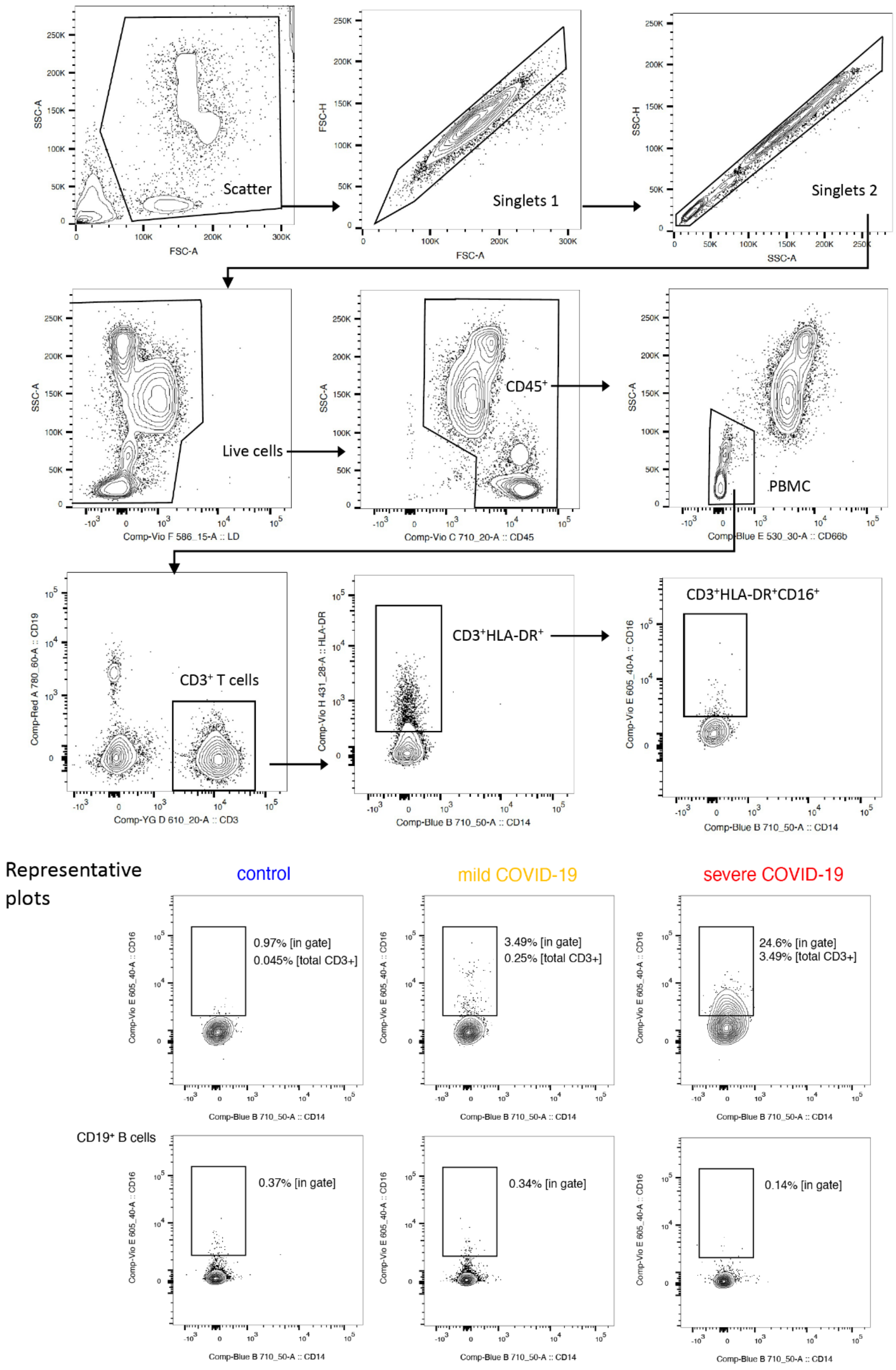


Cluster	0	1	2	3	4	5	6	7	8	9	10	11
control	53.73	39.31	64.67	42.56	41.79	34.74	68.69	69.75	62.73	57.06	30.98	43.72
COVID-19	46.27	60.69	35.33	57.44	58.21	65.26	31.31	30.25	37.27	42.94	69.02	56.28

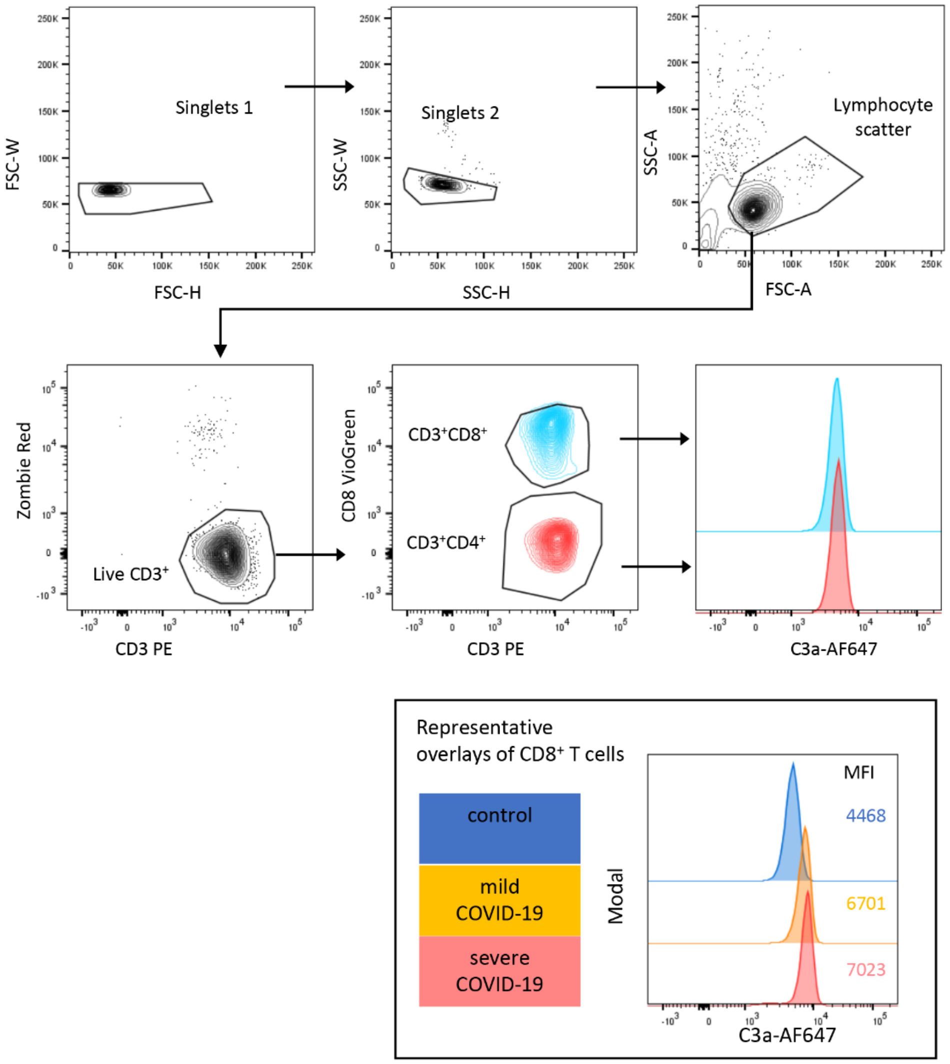
Mendeley Data 1. T cell space analysis of single-cell RNA-seq data from BAL samples. A, UMAP of T cells generated from the BAL sample dataset of Wauters et al. (Wauters et al., 2021), including COVID-19 (n = 22) and control pneumonia (n = 13) samples. **B**, UMAPs of T cell clusters as shown in A with superimposed *CD38*, *HLA-DRA* and *FCGR3A* expression. **C**, Confusion matrix showing the percentage of the relative contribution of each group in each cluster. Each group was normalized to the same total number of cells to avoid biases derived from different cell numbers. **D**, Dot plot of the expression of the genes included in the “Cytotoxicity” signature as applied in the analyses of PBMC samples (Figure 2, S3) and *FCGR3A* in the T cell clusters as shown in A. The dots are colored by the scaled gene expression across the clusters and the size is proportional to the ratio of cells expressing the specific gene.

Gating of CD3⁺HLA-DR⁺CD16⁺ as shown in Figure S1



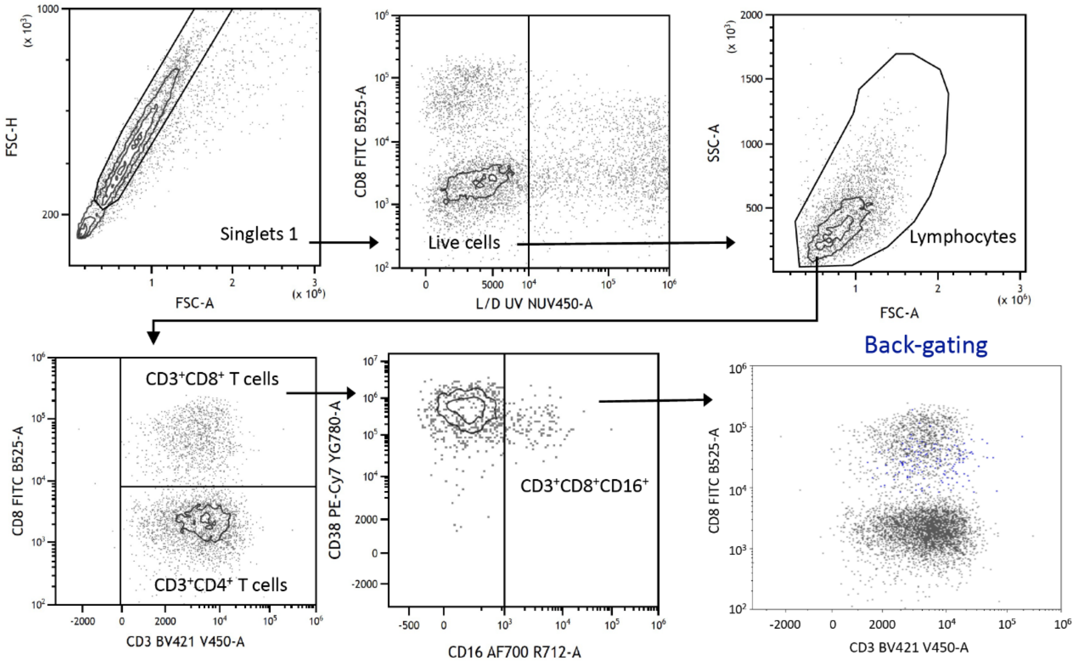
Mendeley Data 2. Gating of CD3⁺HLA-DR⁺CD16⁺ as shown in Figure S1.

Gating of C3a binding capacity of CD3⁺CD4⁺ & CD3⁺CD8⁺ T cells as shown in Figure 5D



Mendeley Data 3. Gating of C3a binding capacity of CD3⁺CD4⁺ & CD3⁺CD8⁺ T cells as shown in Figure 5D.

Gating of in vitro cultured CD3⁺CD4⁺CD16⁺ & CD3⁺CD8⁺CD16⁺ T cells as shown in Figure 5F/G/H



Mendeley Data 4. Gating of in vitro cultured CD3⁺CD4⁺CD16⁺ & CD3⁺CD8⁺CD16⁺ T cells as shown in Figure 5F/G/H.