**SUPPLEMENTARY MATERIALS**

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Fig. S2. Effect of vaccination on the frequencies of spike-specific T cells.

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Data file S1. Raw data file for main figures.

Data file S2. Raw data file for supplementary figures.

Data file S3. Lists of differentially expressed genes.

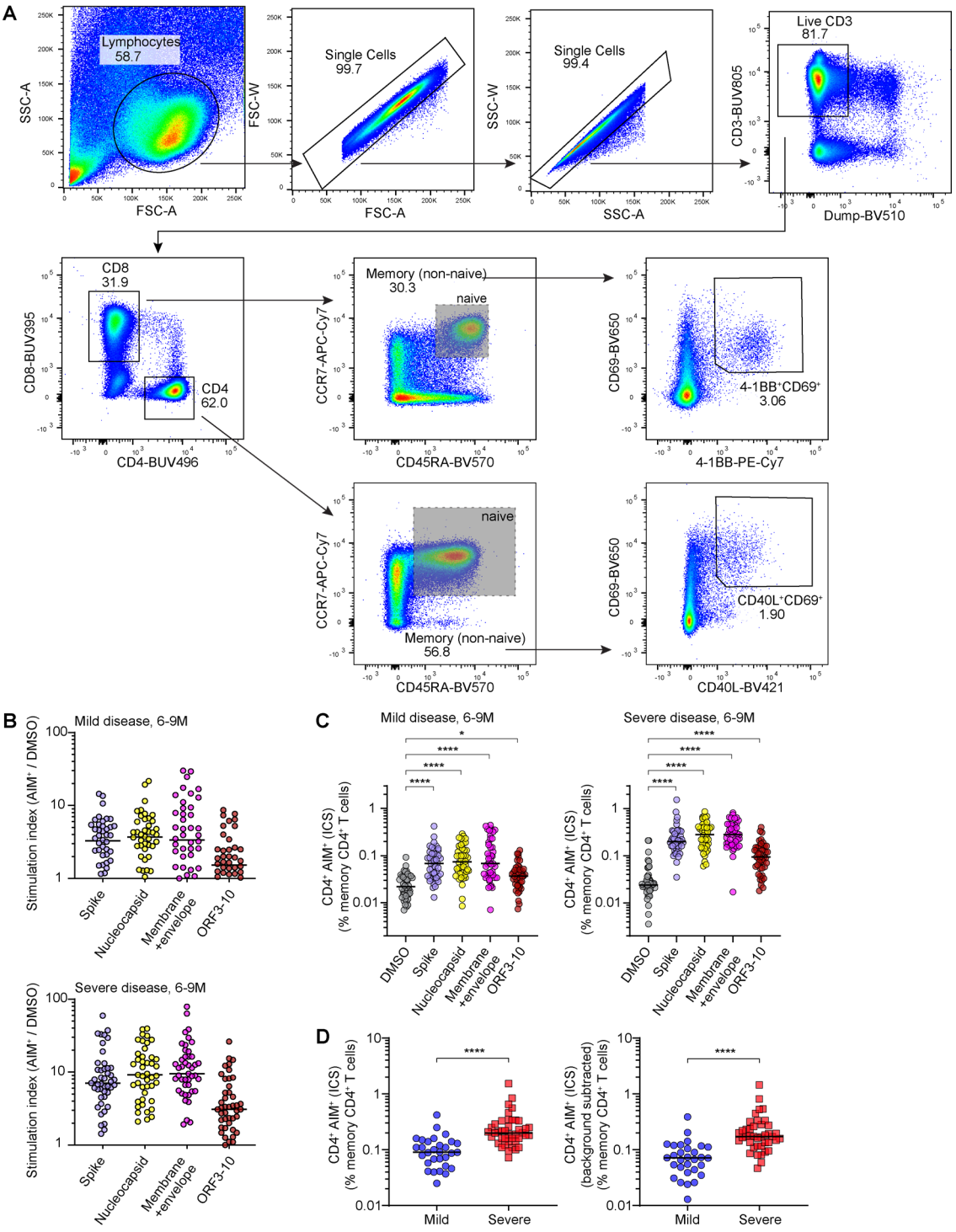


**Fig. S1. Detection of AIM⁺ T cells.** (**A**) Representative flow cytometric gating strategy showing the identification of AIM⁺ memory CD4⁺ and CD8⁺ T cells via flow cytometry. (**B**) Stimulation indices of individual donor responses at 6–9M. (**C**) Frequencies of intracellular AIM⁺ memory CD4⁺ T cells after DMSO and peptide pool stimulation. (**D**) Frequencies of AIM⁺ memory CD4⁺ T cells measured by intracellular staining, plotted with raw values (left) and DMSO background subtracted values (right). Statistical significance was determined by Mann–Whitney U test (C and D). *$P$ < 0.05, **$P$ < 0.01, ***$P$ < 0.001, ****$P$ < 0.0001. Bars shown median.

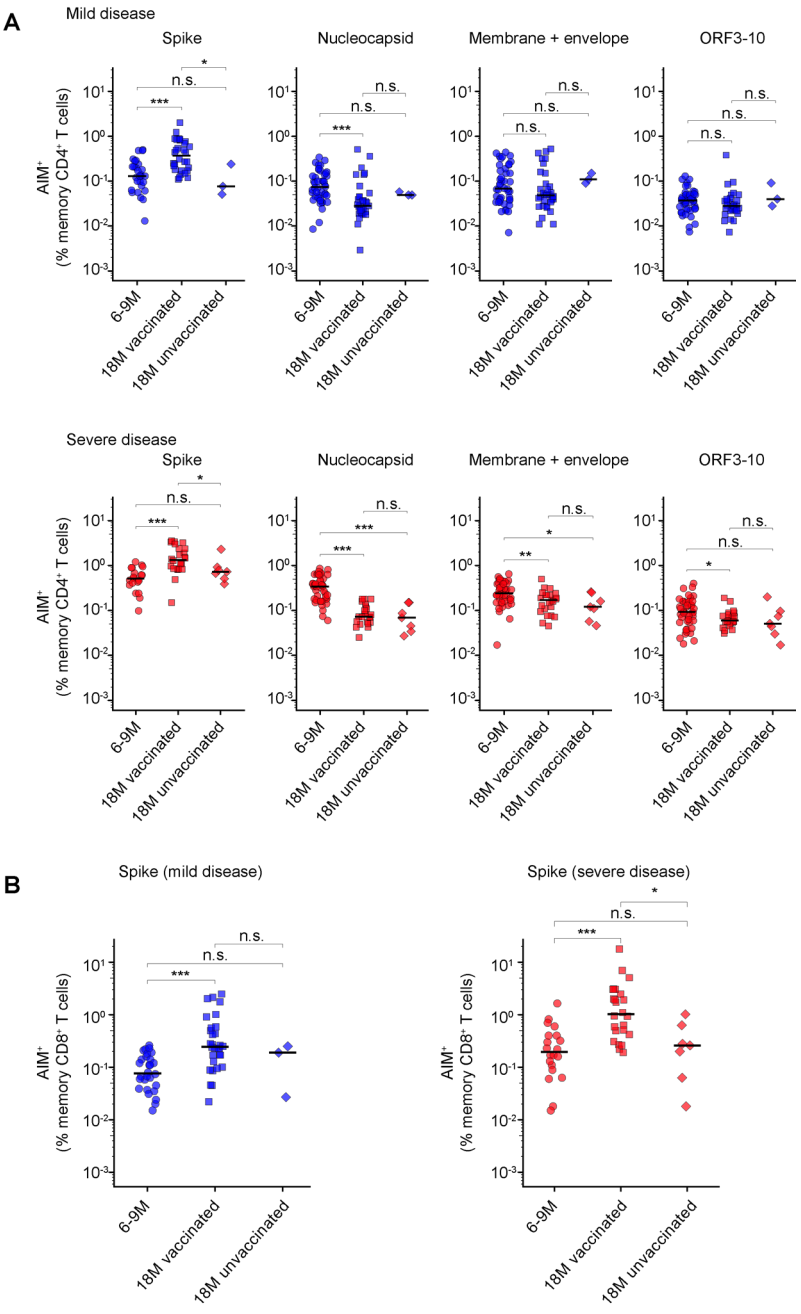


**Fig. S2. Effect of vaccination on the frequency of spike-specific T cells.** (**A**) Frequencies of AIM$^+$ memory CD4$^+$ T cells targeting different regions of SARS-CoV-2. (**B**) Frequencies of AIM$^+$ memory CD8$^+$ T cells targeting the spike protein of SARS-CoV-2. Statistical significance was determined by Mann–Whitney U test (A and B). n.s. = $P > 0.05$, *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ****$P < 0.0001$. Bars shown median.

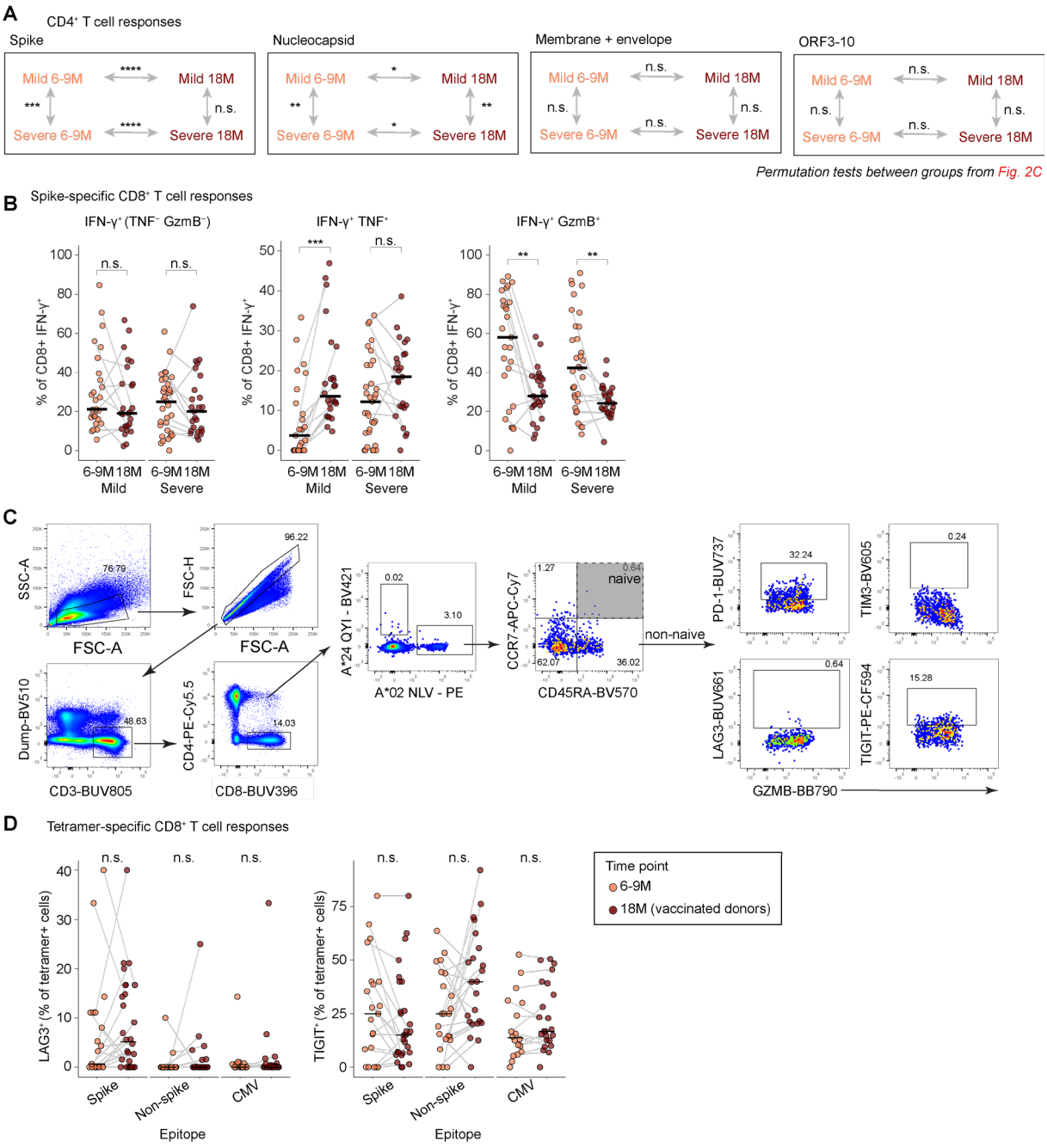


**Fig. S3. Characterization of T cell cytokine production and inhibitory receptor expression.** (**A**) Permutation test comparisons of cytokine expression profiles among AIM⁺ memory CD4⁺ T cells (related to Fig. 2C). (**B**) Percentages of IFN-γ⁺ spike-specific memory CD8⁺ T cells with polyfunctional cytokine and cytotoxic molecule expression after peptide stimulation. (**C**) Representative flow cytometry plots showing the identification of inhibitory receptor expression among tetramer-binding CD8⁺ T cells. (**D**) Percentages of tetramer-binding CD8⁺ T cells with inhibitory receptor expression. Statistical significance was determined by permutation test (A) and Mann–Whitney U test (B and D). n.s. = $P > 0.05$, *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$, ****$P < 0.0001$. Bars shown median.

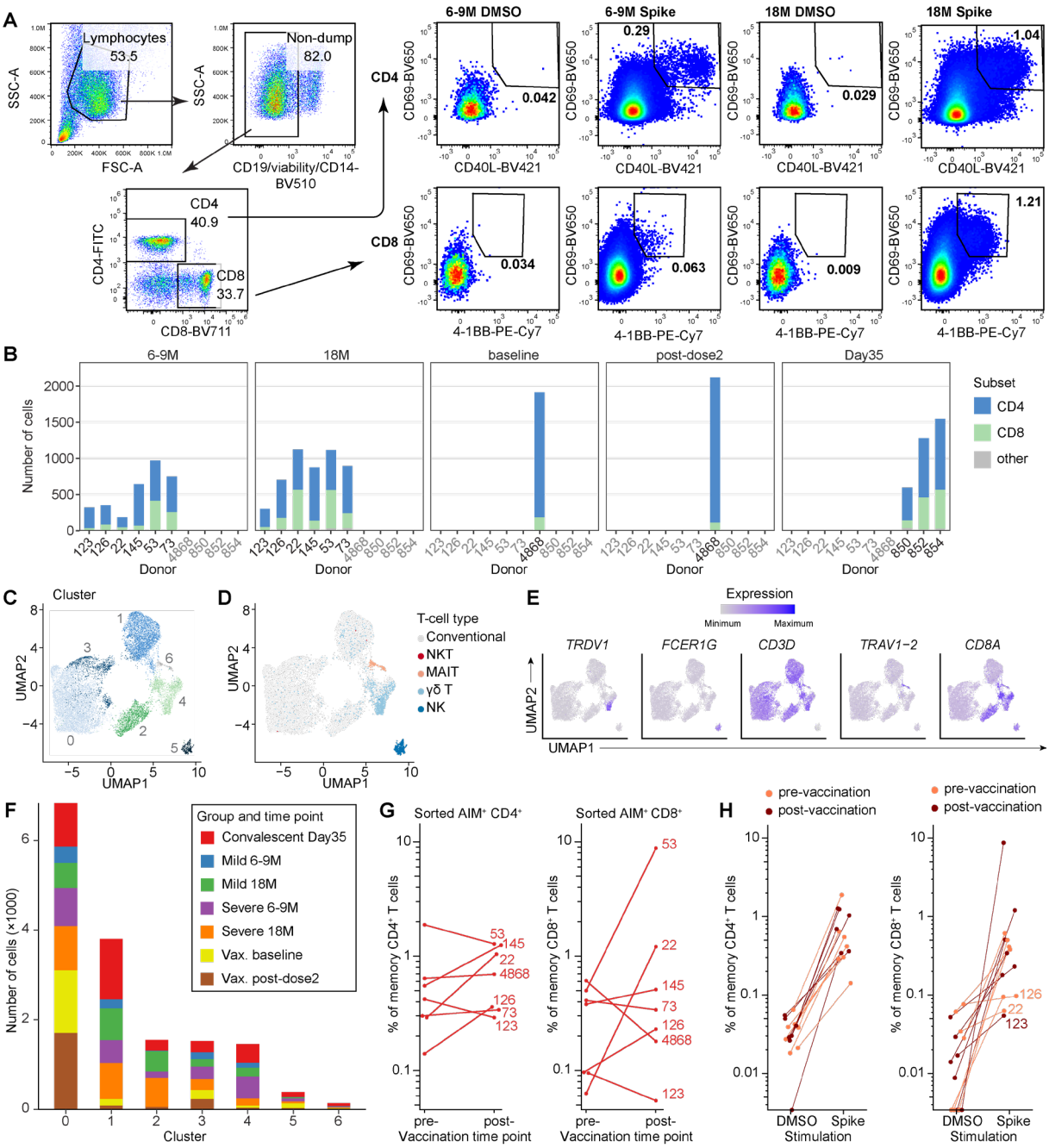


**Fig. S4. Classification of AIM⁺ populations sorted for scRNA-seq.** (**A**) Representative flow cytometric gating strategy for the identification and sorting of AIM⁺ CD4⁺ and CD8⁺ T cells for scRNA-seq. (**B**) Distribution of conventional AIM⁺ cells with CD4 or CD8 protein expression separated by donor and time point. Cells classified as 'other' either lacked expression of CD4 and CD8 or expressed both CD4 and CD8. (**C**) UMAP and clustering of all sorted cells, including NK cells and unconventional T cells. (**D**) Classification of NK cells and unconventional T cells. (**E**) Expression of transcripts corresponding to conventional and unconventional T cell subsets. (**F**) Distribution of donor groups and time points across each UMAP cluster. (**G**) Frequencies of sorted AIM⁺ memory CD4⁺ and CD8⁺ T cells after spike peptide pool stimulation. (**H**) Comparison of frequencies of AIM⁺ populations after DMSO and spike peptide pool stimulation.

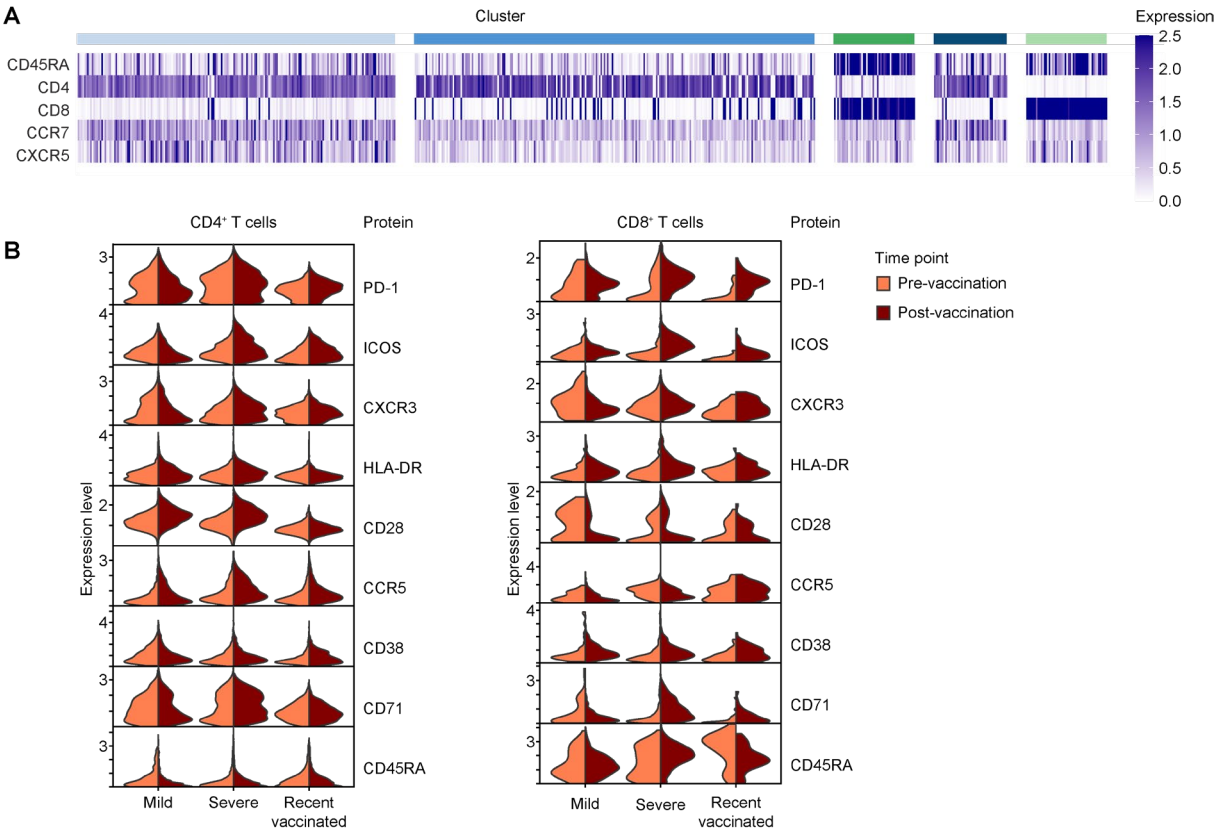


**Fig. S5. Protein expression among spike-specific T cells determined via CITE-seq.** (**A**) Heatmap showing protein expression measured via CITE-seq using a reduced panel for convalescent donors sampled on day 35. (**B**) Violin plots showing the expression of activation markers separated by donor group and time point.

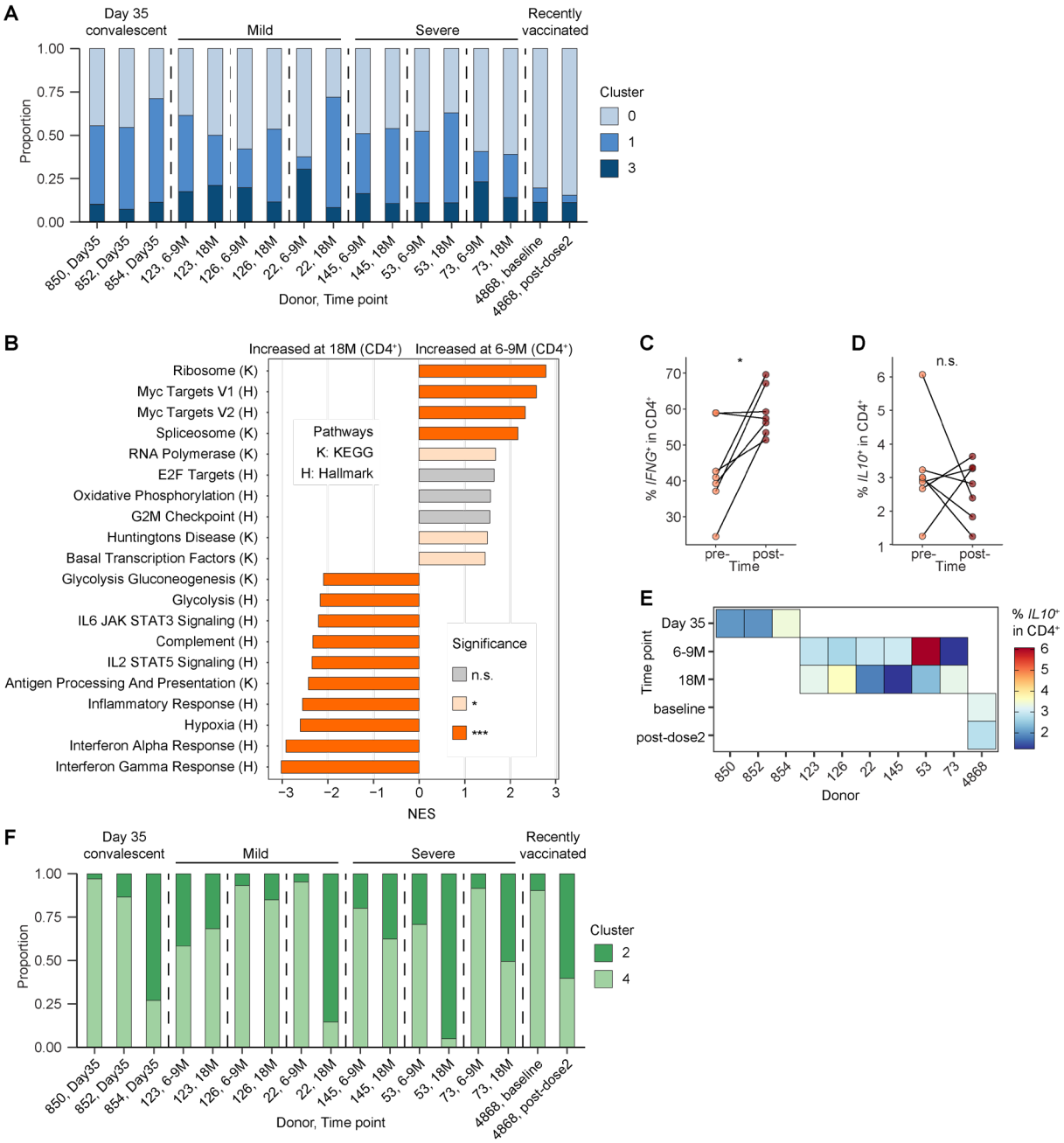


**Fig. S6. Transcriptomic comparison of spike-specific T cells before and after vaccination.** (**A**) Proportions of AIM$^+$ CD4$^+$ T cells from individual donors belonging to each CD4$^+$ T cell cluster. (**B**) GSEA summary of differentially expressed genes between CD4$^+$ T cells at 6-9M versus 18M. (**C**) Dot plots of the percentages of CD4$^+$ T cells from mild, severe and recently vaccinated donors with expression of *IFNG*. (**D**) Dot plots of the percentages of CD4$^+$ T cells from mild, severe and recently vaccinated donors with expression of *IL10*. (**E**) Percentages of CD4$^+$ T cells with expression of *IL10*. (**F**) Proportions of AIM$^+$ CD8$^+$ T cells from individual donors belonging to each CD8$^+$ T cell cluster. Statistical significance was determined by Broad GSEA test (B) and Mann–Whitney U test (C and D). Adjusted p-values calculated using the Benjamini–Hochberg (B) method. n.s. = $P > 0.05$, *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$

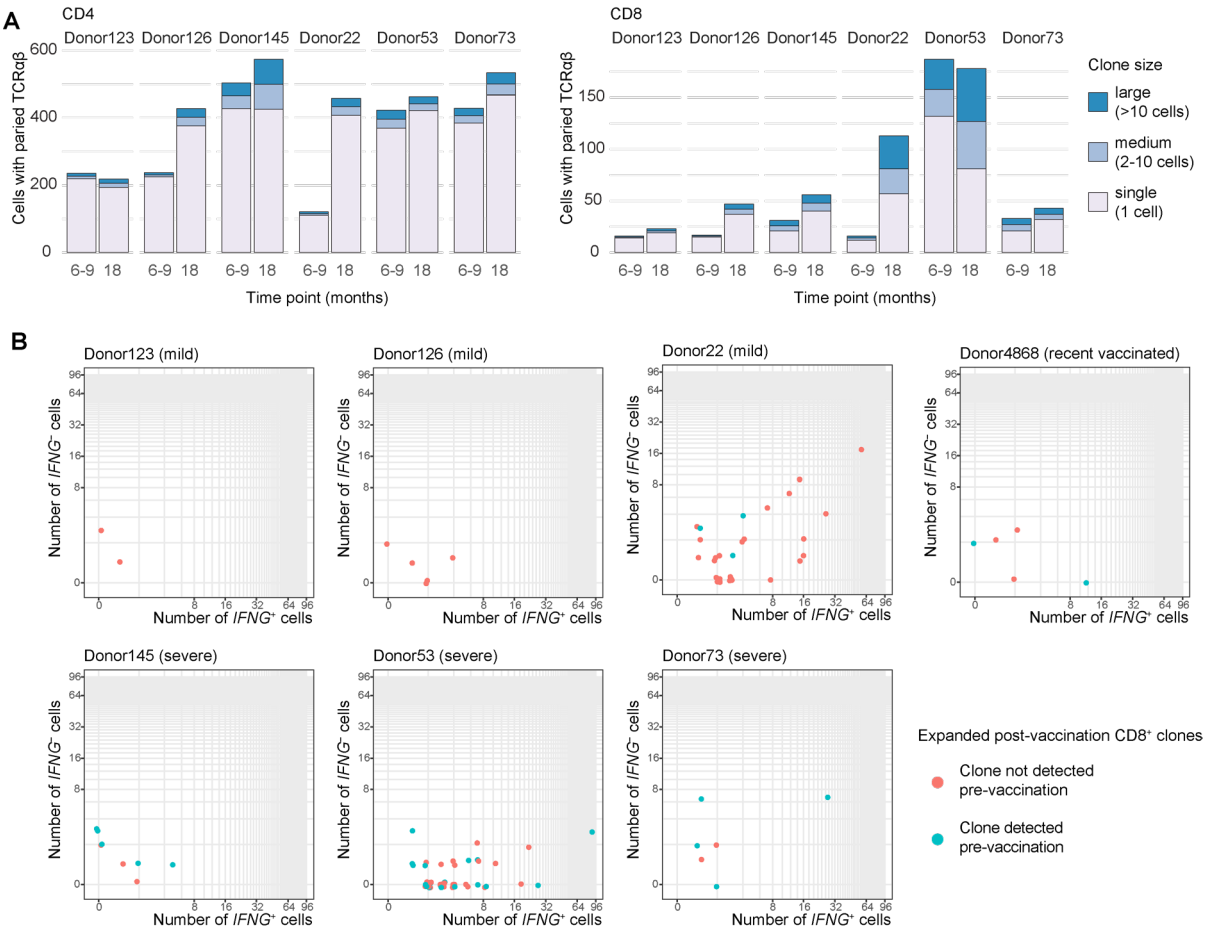


**Fig. S7. Clonal characterization of spike-specific T cells before and after vaccination.** (**A**) Proportions of CD4$^+$ and CD8$^+$ T cells classified by the degree of clonal expansion. (**B**) *IFNG* expression among expanded CD8$^+$ T cell clonotypes after vaccination separated by donor.

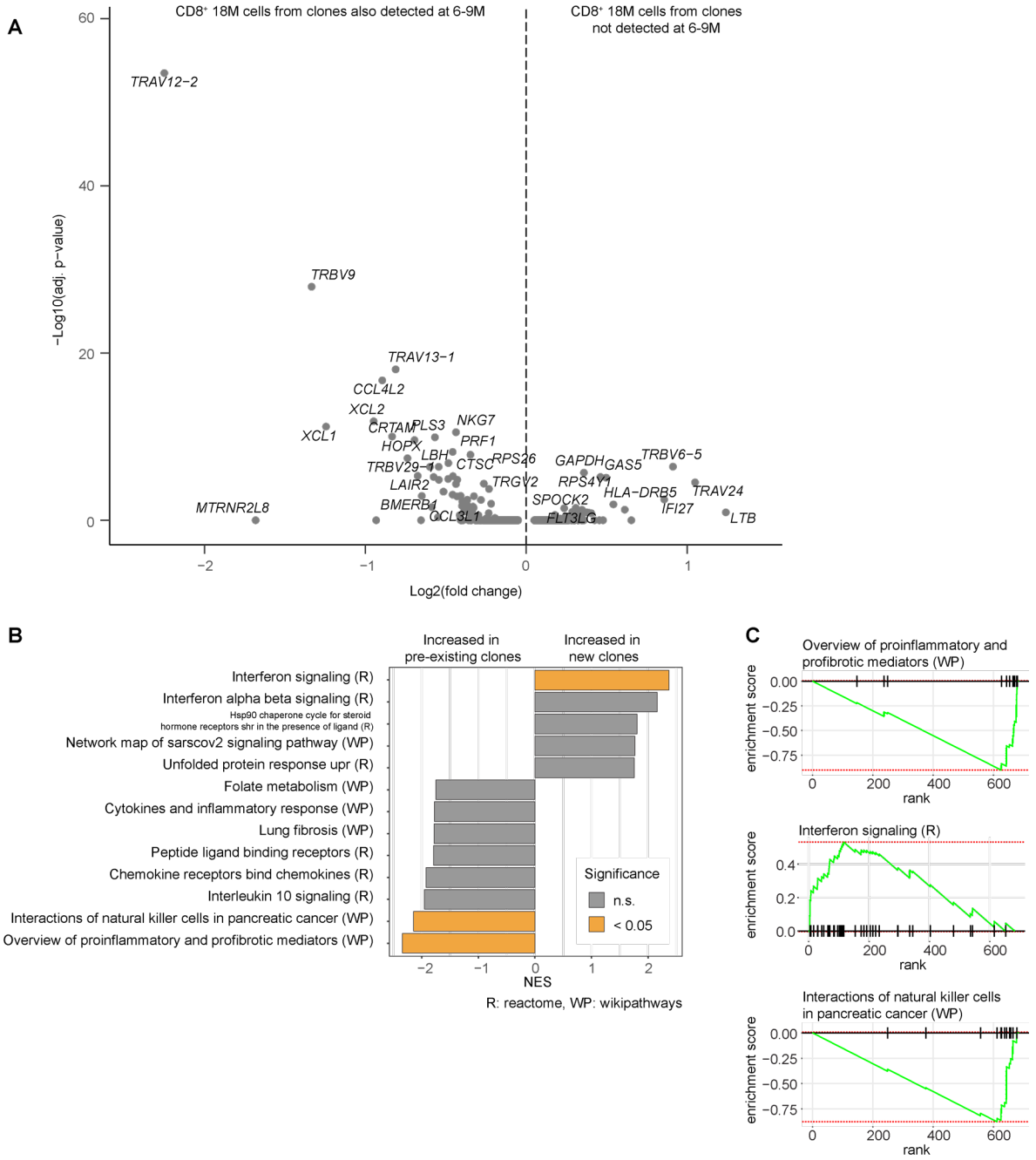


**Fig. S8. Transcriptomic signatures of CD8⁺ T cell clonotypes detected at one or both time points.** (**A**) Volcano plot showing differentially expressed genes between existing and newly detected CD8⁺ T cell clonotypes at 18M. (**B**) GSEA summary of differentially expressed genes between existing and newly detected CD8⁺ T cell clonotypes at 18M. (**C**) GSEA plot showing significantly enriched pathways at 18M. WP: WikiPathways; R: Reactome. Statistical significance was determined by Mann–Whitney U test (A) and Broad GSEA test (C) and. Adjusted p-values calculated using the Bonferroni method (A). n.s. = $P > 0.05$, *$P < 0.05$

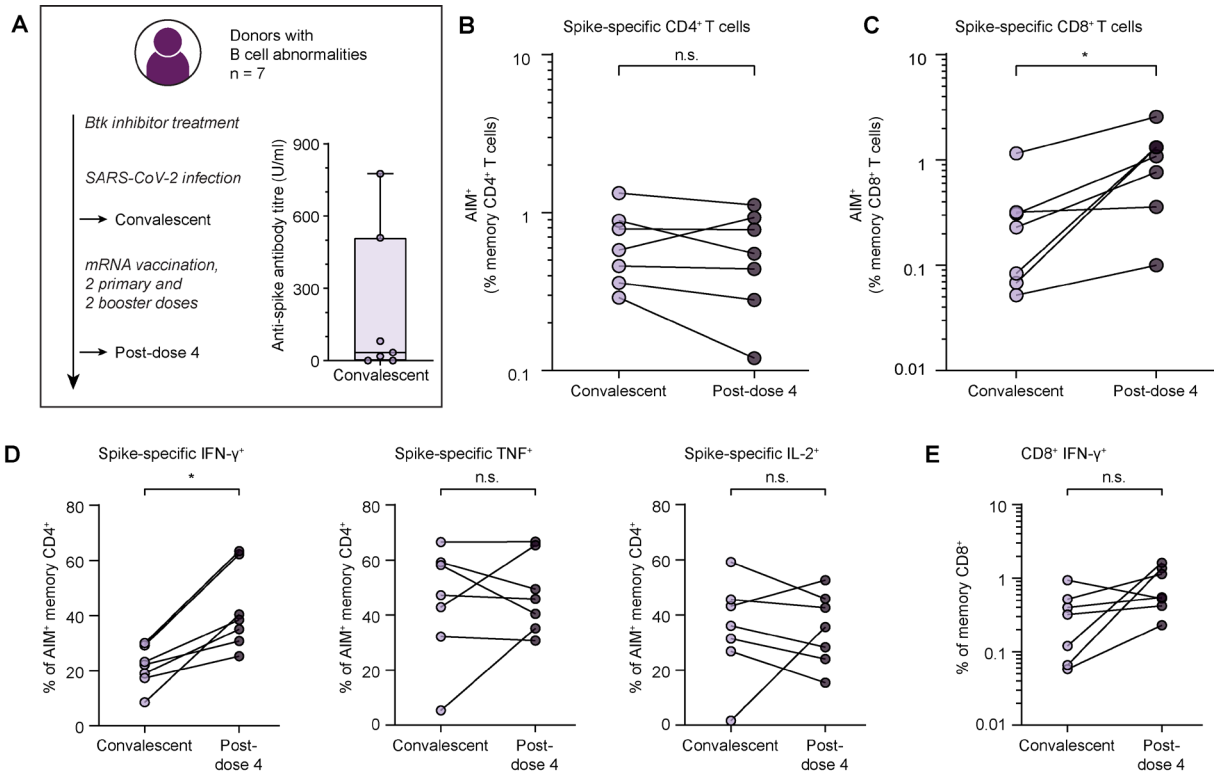


**Fig. S9. Characterization of hybrid spike-specific T cell responses in donors with CLL.** (**A**) Overview of donors and sampling time points from a cohort of patients undergoing treatment for CLL. (**B**) Frequencies of AIM$^+$ memory CD4$^+$ T cells. (**C**) Frequencies of AIM$^+$ memory CD8$^+$ T cells. (**D**) Percentages of AIM$^+$ memory CD4$^+$ T cells expressing cytokines. (**E**) Percentages of total memory CD8$^+$ T cells expressing IFN-γ. Statistical significance was determined by paired Wilcoxon Signed-Rank Test (B, C, D, E). n.s. = $P > 0.05$, *$P < 0.05$

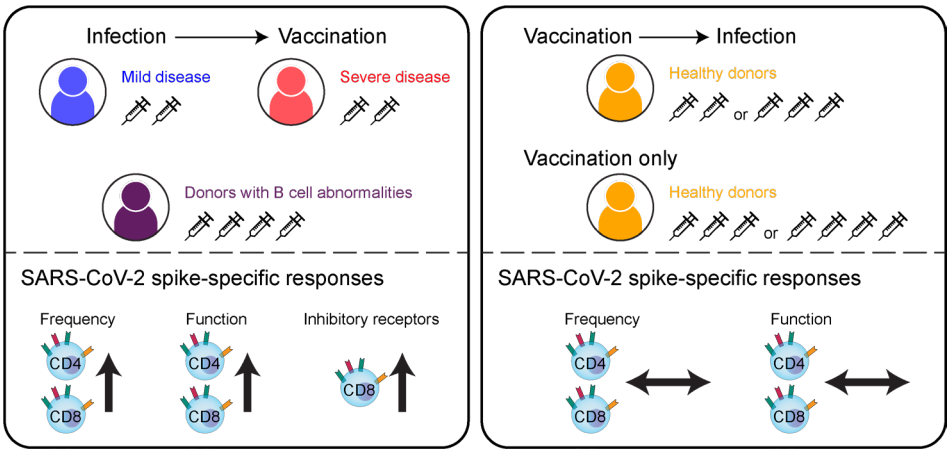


**Fig. S10. Summary of hybrid T cell immunity shaped by infection and vaccination.** Schematic representation of the key findings.

**Table S1. Summary of donors with a history of mild or severe disease.**

| Donor group and time point | Characteristic | Value |
|---|---|---|
| Mild (non-hospitalized) | Total number | 50 |
| | Number with paired time points | 31 |
| 6–9 months convalescence | Total number | 44 |
| | Unvaccinated | 44 |
| | Median age at infection (range) | 54.5 (43−78) |
| | Male / Female | 33 / 11 (75/25 %) |
| 18 months convalescence | Total number | 37 |
| | Unvaccinated | 3 |
| | Vaccinated | 34 |
| | Vaccine platform (Comirnaty, SpikeVax, Vaxzevria, unknown) | 27, 3, 2, 2 |
| | Median age at infection (range) | 57 (43−78) |
| | Male / Female | 28 / 9 (76/24 %) |
| Severe (hospitalized) | Total number | 53 |
| | Number with paired time points | 24 |
| 6–9 months convalescence * | Total number | 45 |
| | Unvaccinated | 45 |
| | Median age at infection (range) | 57 (33−68) |
| | Male / Female * | 34 / 7 (76/16 %) |
| | Admitted to ICU | 26 |
| | Required ventilator | 21 |
| 18 months convalescence | Total number | 32 |
| | Unvaccinated | 7 |
| | Vaccinated | 25 |
| | Vaccine platform (Comirnaty, SpikeVax, Vaxzevria, unknown) | 16, 6, 0, 3 |
| | Median age at infection (range) | 57.5 (33−76) |
| | Male / Female | 23 / 9 (72/28 %) |
| | Admitted to ICU | 18 |
| | Required ventilator | 15 |

The exact date of infection or vaccination was unavailable for four donors with mild disease and two donors with severe disease. *Clinical information was unavailable from four donors. ICU: intensive care unit.

**Table S2. Summary of donors selected for tetramer analysis.**

| Donor group and time point | Characteristic | Value |
|---|---|---|
| Mild (non-hospitalized)<br>• Paired 6–9M and 18M time points for each donor<br>• All donors vaccinated at the 18M time point | Total number | 14 |
| | Median age at infection (range) | 54 (43−66) |
| | Male / Female | 10 / 4 |
| | HLA combinations | |
| | A24 | 3 |
| | A2 A24 | 6 |
| | A2 B7 | 2 |
| | A24 B7 | 2 |
| | A2 A24 B7 | 1 |
| Severe (hospitalized)<br>• Paired 6–9M and 18M time points for each donor<br>• All donors vaccinated at the 18M time point | Total number | 14 |
| | Median age at infection (range) | 57.5 (33−68) |
| | Male / Female | 11 / 3 |
| | HLA combinations | |
| | A2 | 5 |
| | A24 | 5 |
| | A2 A24 | 2 |
| | A2 B7 | 1 |
| | A2 A24 B7 | 1 |

**Table S3. Summary of donors selected for single-cell RNA-sequencing (scRNA-seq).**

| Donor group and time point | Characteristic | Value |
|---|---|---|
| Mild<br>• Non-hospitalized<br>• 6–9 months convalescence<br>• 18 months convalescence | Donor IDs | 22, 123, 126 |
| | Age | 67, 59, 57 |
| | Sex | M, M, M |
| | Vaccine platform | |
| | Vaxzevria (Donor IDs) | 22 |
| | Comirnaty (Donor IDs) | 123, 126 |
| Severe<br>• Non-hospitalized<br>• 6–9 months convalescence<br>• 18 months convalescence | Donor IDs | 53, 73, 145 |
| | Age | 56, 62, 56 |
| | Sex | M, F, F |
| | Vaccine platform | |
| | Comirnaty (Donor IDs) | 53, 73 |
| | Unknown (Donor IDs) | 145 |
| Recently vaccinated<br>• Non-hospitalized<br>• Baseline: 2 weeks before vaccination or 13 months convalescence<br>• Dose 2+: 2 weeks after second dose vaccination or 15 months convalescence | Donor IDs | 4868 |
| | Age | 54 |
| | Sex | F |
| | Vaccine platform | |
| | SpikeVax (Donor IDs) | 4868 |
| Recently convalescent<br>• Non-hospitalized<br>• Day 35 convalescence<br>• Unvaccinated | Donor IDs | 850, 852, 854 |
| | Unvaccinated | 3 |
| | Age | Unavailable |
| | Sex | F, F, M |

**Table S4. Summary of donors with B cell abnormalities (CLL).**

| Donor group and time point | Characteristic | Value |
|---|---|---|
| B cell abnormality<br>• Treated with BTK inhibition for CLL<br>• Convalescent<br>• Post-dose 4 | Total number<br>Median age at convalescent time point (range)<br>Male / Female<br>Hospitalized | 7<br>69 (46−77)<br>4 / 3<br>6 |

CLL: chronic lymphocytic leukemia; BTK: Bruton's tyrosine kinase

**Table S5. Summary of healthy vaccinated donors.**

| Donor group and time point | Characteristic | Value |
|---|---|---|
| Vaccinated healthy controls<br>• 3 month post-vaccination follow-up (two doses received)<br>• 18 month post-vaccination follow-up (three or four doses received) | Total number | 14 |
| With breakthrough infection | Total number<br>Median age at vaccination (range)<br>Male / Female<br>Vaccine platform<br>Comirnaty only<br>Comirnaty and SpikeVax<br>Clinical history<br>Two doses > breakthrough<br>Two doses > breakthrough > third dose<br>Three doses > breakthrough | 5<br>32 (26−55)<br>2 / 3<br><br>2<br>3<br><br>1<br>1<br>3 |
| Without breakthrough infection<br>• All received four vaccine doses by the 18 month follow-up | Total number<br>Median age at vaccination (range)<br>Male / Female<br>Vaccine platform<br>Comirnaty only<br>Comirnaty and SpikeVax | 9<br>46 (28−59)<br>4 / 5<br><br>6<br>3 |

**Table S6. Surface staining protocol for flow cytometry.**

| STEP 1: Stain for viability at room temperature for 10 minutes. | | | | | |
|---|---|---|---|---|---|
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| LIVE/DEAD Fixable Aqua | For 405 nm excitation | Invitrogen | 1X in PBS | L34957 | - |
| STEP 2: Stain for chemokine receptors at 37°C for 10 minutes. | | | | | |
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| CCR7 | APC-Cy7 | BioLegend | 1:50 | 353212 | G043H7 |
| CCR4 | BB700 | BD | 1:50 | 566475 | 1G1 |
| CCR6 | BUV737 | BD | 1:75 | 612780 | 11A9 |
| CXCR3 | AF647 | BioLegend | 1:100 | 353712 | G025H7 |
| STEP 3: Stain with remaining antibodies at room temperature for 30 minutes in BD Brilliant Stain Buffer Plus. | | | | | |
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| CD40L | BV421 | BioLegend | 1:25 | 310824 | 24-31 |
| 4-1BB | PE-Cy7 | BioLegend | 1:25 | 309818 | 4B4-1 |
| CD4 | BUV496 | BD | 1:25 | 612936 | SK3 |
| CD14 | BV510 | BioLegend | 1:100 | 301842 | M5E2 |
| CD19 | BV510 | BioLegend | 1:100 | 302242 | HIB19 |
| CD45RA | BV570 | BioLegend | 1:200 | 304132 | HI100 |
| CD69 | BV650 | BioLegend | 1:50 | 310934 | FN50 |
| CD3 | BUV805 | BD | 1:50 | 612895 | UCHT1 |
| CD8 | BUV395 | BD | 1:250 | 563795 | RPA-T8 |
| STEP 4: Wash and fix cells in 1% paraformaldehyde. | | | | | |

**Table S7. Surface and intracellular staining protocol for flow cytometry.**

| STEP 1: Stain for chemokine receptors at 37°C for 10 minutes. | | | | | |
|---|---|---|---|---|---|
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| CCR7 | APC-Cy7 | BioLegend | 1:50 | 353212 | G043H7 |
| CCR4 | BB700 | BD | 1:50 | 566475 | 1G1 |
| CCR6 | BUV737 | BD | 1:75 | 612780 | 11A9 |
| CXCR3 | AF647 | BioLegend | 1:50 | 353712 | G025H7 |
| STEP 2: Stain with surface antibodies and viability dye at room temperature for 30 minutes in BD Brilliant Stain Buffer Plus. | | | | | |
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| PD-1 | BV711 | BioLegend | 1:25 | 329928 | EH12.2H7 |
| CD4 | BUV496 | BD | 1:25 | 612936 | SK3 |
| CD14 | BV510 | BioLegend | 1:100 | 301842 | M5E2 |
| CD19 | BV510 | BioLegend | 1:100 | 302242 | HIB19 |
| CD45RA | BV570 | BioLegend | 1:200 | 304132 | HI100 |
| CD8 | BUV395 | BD | 1:250 | 563795 | RPA-T8 |
| LIVE/DEAD Fixable Aqua | For 405 nm excitation | Invitrogen | 1:1667 | L34957 | - |
| CD38 | APC-R700 | BD | 1:50 | 564979 | HIT2 |
| STEP 3: Fix and permeabilize with FoxP3 Transcription Factor Staining Buffer Set (Invitrogen, #00-5523-00) according to the provided protocol. | | | | | |
| STEP 4: Stain with intracellular antibodies at room temperature for 30 minutes in BD Brilliant Stain Buffer Plus and 1X Permeabilization Buffer. | | | | | |
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| CD40L | BV421 | BioLegend | 1:25 | 310824 | 24-31 |
| IL-17A | eFluor660 | Invitrogen | 1:25 | 50-7178-42 | eBio64CAP17 |
| IL-2 | PE-Dazzle594 | BioLegend | 1:33 | 500344 | MQ1-17H12 |
| 4-1BB | PE-Cy7 | BioLegend | 1:100 | 309818 | 4B4-1 |
| TNFa | BV650 | BD | 1:166 | 563418 | MAb11 |
| CD3 | BUV805 | BD | 1:250 | 612895 | UCHT1 |
| CD69 | BUV563 | BD | 1:200 | 748764 | FN50 |
| IFN-γ | PE | BioLegend | 1:400 | 506507 | B27 |
| Granzyme B | BB790 | BD | 1:500 | 624296 | GB11 |
| STEP 5: Wash and fix cells in 1% paraformaldehyde. | | | | | |

**Table S8. Tetramer, surface and intracellular staining protocol for flow cytometry.**

| STEP 1: Incubate with dasatinib at room temperature for 10 minutes. | | | | | |
|---|---|---|---|---|---|
| **Reagent** | **Fluorophore** | **Supplier** | **Final conc.** | **Product number** | **Clone** |
| Dasatinib | - | STEMCELL | 50 µM | 73082 | - |
| STEP 2: Incubate with one relevant PE tetramer/tetramer pool at room temperature for 20 minutes. Each tetramer should be equivalent to 0.2 µl of pMHC (0.5 µg/ml, total 10µl volume). | | | | | |
| **Reagent** | | | | **Fluorophore** | |
| Tetramer pool consisting of:<br>SARS-CoV-2 nucleocapsid A*0201 LLLDRLNQL<br>SARS-CoV-2 ORF3a A*0201 ALSKGVHFV<br>SARS-CoV-2 ORF3 A*0201 LLYDANYFL | | | | PE | |
| SARS-CoV-2 nucleocapsid B*0702 SPRWYFYYL | | | | PE | |
| CMV pp65 B*0702 TPRVTGGGAM | | | | PE | |
| CMV pp65 A*0201 NLVPMVATV | | | | PE | |
| STEP 3: Incubate with one relevant BV421 tetramer at room temperature for 20 minutes. | | | | | |
| **Reagent** | | | | **Fluorophore** | |
| SARS-CoV-2 spike A*0201 YLQPRTFLL | | | | BV421 | |
| SARS-CoV-2 spike A*2402 QYIKWPWYI | | | | BV421 | |
| SARS-CoV-2 spike B*0702 SPRRARSVA | | | | BV421 | |
| CMV pp65 A*0201 NLVPMVATV | | | | BV421 | |
| STEP 4: Wash cells. Stain for viability at room temperature for 10 minutes. | | | | | |
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| LIVE/DEAD Fixable Aqua | For 405 nm excitation | Invitrogen | 1X in PBS | L34957 | - |
| STEP 5: Stain for chemokine receptors at 37°C for 10 minutes. | | | | | |
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| CCR7 | APC-Cy7 | BioLegend | 1:50 | 353212 | G043H7 |
| CXCR3 | PE-Cy5 | BioLegend | 1:200 | 353756 | G025H7 |
| CX3CR1 | BUV615 | BioLegend | 1:100 | 750690 | 2A9-1 |
| STEP 6: Stain with surface antibodies at room temperature for 30 minutes in BD Brilliant Stain Buffer Plus. | | | | | |
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| CD8 | BUV396 | BioLegend | 1:200 | 563795 | RPA-T8 |
| CD38 | BUV496 | BD | 1:200 | 612946 | HIT2 |
| LAG3 | BUV661 | BD | 1:200 | 624285 | T47-530 |
| PD-1 | BUV737 | BD | 1:50 | 612791 | EH12.1 |
| CD3 | BUV805 | BD | 1:50 | 612895 | UCHT1 |
| CD14 | BV510 | BioLegend | 1:100 | 301842 | M5E2 |
| CD19 | BV510 | BioLegend | 1:100 | 302242 | HIB19 |
| CD45RA | BV570 | BioLegend | 1:200 | 304132 | HI100 |
| TIM3 | BV605 | BioLegend | 1:100 | 502936 | 344823 |
| HLA-DR | BV650 | BD | 1:100 | 564231 | G46-6 |
| TIGIT | PE-Dazzle594 | BioLegend | 1:100 | 372715 | A15153G |
| CD127 | BB630 | BD | 1:100 | Custom | HIL-7R-M21 |
| CD27 | BV786 | BioLegend | 1:50 | 302832 | O323 |
| CD4 | PE-Cy5.5 | Invitrogen | 1:400 | 35-0042-82 | RMA-4.5 |
| CD95 | BB700 | BioLegend | 1:50 | 305634 | DX2 |
| CD39 | BV711 | BioLegend | 1:100 | 328228 | A1 |
| STEP 5: Wash and fix cells in 1% paraformaldehyde. | | | | | |

**Table S9. Surface and oligo-conjugated antibody staining protocol for single-cell sorting and CITE-seq.**

| STEP 1: Stain for viability at room temperature for 10 minutes. | | | | | |
|---|---|---|---|---|---|
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| LIVE/DEAD Fixable Aqua | For 405 nm excitation | Invitrogen | 1X in PBS | L34957 | - |
| STEP 2: Stain for chemokine receptors at 37°C for 10 minutes. | | | | | |
| **Marker** | **Conjugate** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| CCR7 | TotalSeq-C0148 | BioLegend | 1:300 | 353251 | G043H7 |
| CXCR5 | TotalSeq-C0144 | BioLegend | 1:500 | 356939 | J252D4 |
| CXCR3 | TotalSeq-C0140 | BioLegend | 1:500 | 353747 | G025H7 |
| CX3CR1 | TotalSeq-C0179 | BioLegend | 1:500 | 355705 | K0124E1 |
| CCR4 | TotalSeq-C0071 | BioLegend | 1:500 | 359425 | L291H4 |
| CCR5 | TotalSeq-C0141 | BioLegend | 1:500 | 359137 | J418F1 |
| CCR6 | TotalSeq-C0143 | BioLegend | 1:500 | 353440 | G034E3 |
| CXCR6 | TotalSeq-C0804 | BioLegend | 1:500 | 356023 | K041E5 |
| STEP 3: Stain with remaining antibodies at room temperature for 30 minutes in BD Brilliant Stain Buffer Plus. Use one hashing antibody per sample. | | | | | |
| **Marker** | **Fluorophore** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| CD40L | BV421 | BioLegend | 1:25 | 310824 | 24-31 |
| 4-1BB | PE-Cy7 | BioLegend | 1:25 | 309818 | 4B4-1 |
| CD4 | FITC | BD | 1:25 | 345768 | SK3 |
| CD14 | BV510 | BioLegend | 1:100 | 301842 | M5E2 |
| CD19 | BV510 | BioLegend | 1:100 | 302242 | HIB19 |
| CD69 | BV650 | BioLegend | 1:50 | 310934 | FN50 |
| CD8 | BV711 | BioLegend | 1:50 | 301044 | RPA-T8 |
| **Marker** | **Conjugate** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| CD4 | TotalSeq-C0072 | BioLegend | 1:1250 | 300567 | RPA-T4 |
| CD8 | TotalSeq-C0046 | BioLegend | 1:10000 | 344753 | SK1 |
| CD45RA | TotalSeq-C0063 | BioLegend | 1:4000 | 304163 | HI100 |
| CD127 | TotalSeq-C0390 | BioLegend | 1:333 | 351356 | A019D5 |
| CD27 | TotalSeq-C0154 | BioLegend | 1:500 | 302853 | O323 |
| PD-1 | TotalSeq-C0088 | BioLegend | 1:500 | 329963 | EH12.2H7 |
| ICOS | TotalSeq-C0171 | BioLegend | 1:500 | 313553 | C398.4A |
| HLA-DR | TotalSeq-C0159 | BioLegend | 1:500 | 307663 | L243 |
| CD122 | TotalSeq-C0246 | BioLegend | 1:500 | 339021 | TU27 |
| CD28 | TotalSeq-C0386 | BioLegend | 1:500 | 302963 | CD28.2 |
| CD95 | TotalSeq-C0156 | BioLegend | 1:500 | 305651 | DX2 |
| CD38 | TotalSeq-C0389 | BioLegend | 1:500 | 303543 | HIT2 |
| CD71 | TotalSeq-C0394 | BioLegend | 1:500 | 334125 | CY1G4 |
| **Hashtag** | **Conjugate** | **Supplier** | **Dilution** | **Product number** | **Clone** |
| Hashtag 1 | TotalSeq-C0251 | BioLegend | 1:100 | 394661 | LNH-94; 2M2 |
| Hashtag 2 | TotalSeq-C0252 | BioLegend | 1:100 | 394663 | LNH-94; 2M2 |
| Hashtag 3 | TotalSeq-C0253 | BioLegend | 1:100 | 394665 | LNH-94; 2M2 |
| Hashtag 4 | TotalSeq-C0254 | BioLegend | 1:100 | 394667 | LNH-94; 2M2 |