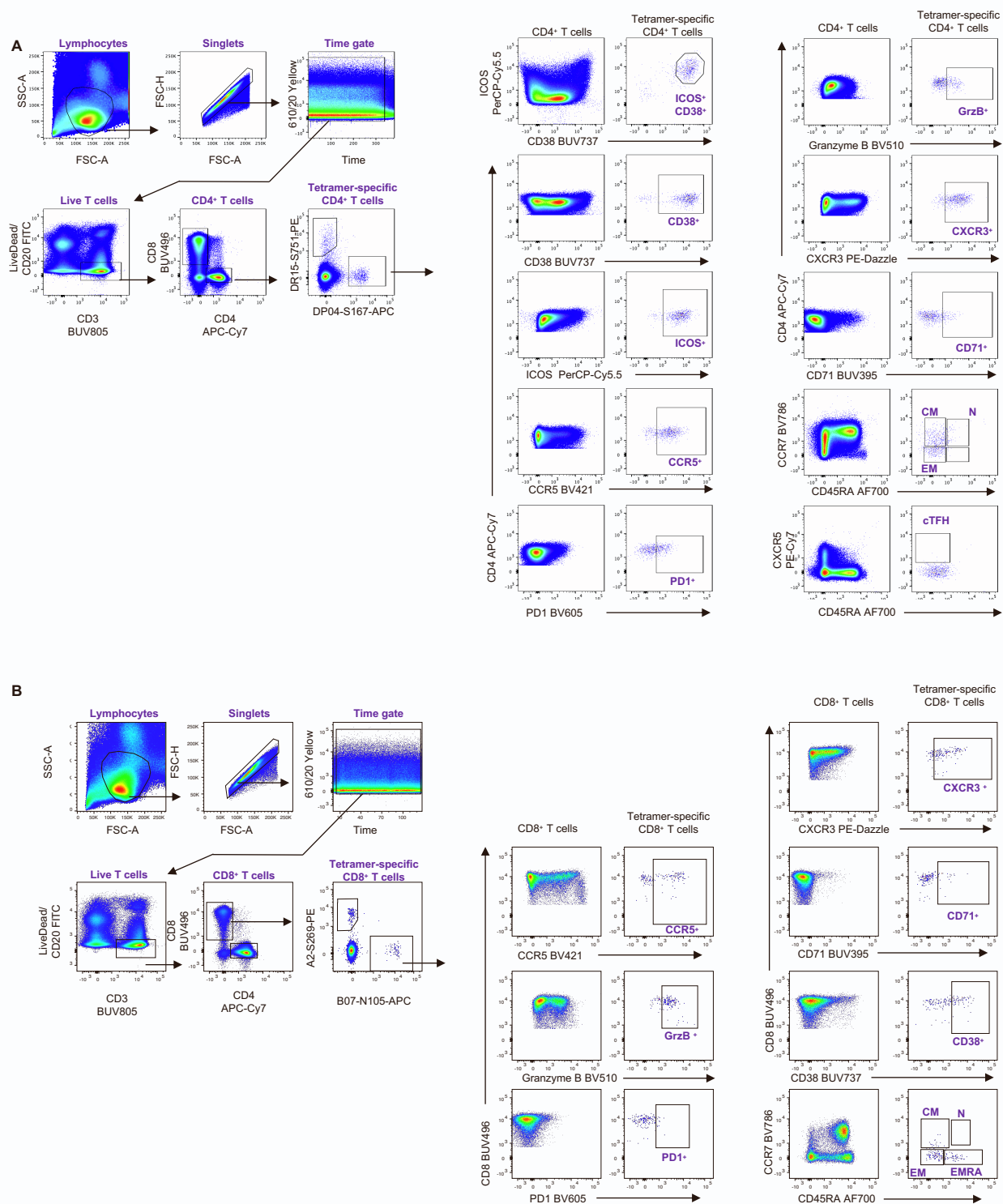


**Supplemental information**

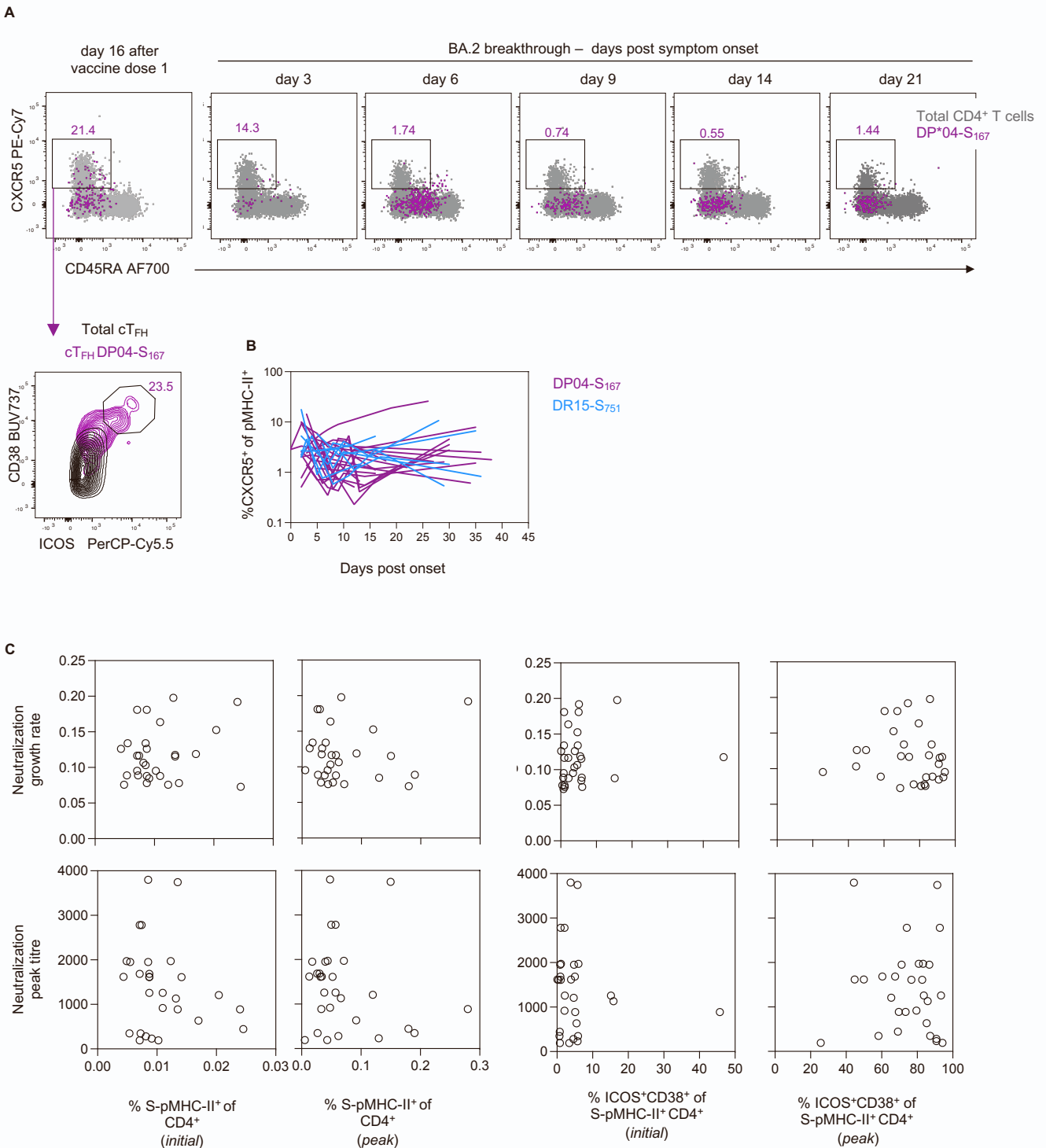
**SARS-CoV-2 breakthrough infection induces rapid  
memory and *de novo* T cell responses**

**Marios Koutsakos, Arnold Reynaldi, Wen Shi Lee, Julie Nguyen, Thakshila Amarasena, George Taiaroa, Paul Kinsella, Kwee Chin Liew, Thomas Tran, Helen E. Kent, Hyon-Xhi Tan, Louise C. Rowntree, Thi H.O. Nguyen, Paul G. Thomas, Katherine Kedzierska, Jan Petersen, Jamie Rossjohn, Deborah A. Williamson, David Houry, Miles P. Davenport, Stephen J. Kent, Adam K. Wheatley, and Jennifer A. Juno**

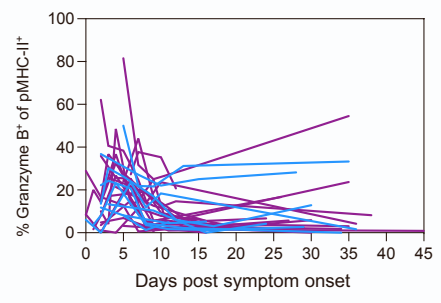
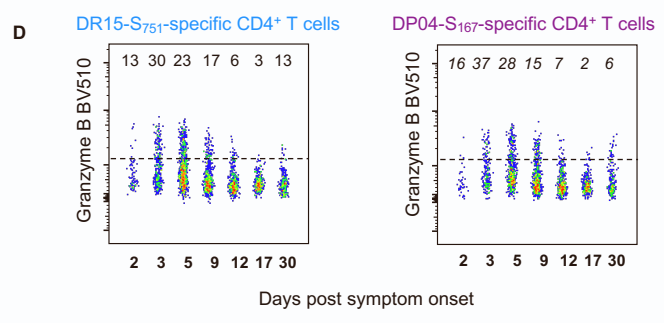
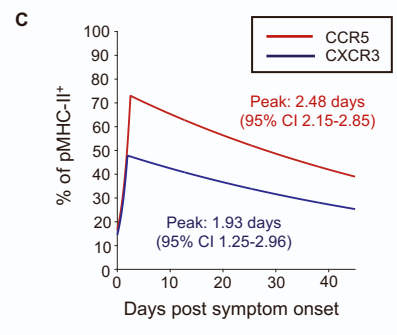
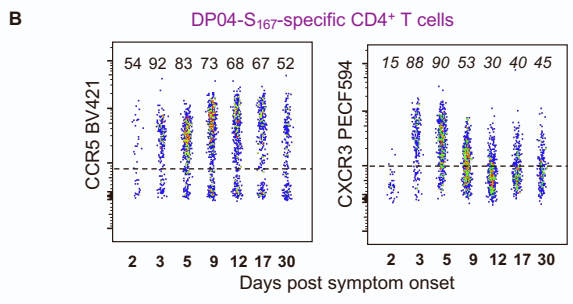
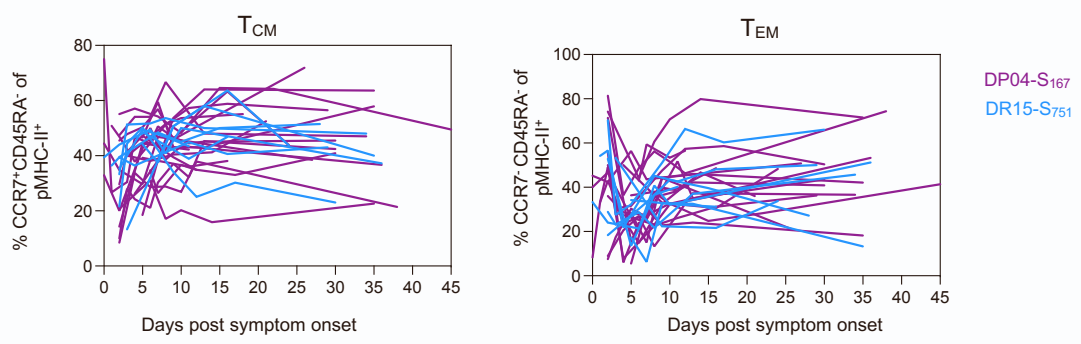
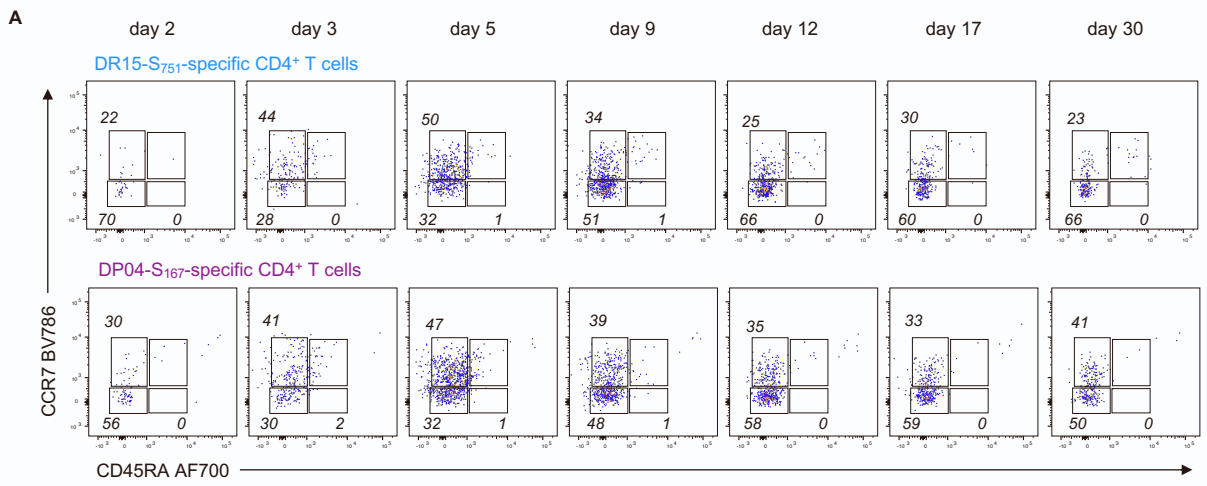
**Supplementary Figures 1-6**  
**Supplementary Tables 1-6**



**Figure S1. Gating strategy for the identification of pMHC-specific CD4<sup>+</sup> and CD8<sup>+</sup> T cells and their phenotypic characterisation, related to Figures 1-4. (A)** Lymphocytes were identified by FSC-A vs SSC-A gating, followed by doublet exclusion (FSC-A vs FSC-H), a time gate and then gating on live T cells (CD3<sup>+</sup>CD19<sup>-</sup>) and subsequently CD4<sup>+</sup>CD8<sup>-</sup> cells. HLA-DR\*15-S<sub>751</sub> and HLA-DP\*04-S<sub>167</sub>-specific cells were identified within CD4<sup>+</sup> T cells, and phenotyped as indicated, with the total CD4<sup>+</sup> T cell population serving as a reference for gating of phenotypic markers. **(B)** CD8<sup>+</sup> T cell were identified as CD4<sup>-</sup>CD8<sup>+</sup> within live T cells gated as in (A). HLA-A\*02-S<sub>269</sub>, HLA-A\*03-S<sub>378</sub> and HLA-A\*24-S<sub>1208</sub> and HLA-B\*07-N<sub>105</sub>-specific CD8<sup>+</sup> T cells were identified within CD8<sup>+</sup> T cells and phenotyped as indicated, with the total CD8<sup>+</sup> T cell population serving as a reference for gating of phenotypic markers.

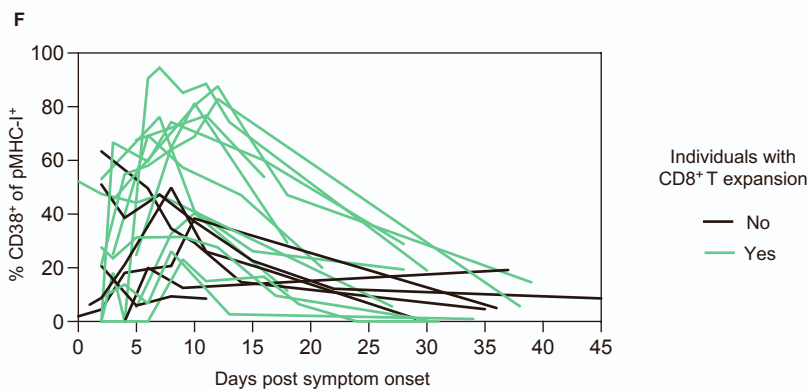
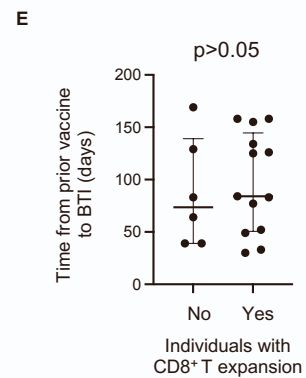
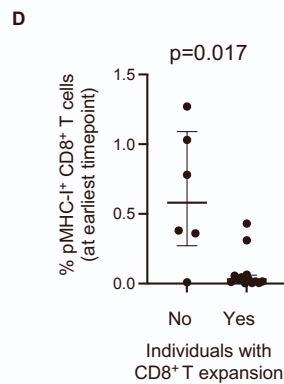
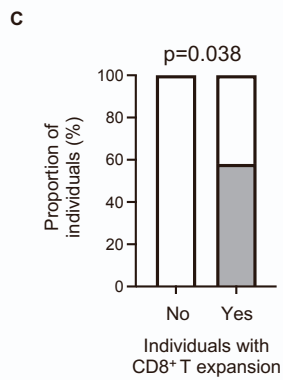
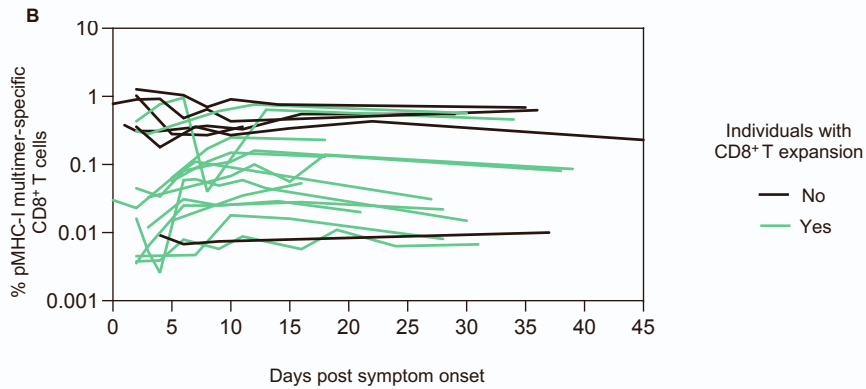
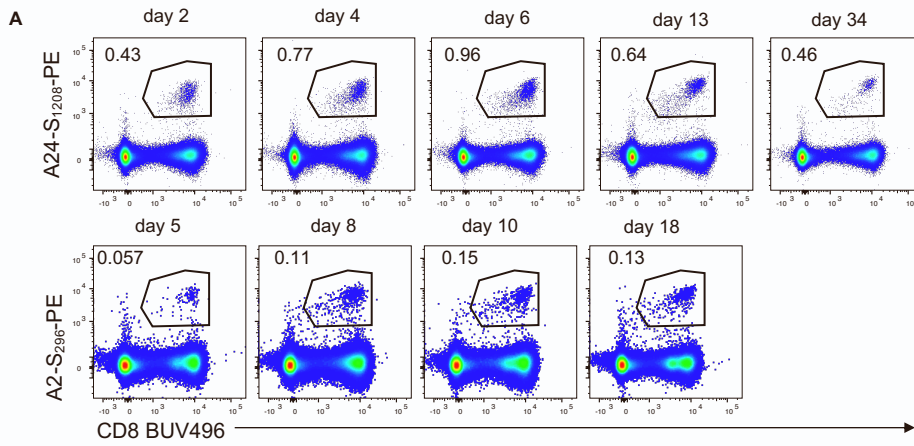


**Figure S2. Limited cTFH phenotype following BTI, related to Figure 2. (A)** Representative flow cytometry plots of the cTFH phenotype (CXCR5<sup>+</sup>CD45RA<sup>-</sup>) for HLA-DP\*04-S<sub>167</sub>-specific CD4<sup>+</sup> T cells. A post-vaccination sample was included in acquisition and analysis, serving as a reference for the cTFH activation and cTFH activation (CD38/ICOS expression). **(B)** Kinetics of CXCR5<sup>+</sup> cells for both pMHC-II populations, n=19 for DP\*04-S<sub>167</sub> and n=9 for DR\*15-S<sub>751</sub>. **(C)** Correlations between the initial or peak frequency of S-pMHC-II<sup>+</sup> CD4<sup>+</sup> T cells and initial or peak frequency of ICOS<sup>+</sup>CD38<sup>+</sup> S-pMHC-II<sup>+</sup> CD4<sup>+</sup> T cells with the growth rate and peak value of neutralising antibody titres. Spearman correlation coefficient and p-values along with a linear regression line are shown for statistically significant comparisons (p<0.05), n=29 datapoints, pooled for both S-pMHC-II<sup>+</sup> CD4<sup>+</sup> T cell populations.



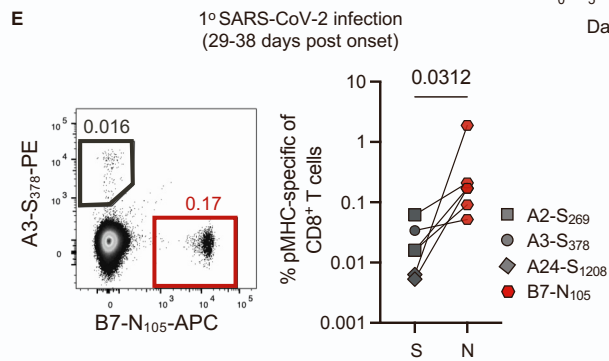
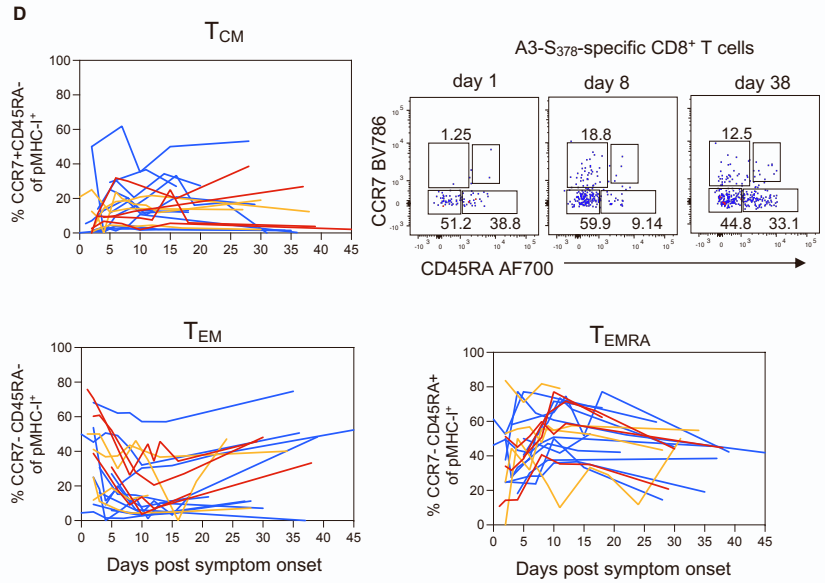
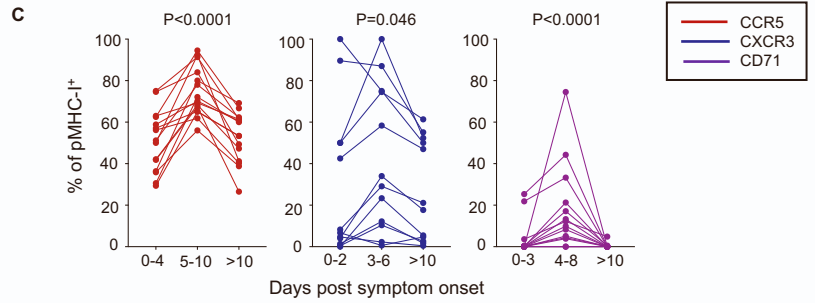
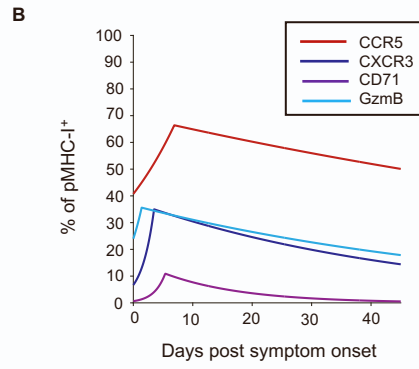
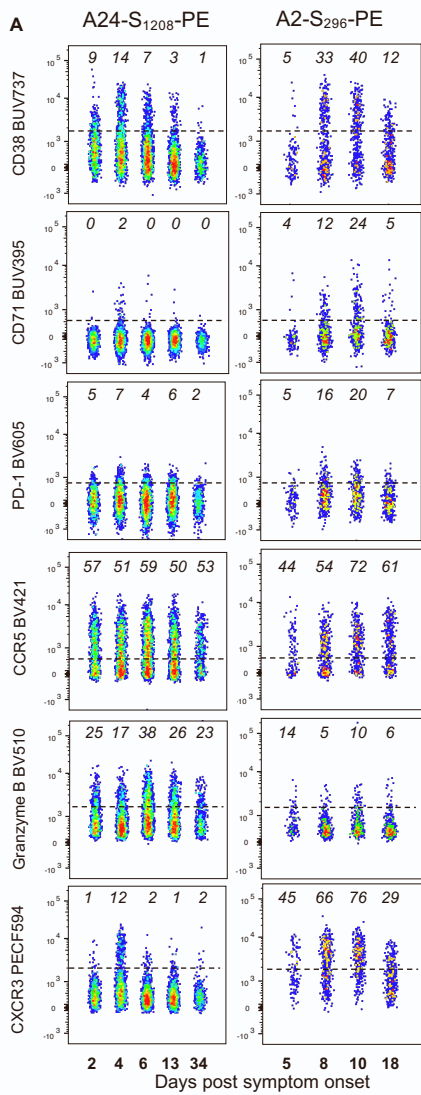
**Figure S3. Phenotype of S-specific CD4<sup>+</sup> T cells, related to Figure 2.**

**(A)** Representative flow cytometry plots of HLA-DR\*15-S<sub>751</sub> and HLA-DP\*04-S<sub>167</sub>-specific CD4<sup>+</sup> T cells from a single participant showing co-expression of CCR7 and CD45RA. Kinetics of T<sub>CM</sub> and T<sub>EM</sub> for both pMHC-II populations. **(B)** Flow cytometry plots of HLA-DP\*04-S<sub>167</sub>-specific CD4<sup>+</sup> T cells from a single participant for CCR5 and CXCR5 expression, representative of the data shown in Fig 2. **(C)** Estimated kinetics of CCR5 and CXCR3 expression. The lines indicate the mean estimate for measurement from the piecewise linear regression model, using pooled data from both pMHC-II populations as no significant differences were found between the two. **(D)** Flow cytometry plots of HLA-DR\*15-S<sub>751</sub> and HLA-DP\*04-S<sub>167</sub>-specific CD4<sup>+</sup> T cells from a single participant showing expression of Granzyme B, with kinetics from all participants shown both pMHC-II populations. Throughout the figure, coloured lines represent individual donors for each pMHC-specific population, n=19 for DP\*04-S<sub>167</sub> and n=9 for DR\*15-S<sub>751</sub>.

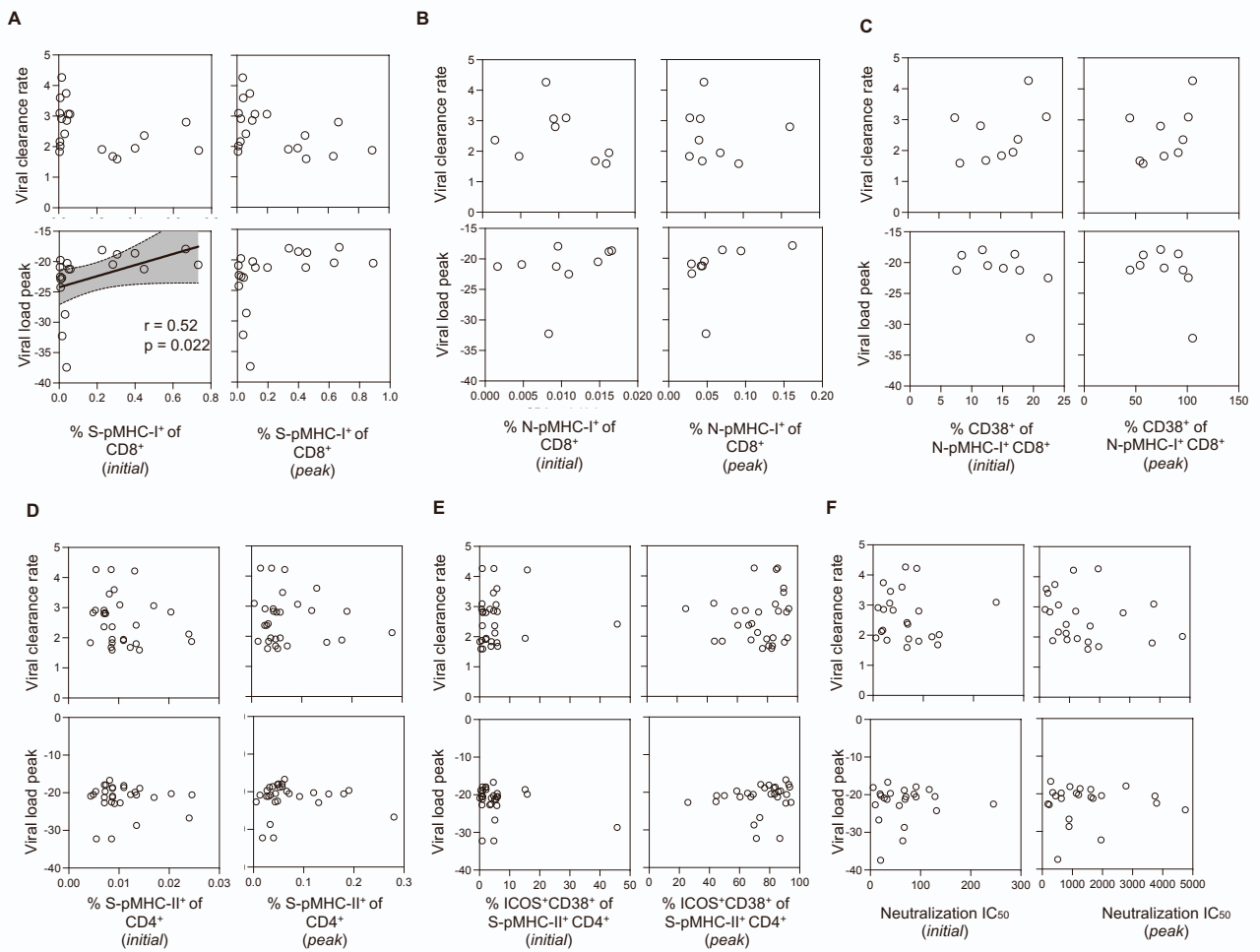


**Figure S4. CD8<sup>+</sup> T cell responses following BTI, related to Figure 3.** (A) Representative flow cytometry plots of HLA-A\*02-S<sub>269</sub> and HLA-A\*24-S<sub>1208</sub> -specific CD8<sup>+</sup> T cell kinetics. (B) pMHC-I<sup>+</sup> CD8<sup>+</sup> T cell kinetics colour coded for individuals with an observable expansion and those without. (C) Vaccination history of individuals with an observable expansion and those without. (D) pMHC-I<sup>+</sup> CD8<sup>+</sup> T cell frequency at earliest available timepoint for individuals with an observable expansion and those without. (E) Time from last vaccination to BTI for individuals with an observable and those without. (F) CD38<sup>+</sup> phenotype for pMHC-I<sup>+</sup> CD8<sup>+</sup> T cell kinetics colour coded for individuals with an observable expansion and those without.





**Figure S5. Phenotype of S-specific CD8<sup>+</sup> T cells, related to Figures 3 and 4.** (A) Flow cytometry plots of HLA-A\*02-S<sub>269</sub> and HLA-A\*24-S<sub>1208</sub>-specific CD8<sup>+</sup> T cells from a single participant for different phenotypic markers, representative of the data shown in Fig 3. (B) Estimated kinetics of CCR5, CXCR3, CD71 and GzmB expression. The lines indicate the mean estimate for measurement from the piecewise linear regression model, using pooled data from both pMHC-I populations as no significant differences were found between the two. (C) Changes in CCR5, CXCR3 and CD71 expression during the course of BTI, binned according to the kinetics estimated by linear regression (n=12-15). Statistics assessed by Friedman test. Data are shown for individuals with samples available at all timepoints indicated. (D) Representative flow cytometry plots of HLA-A\*03-S<sub>378</sub> -specific CD8<sup>+</sup> T cells from a single participant showing co-expression of CCR7 and CD45RA. Kinetics of T<sub>CM</sub>, T<sub>EM</sub> and T<sub>EMRA</sub> for all 3 pMHC-I populations. Throughout the figure, coloured lines represent individual donors for each pMHC-I-specific population, n=11 for A\*02-S<sub>269</sub>, n=4 A\*03-S<sub>378</sub> and n=4 for A\*24-S<sub>1208</sub>. (E) Frequency of spike-specific and nucleoprotein-specific CD8<sup>+</sup> T cells in convalescent samples from primary SARS-CoV-2 infection. For (C), n=6 donors with paired analysis of spike-specific CD8<sup>+</sup> T cells (either A\*02, A\*03 and A\*24) and B\*07-N<sub>105</sub>.



**Figure S6. Correlations between immune recall and viral clearance, related to Figure 5.** Correlations between the initial or peak frequency of **(A)** S-pMHC-I<sup>+</sup> CD8<sup>+</sup> T cells, **(B)** N-pMHC-I<sup>+</sup> CD8<sup>+</sup> T cells or **(C)** CD38<sup>+</sup> N-pMHC-I<sup>+</sup> CD8<sup>+</sup> T cells, **(D)** S-pMHC-II<sup>+</sup> CD4<sup>+</sup> T cells, **(E)** ICOS<sup>+</sup>CD38<sup>+</sup>S-pMHC-II<sup>+</sup> CD4<sup>+</sup> T cells, **(F)** neutralisation IC<sub>50</sub> titre against infecting or antigenically similar live virus and viral clearance rate or peak Ct value (amongst available timepoints). Throughout the figure Spearman correlation coefficient and p-values along with a linear regression line are shown for statistically significant comparisons (p<0.05), n=19 for (A), n=9 for (B-C), n=29 datapoints, pooled for both S-pMHC-II<sup>+</sup> CD4<sup>+</sup> T cell populations for (D-E), n=23 for (F).

**Supplementary Table 1.** Cohort demographics, related to Figure 1

Subject	Gender	Age	# Prior Vaccine doses	Last vaccine to symptom onset (days)	Class I Alleles (relevant to this study)	Class II Alleles (relevant to this study)	VOC
CP105	M	29	2	N.D.	A*02:01	--	Delta
CP106	F	30	2	139	--	DP*04:01	Delta
CP107	F	31	2	77-106	A*02:01	DP*04:01	Delta
CP108	M	29	2	132	--	DP*04:01	Delta
COR034	M	31	2	126	A*02:01, B*07:02	DR*15:01, DP*04:01	Delta
COR136	F	50	2	158	A*02:01, A*03:01	DP*04:01	Delta
COR015	F	27	3	39	A*02:01	--	BA.1
COR032	F	23	3	33	A*24:02, B*07:02	DR*15:01, DP*04:01	BA.1
CP110	M	24	2	84	A*02:01	DP*04:01	BA.1
CP111	M	34	2	83	A*24:02	--	BA.1
CP112	F	35	2	90	A*02:01 <sup>^</sup>	DP*04:01	BA.1
COR198	F	60	3	39	A*02:01	DP*04:02	BA.1
CP69*	F	36	2	111	A*02:01	DR*15:01, DP*04:01	BA.1
CP40*	M	63	3	49	--	DR*15:01, DP*04:01	BA.2
COR291	M	50	3	134	A*02:01	DR*15:01	BA.2
COR043	F	55	3	64	A*02:01	DP*04:01	BA.2
CP117	M	40	3	52	A*03:01, B*07:02	DR*15:01, DP*04:01	BA.2
COR281	F	43	3	129	A*03:01, B*07:02	DR*15:01, DP*04:01	BA.2
CP118	M	66	3	100	--	DP*04:01	BA.2
COR274	F	57	3	155	A*03:01	DP*04:01, 04:02	BA.2
COR275	M	62	3	83	A*02:01, B*07:02	DR*15:01, DP*04:01	BA.2
COR215	F	55	3	125	A*24:02, B*07:02	DR*15:01, DP*04:01	BA.2
COR039	F	58	3	169	A*24:02, B*07:02	DR*15:01, DP*04:01	BA.2

\*Previously infected during Hu-1 wave. <sup>^</sup>Data not shown, due to lack of A\*02:01 pentamer binding in any longitudinal samples from participant; N.D., not determined.

**Supplementary Table 2.** Piecewise linear regression parameters of viral kinetics and neutralising antibodies (with 95% CI), related to Figure 1. Values in bold indicate a significant difference between VOCs.

		<b>Initial value</b>	<b>Delay (days PSO)</b>	<b>Growth Rate (per day)</b>	<b>Peak Time (days PSO)</b>	<b>Decay Rate (per day)</b>
Viral RNA ( $\Delta$ Ct)	Delta	36.5 (44.71 – 28.29)	N/A	5.47 (2.83 – 10.57)	3.22 (2.53 – 4.1)	<b>3.97</b> (3.03 – 5.22)
	BA.1	31.79 (49.98 – 13.6)	N/A	4.41 (0.82 – 23.77)	2.43 (1.24 – 4.78)*	<b>2.13</b> (1.03 – 4.43)
	BA.2	24.2 (49.5 – 1.1)	N/A	6.73 (0.32 – 139.23)	1.12 (0.47 – 2.63)	<b>2.04</b> (1.12 – 3.73)
	Nab (IC <sub>50</sub> )	51.29 (30.52 – 86.18)	4.3 (2.2 – 8.42)	0.12 (0.084 – 0.18)	14.58 (12.23 – 17.39)	N/A

**Supplementary Table 3.** Estimates of spike-specific CD4<sup>+</sup> T cell expansion, activation and phenotypic parameters (with 95% CI), related to Figures 2 and 5. Pooled estimates from both epitopes are shown if the epitope-specific estimates were not significantly different for any parameter. Separate epitope-specific estimates are shown if at least one of the parameters of that makers were significantly different between epitopes. Values in bold indicate a significant difference between epitopes for the indicated marker.

	<b>Initial (%)</b>	<b>Delay (days PSO)</b>	<b>Growth Rate (per day)</b>	<b>Peak Time (days PSO)</b>	<b>Decay Rate (per day)</b>
%pMCH <sup>+</sup> of CD4 <sup>+</sup>	0.0093 (0.0071 – 0.012)	2.51 (1.86 – 3.4)	0.24 (0.16 – 0.35)	5.42 (4.81 – 6.1)	0.014 (0.01 – 0.019)
%CD38 <sup>+</sup> ICOS <sup>+</sup> of pMCH <sup>+</sup>	2.44 (1.1 – 5.42)	1.12 (0.7 – 1.8)	0.62 (0.5 – 0.76)	3.60 (3.22 – 4.01)	0.057 (0.051 – 0.063)

	<b>Initial (%)</b>	<b>Growth Rate (per day)</b>	<b>Peak Time (days PSO)</b>	<b>Decay Rate (per day)</b>
%CCR5 <sup>+</sup> ( <i>pooled epitopes</i> )	16.59 (12 – 22.96)	0.26 (0.19 0 0.35)	2.48 (2.15 – 2.85)	0.0064 (0.0043 – 0.0095)
%CXCR3 <sup>+</sup> ( <i>pooled epitopes</i> )	14.4 (7.51 – 27.8)	0.27 (0.13 – 0.54)	1.93 (1.25 – 2.96)	0.0064 (0.0032 – 0.013)
%GzmB <sup>+</sup> ( <i>pooled epitopes</i> )	7.34 (4.27 – 12.62)	0.13 (0.04 – 0.4)	1.97 (0.88 – 4.38)	0.019 (0.013 – 0.029)
%PD-1 <sup>+</sup> ( <i>DP04</i> )	22.38 (10.49 – 47.78)	0.11 (0.05 – 0.26)	4.05 (3.29 – 5)	<b>0.0078</b> (0.004 – 0.015)
%PD-1 <sup>+</sup> ( <i>DR15</i> )	34.04 (6.7 – 172.82)	0.12 (0.019 – 0.78)	2.71 (1.46 – 5.03)	<b>0.00047</b> (0.00023 – 0.0093)
%CD71 <sup>+</sup> ( <i>DP04</i> )	1.05 (0.39 – 2.86)	0.38 (0.23 – 0.62)	3.35 (2.73 – 4.11)	<b>0.077</b> (0.056 – 0.11)
%CD71 <sup>+</sup> ( <i>DR15</i> )	1.32 (0.08 – 21.71)	0.45 (0.00011 – 1.821)	1.64 (0.001 – 2.588)	<b>0.038</b> (0.014 – 0.1)

**Supplementary Table 4.** Estimates of S-specific CD8<sup>+</sup> T cell expansion and activation (with 95% CI), related to Figures 3 and 5. Pooled estimates from all three epitopes are shown.

	<b>Initial (%)</b>	<b>Delay (days PSO)</b>	<b>Growth Rate (per day)</b>	<b>Peak Time (days PSO)</b>	<b>Decay Rate (per day)</b>
%pMCH <sup>+</sup> of CD8 <sup>+</sup>	0.055 (0.024 – 0.12)	4.39 (3.4 – 5.68)	0.15 (0.07 – 0.3)	5.81 (4.87 – 6.94)	0.00068 (4.7e-7 – 0.98)
%CD38 <sup>+</sup> of pMCH <sup>+</sup>	15.85 (10.82 – 23.21)	0.24 (0.019 – 3.06)	0.082 (0.055 – 0.12)	7.1 (5.86 – 8.6)	0.036 (0.028 – 0.046)

	<b>Initial (%)</b>	<b>Growth Rate (per day)</b>	<b>Peak Time (days PSO)</b>	<b>Decay Rate (per day)</b>
%CCR5 <sup>+</sup>	40.74 (34.41 – 48.23)	0.031 (0.018 – 0.052)	6.89 (5.17 – 9.17)	0.0032 (0.0015 – 0.0068)
%CXCR3 <sup>+</sup>	6.68 (2.93 – 15.26)	0.2 (0.12 – 0.34)	3.49 (2.56 – 4.75)	0.0093 (0.0049 – 0.017)
%GzmB <sup>+</sup>	23.99 (13.77 – 41.79)	0.12 (0.007 – 2.14)	1.4 (0.15 – 12.58)	0.0069 (0.0039 – 0.012)
%CD71 <sup>+</sup>	0.64 (0.2 – 2)	0.23 (0.14 – 0.38)	5.36 (4.25 – 6.77)	0.033 (0.022 – 0.049)
%PD-1 <sup>+</sup>	7.52 (4.53 – 12.46)	0.096 (0.04 – 0.23)	3.32 (2.14 – 5.16)	0.0079 (0.0047 – 0.013)

**Supplementary Table 5.** Estimates of S- and N-specific CD8<sup>+</sup> T cell expansion and activation (with 95% CI), related to Figures 4 and 5. Values in bold indicate a significant difference between epitopes for the indicated marker.

	<b>Initial (%)</b>	<b>Delay (days PSO)</b>	<b>Growth Rate (per day)</b>	<b>Peak Time (days PSO)</b>	<b>Decay Rate (per day)</b>
%pMCH <sup>+</sup> of CD8 <sup>+</sup> <b>(S)</b>	<b>0.098</b> (0.012 – 0.82)	6.29 (1.49 – 26.46)	0.087 (0.013 – 0.556)	7.69 (3.56 – 16.57)	0 (NA)
%pMCH <sup>+</sup> of CD8 <sup>+</sup> <b>(N)</b>	<b>0.012</b> (0.0048 – 0.03)	3.06 (1.62 -5.81)	0.12 (0.071 – 0.2)	8.17 (6.32 – 10.56)	0 (NA)
%CD38 <sup>+</sup> <b>(S)</b>	10.16 (1.66 – 62.36)	0.95 (0.001 – 86.85)	0.073 ( 0.01 – 0.52)	8.29 (4.45 – 15.43)	<b>0.047</b> (0.014 – 0.16)
%CD38 <sup>+</sup> <b>(N)</b>	17.78 (9.58 – 33)	3.63 (2.28 – 5.79)	0.19 (0.077 – 0.45)	6.89 (5.26 – 9.02)	<b>0.019</b> (0.011 – 0.034)



**Supplementary Table 6.** Estimates of S- and N-specific CD8<sup>+</sup> T cell phenotypic parameters (with 95% CI) for individuals presented in Figure 4. Estimates for N-specific CD8<sup>+</sup> T cells only are shown if the S -and N-specific estimates were not significantly different for any parameter (estimates for S only are shown in Supplementary Table 6. Separate epitope-specific estimates are shown if at least one of the parameters of that makers were significantly different between epitopes. Values in bold indicate a significant difference between epitopes for the indicated marker. Growth and decay parameters for PD-1 expression kinetics could not be determined.

	<b>Initial (%)</b>	<b>Growth Rate (per day)</b>	<b>Peak Time (days PSO)</b>	<b>Decay Rate (per day)</b>
%GzmB <sup>+</sup> ( <b>S</b> )	<b>22.75</b> (4.81 – 135.88)	0.100 (0.0002 – 5.43)	1.22 (0.01 – 141.04)	0.0081 (0.0015 – 0.042)
%GzmB <sup>+</sup> ( <b>N</b> )	<b>6.83</b> (3.4 – 13.76)	0.08 (0.045 – 0.17)	5.26 (3.14 – 8.81)	0.021 (0.012 – 0.038)
<hr/>				
%CCR5 <sup>+</sup> ( <b>S</b> )	<b>40.93</b> (14.96 – 111.96)	<b>0.017</b> (0.0043 – 0.071)	7.52 (2.69 – 21.05)	0.0002 (1e-13 – 3.6)
%CCR5 <sup>+</sup> ( <b>N</b> )	<b>2.15</b> (1.32 – 3.48)	<b>0.29</b> (0.2 – 0.41)	4.95 (3.75 – 6.52)	0.01 ( 0.0066 – 0.016)
<hr/>				
%CD71 <sup>+</sup> ( <b>N</b> )	0.74 (0.11 - 5.05)	0.36 (0.16 - 0.85)	4.13 (3.09 - 5.54)	0.045 (0.027 - 0.073)
%CXCR3 <sup>+</sup> ( <b>N</b> )	12.89 (6.79 - 24.45)	0.13 (0.062 - 0.28)	4.75 (3.08 - 7.33)	0.0038 (0.0006 - 0.025)