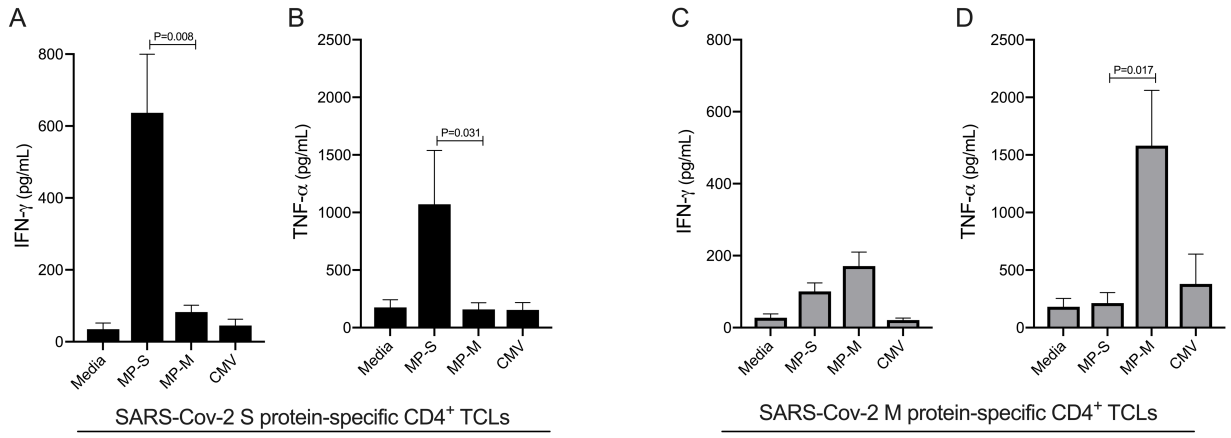
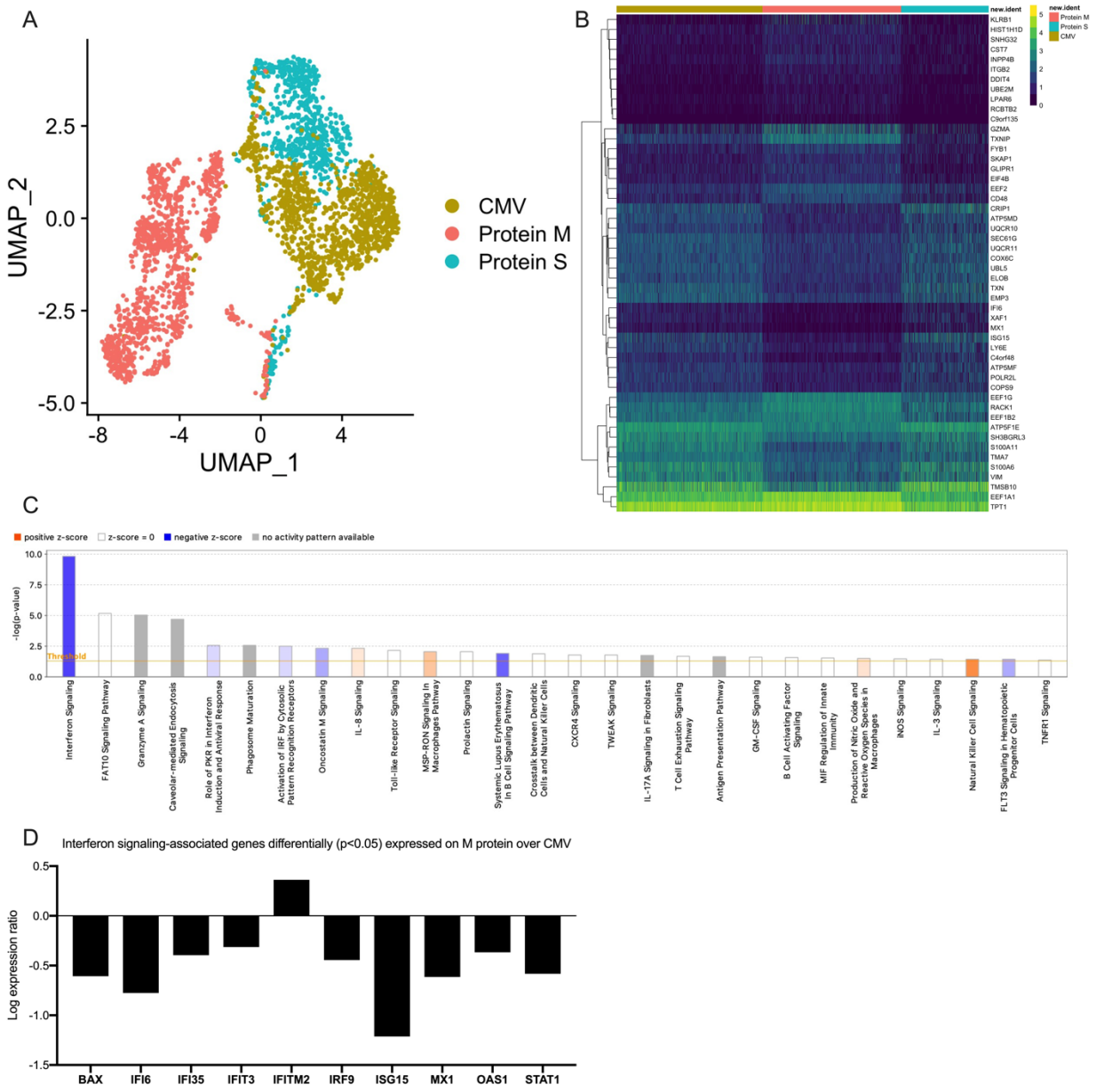
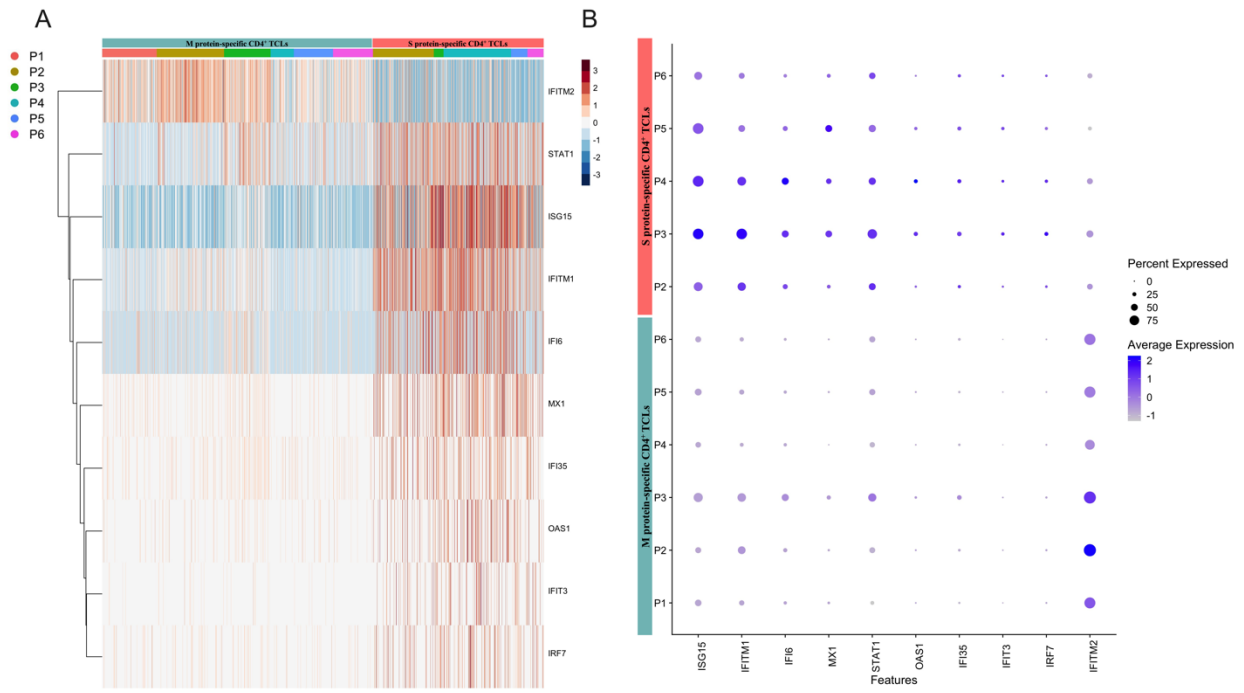


Supplemental figure 1. SARS-CoV-2 S and M proteins-specific CD4$^+$ TCLs reactivity and specificity. 2 x10^5 S-reactive TCLs (A) and 2 x10^5 M-reactive TCLs (B) from the 6 donors were incubated with 2 x10^5 autologous irradiated PBMCs and stimulated separately in the absence (media) or in the presence of MP-S (1µg/mL) and MP-M (1µg/mL) and CMV MP (1µg/mL) for 48 hours at 37°C and 5% CO_2. IFN-γ and TNF-α levels were measured in the culture supernatant by Luminex platform. All differences by Wilcoxon matched-pairs test with $P < 0.05$ are indicated in the graph.



Supplemental figure 2. Single-cell transcriptional profiling of SARS-CoV-2 S, M and CMV-specific CD4$^+$ T cells (A). Heatmap showing expression of the most significantly 50 enriched transcripts in M protein-specific CD4$^+$ T cell lines over S protein- and CMV-specific CD4$^+$ T cell lines (B). Canonical signaling pathways (IPA, QIAGEN) of immunological relevance affected in M protein-specific TCLs over CMV-specific TLCs indicating a marked suppression of interferon signaling pathway (C), with the associated gene expression levels and directions presented individually (D).



Supplemental figure 3. Heatmap (A) and the feature dot plot graph (B) showing the average expression and the percent expression of the interferon signaling pathway genes in the respective S-protein-specific CD4$^+$ T cell lines and M-protein-specific CD4$^+$ T cell lines by a donor-specific manner (colored from P1-P6).