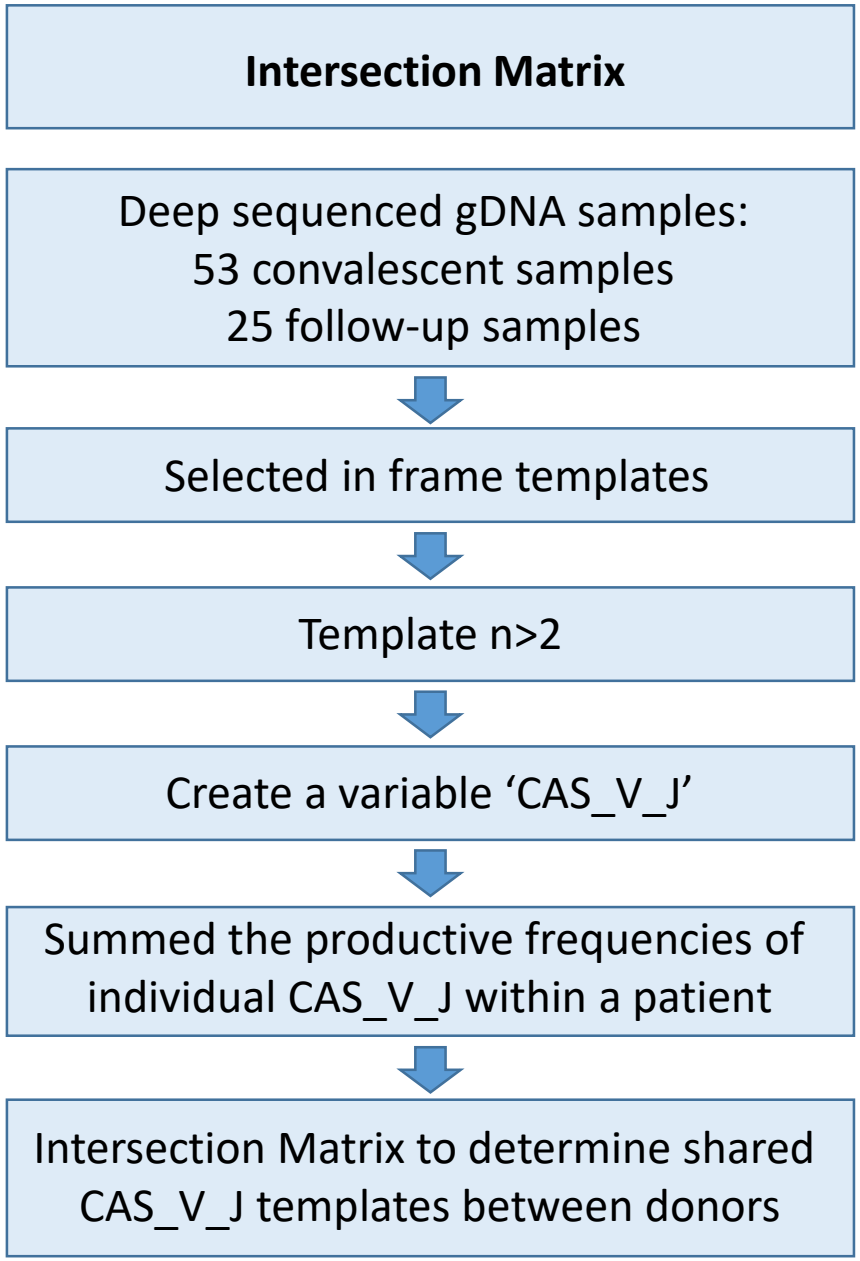
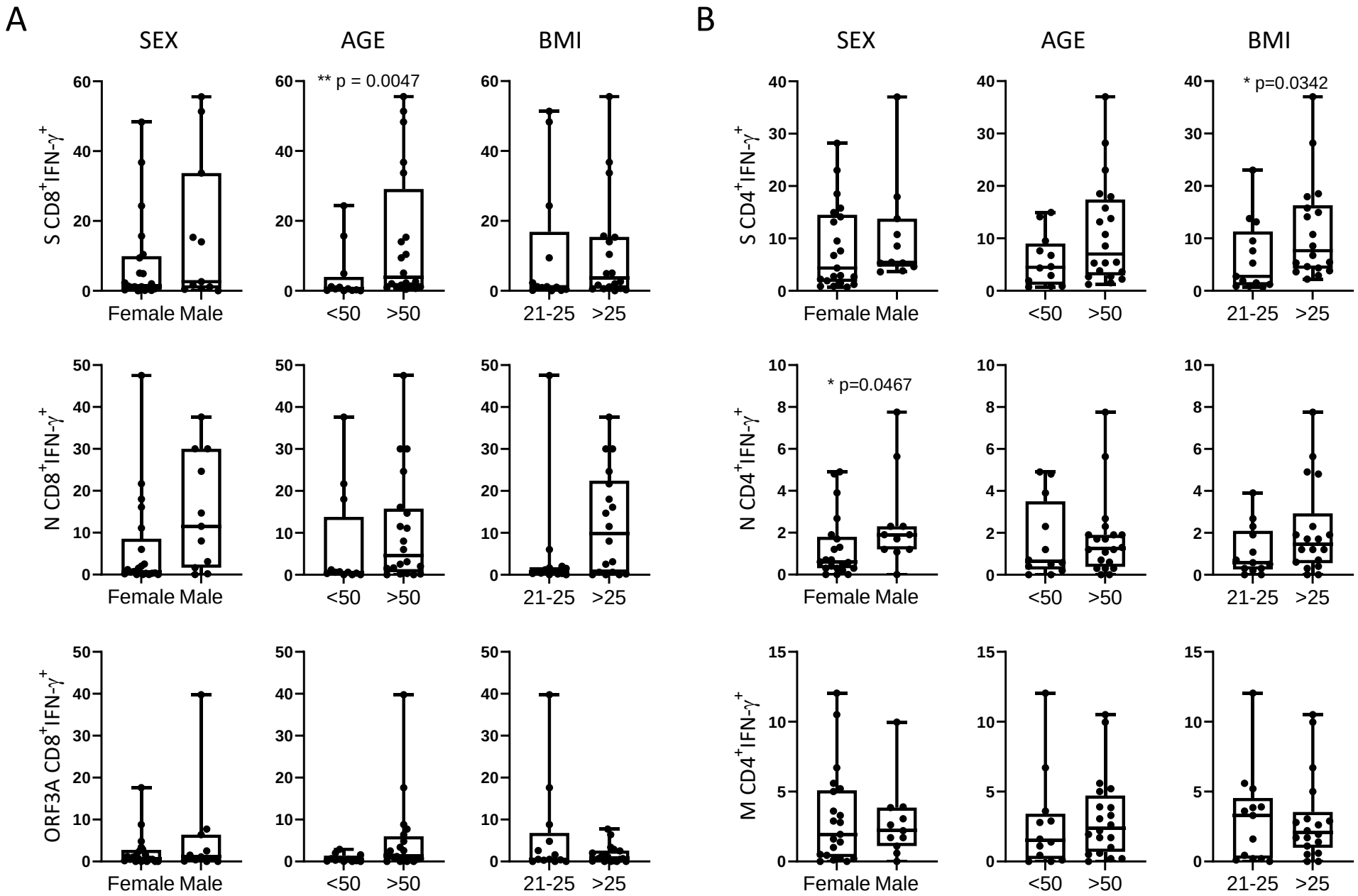
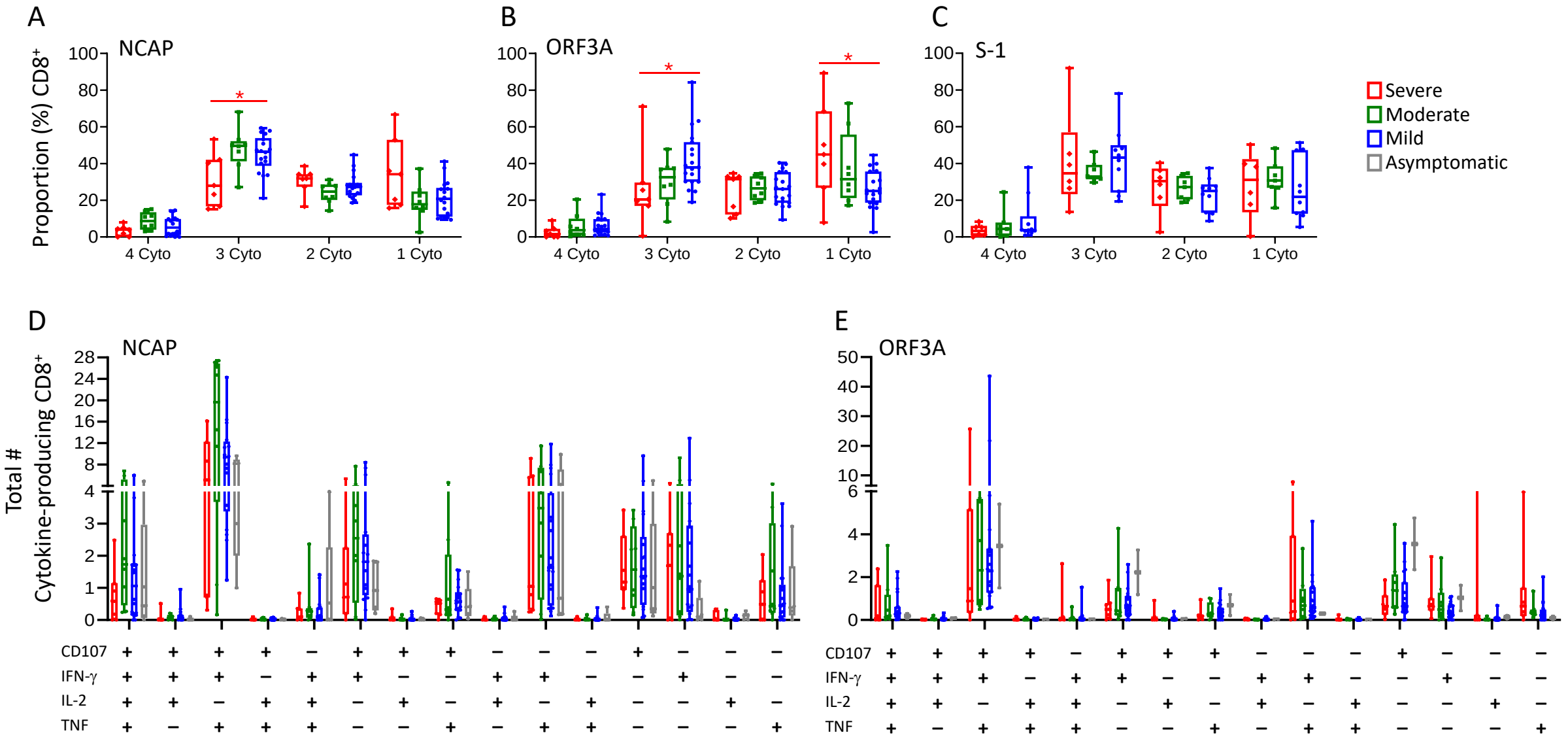


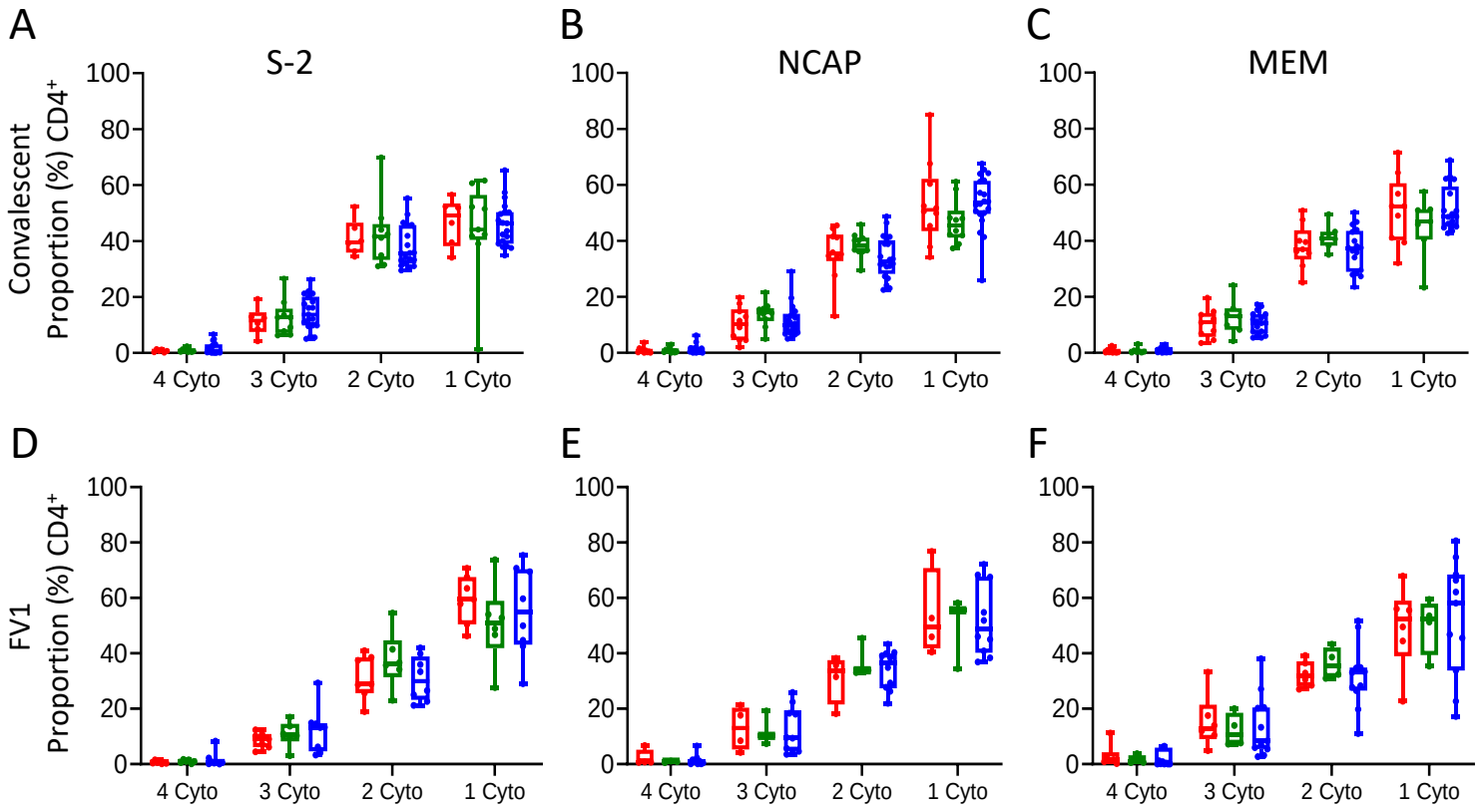
Supplementary Figure 1. Flow chart of the intersection matrix analysis.



Supplementary Figure 2. Impact of Sex, Age and BMI on the SARS-CoV-2 T cell responses. Data represents the frequency of **(A)** $CD8^{+}IFN\text{-}\gamma^{+}$ T cells and **(B)** CD4+IFN-γ^{+} T cells

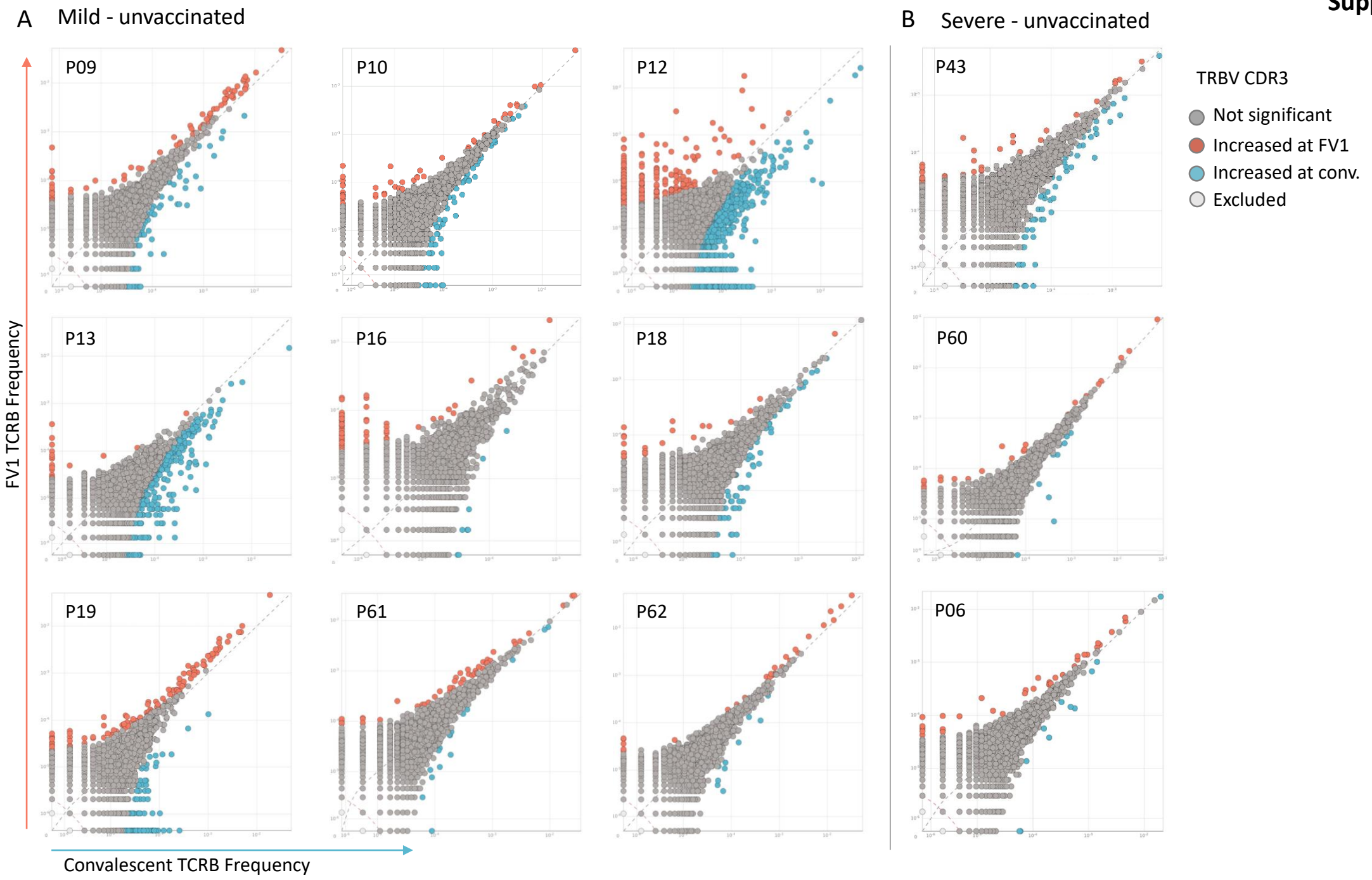


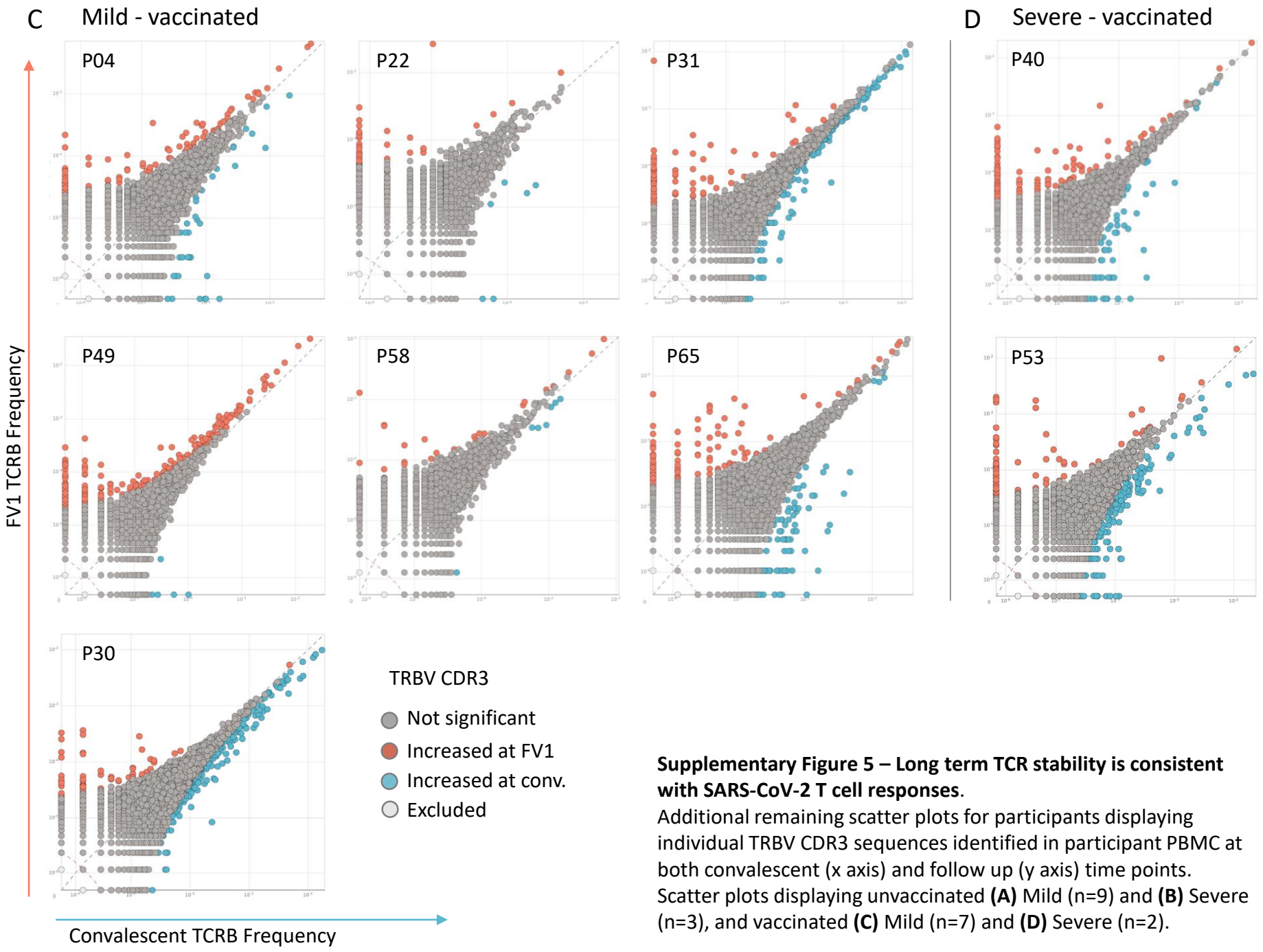
Supplementary Figure 3. SARS-CoV-2 convalescent CD8⁺ T cell responses show increased polyfunctionality. Data represents the polyfunctional cytokine (cyto) profile of **(A)** NCAP-specific, **(B)** ORF3A-specific and **(C)** S-1 specific T cells. Data in **(F)** NCAP-specific and **(E)** ORF3A-specifi, represents the total number of cytokine-producing CD8⁺ T cells



Supplementary Figure 4. SARS-CoV-2 CD4⁺ T cell responses show reduced polyfunctionality that persists long-term. Data represents the polyfunctional cytokine (cyto) profile of **(A&D)** S-2 specific T cells, **(B&E)** NCAP-specific T cells and **(C&F)** Mem-specific T cells at the convalescent (top panels) and follow-up (bottom panels) timepoints.

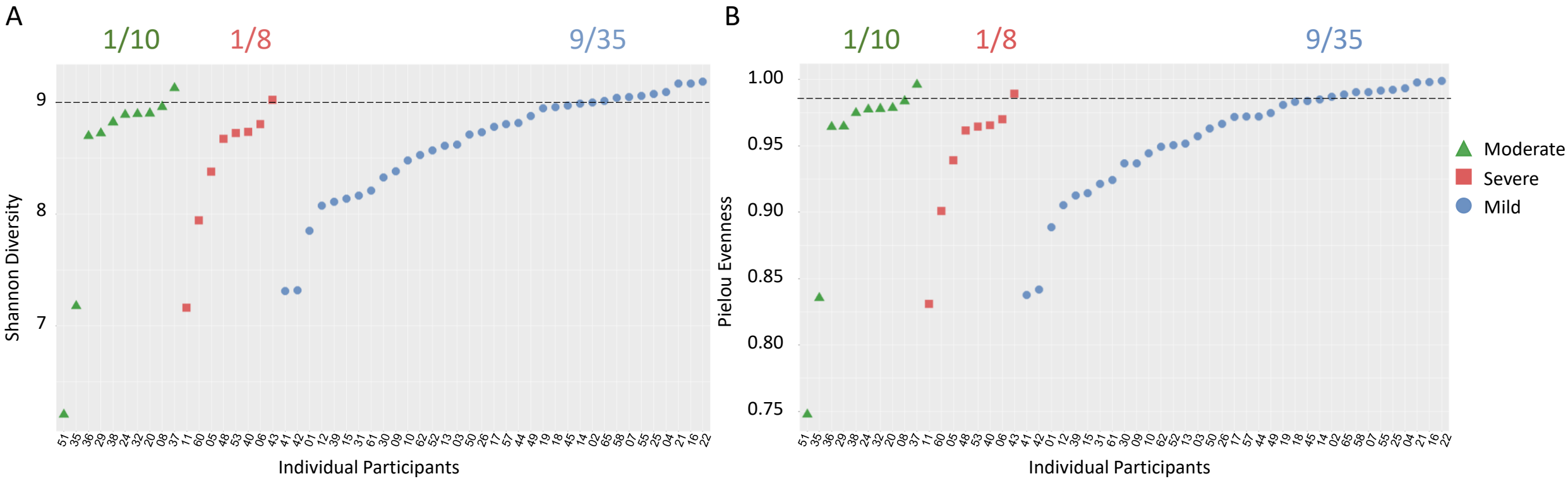
Supplementary Figure 5



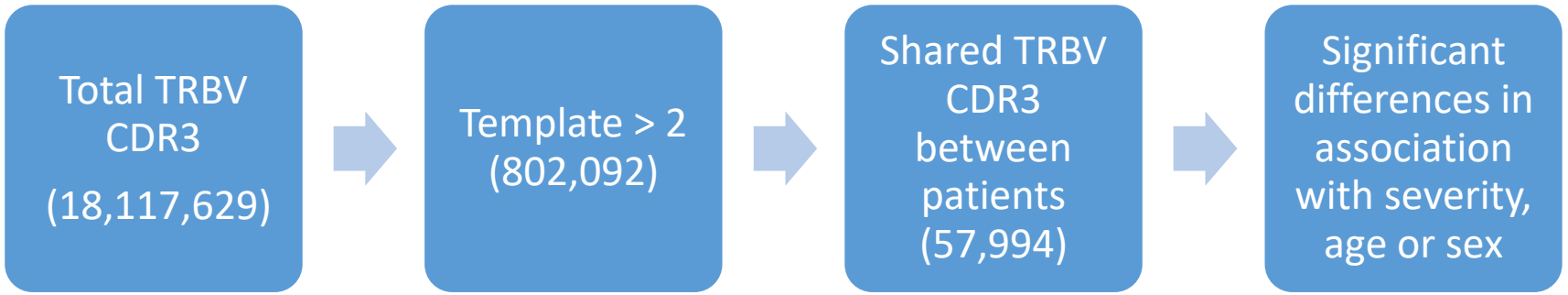


Supplementary Figure 5 – Long term TCR stability is consistent with SARS-CoV-2 T cell responses.
Additional remaining scatter plots for participants displaying individual TRBV CDR3 sequences identified in participant PBMC at both convalescent (x axis) and follow up (y axis) time points. Scatter plots displaying unvaccinated **(A)** Mild (n=9) and **(B)** Severe (n=3), and vaccinated **(C)** Mild (n=7) and **(D)** Severe (n=2).

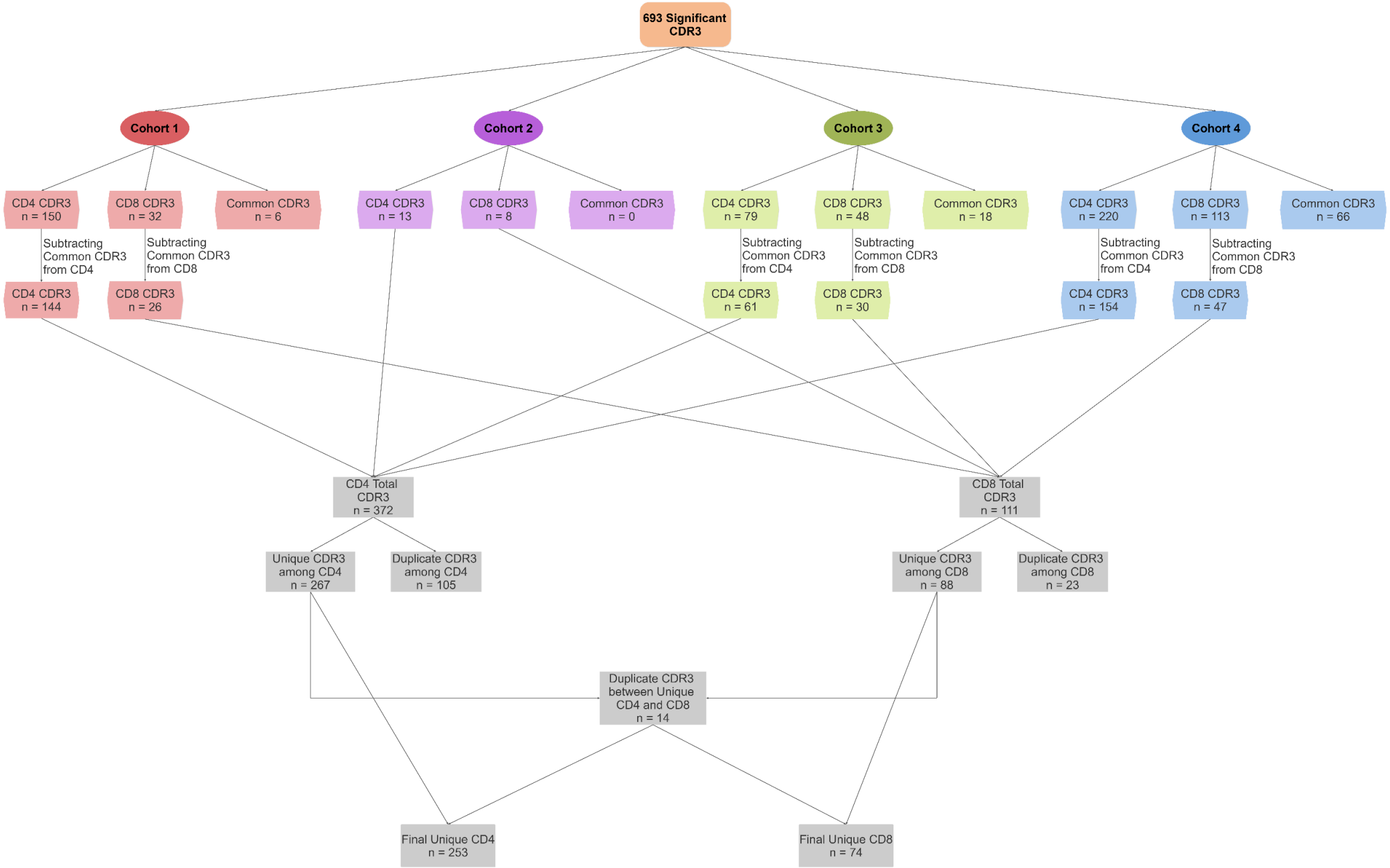
Supplementary Figure 6



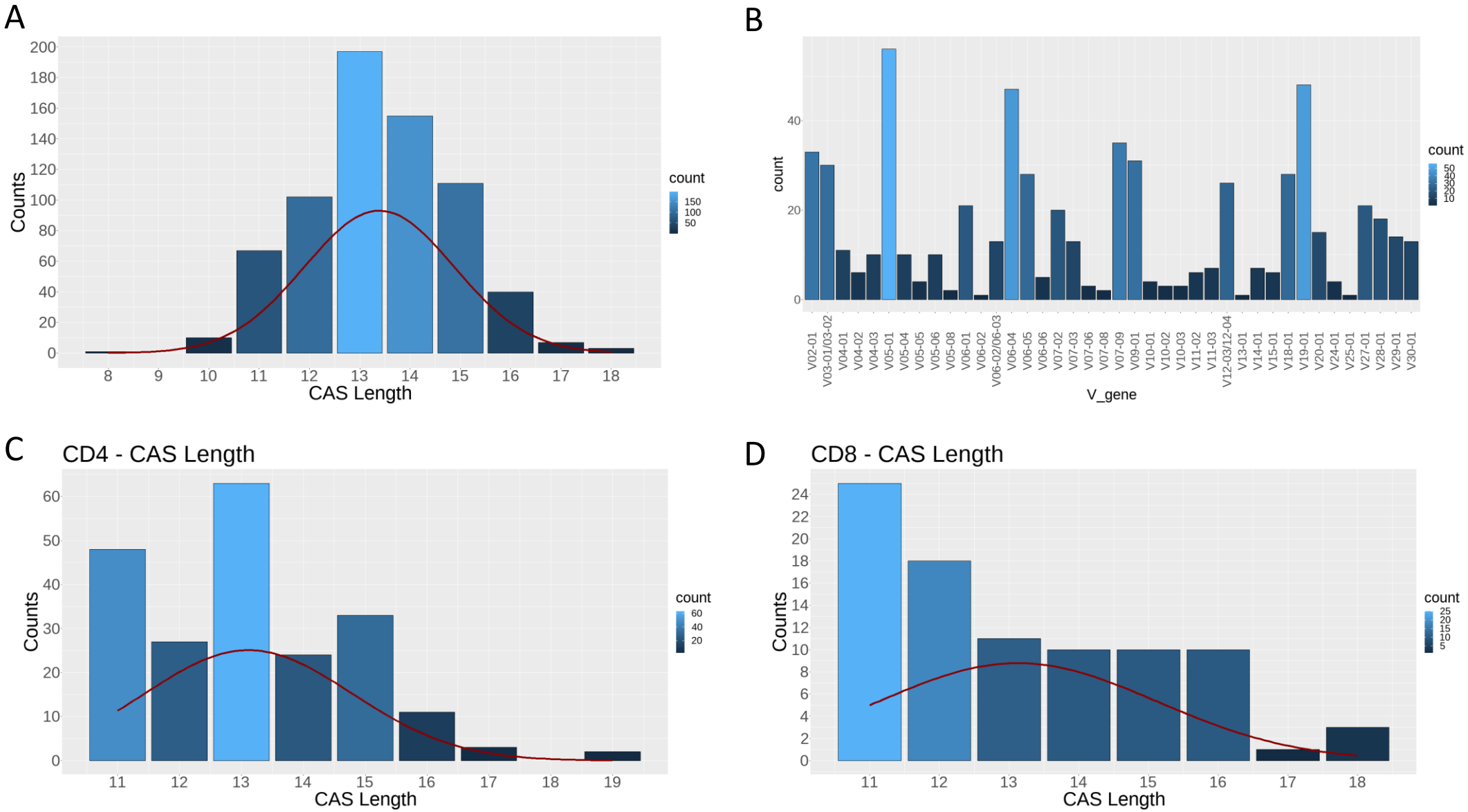
Supplementary Figure 6: Scatter plots comparing the Shannon Diversity **(A)** and Pielou Evenness **(B)** between moderate (green, n=10), severe (red, n=8), and mild (blue, n=35) COVID-19 severity cohorts. The dotted black line indicates the 80th percentile in each dataset. Graphs were prepared using R software.



Supplementary Figure 7. Flowchart of the total number of TRBV CDR3 sequences defined during the intersectional matrix analysis used to identify shared sequences between participants.



Supplementary Figure 8. Prevalence of severity associated TRBV CDR3 in the CD4⁺ or CD8⁺ T cell compartment. TRBV CDR3 sequences identified in four different cohorts contained separate CD4⁺ and CD8⁺ population analysis were assessed for the presence of the severity-associated TRBV sequences. Common TRBV CDR3 sequences in both CD4⁺ and CD8⁺ populations were subtracted from the final analysis.



Supplementary Figure 9. Bar graphs displaying the **(A)** standard length distribution and **(B)** distribution of V-gene usage for the TRBV CDR3 (n=693) identified to be significantly increased in association with disease severity. And, the standard length distribution for **(C)** SARS-CoV-2-specific CD4 TRBV CRD3 and **(D)** SARS-CoV-2-specific CD8 TRBV CDR3 sequences.