

Supplemental information

**Robust SARS-CoV-2 T cell responses with common
TCR $\alpha\beta$ motifs toward COVID-19 vaccines in patients
with hematological malignancy impacting B cells**

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SUPPLEMENTAL INFORMATION

Robust T cell responses with common TCR $\alpha\beta$ motifs towards COVID-19 vaccines in haematological malignancy patients with impacted B cell immunity

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Table S1. Cohort demographics and clinical summary, refer to Figure 1.

Figure S1. Haematology patients grouped by low, normal or high B cell numbers.

Figure S2. FACS gating strategies to measure cellular vaccine responses.

Figure S3. Correlations of whole blood subsets.

Figure S4. Functional spike-specific CD4⁺ and CD8⁺ T cell responses in haematology patients and healthy individuals.

Figure S5. Spike-specific CD4⁺ and CD8⁺ T cell responses by vaccine type.

Figure S6. Volcano plots comparing healthy individuals and haematology patients.

Figure S7. *Ex vivo* SARS-CoV-2-specific tetramer⁺ T cell responses following COVID-19 vaccination.

Figure S8. Vaccine responses in donors with breakthrough SARS-CoV-2 infections.

Figure S9. *Ex vivo* paired spike and non-spike-specific tetramer⁺ CD8⁺ T cell responses following breakthrough COVID-19.

Figure S10. V and J gene segment usage and covariation in epitope-specific responses.

Figure S11. TCR logo representations of CDR3 α and β sequence motifs for DPB4/S₁₆₇, A2/S₂₆₉ and A24/S₁₂₀₈.

Figure S12. Individual patient's immune response following COVID-19 vaccination.

Supplementary Tables

Table S1. Cohort demographics and clinical summary, refer to Figure 1.

	Healthy individuals	Haematology patients	BNT162b2, mRNA-1273	ChAdOx1
Number of individuals, <i>n</i>	58	95	25	70
Age, mean (range)	44 (20-80)	65 (19-91)	51 (19-80)	70 (51-91)
Female, <i>n</i> (%)	41 (71%)	28 (29%)	-	-
Vaccine (2 doses), <i>n</i> (%)				
ChAdOx1 (AstraZeneca)	26 (45%)	70 (74%)	-	-
Age, mean (range)	51 (20-80)	70 (51-91)	-	-
BNT162b2 Comirnaty (Pfizer)	32 (55%)	24 (25%)	-	-
Age, mean (range)	38 (23-60)	50 (19-80)	-	-
mRNA-1273 (Moderna)	0	1 (1%)	-	-
Vaccine (3 rd dose), <i>n</i> (%)				
ChAdOx1 (AstraZeneca)	1 (2%)	5 (5%)	-	-
BNT162b2 Comirnaty (Pfizer)	20 (34%)	63 (66%)	-	-
mRNA-1273 (Moderna)	1 (2%)	10 (11%)	-	-
Novavax	1 (2%)	0 (0%)	-	-
Unknown due to lost follow-up	35 (60%)	17 (18%)	-	-
Cellular therapy, <i>n</i> (%)				
Allogeneic SCT	-	33 (34%)	17 (68%)	16 (23%)
Autograft	-	5 (5%)	4 (16%)	1 (1%)
CAR T-cell	-	21(22%)	9 (36%)	12 (17%)
CAR T-cell	-	7 (7%)	4 (16%)	3 (5%)
Days post-cellular therapy, mean (range)	-	177 (45-393)	185 (45-393)	167 (73-337)
Malignancy/treatment, <i>n</i> (%)				
CLL/naive	-	14 (15%)	2 (8%)	12 (17%)
CLL/venetoclax	-	5 (5%)	1 (4%)	4 (6%)
CLL/zanubrutinib	-	25 (26%)	1 (4%)	24 (34%)
WM/naive	-	1 (1%)	0	1 (1%)
WM/zanubrutinib	-	10 (11%)	1 (4%)	9 (13%)
Myeloma	-	7 (7%)	3 (12%)	4 (6%)
Previous SARS-CoV-2 infection, <i>n</i>	1	0	0	0
SARS-CoV-2 infection during the study, <i>n</i>	8	12	5	7

Abbreviations: CAR T-cell, chimeric antigen receptor T-cell; CLL, chronic lymphocytic leukemia; SCT, stem cell transplantation; WM, Waldenstrom macroglobulinemia. Clinical information and limited immune data have been described for a subset of CLL patients.⁴¹

SUPPLEMENTARY FIGURES

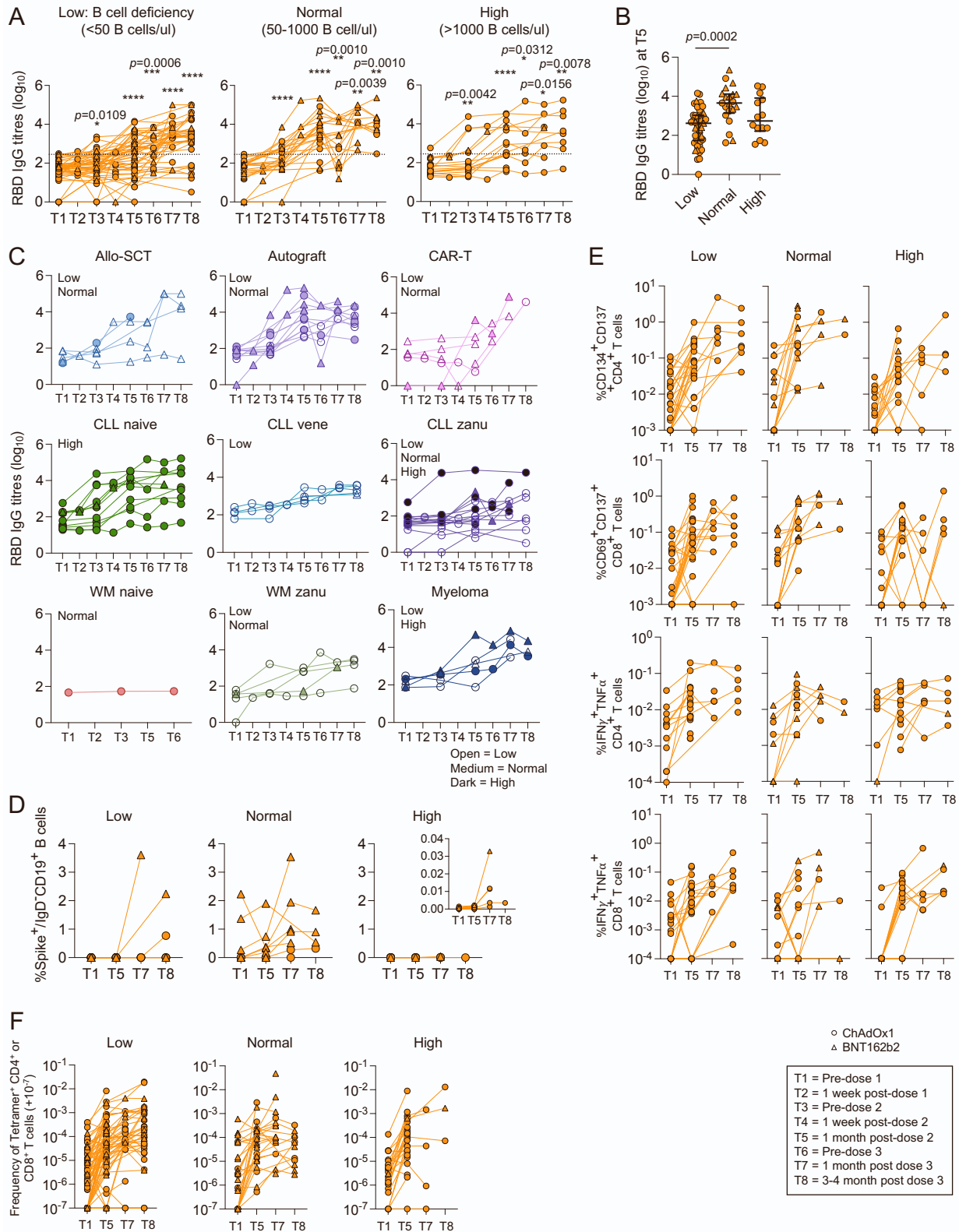


Figure S1. Haematology patients grouped by low, normal or high B cell numbers. End-point IgG titres of ancestral RBD antibodies (A) across sampling timepoints, (B) at T5, and (C) per malignancy and treatment group. (D) Spike-specific memory B cells in haematology patients grouped by low, normal or high B cell numbers. (E) AIM and ICS frequencies and (F) tetramer⁺ spike-specific CD4⁺ and CD8⁺ T cells grouped by low, normal or high B cell numbers. Due to limited sample availability, experiments were performed once for each sample. Related to Figure 1, 3, 4.

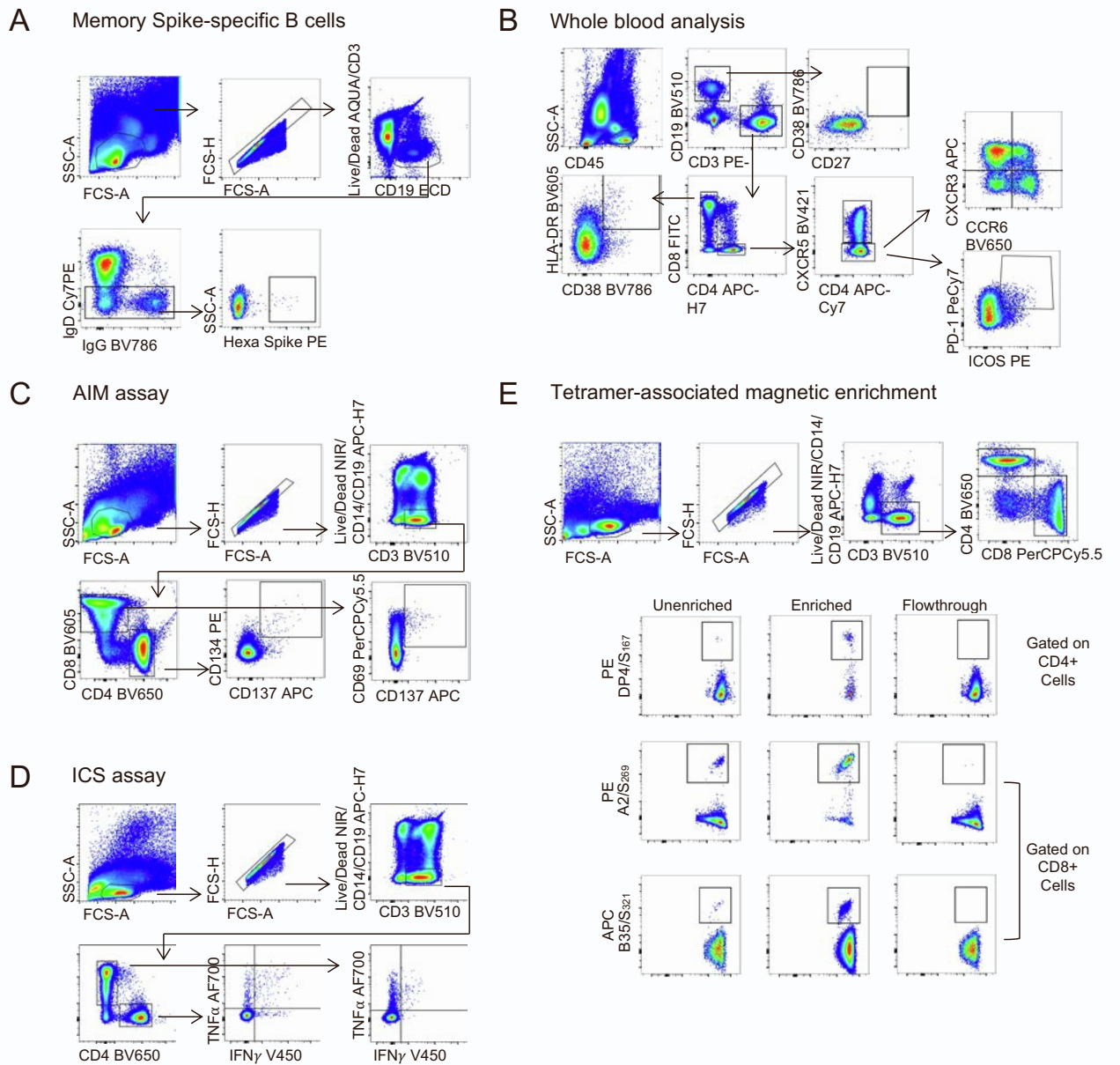


Figure S2. FACS gating strategies to measure cellular vaccine responses. Gating strategy for (A) memory spike-specific B cells, (B) whole blood analysis, (C) AIM and (D) ICS assay, and (E) TAME. Related to Figure 1, 2, 3 and 4.

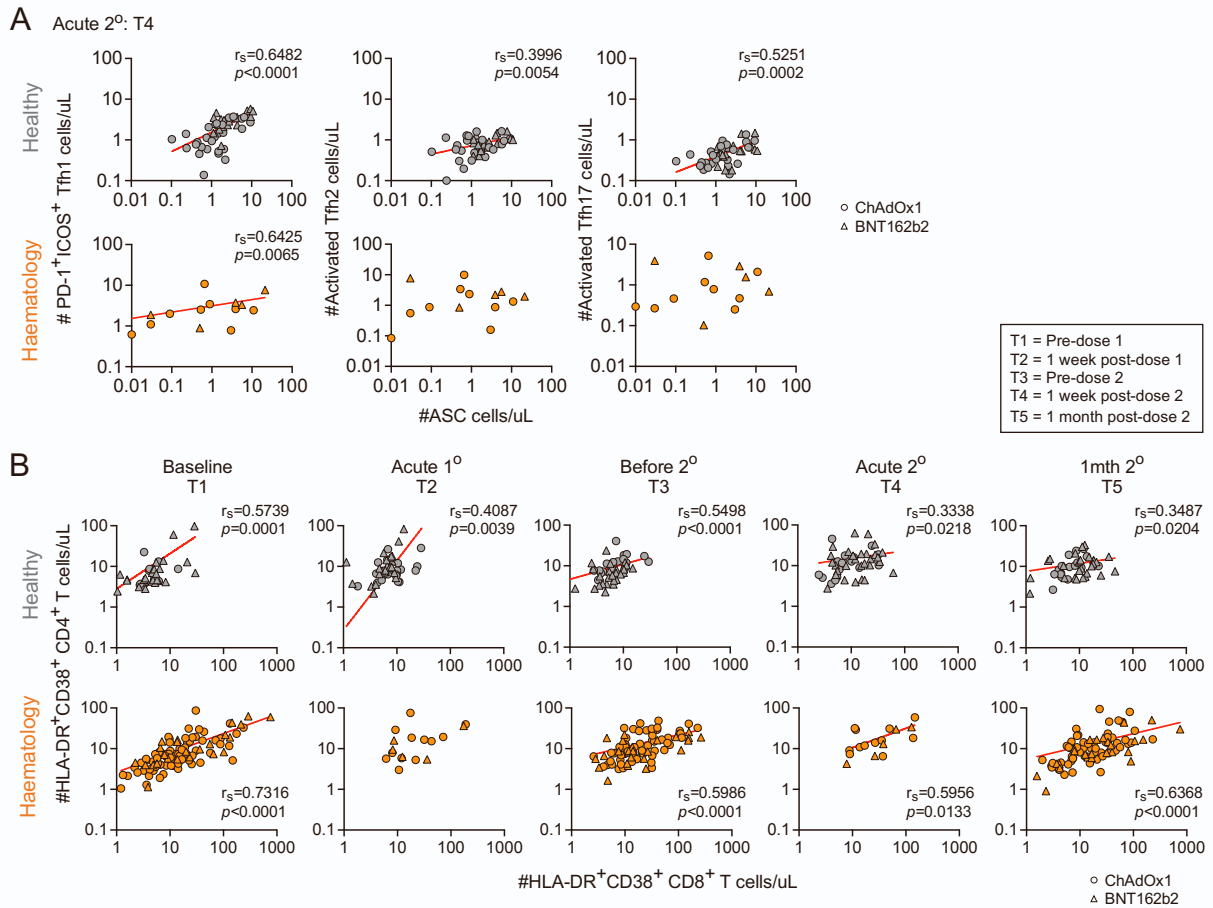


Figure S3. Correlations of whole blood subsets. (A) Spearman's correlation (r_s) of ASCs and Tfh1, Tfh2 and Tfh17 subsets at T4. (B) Spearman's correlation (r_s) of activated CD4⁺ and CD8⁺ T cells at T1-T5. Due to limited sample availability, experiments were performed once for each sample. Related to Figure 2.

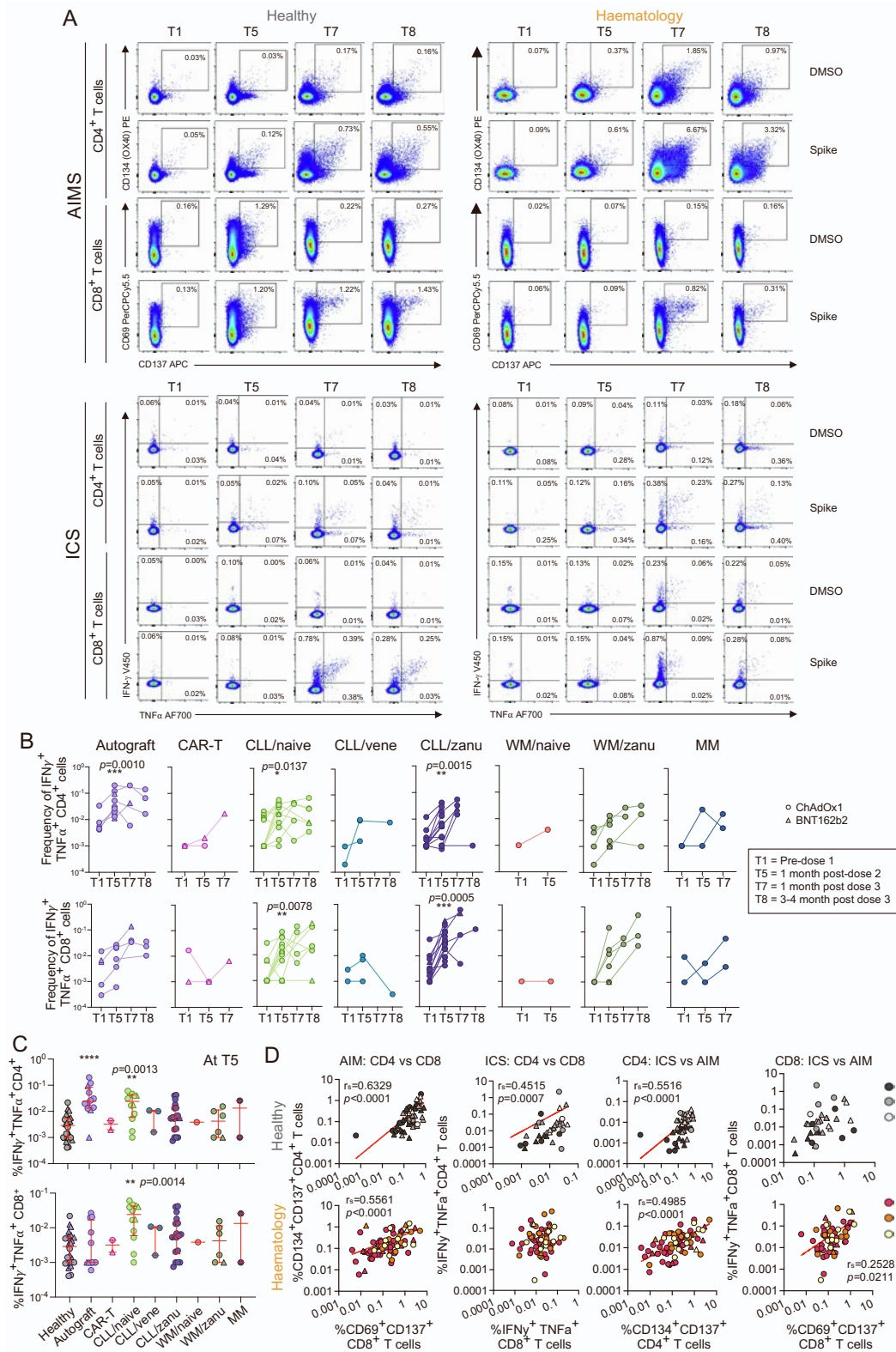


Figure S4. Functional spike-specific CD4⁺ and CD8⁺ T cell responses in haematology patients and healthy individuals. (A) Representative AIM and ICS FACS plots including DMSO controls. (B) ICS frequency per malignancy and treatment group at all timepoints measured and (C) at T5 where median and IQR are shown. Statistical significance determined by Dunn's multiple comparisons set on healthy versus all other disease groups. (D) Spearman correlations of CD4⁺ and CD8⁺ T cell responses via AIM and ICS assays. Statistical significance determined by Wilcoxon test for timepoint comparisons against T1 (floating values). Exact p values $0.0001 < p < 0.05$ are shown except $p < 0.0001 = ****$. Due to limited sample availability, experiments were performed once for each sample. Related to Figure 3.

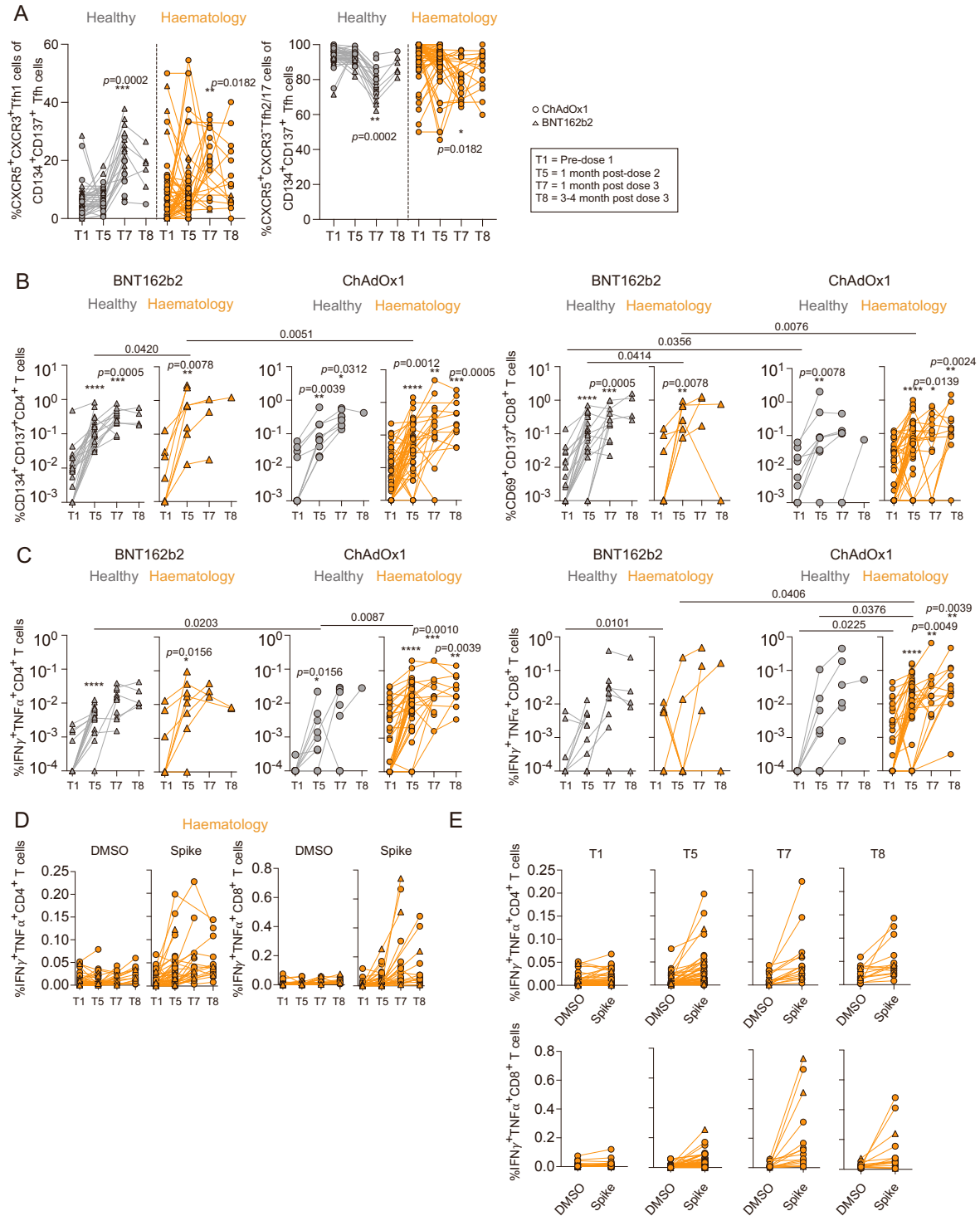


Figure S5. Spike-specific CD4⁺ and CD8⁺ T cell responses by vaccine type. (A) Frequency of Tfh1 and Tfh2/17 AIM⁺ responses of total AIM⁺ CXCR5⁺CD4⁺ Tfh cell response. (B) AIM and (C) ICS frequencies of CD4⁺ and CD8⁺ T cells in healthy and haematology per vaccine type. (D, E) Raw percentages of IFN_γ⁺TNF_α⁺ in DMSO and spike ICS cultures. Statistical significance determined by Wilcoxon test for timepoint comparisons against T1 (floating values) or by Mann-Whitney for comparisons between healthy and patient timepoints or between vaccine type (connecting line). Exact p values $0.0001 < p < 0.05$ are shown except $p < 0.0001 = ****$. Due to limited sample availability, experiments were performed once for each sample. Related to Figure 3.

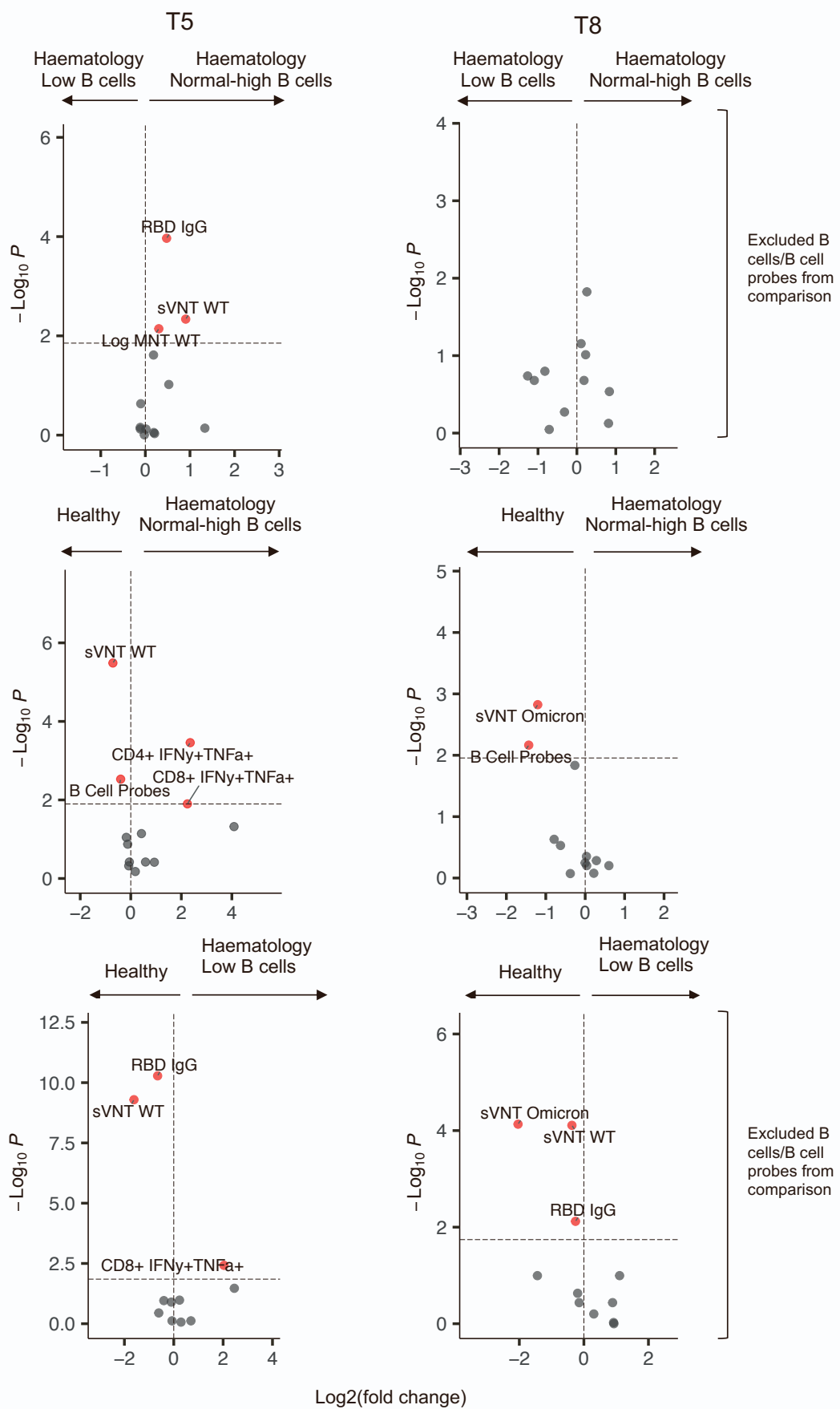


Figure S6. Volcano plots comparing healthy individuals and haematology patients. Related to Figure 3.

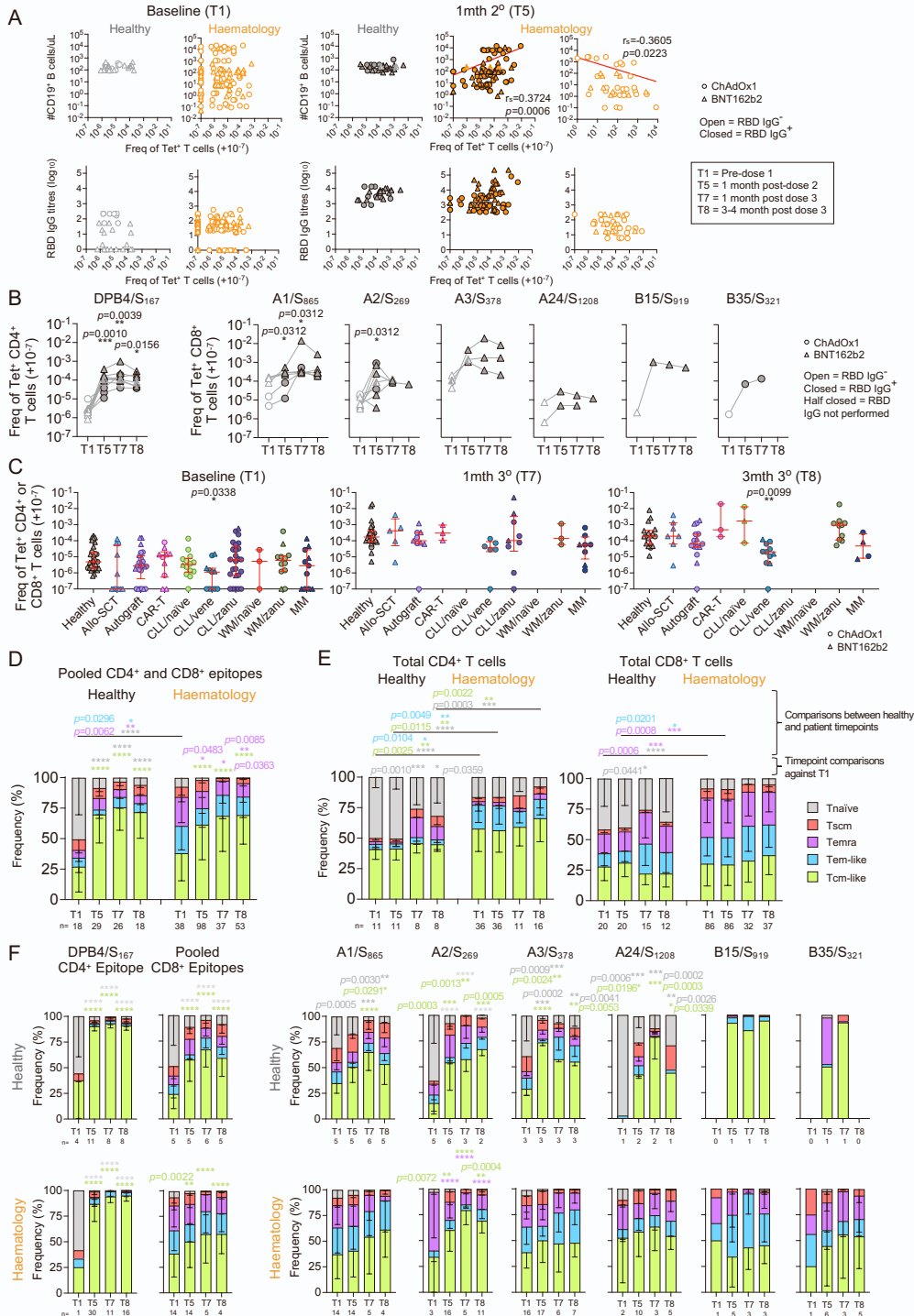


Figure S7. *Ex vivo* SARS-CoV-2-specific tetramer⁺ T cell responses following COVID-19 vaccination. (A) Spearman's correlation (r_s) of tetramer frequencies versus B cell numbers and RBD IgG titres at T1 and T5. (B) Tetramer CD4⁺ and CD8⁺ T cell frequencies of healthy individuals per SARS-CoV-2 epitope. (C) Tetramer frequencies at T1, T7 and T8 where median and IQR are shown. (D) Phenotype profiles of pooled tetramer⁺ cells, (E) total CD4⁺ T cells and CD8⁺ T cells and (F) per SARS-CoV-2 epitope. The frequency of tetramer⁺ cells have been right-shifted by 10^{-7} (i.e. no detected tetramer⁺ events displayed as 10^{-7}) to allow for visibility on the logarithmic y axis. Only samples with 10 or more tetramer⁺ events are included in the phenotypic analysis (Figure D, E and F). Statistical significance determined by Wilcoxon test for timepoint comparisons against T1 ((B) floating values), Dunn's multiple comparisons set on healthy versus all other disease groups (c), Tukey's multiple comparison test (floating values are timepoint comparisons against T1; connecting line are comparisons between healthy and patient timepoints) (D,E), and Dunnett's multiple comparison test for timepoint comparisons against T1 (F). Exact p values $0.0001 < 0.05$ are shown except $p < 0.0001 = ****$. Due to limited sample availability, experiments were performed once for each sample. Related to Figure 4.

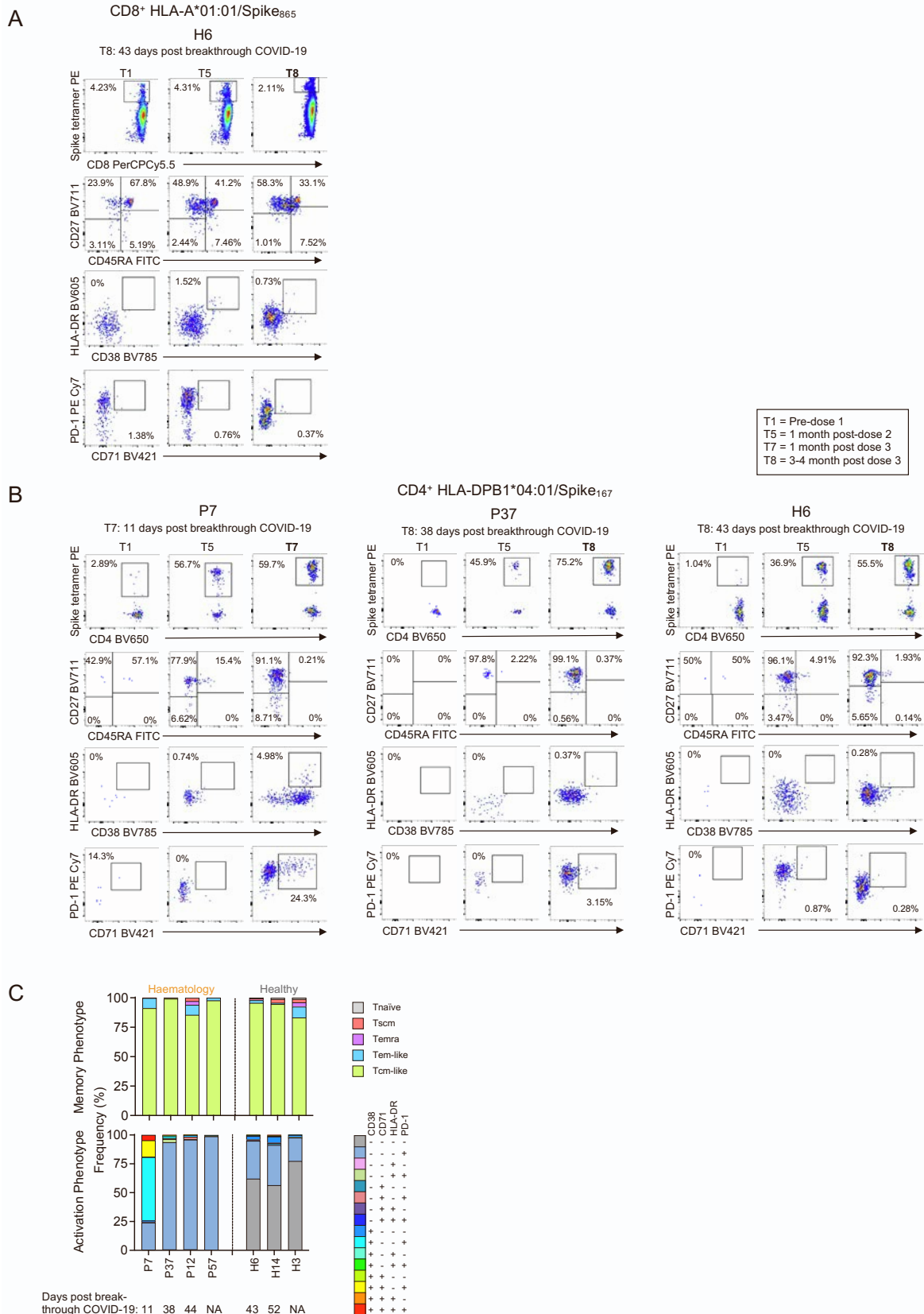


Figure S8. Vaccine responses in donors with breakthrough SARS-CoV-2 infections. Representative TAME enriched FACS plots gated on CD8⁺ (A) and CD4⁺ (B) T cells depicting tetramer, and memory and activation phenotypes. (C) Memory and activation phenotypes of DPB4/S₁₆₇-specific CD4⁺ T cells from individuals with breakthrough COVID-19. Due to limited sample availability, experiments were performed once for each sample. Related to Figure 5.

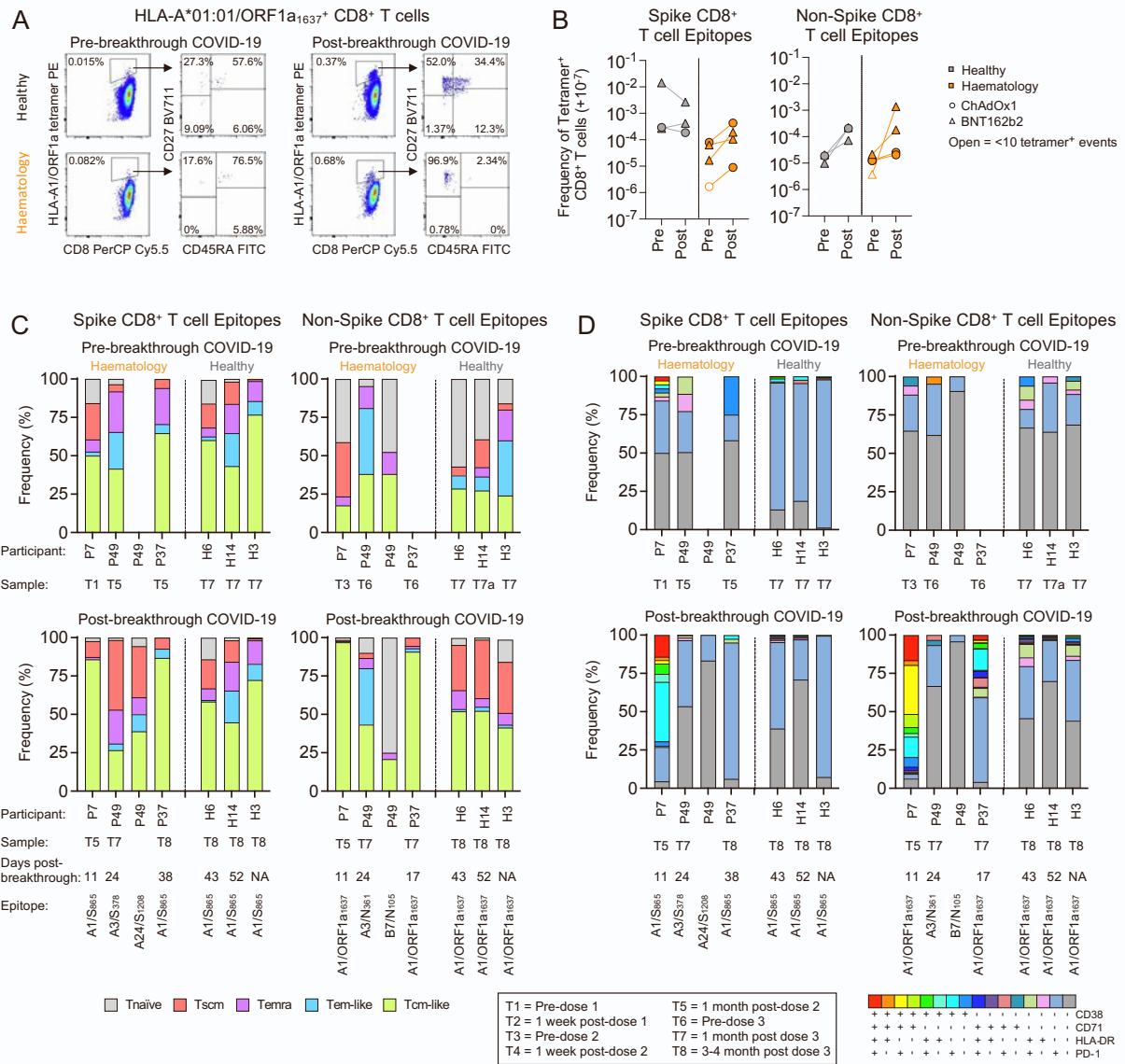


Figure S9. *Ex vivo* paired spike and non-spike-specific tetramer⁺ CD8⁺ T cell responses following breakthrough COVID-19. (A) Representative FACS plots of TAME-enriched non-spike-specific CD8⁺ tetramer populations. (B) Paired tetramer CD8⁺ T cell frequencies of healthy and haematology participants pre- and post-COVID-19 breakthrough. Any samples with < 10 tetramer⁺ events are shown as open symbols. (C) Memory and (D) activation phenotype profiles for spike and non-spike-specific CD8⁺ T cells for individuals with breakthrough COVID-19. The frequency of tetramer⁺ cells have been right-shifted by 10^{-7} (i.e. no detected tetramer⁺ events displayed as 10^{-7}) to allow for visibility on the logarithmic y axis. Only samples with 10 or more tetramer⁺ events are included in the phenotypic analysis (Figure C and D). Due to limited sample availability, experiments were performed once for each sample. Related to Figure 5.

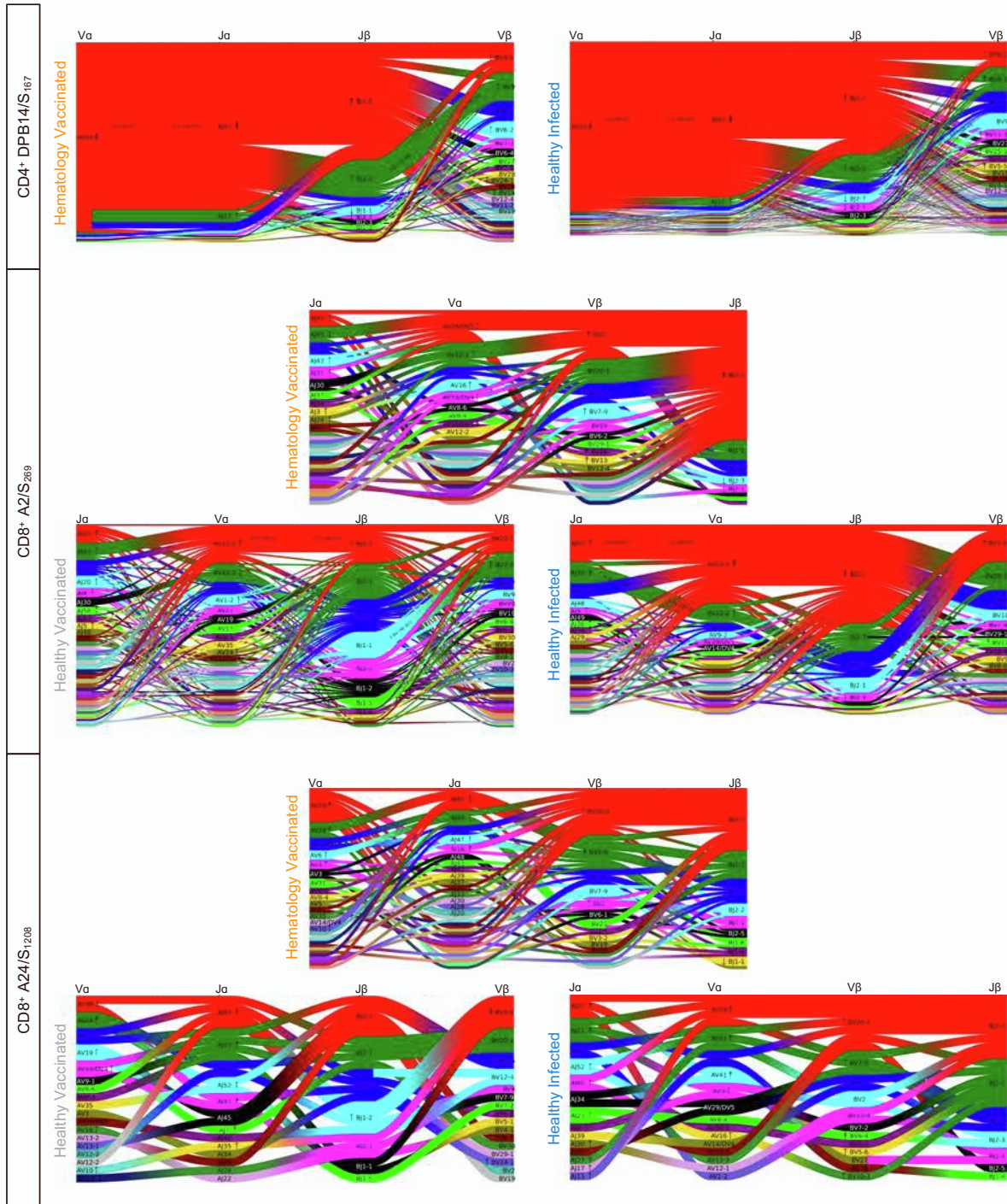


Figure S10. V and J gene segment usage and covariation in epitope-specific responses. Gene-gene pairing landscapes are depicted by curves between vertical gene segment stacks (thickness proportional to the number of TCRs with the gene pairing). Vertical arrows indicate the enrichment of gene segments relative to background frequencies, each arrowhead indicates a 2-fold enrichment. The clonally expanded TCRs were reduced to a single data point for this analysis. Genes are coloured based on frequency: red (most frequent), green (second most frequent), blue, cyan, magenta, and black, followed by assorted colours for rare frequencies. Related to Figure 6.

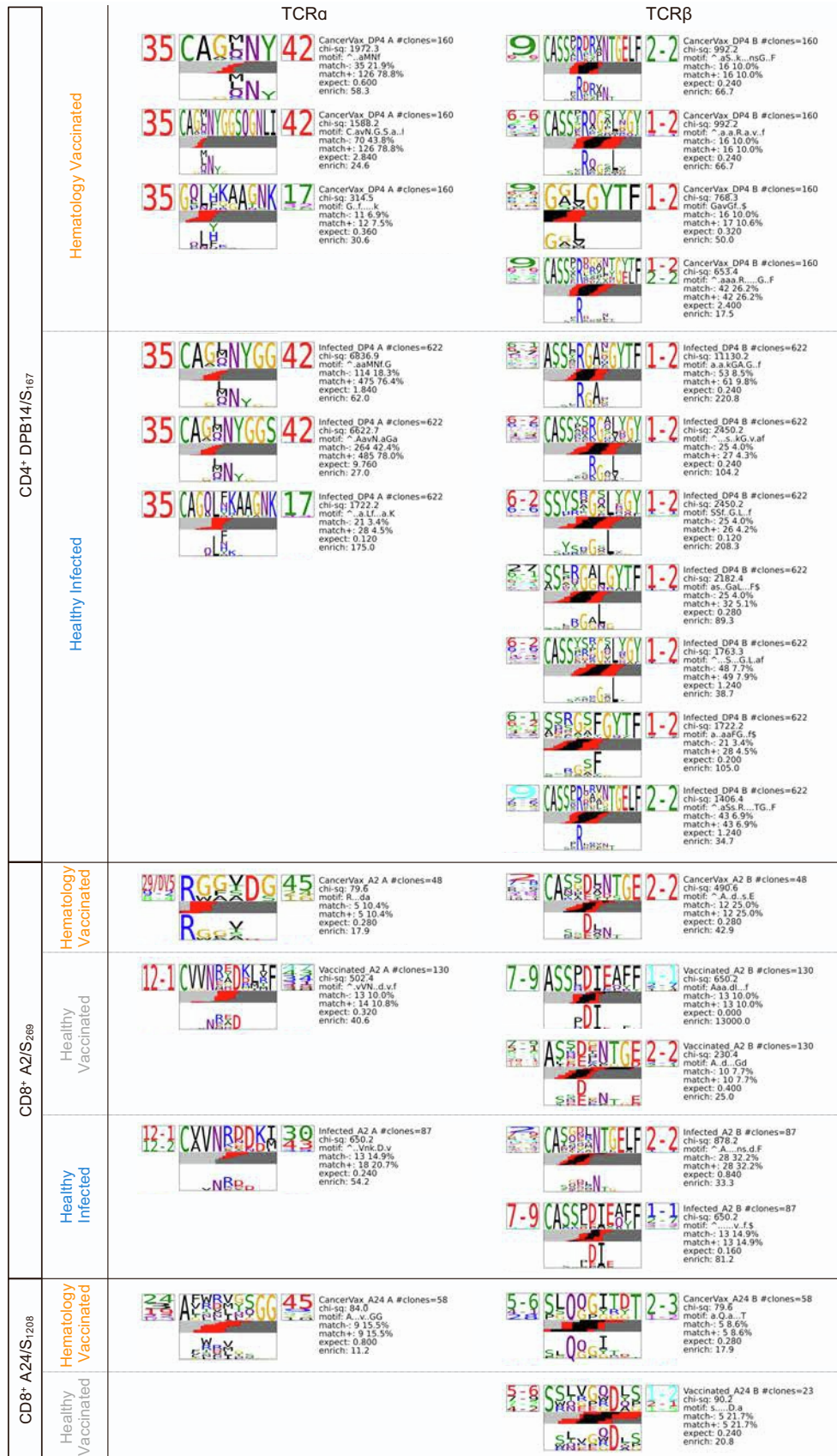
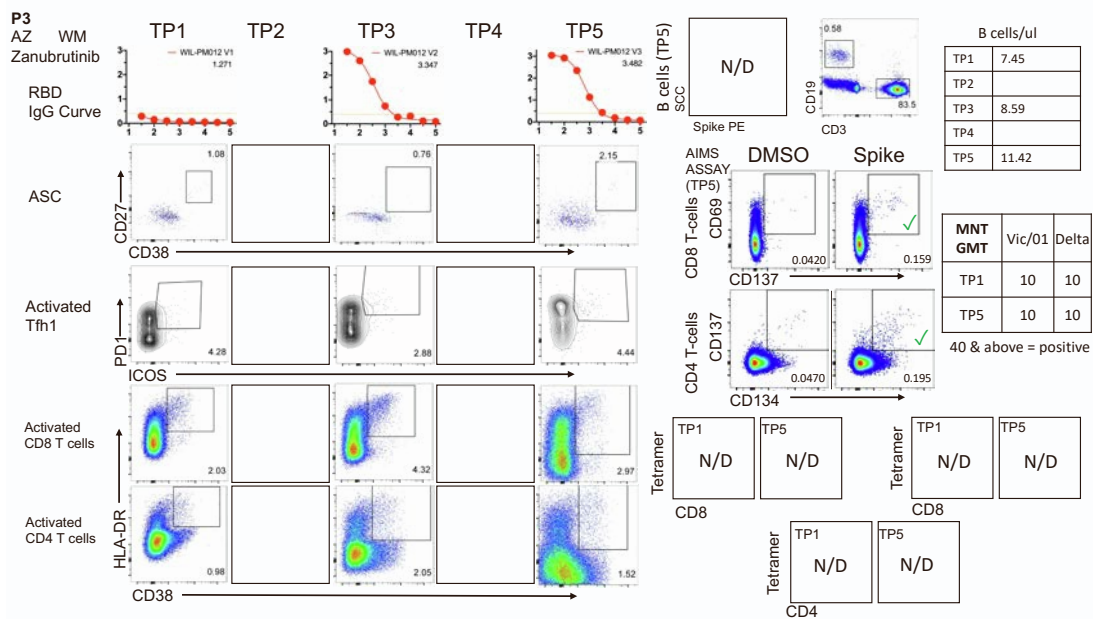
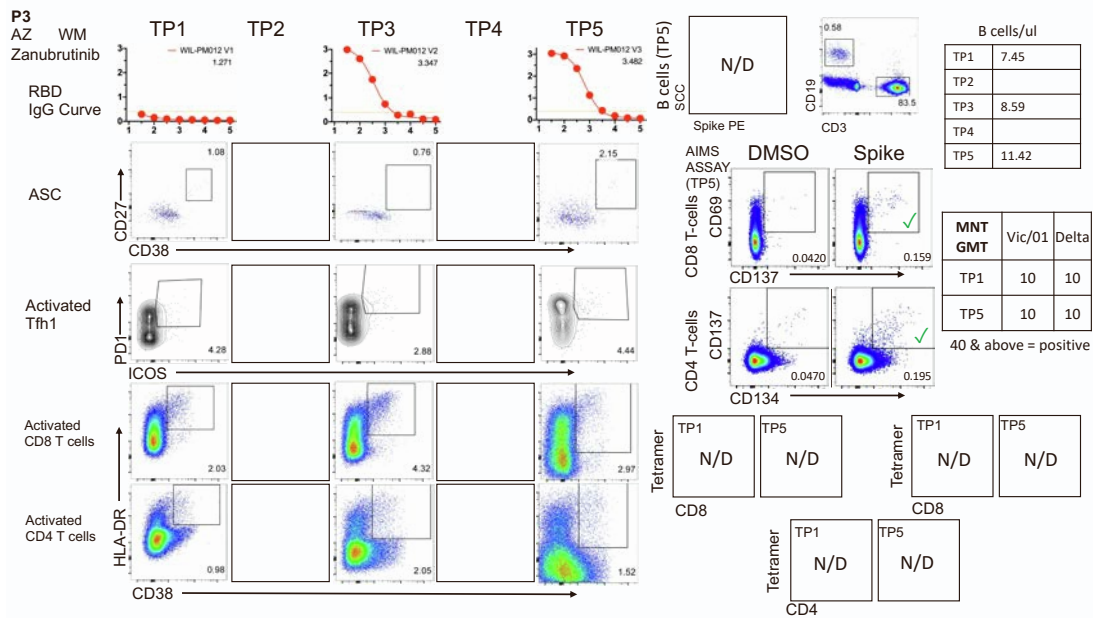
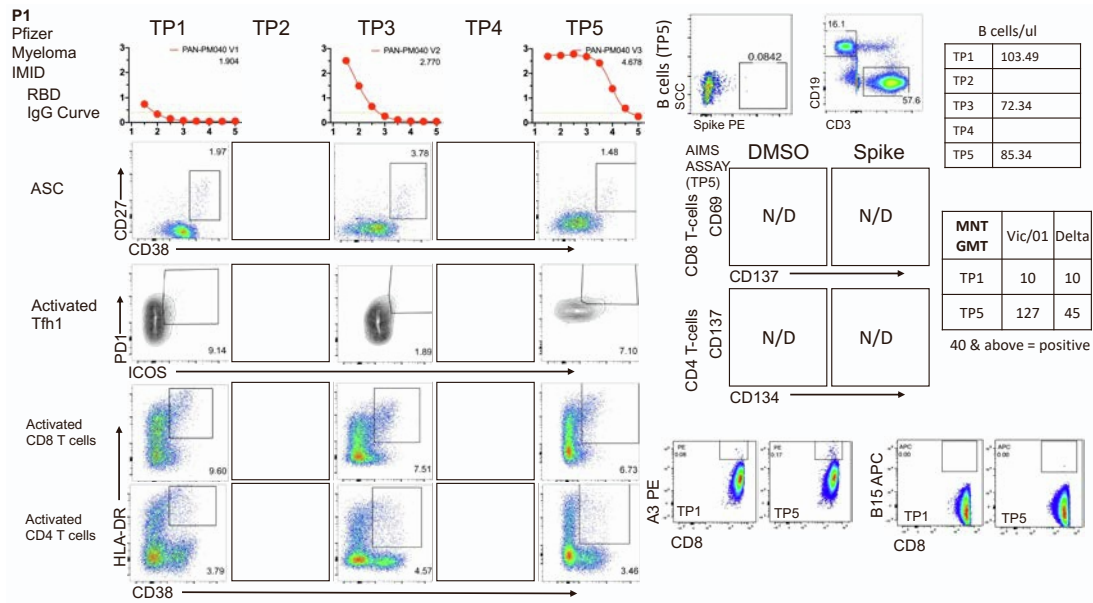
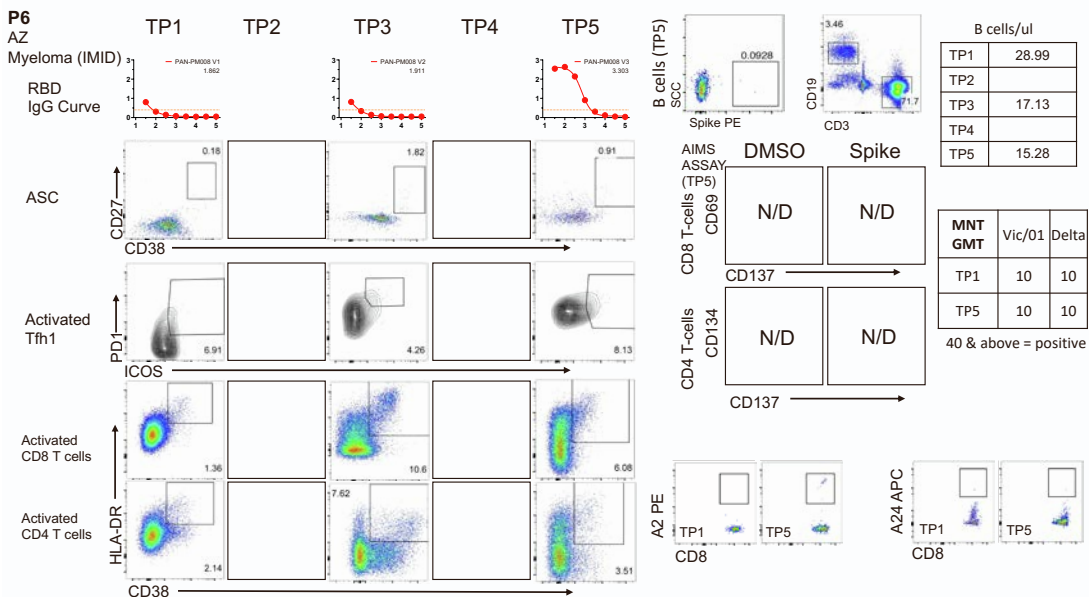
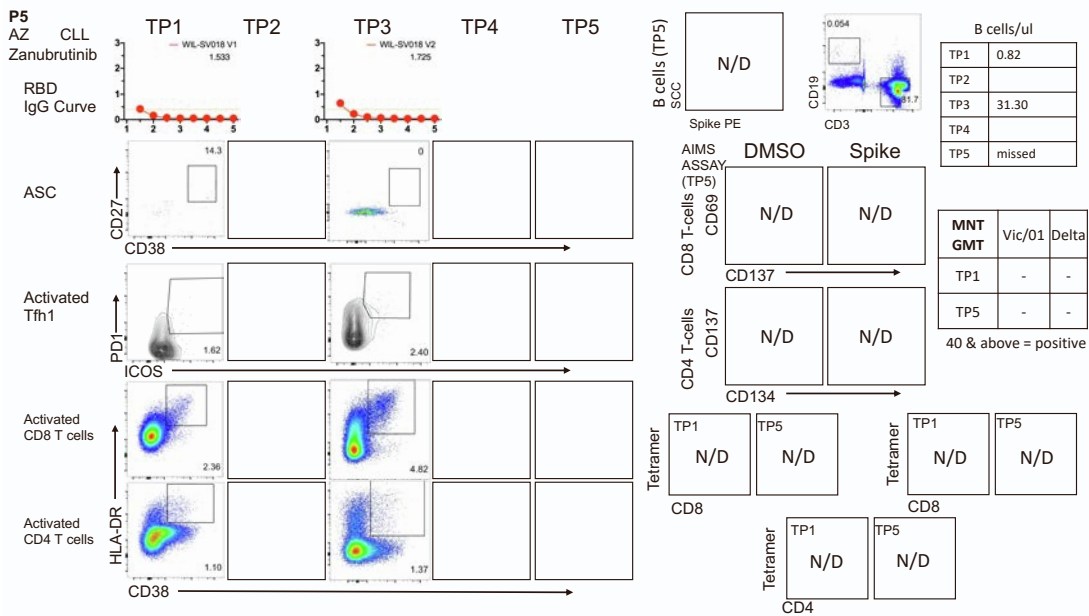
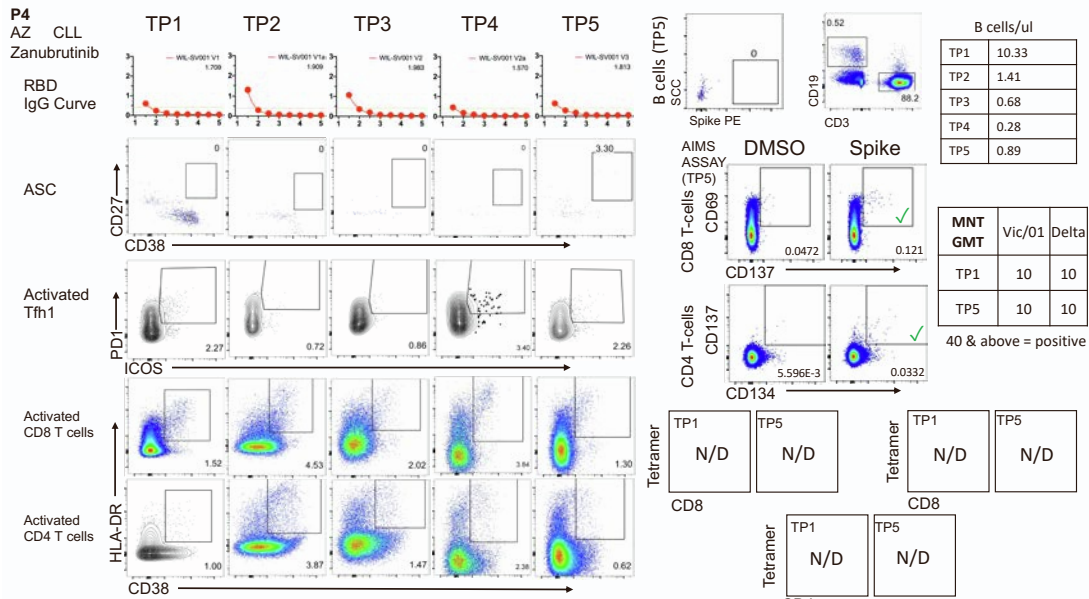
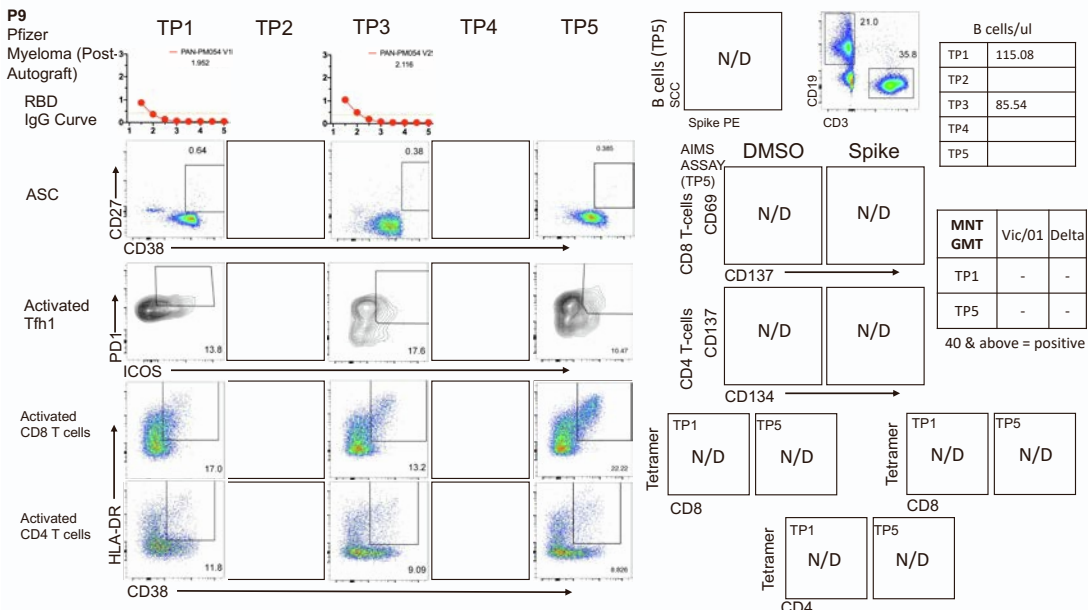
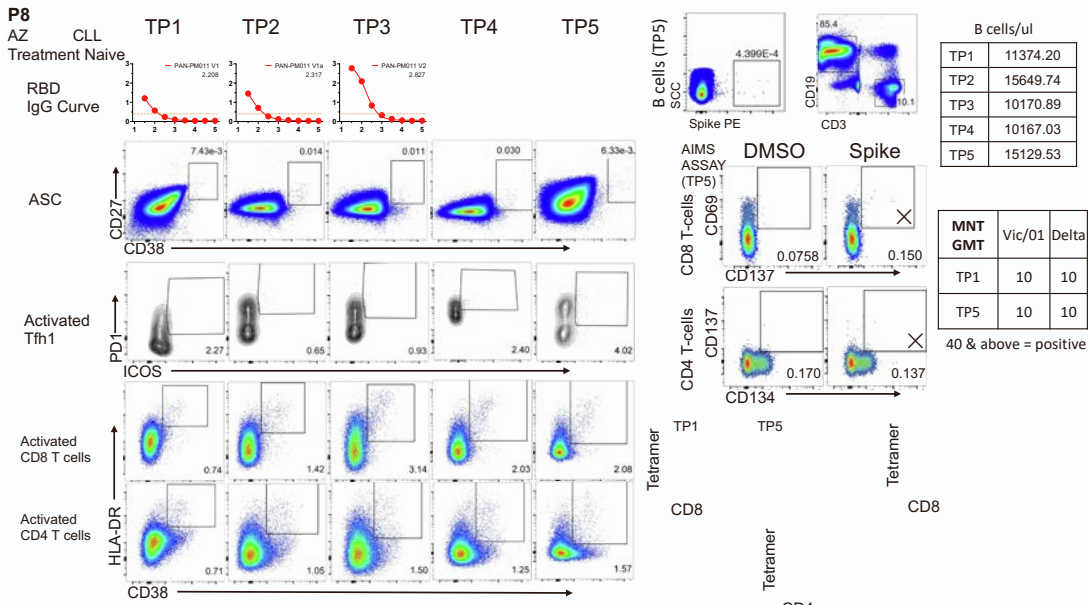
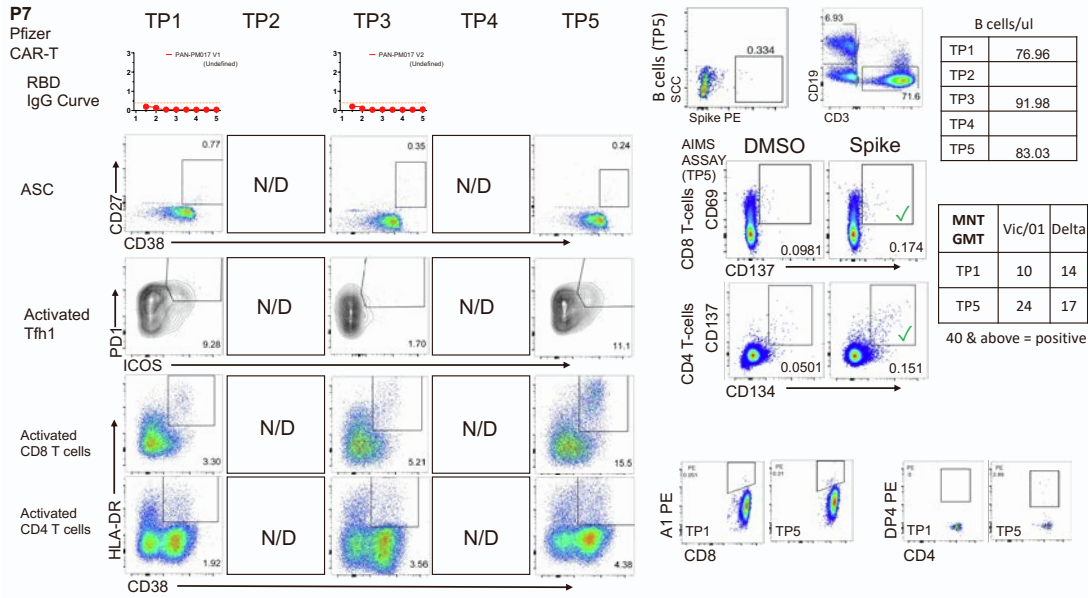
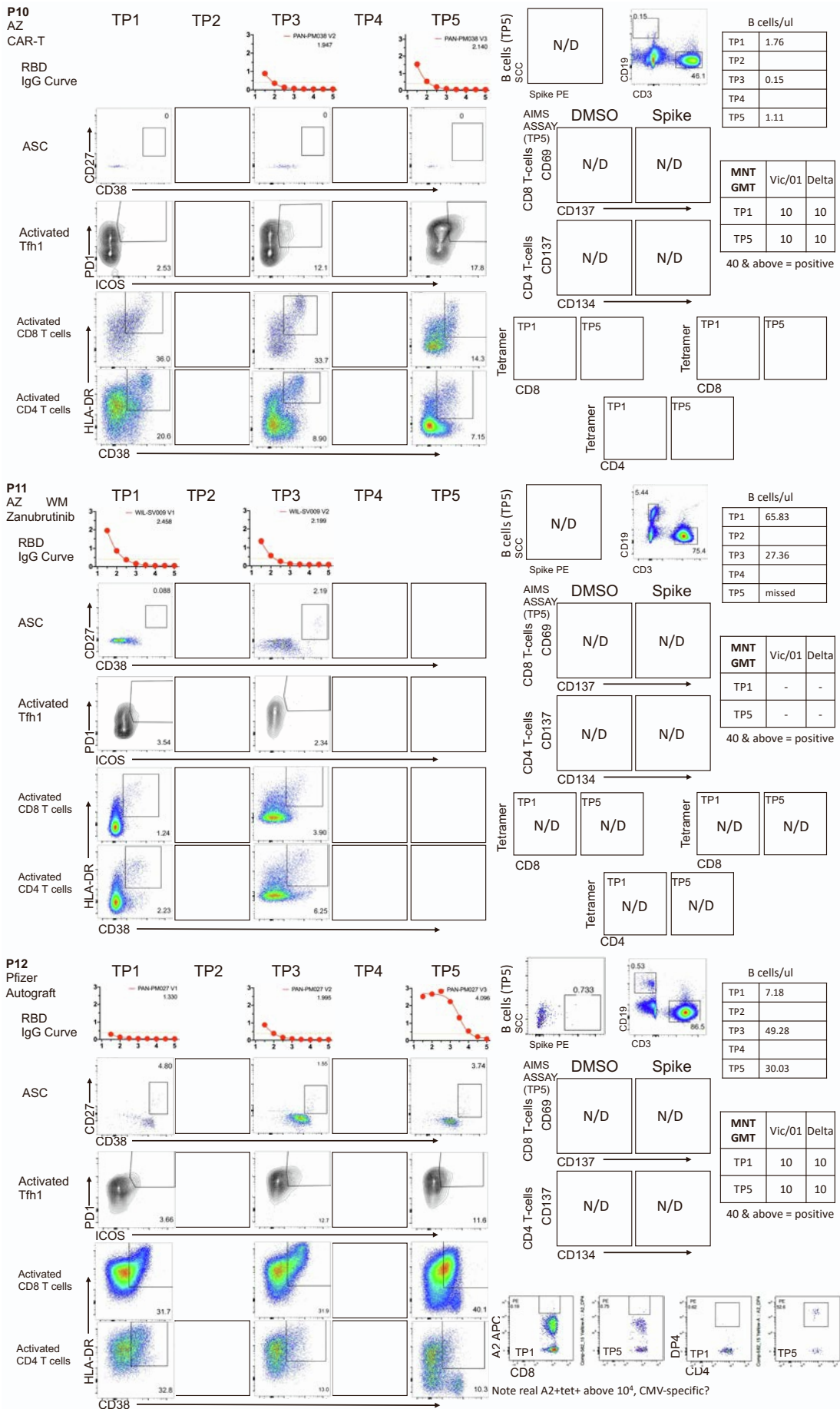


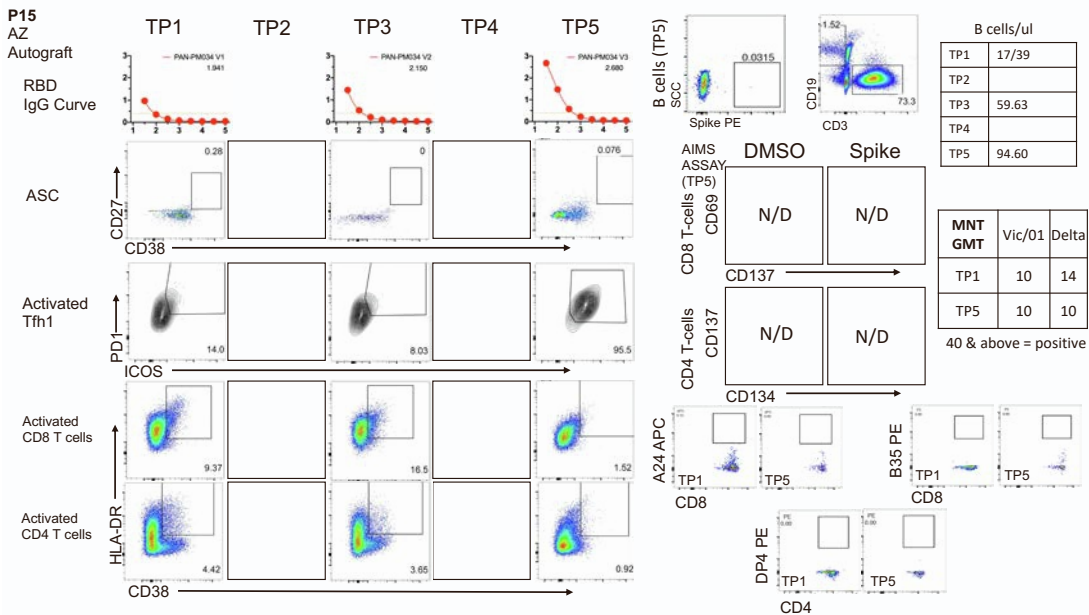
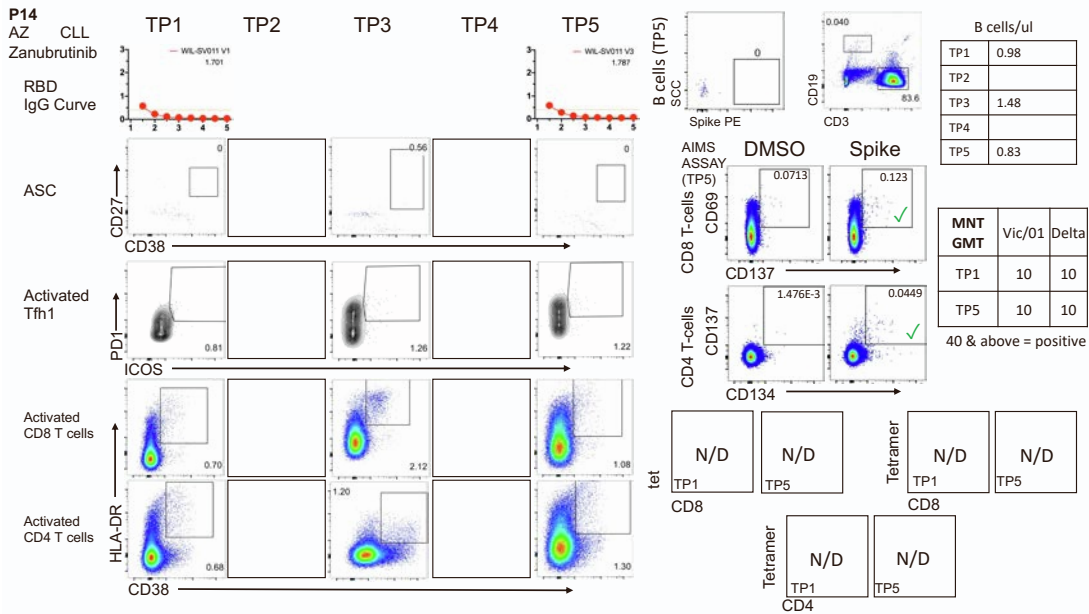
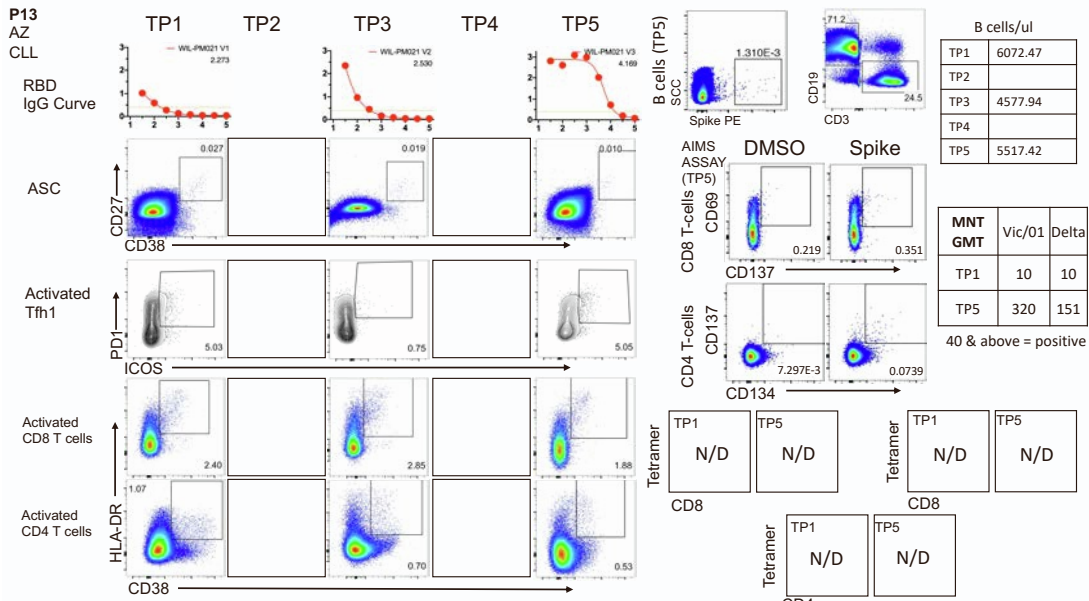
Figure S11. TCR logo representations of CDR3α and β sequence motifs for DPB4/S₁₆₇, A2/S₂₆₉ and A24/S₁₂₀₈. Each TCR motif depicts the V (left side) and J (right side) gene frequencies, the CDR3 amino acid sequence (middle), and the inferred rearrangement structure (bottom bars coloured by source region; V-region, light grey; insertions, red; diversity (D)-region, black; and J-region dark grey). The motif scores with chi-squared values greater than 90 were considered highly significant. Related to Figure 6.







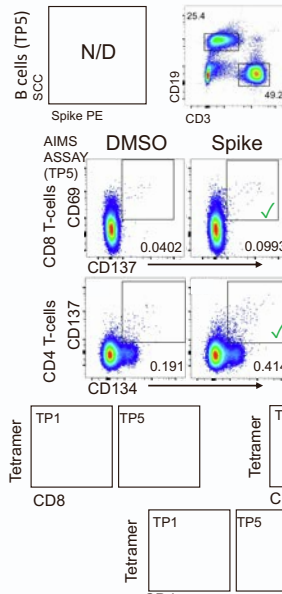
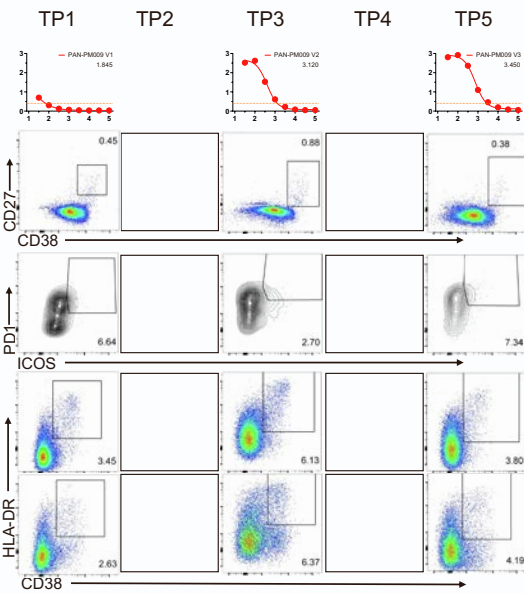




P16

AZ

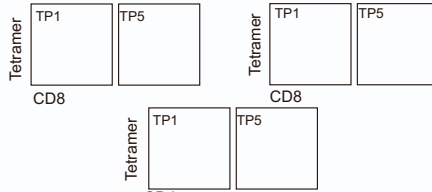
Autograf
RBD
IgG Curve



B cells/ul	
TP1	284.54
TP2	
TP3	267.21
TP4	
TP5	275.54

MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	10
TP5	28	10

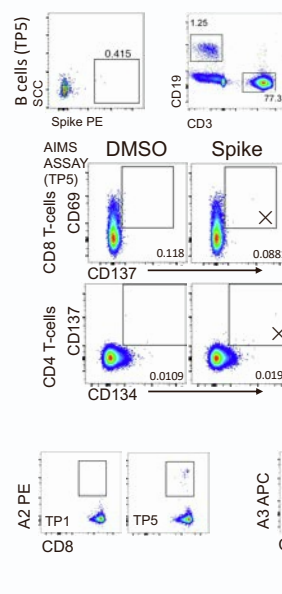
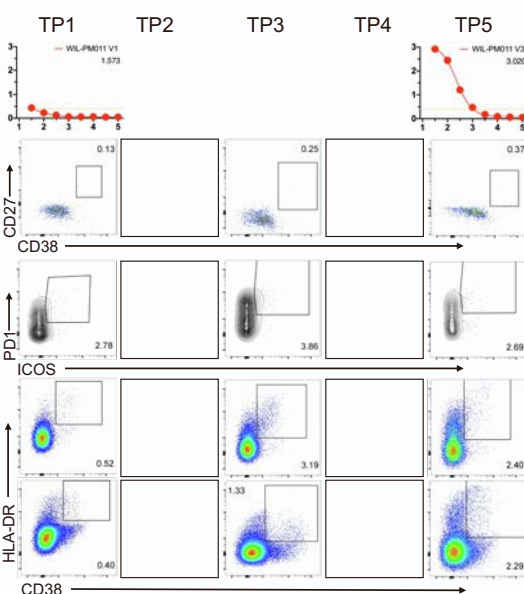
40 & above = positive



P17

AZ WM

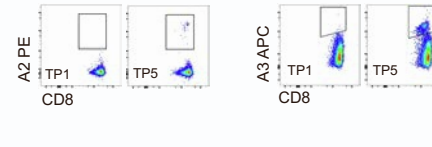
Zanubrutinib
RBD
IgG Curve



B cells/ul	
TP1	14.24
TP2	
TP3	19.01
TP4	
TP5	16.89

MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	10
TP5	40	10

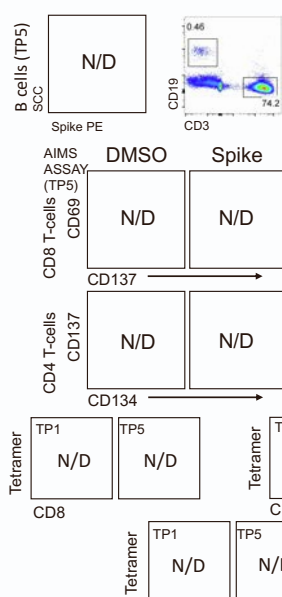
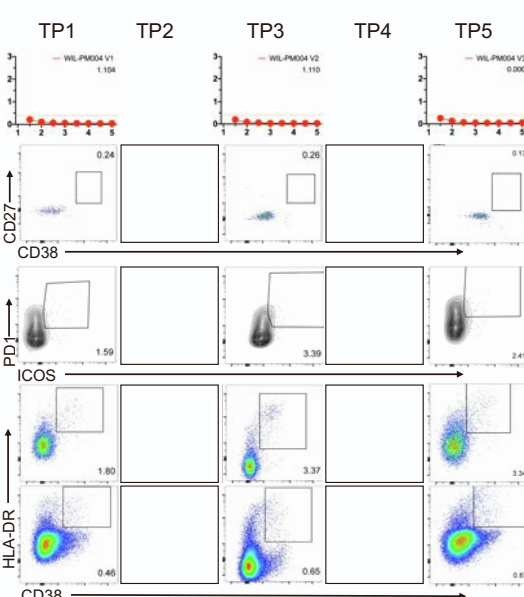
40 & above = positive



P18

AZ CLL

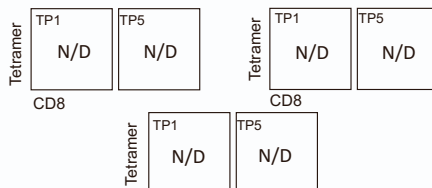
Zanubrutinib
RBD
IgG Curve

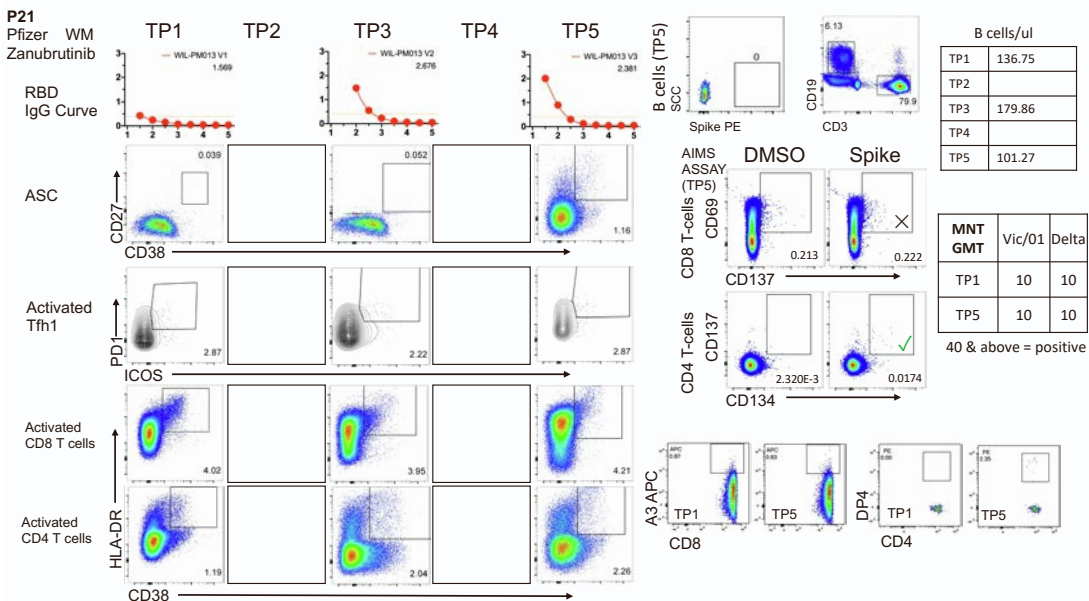
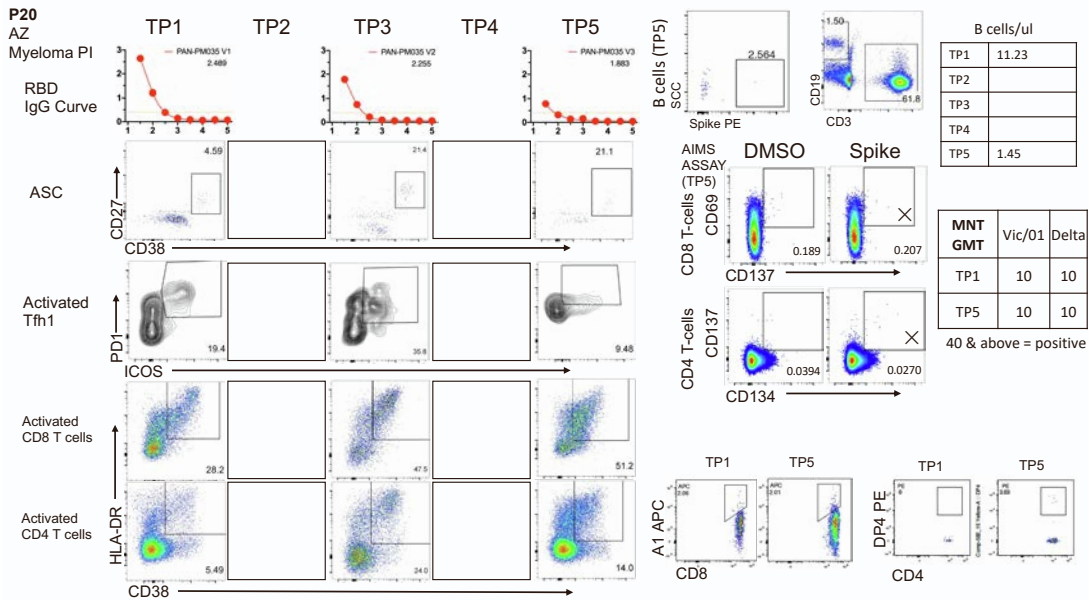
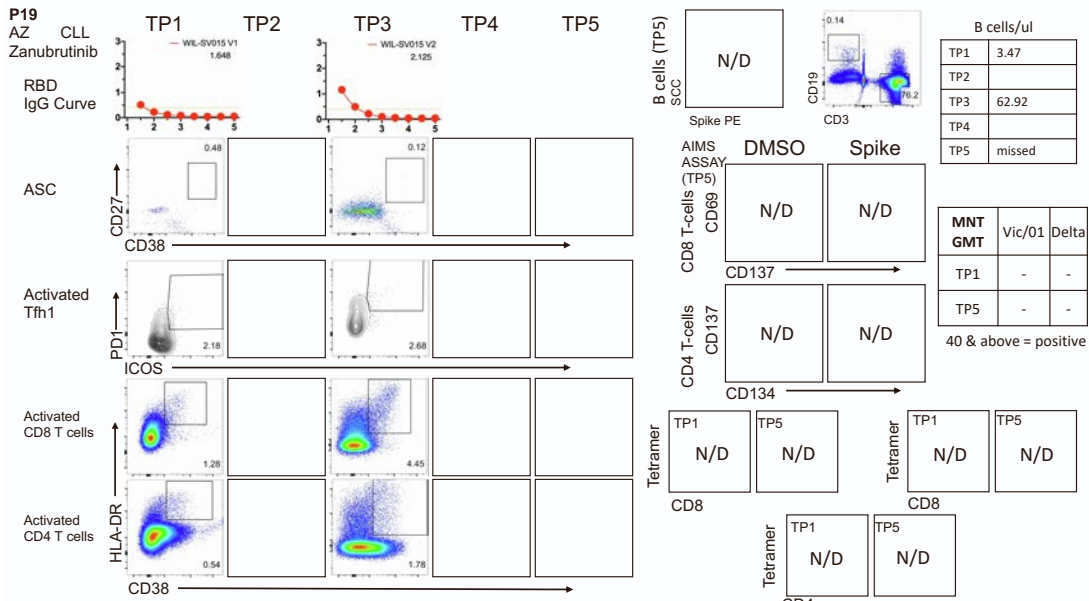


B cells/ul	
TP1	3.69
TP2	
TP3	9.81
TP4	
TP5	10.02

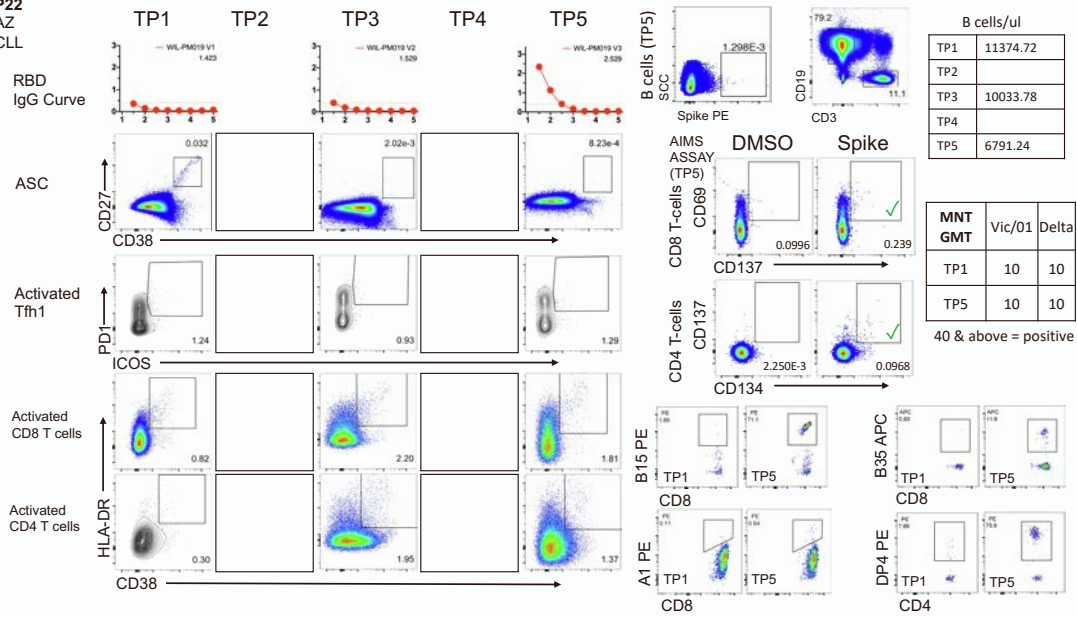
MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	10
TP5	10	10

40 & above = positive

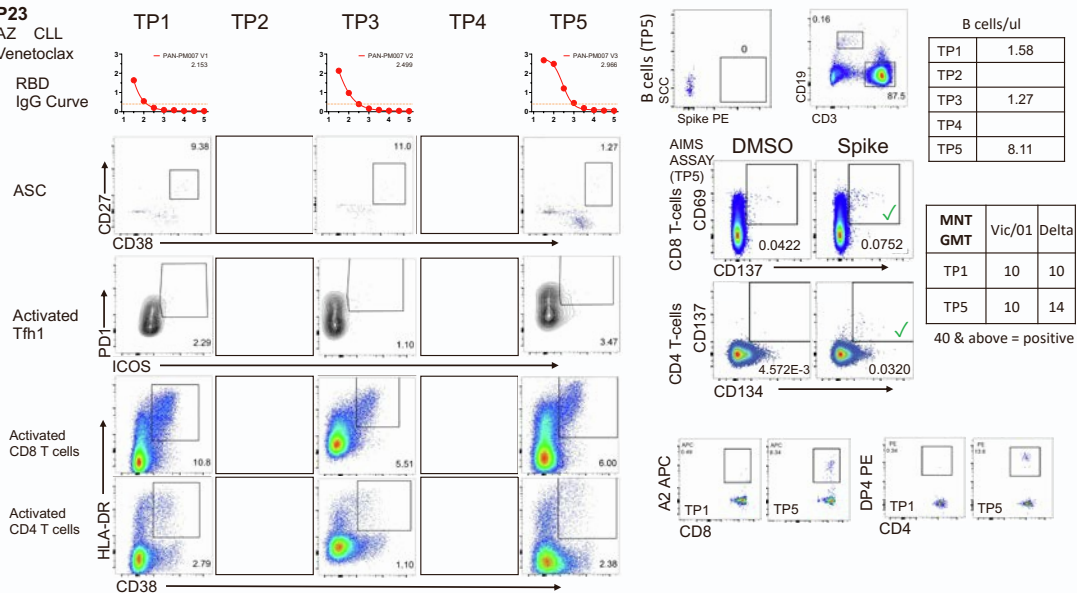




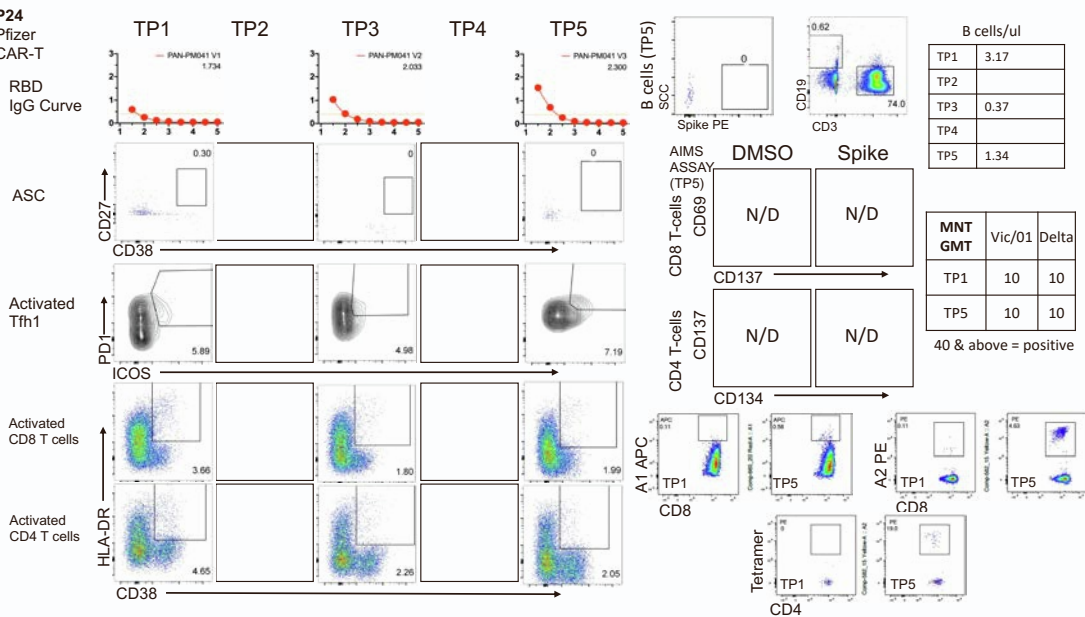
P22
AZ
CLL

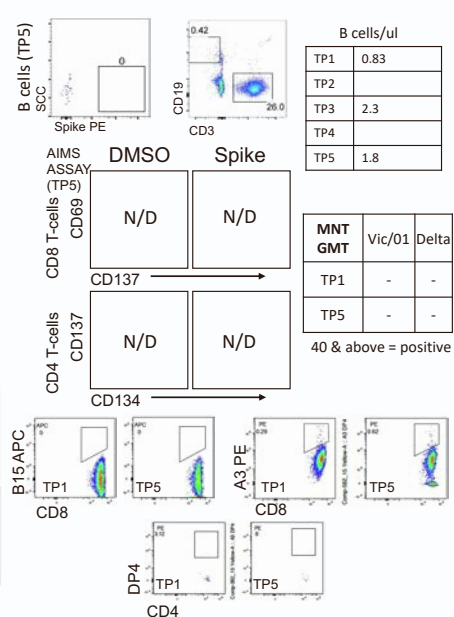
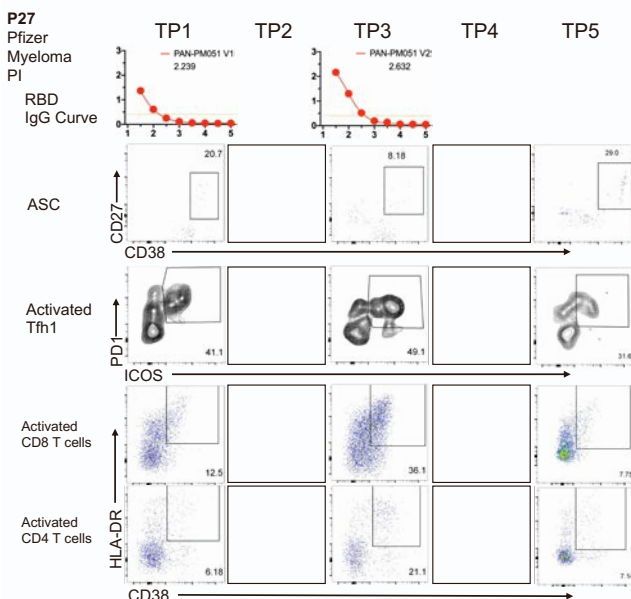
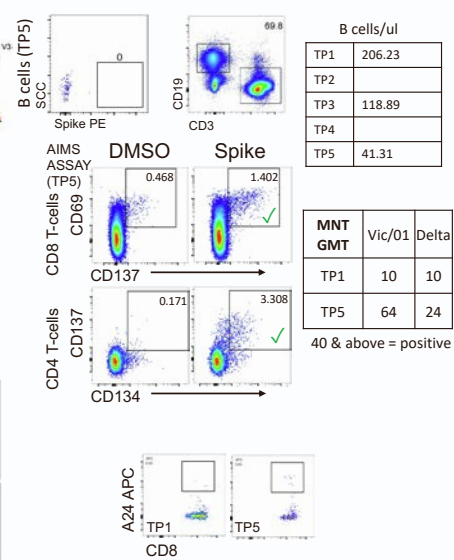
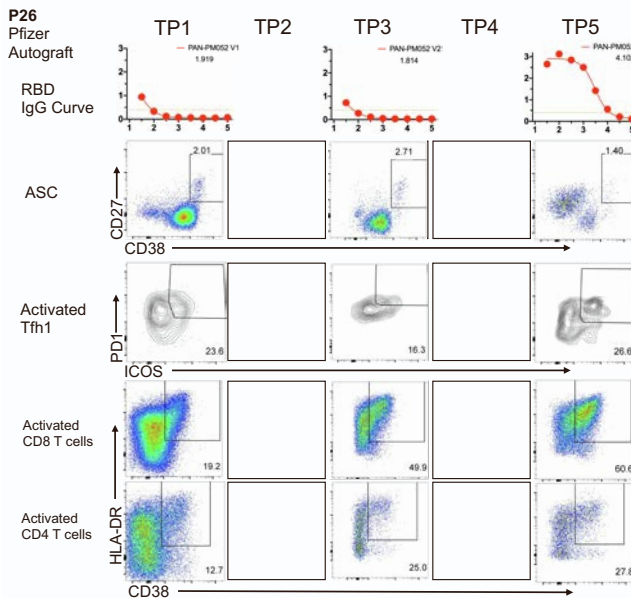
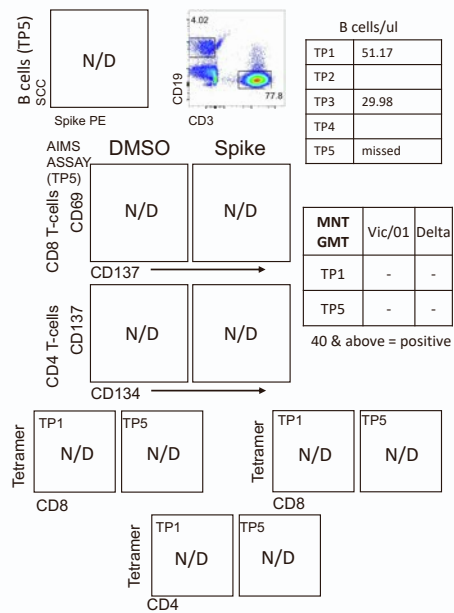
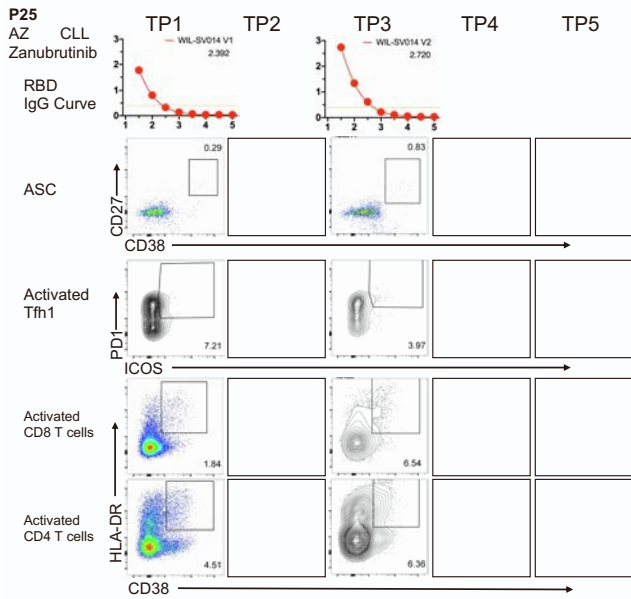


P23
AZ CLL
Venetoclax



P24
Pfizer
CAR-T





P28

AZ
Autograft

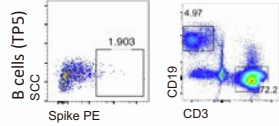
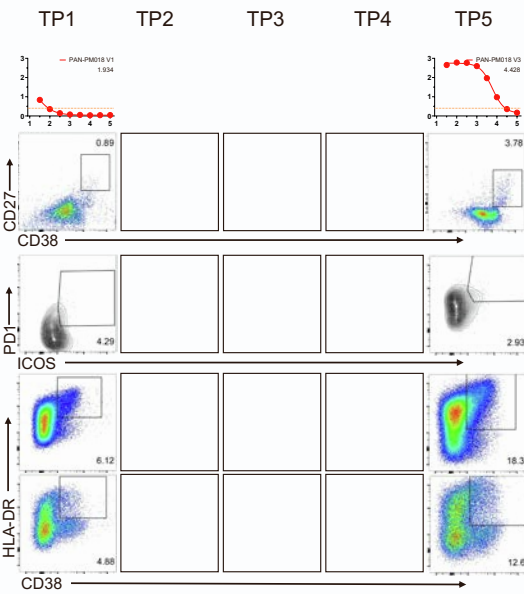
RBD
IgG Curve

ASC

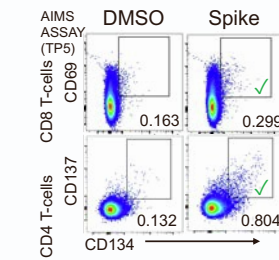
Activated
Tfh1

Activated
CD8 T cells

Activated
CD4 T cells

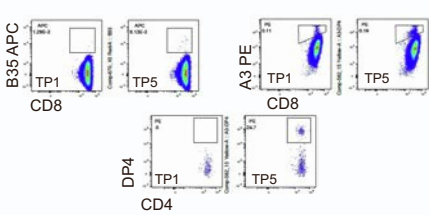


B cells/ul	
TP1	84.03
TP2	
TP3	
TP4	
TP5	118.38



MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	14
TP5	10	10

40 & above = positive



P29

AZ
CLL

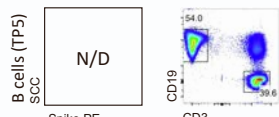
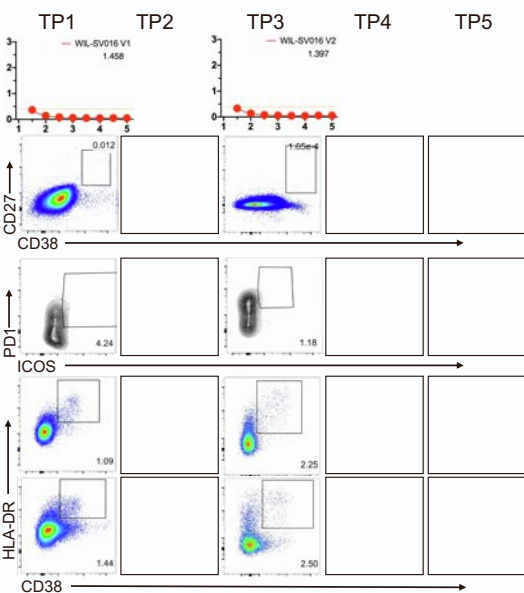
RBD
IgG Curve

ASC

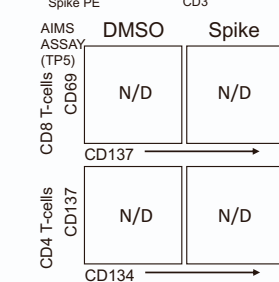
Activated
Tfh1

Activated
CD8 T cells

Activated
CD4 T cells

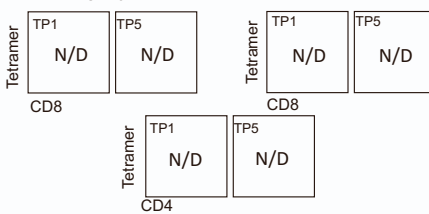


B cells/ul	
TP1	2704.92
TP2	
TP3	78471.47
TP4	
TP5	missed



MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	-	-
TP5	-	-

40 & above = positive



P30

AZ
Autograft

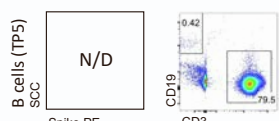
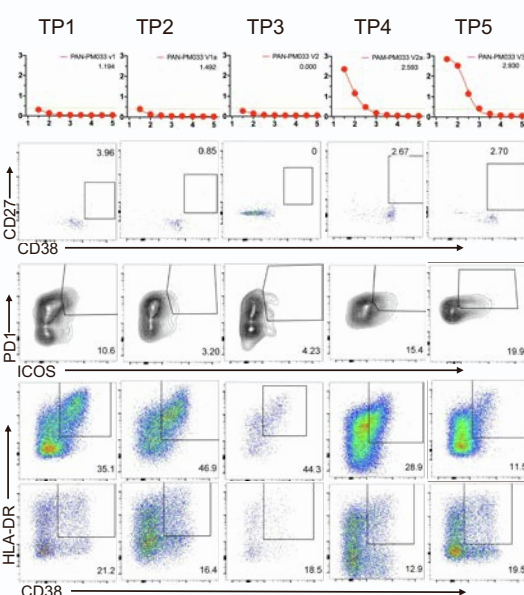
RBD
IgG Curve

ASC

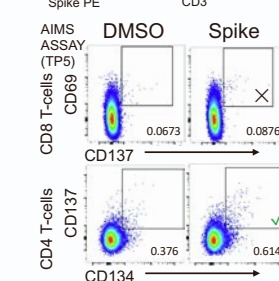
Activated
Tfh1

Activated
CD8 T cells

Activated
CD4 T cells

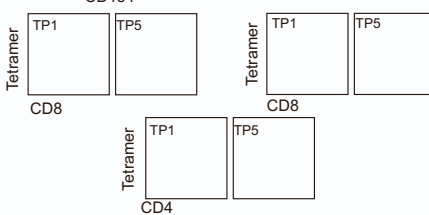


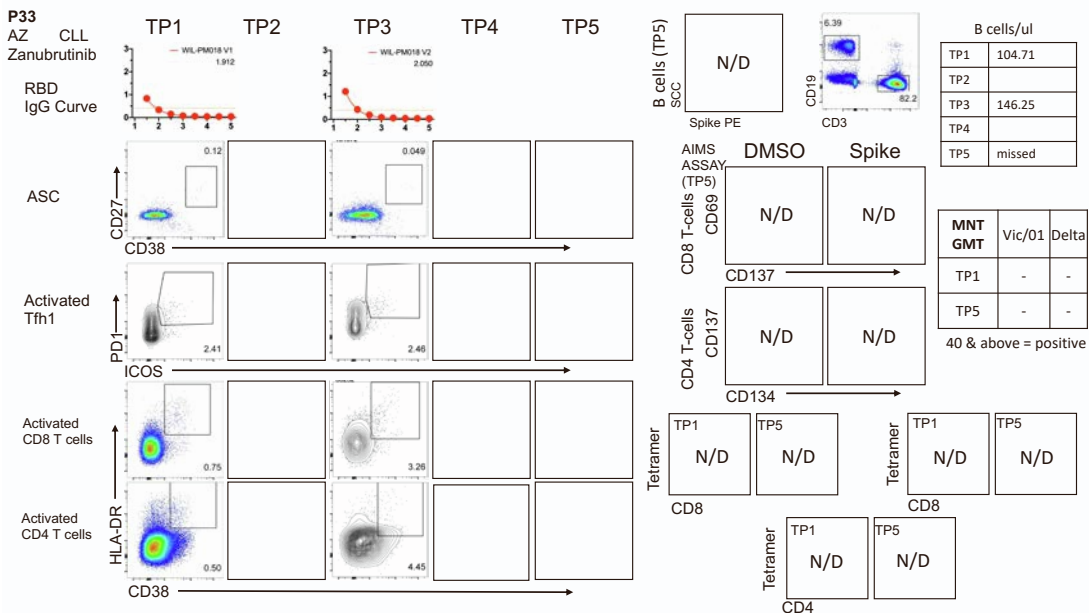
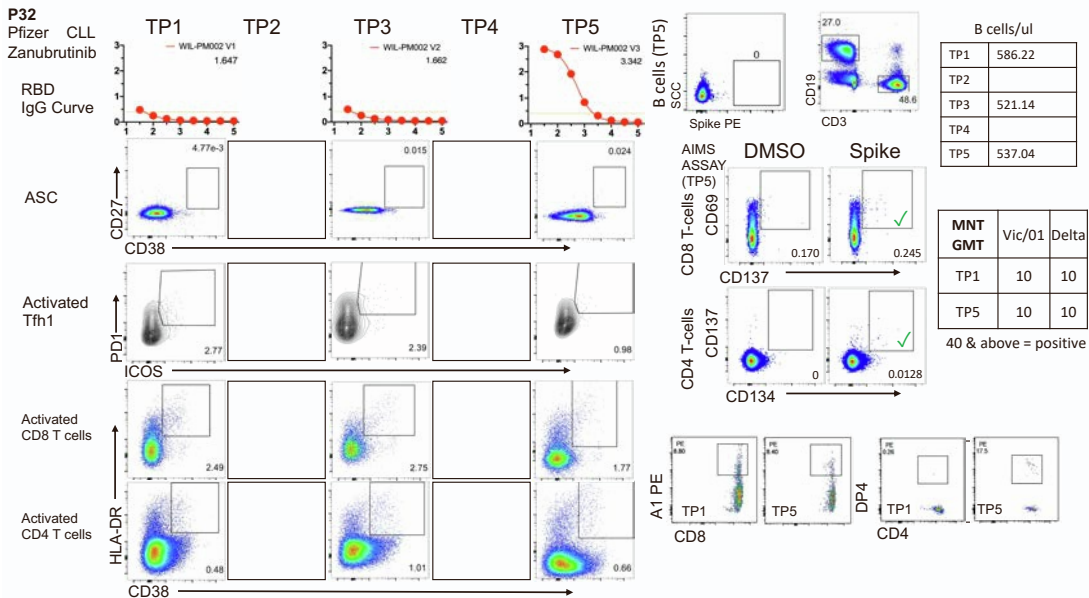
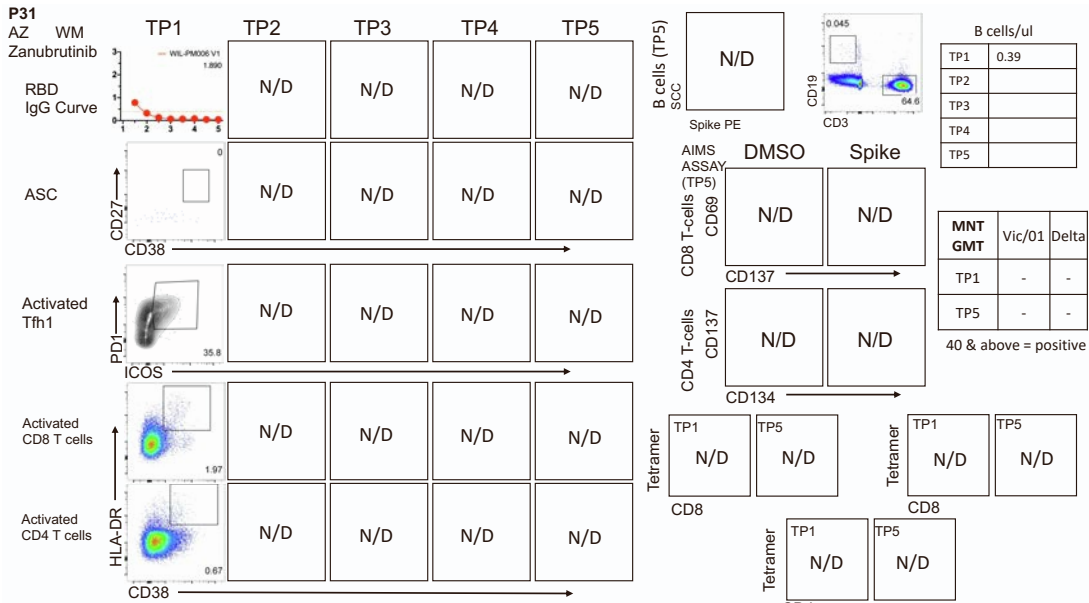
B cells/ul	
TP1	1.7
TP2	1.84
TP3	44.91
TP4	3.48
TP5	2.11



MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	10
TP5	28	10

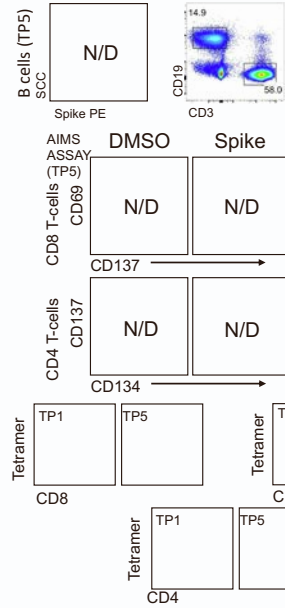
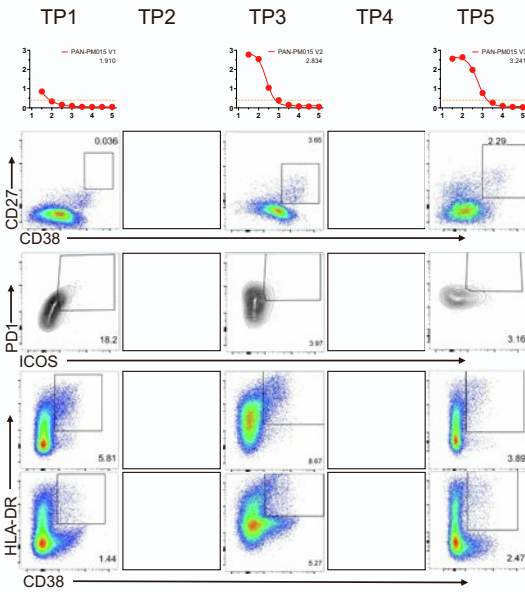
40 & above = positive





P34
AZ

Myeloma
RBD
IgG Curve



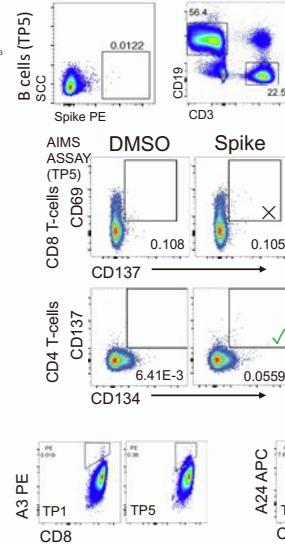
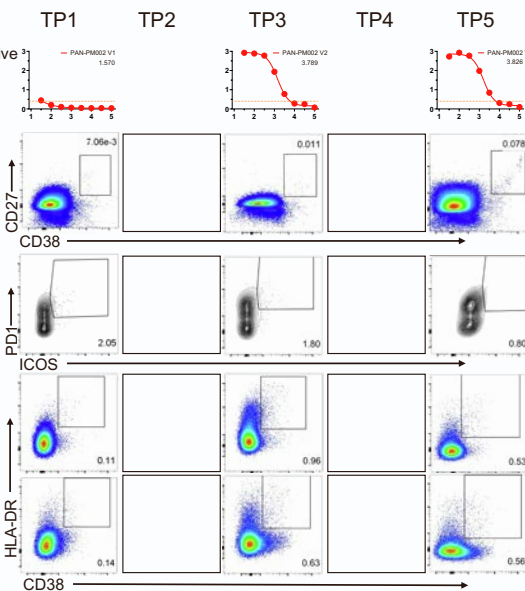
B cells/ul	
TP1	321.92
TP2	
TP3	181.14
TP4	
TP5	209.00

MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	10
TP5	40	10

40 & above = positive

P35
AZ

CLL
Treatment naive
RBD
IgG Curve



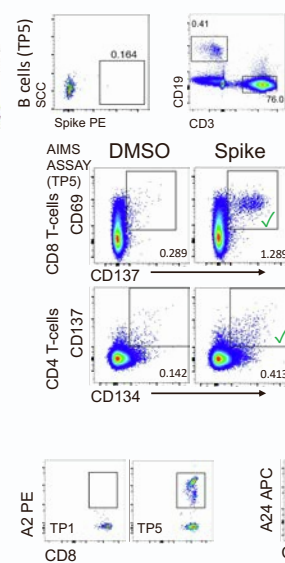
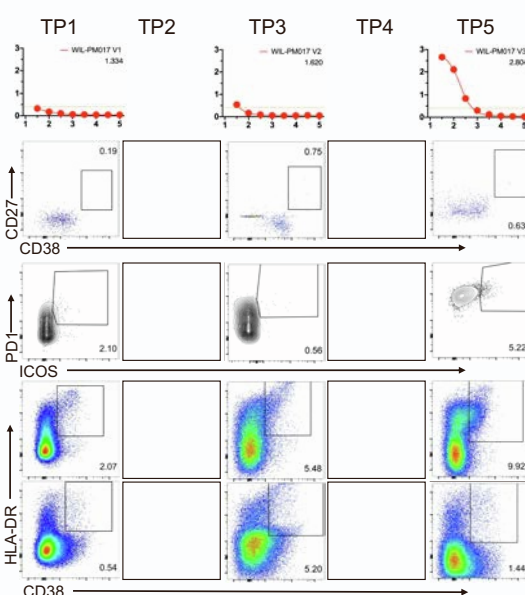
B cells/ul	
TP1	4892.95
TP2	
TP3	4057.83
TP4	
TP5	3455.95

MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	10
TP5	107	45

40 & above = positive

P36
AZ

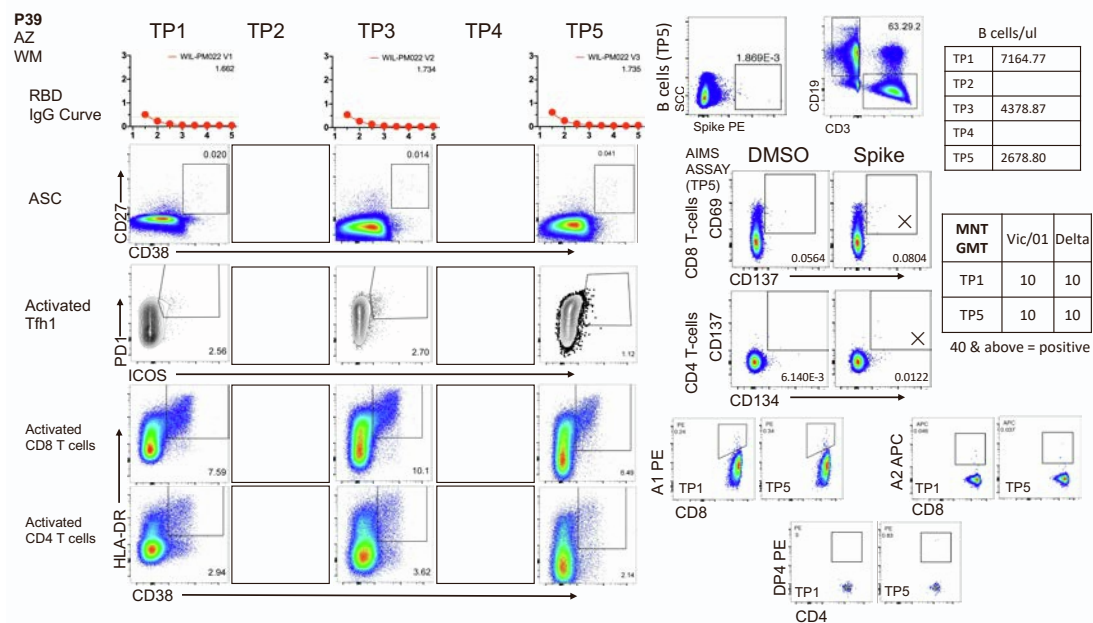
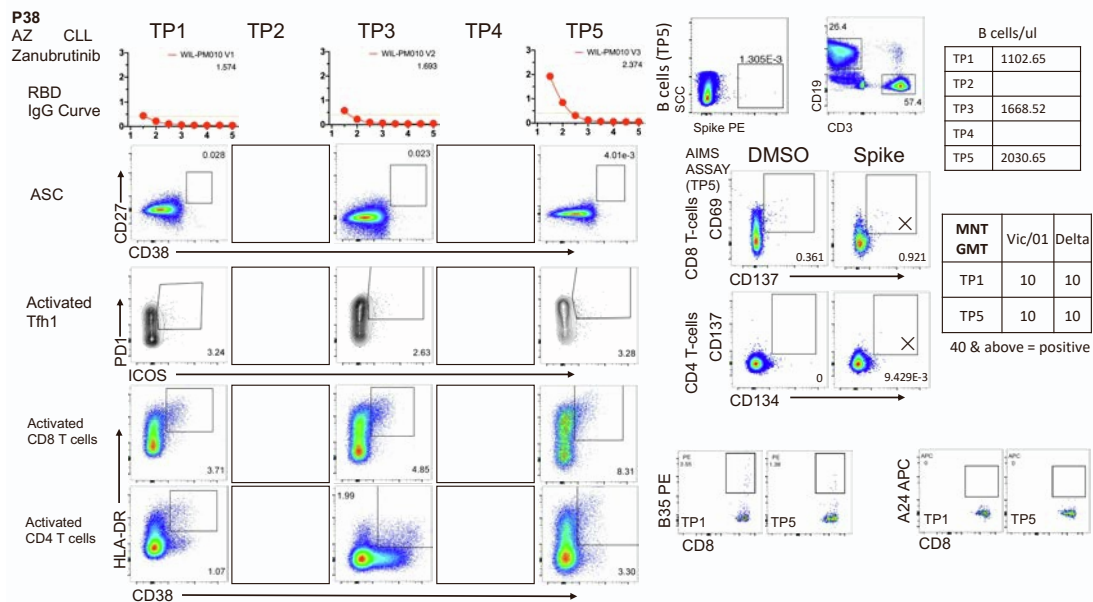
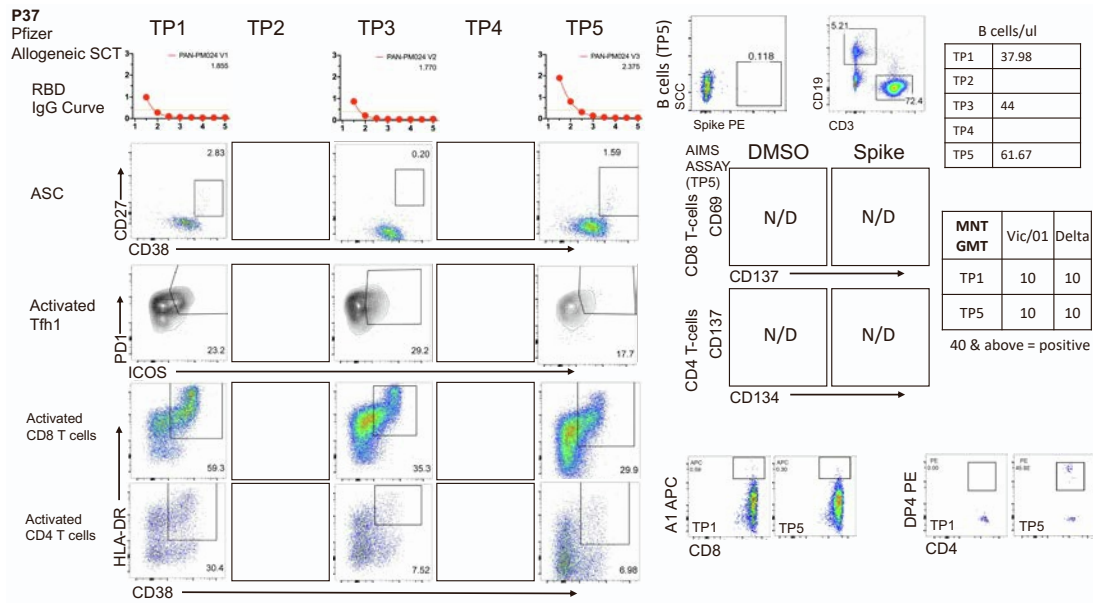
WM
Zanubrutinib
RBD
IgG Curve



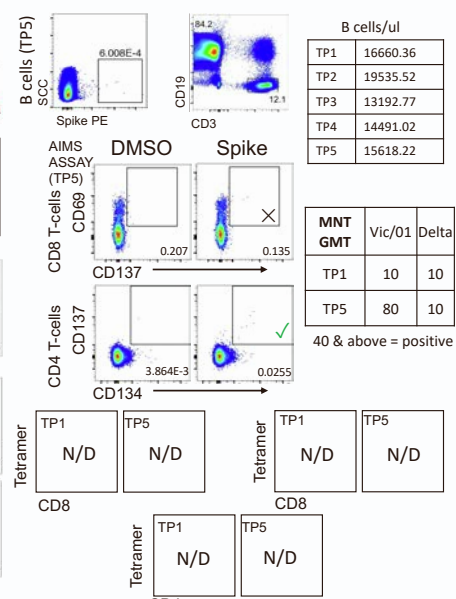
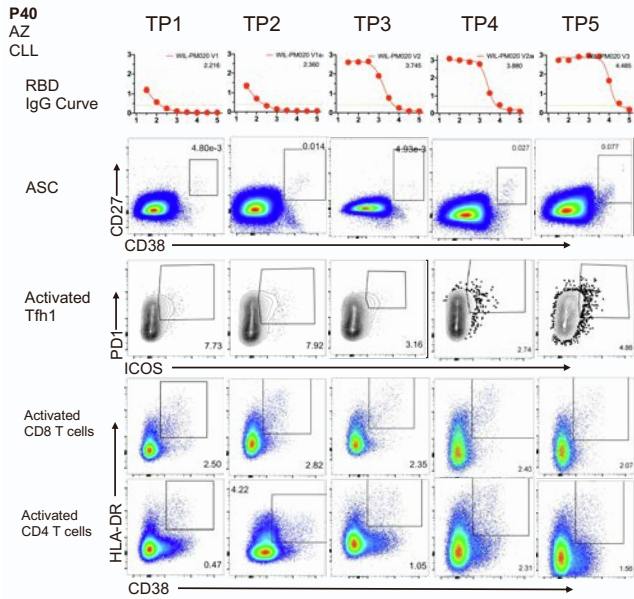
B cells/ul	
TP1	9.76
TP2	
TP3	14.96
TP4	
TP5	12.12

MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	10
TP5	10	10

40 & above = positive



P40
AZ
CLL



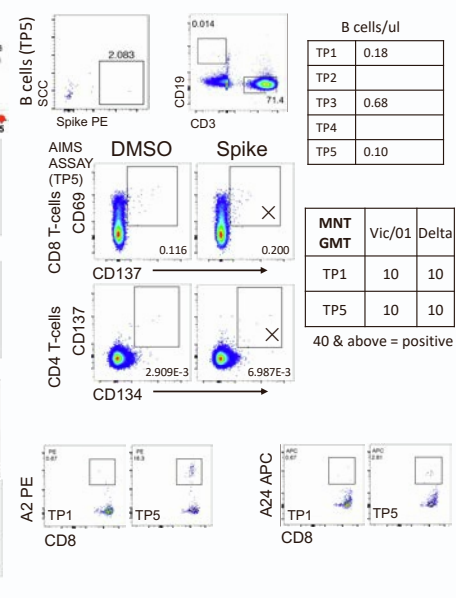
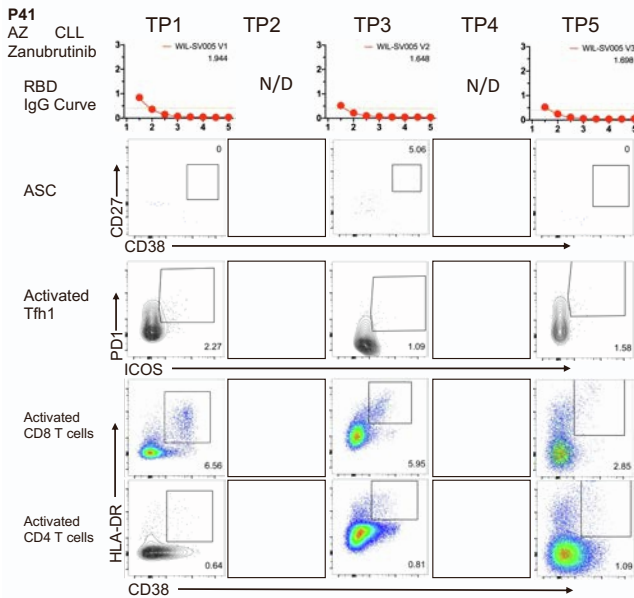
	TP1	TP2	TP3	TP4	TP5
B cells/ul	16660.36	19535.52	13192.77	14491.02	15618.22

MNT GMT	Vic/01	Delta
TP1	10	10
TP5	80	10

40 & above = positive

Tetramer	TP1	TP5
CD8	N/D	N/D
CD4	N/D	N/D

P41
AZ
CLL

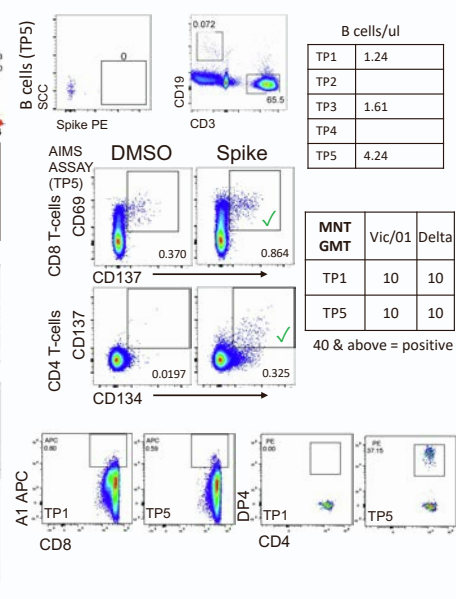
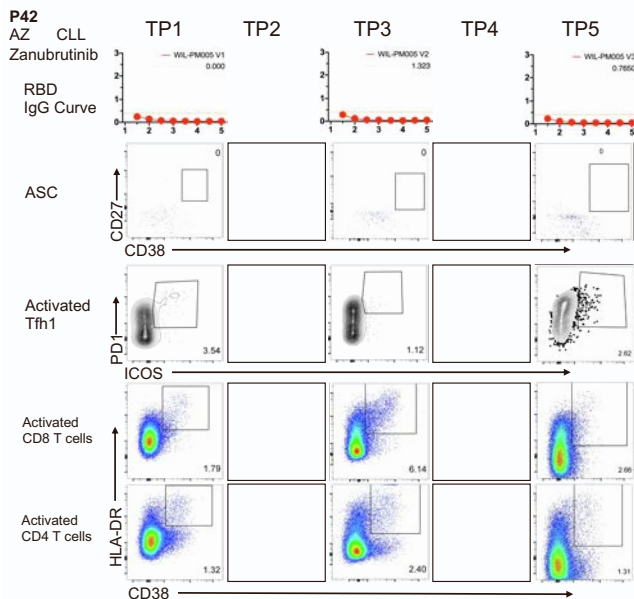


	TP1	TP2	TP3	TP4	TP5
B cells/ul	0.18		0.68		0.10

MNT GMT	Vic/01	Delta
TP1	10	10
TP5	10	10

40 & above = positive

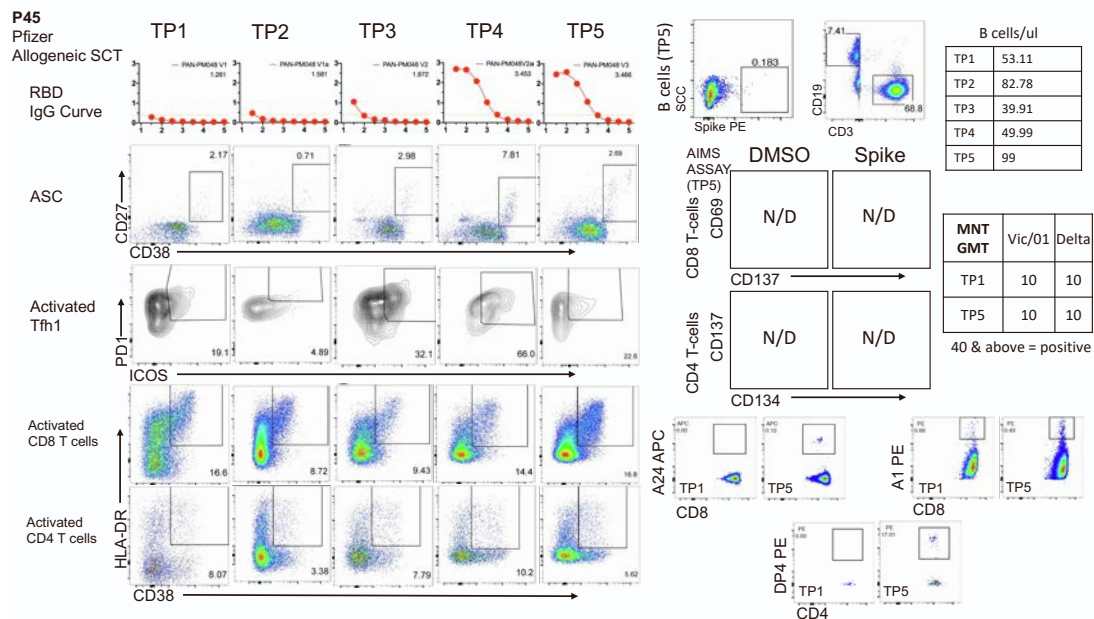
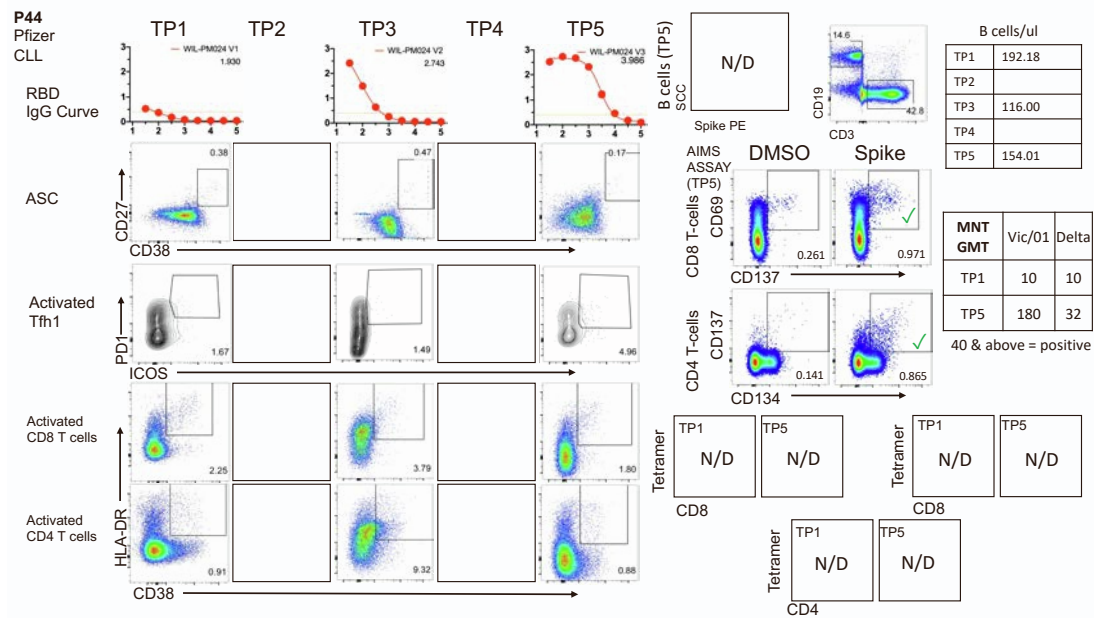
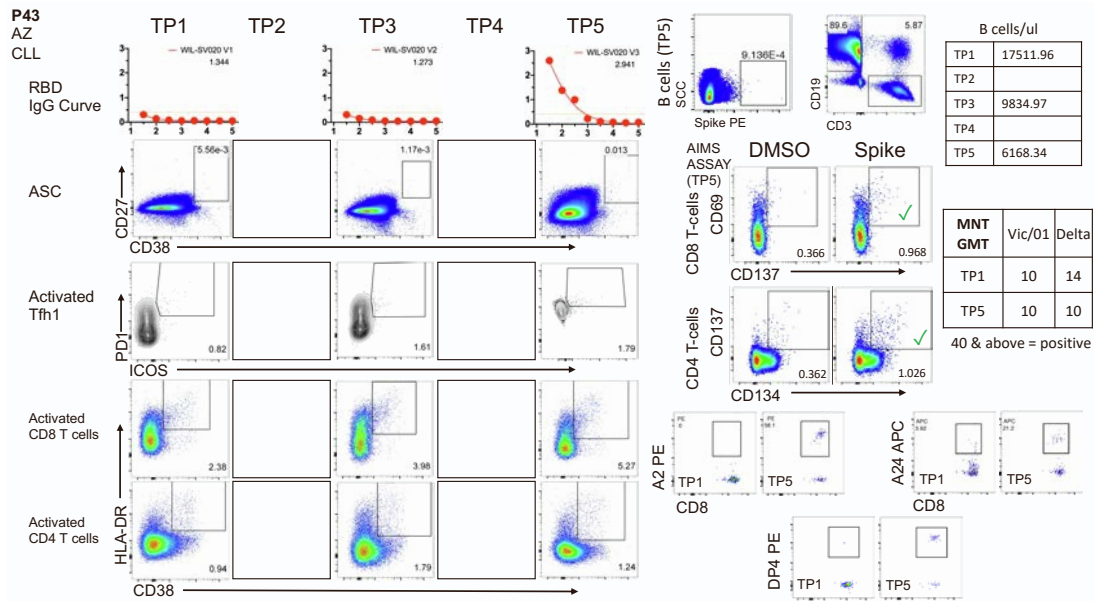
P42
AZ
CLL

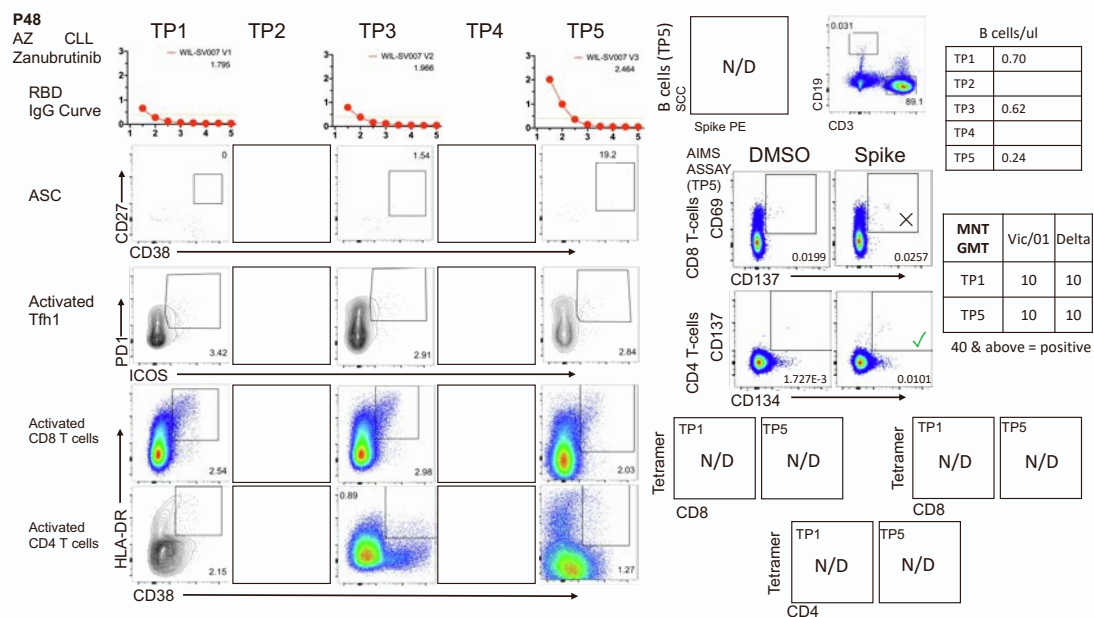
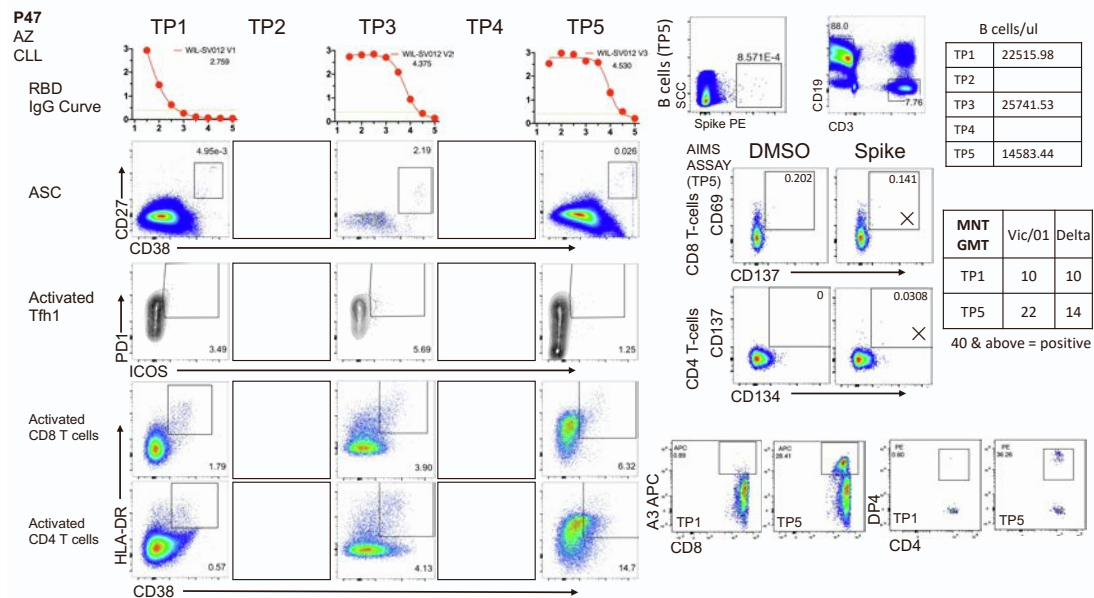
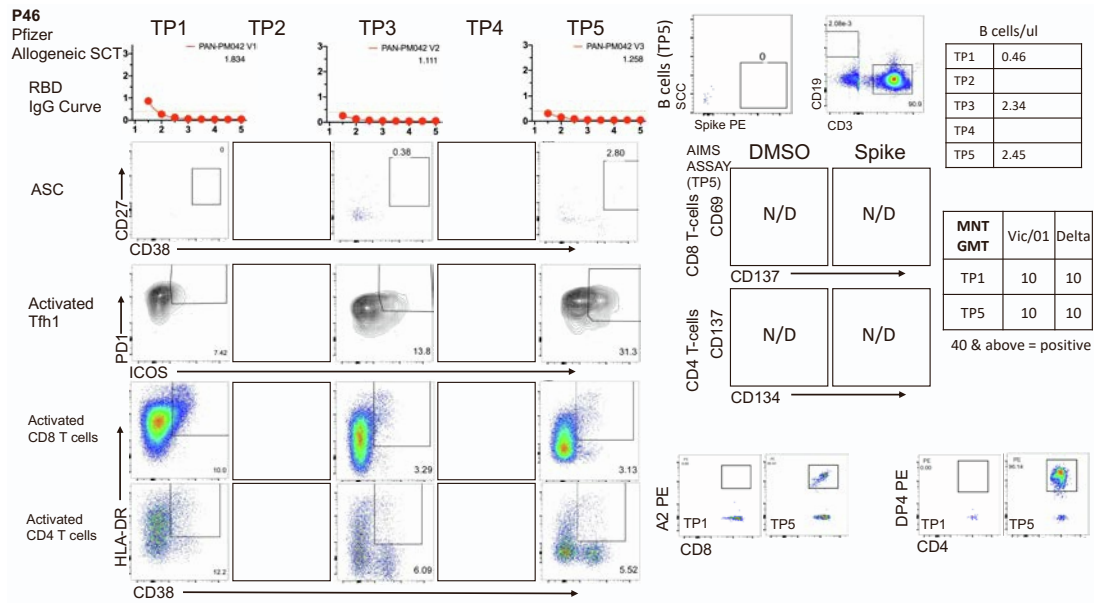


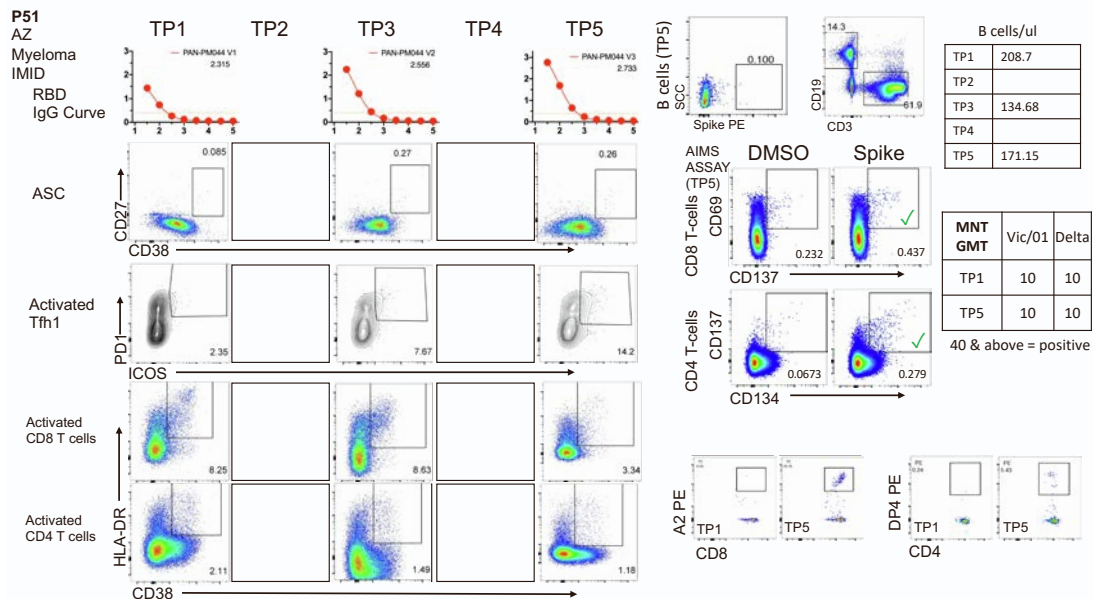
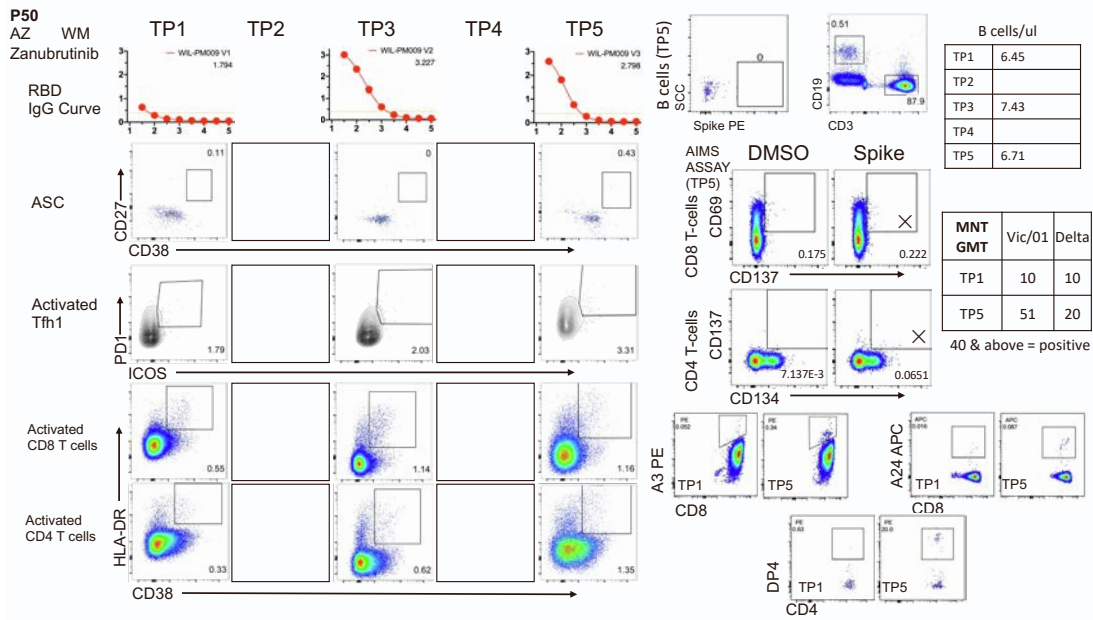
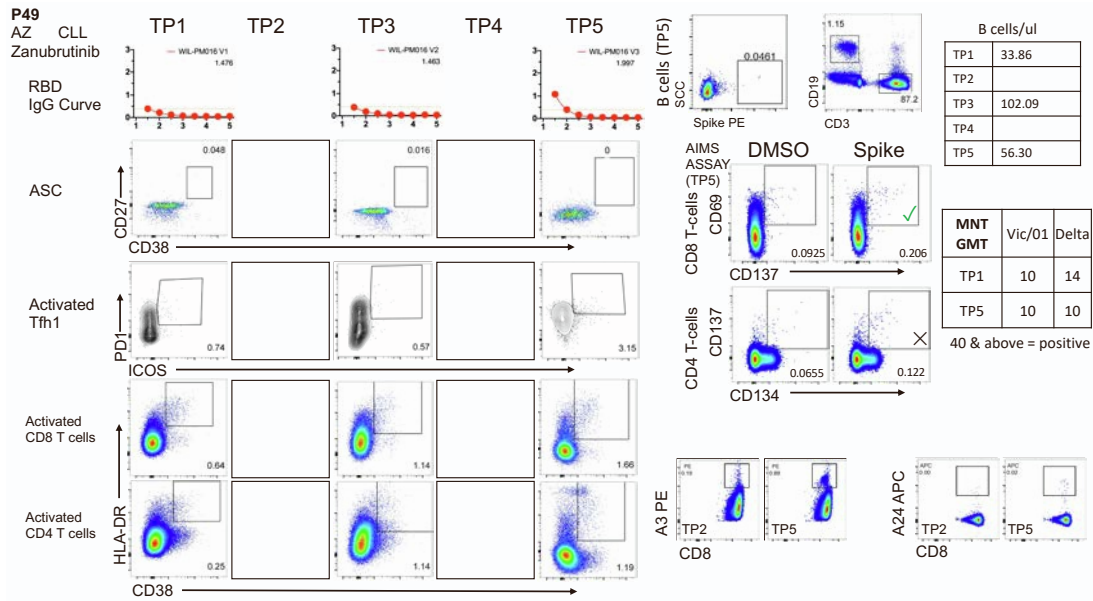
	TP1	TP2	TP3	TP4	TP5
B cells/ul	1.24		1.61		4.24

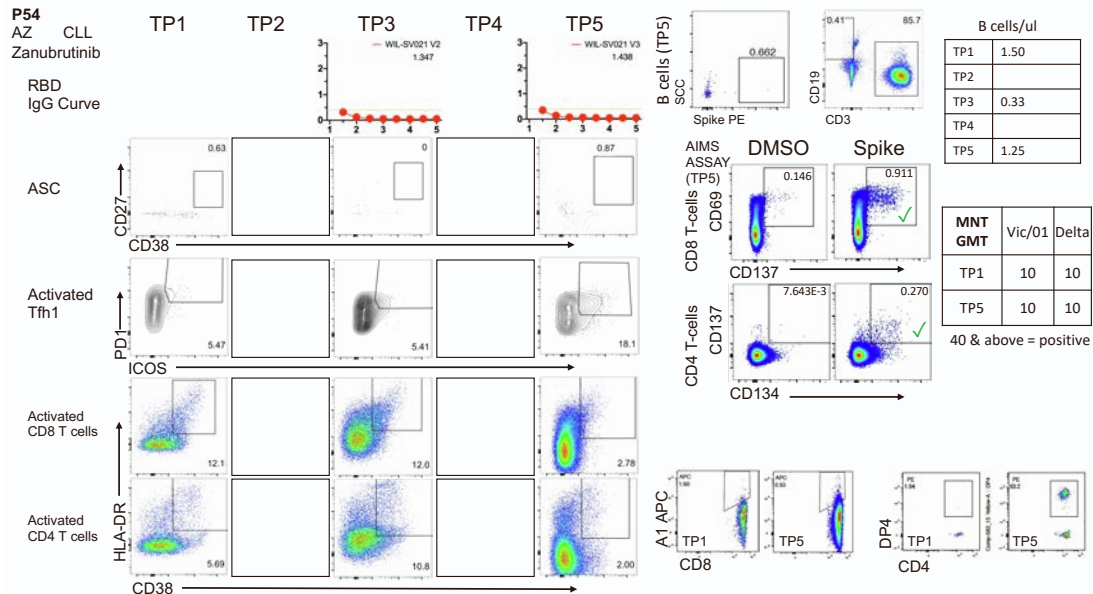
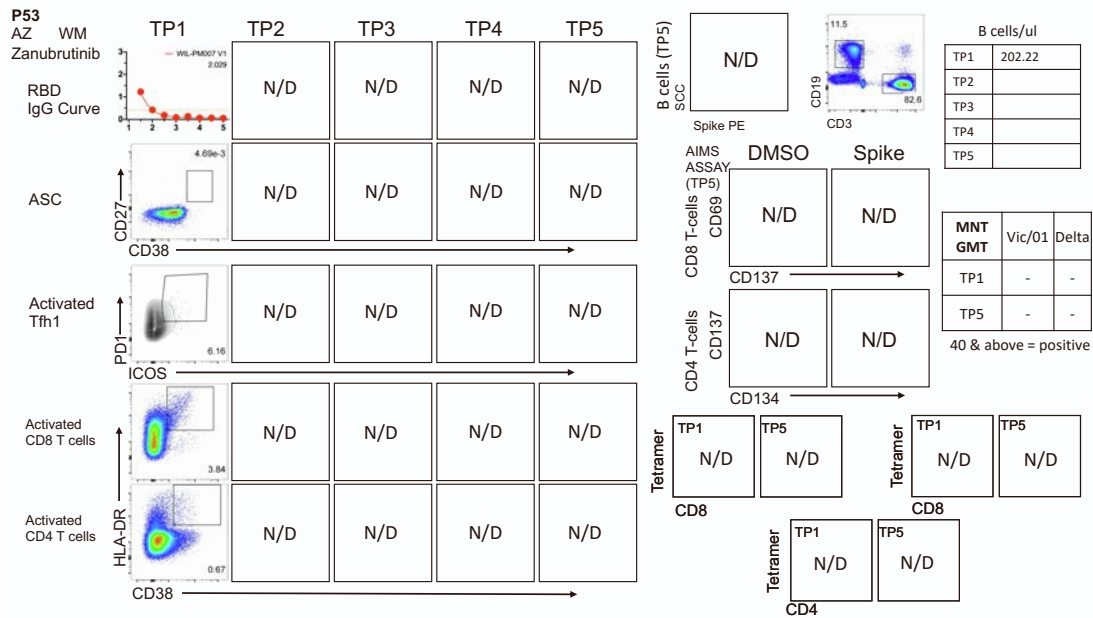
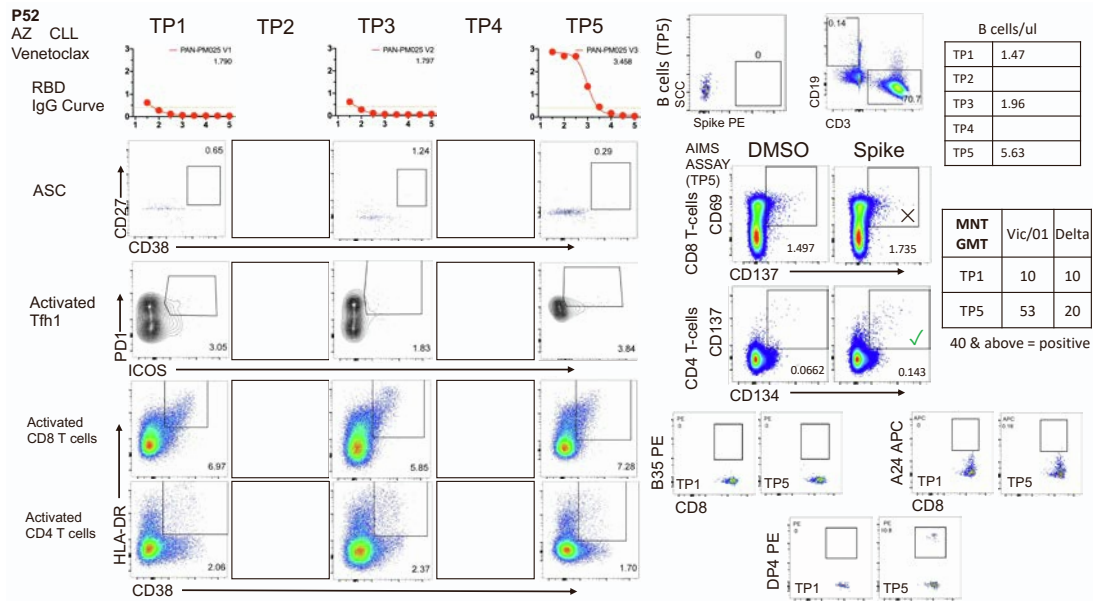
MNT GMT	Vic/01	Delta
TP1	10	10
TP5	10	10

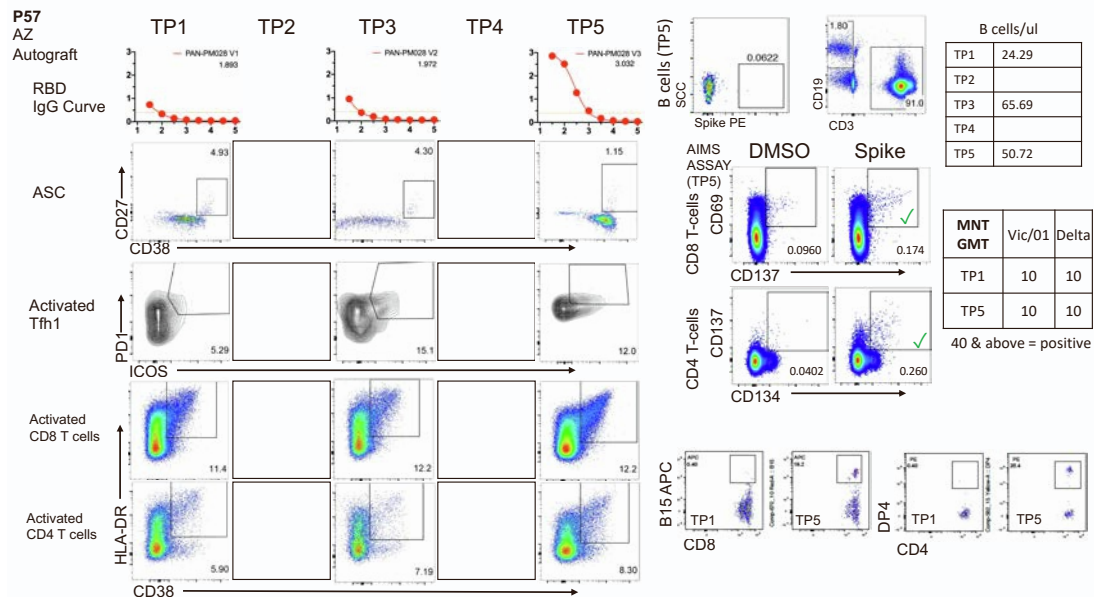
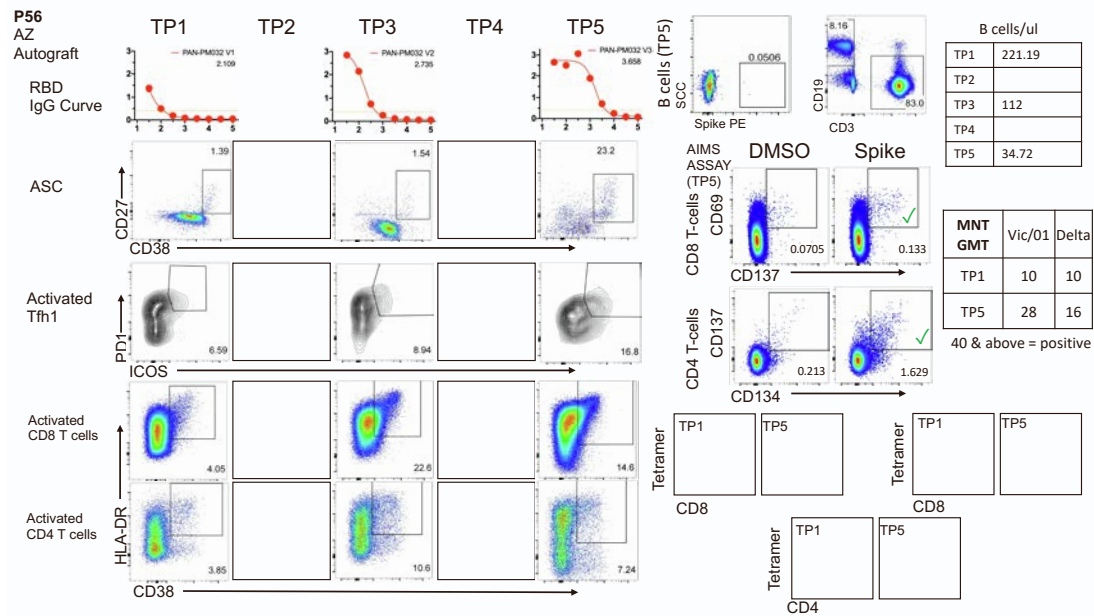
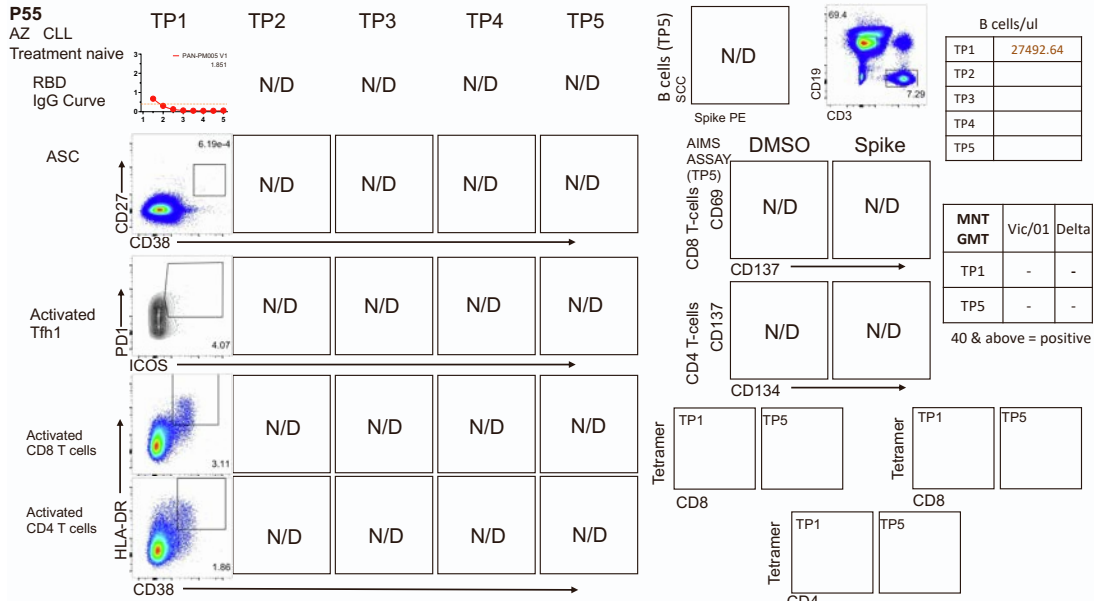
40 & above = positive

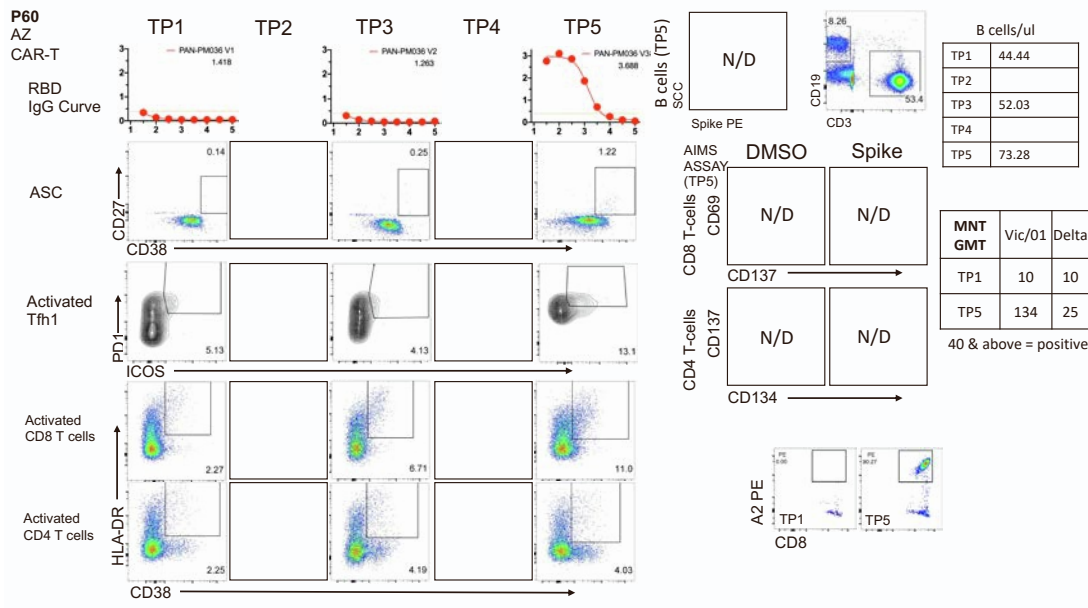
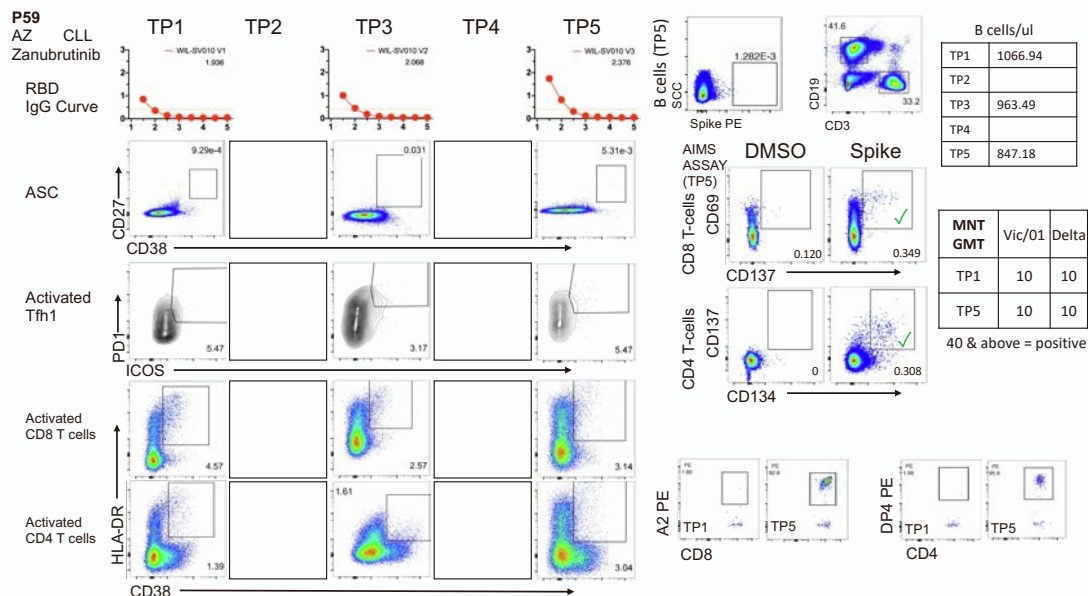
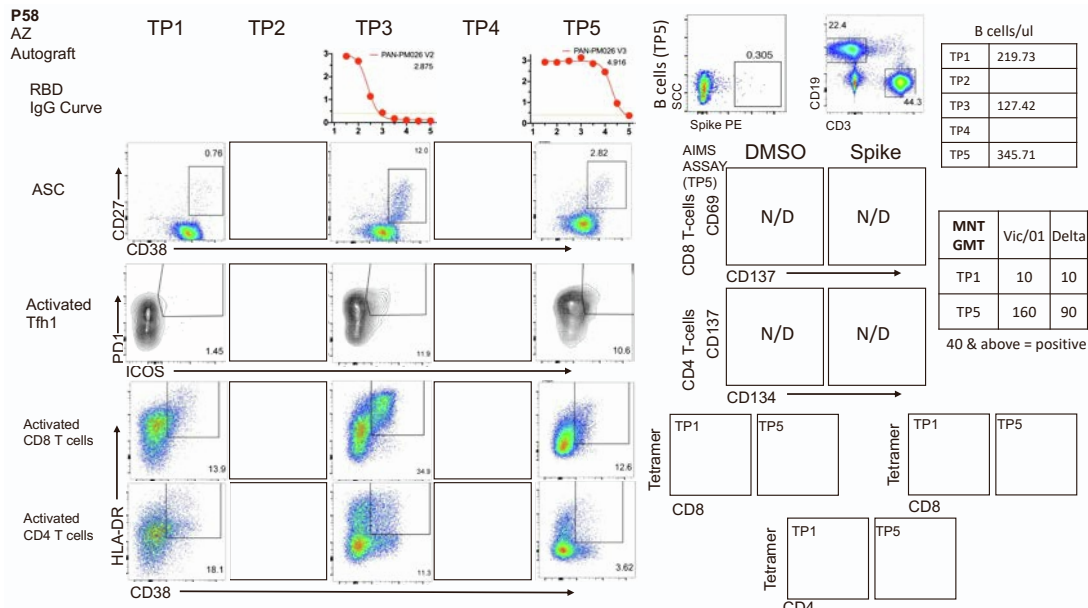


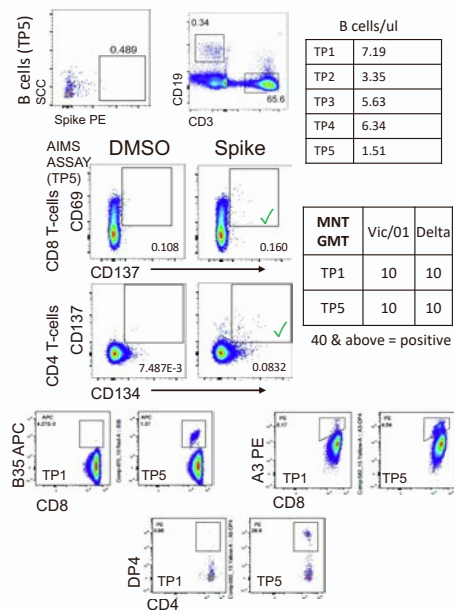
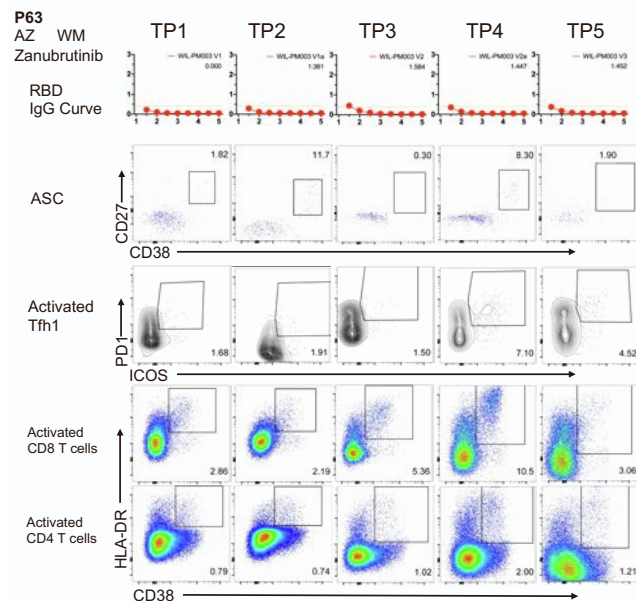
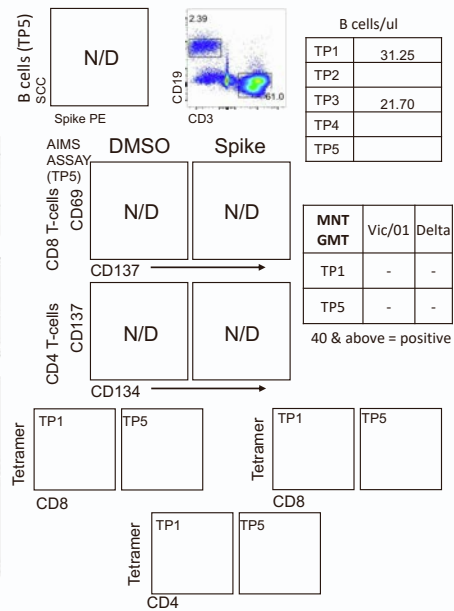
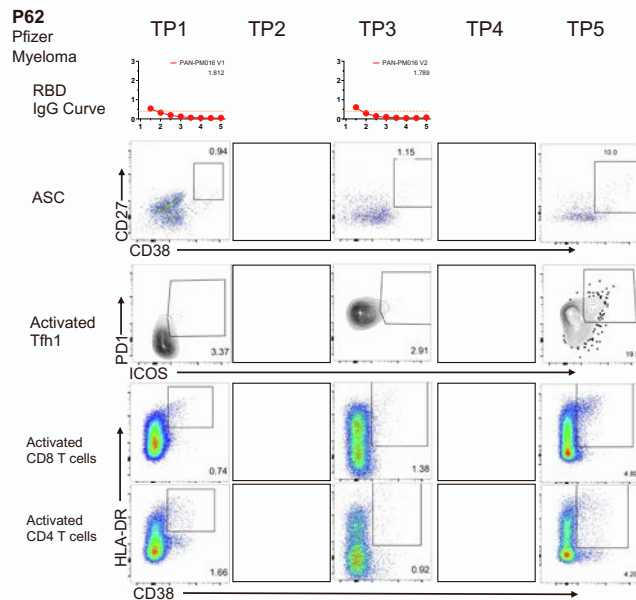
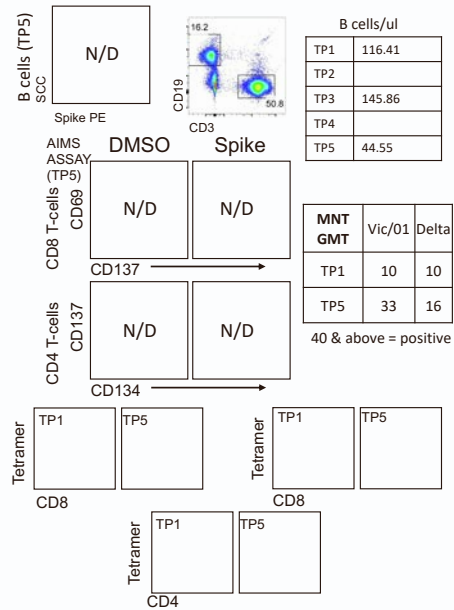
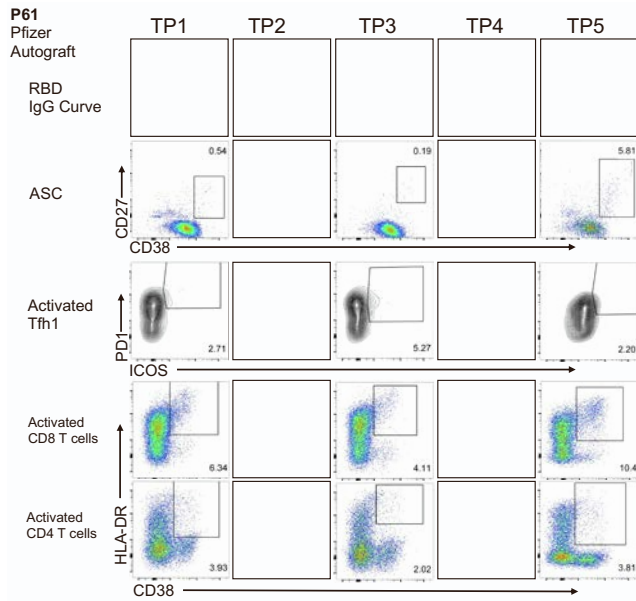






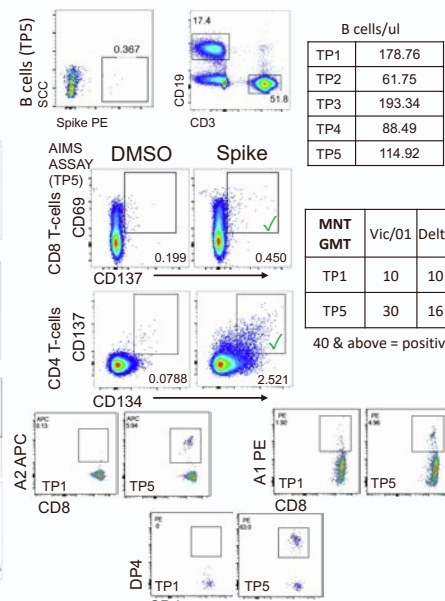
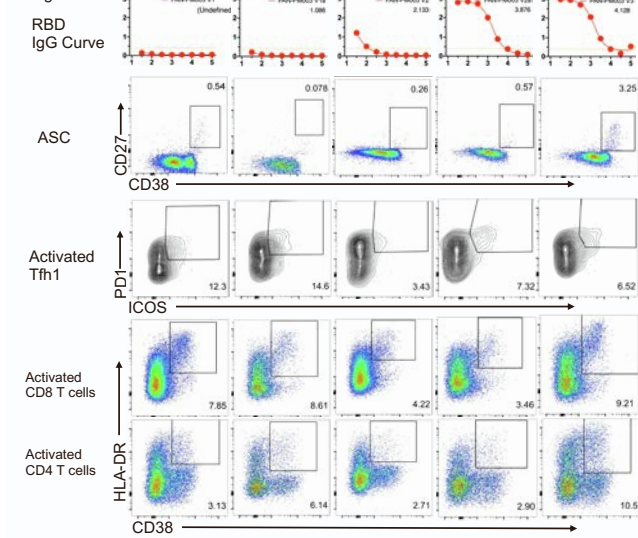






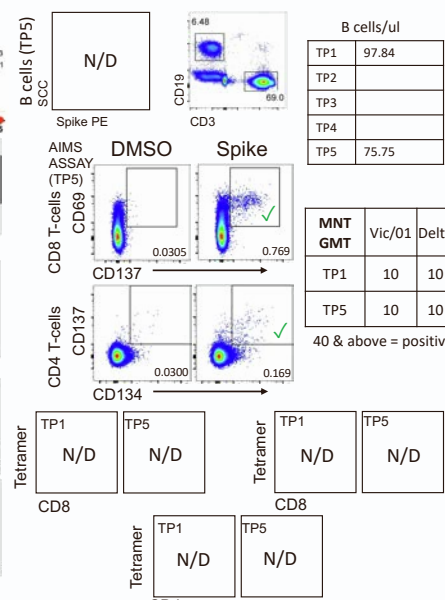
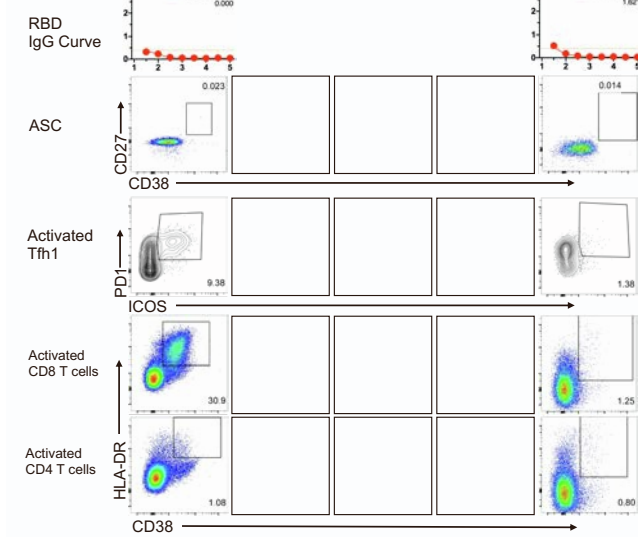
P64

Pfizer
Autograft



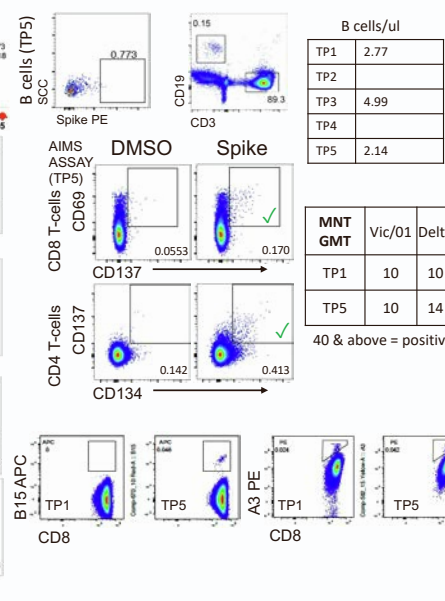
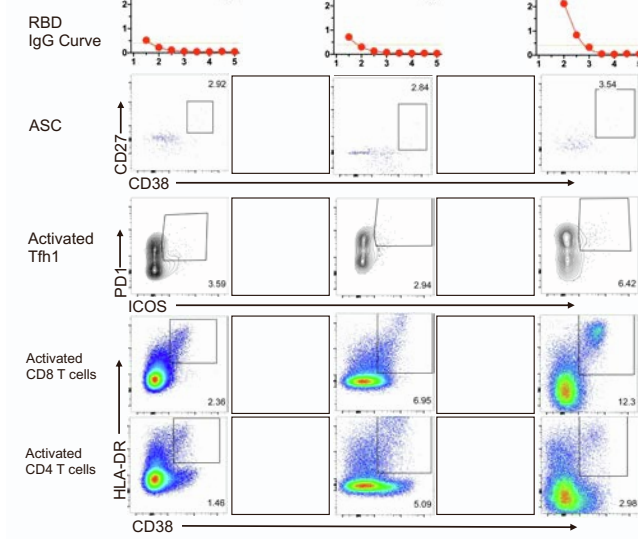
P65

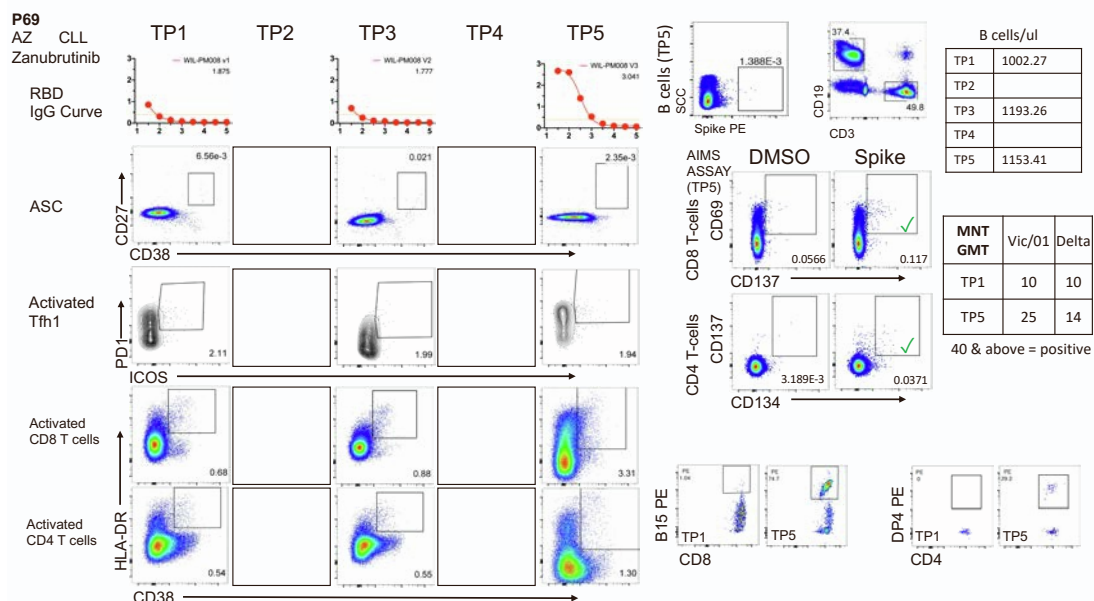
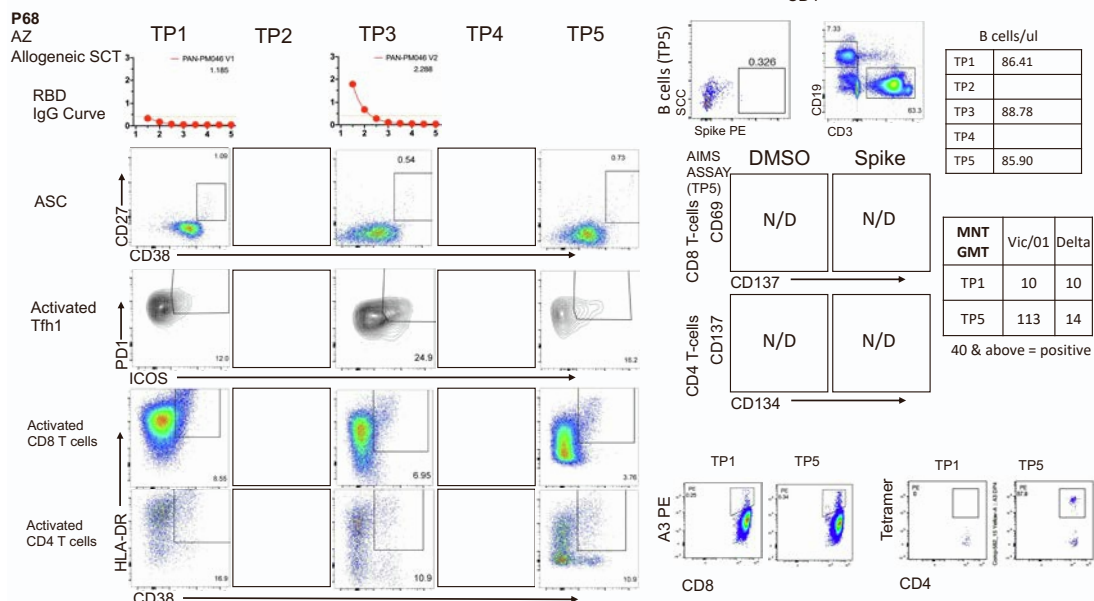
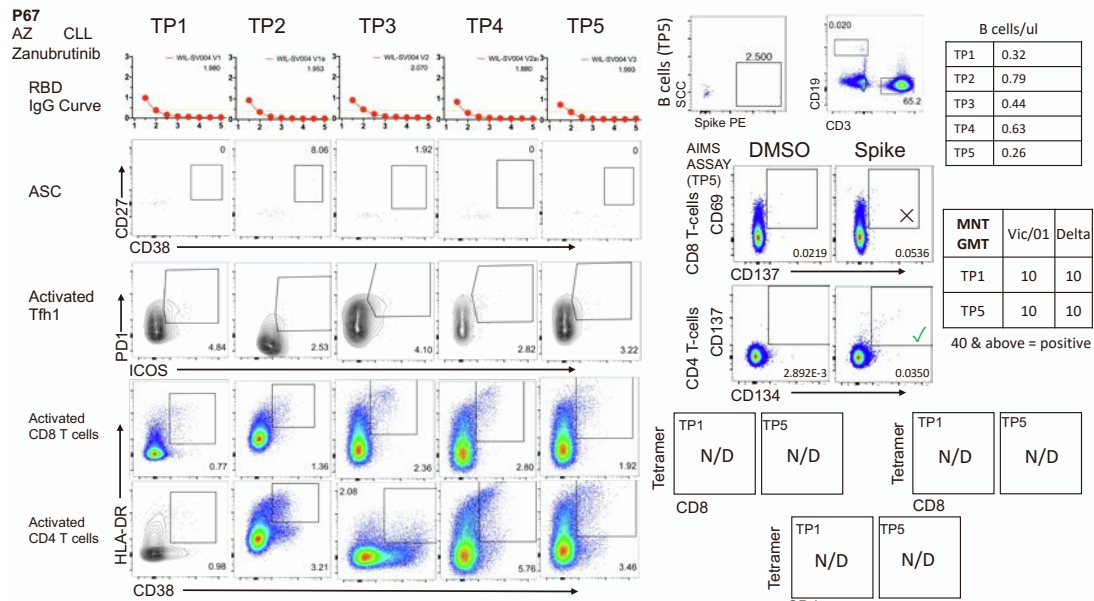
AZ CLL
Zanubrutinib

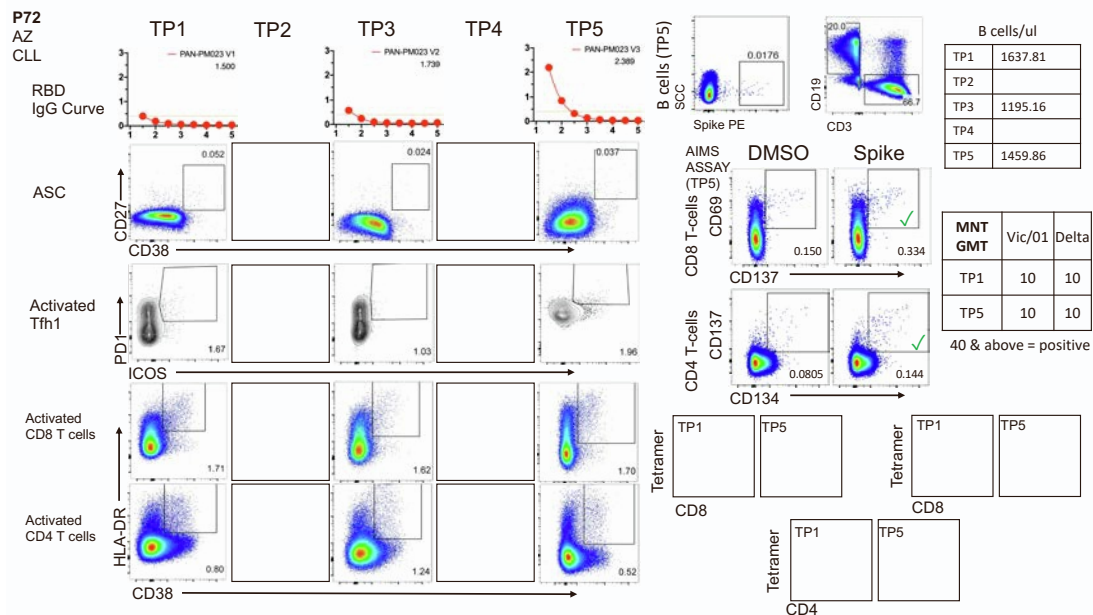
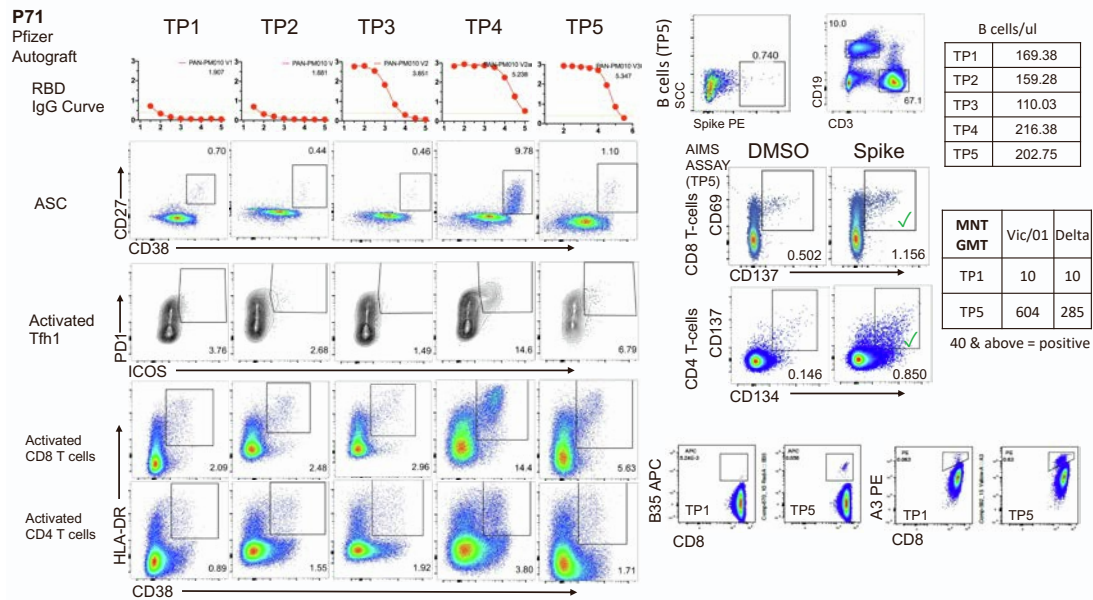
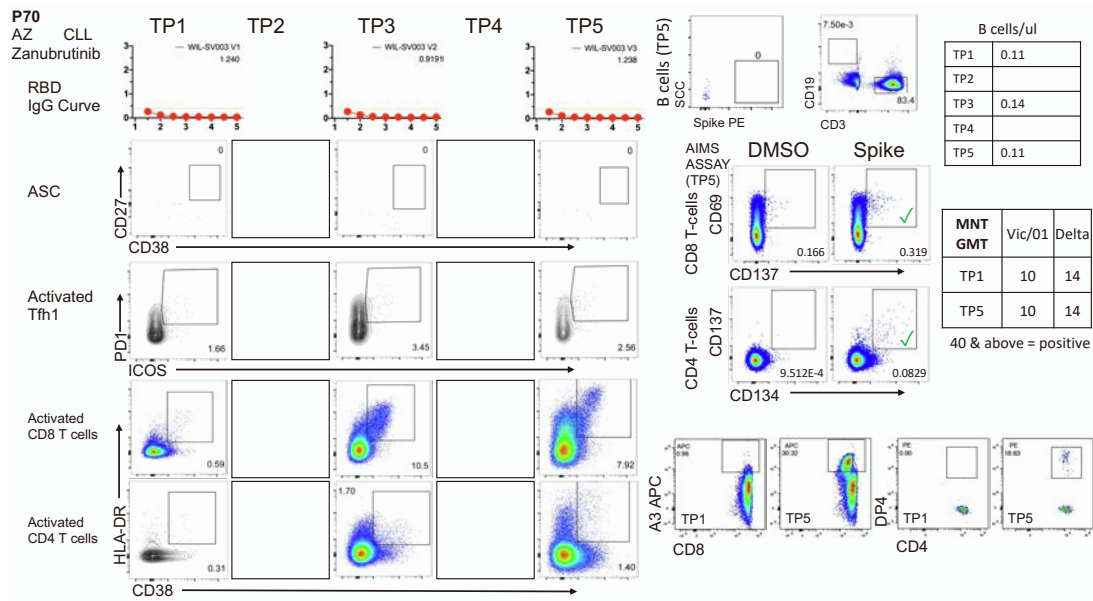


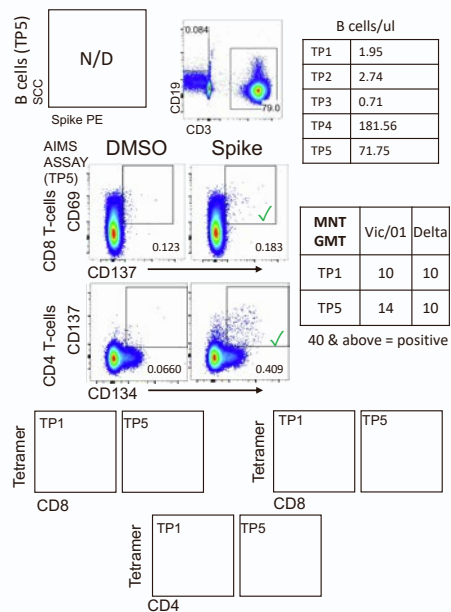
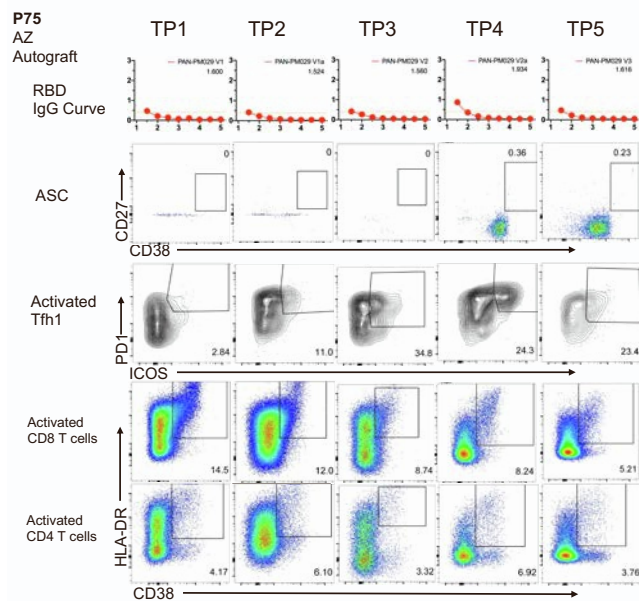
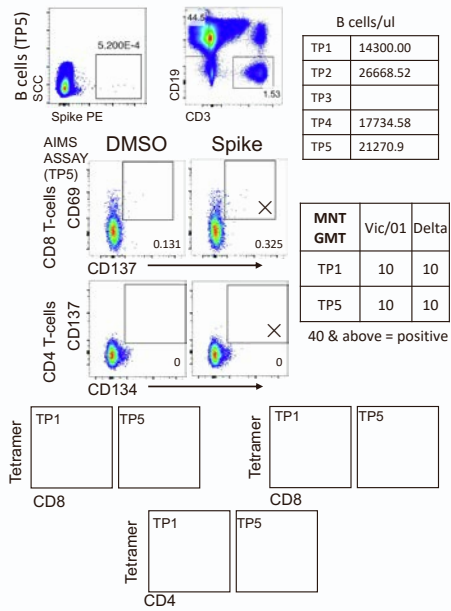
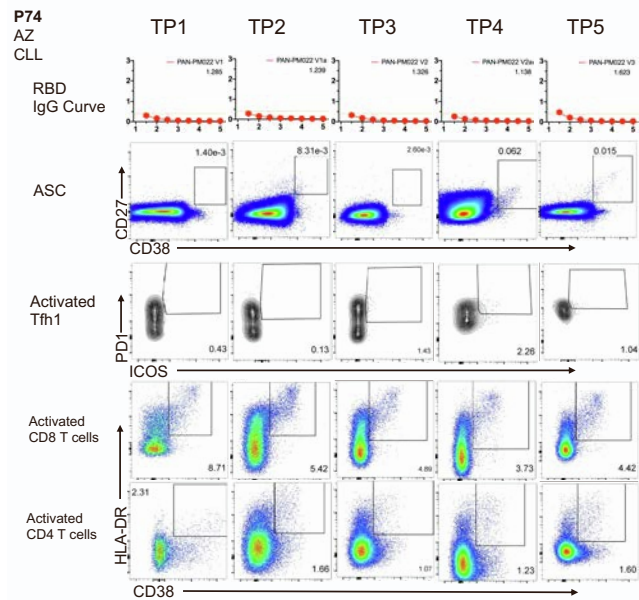
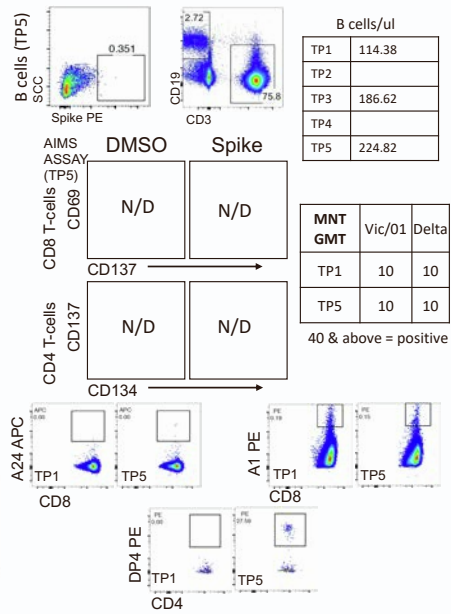
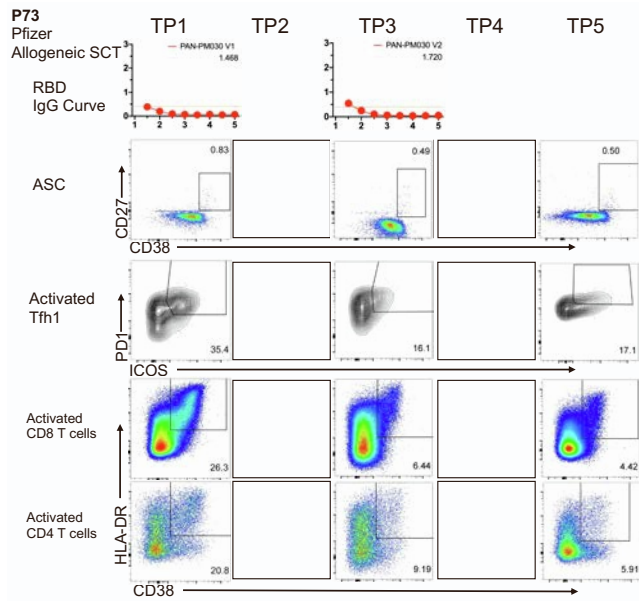
P66

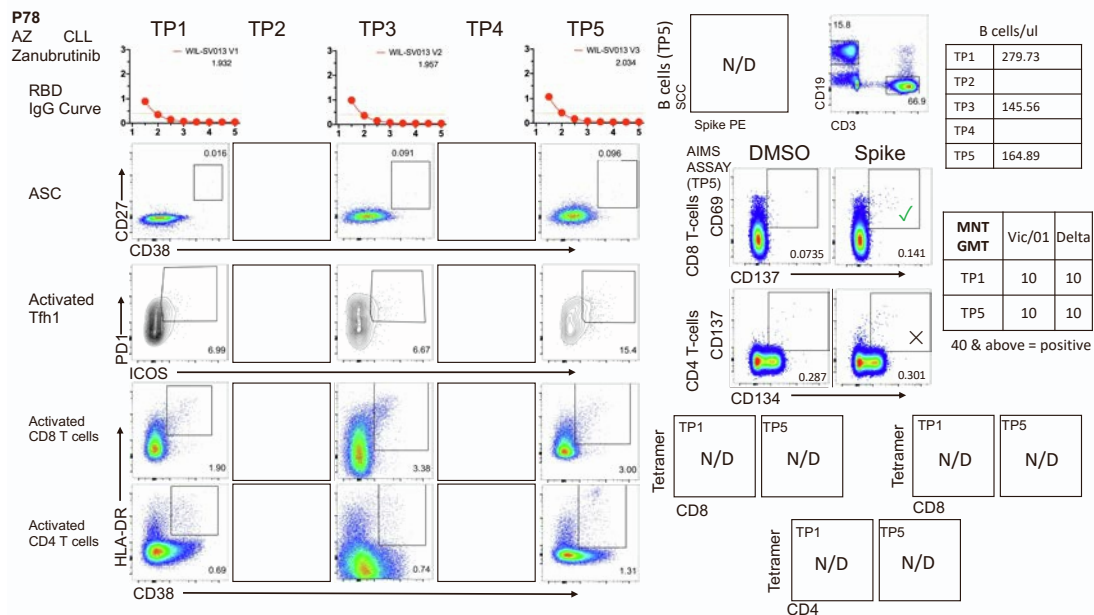
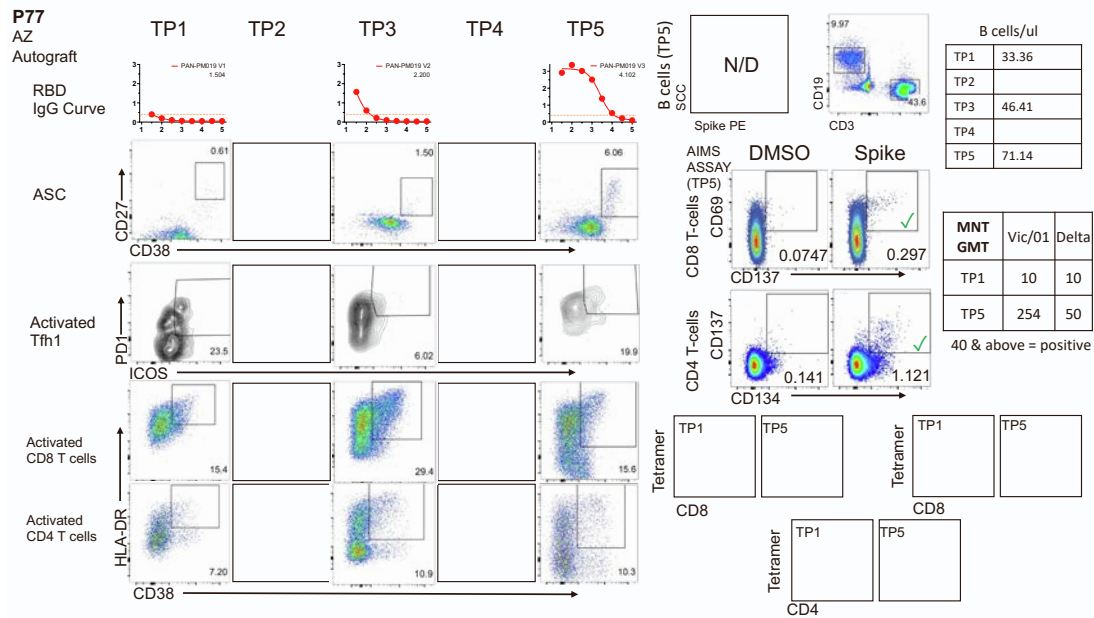
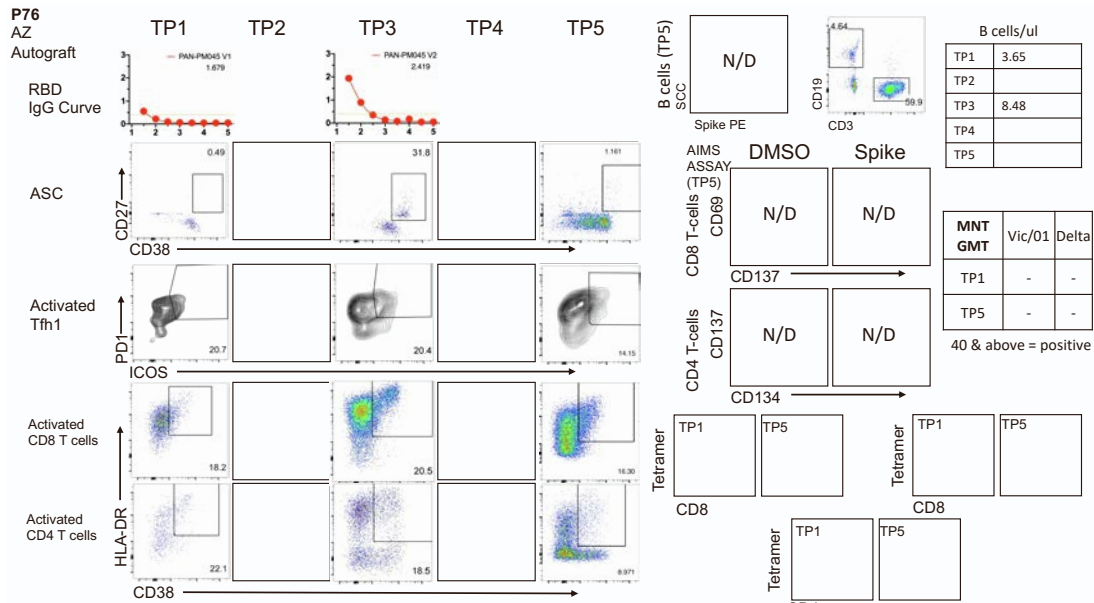
AZ CLL
Zanubrutinib







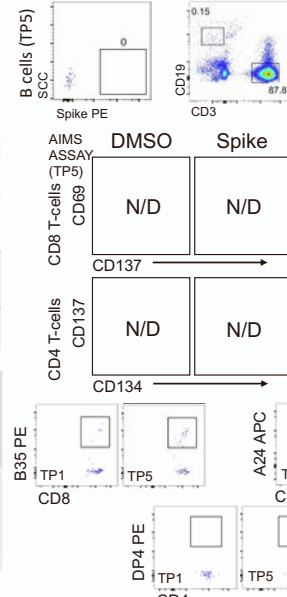
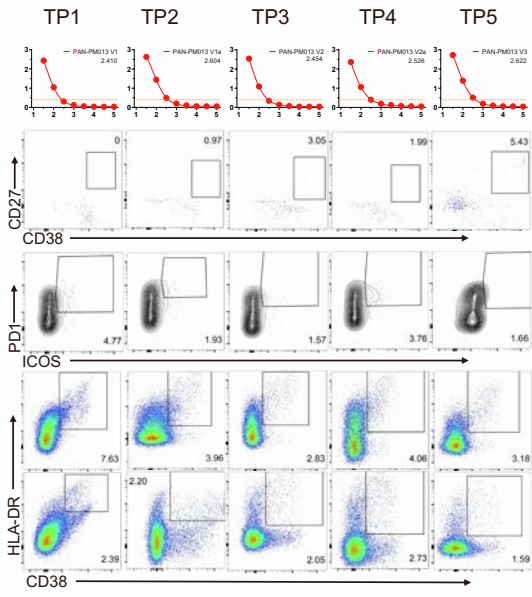




P79

AZ CLL
Venetoclax

RBD
IgG Curve



B cells/ul	
TP1	1.05
TP2	0.98
TP3	1.81
TP4	1.68
TP5	4.32

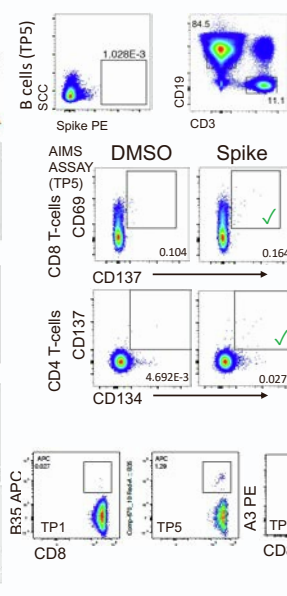
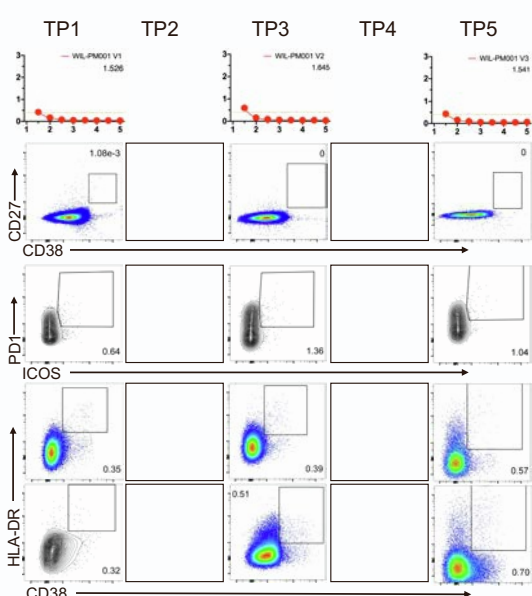
MNT GMT	Vic/01 Delta	
	TP1	10
TP5	10	10

40 & above = positive

P80

AZ CLL
Zanubrutinib

RBD
IgG Curve



B cells/ul	
TP1	13907.62
TP2	
TP3	4838.71
TP4	
TP5	596.82

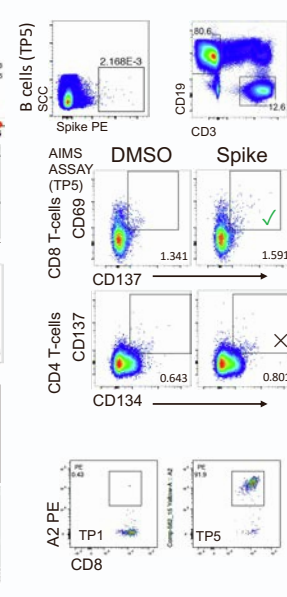
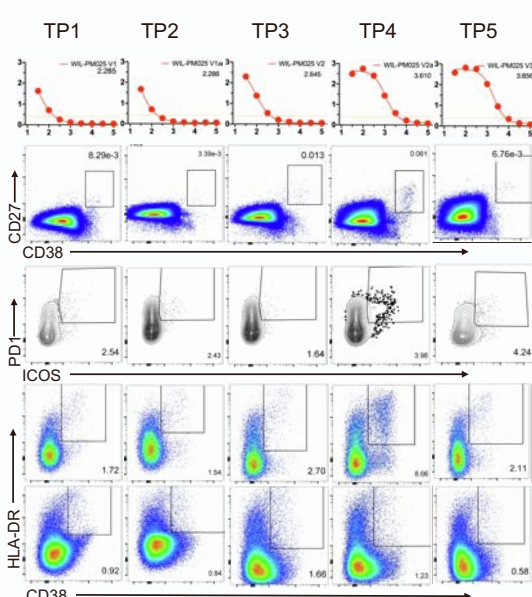
MNT GMT	Vic/01 Delta	
	TP1	10
TP5	10	10

40 & above = positive

P81

Pfizer
CLL

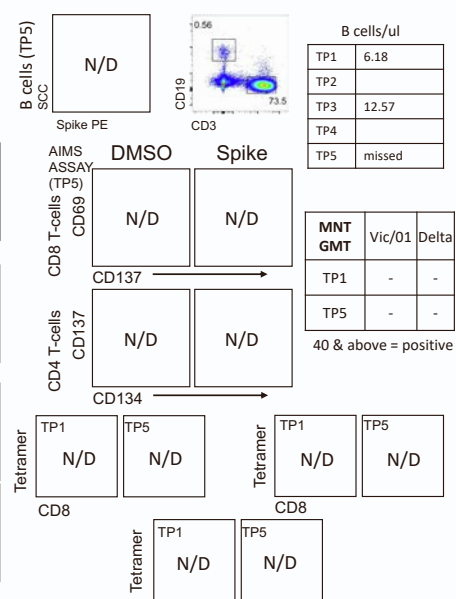
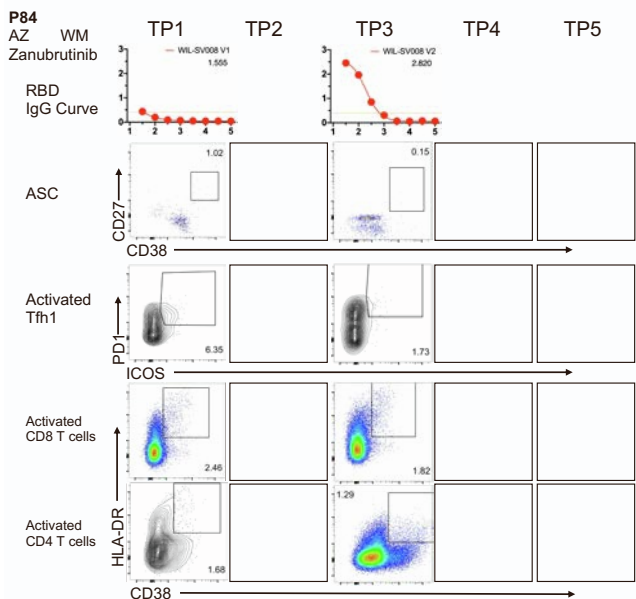
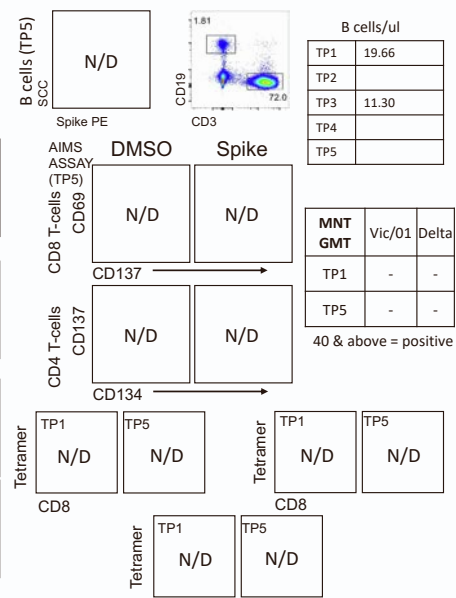
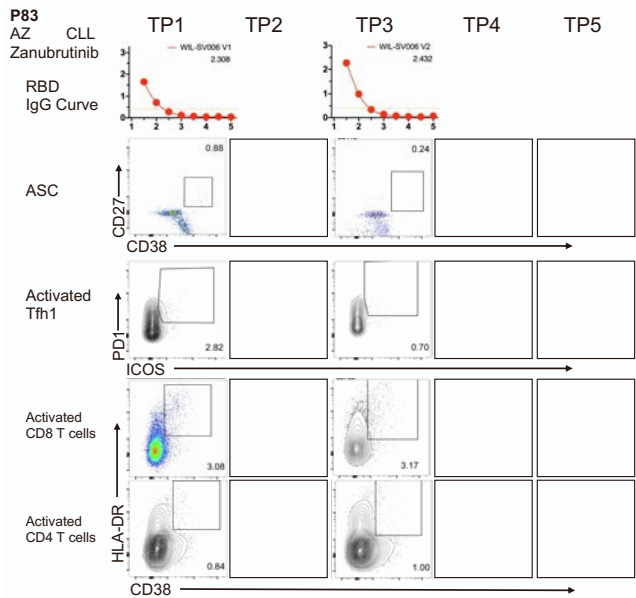
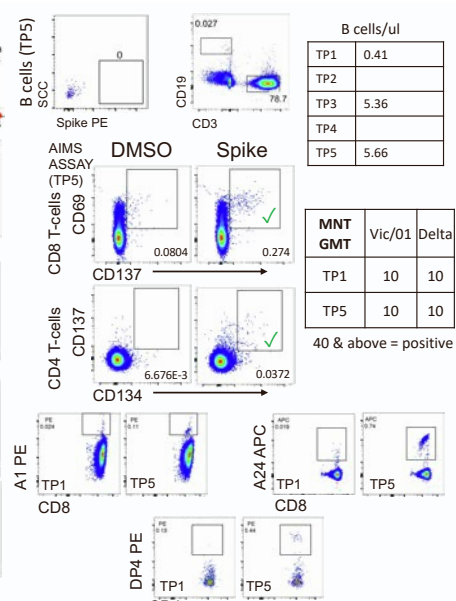
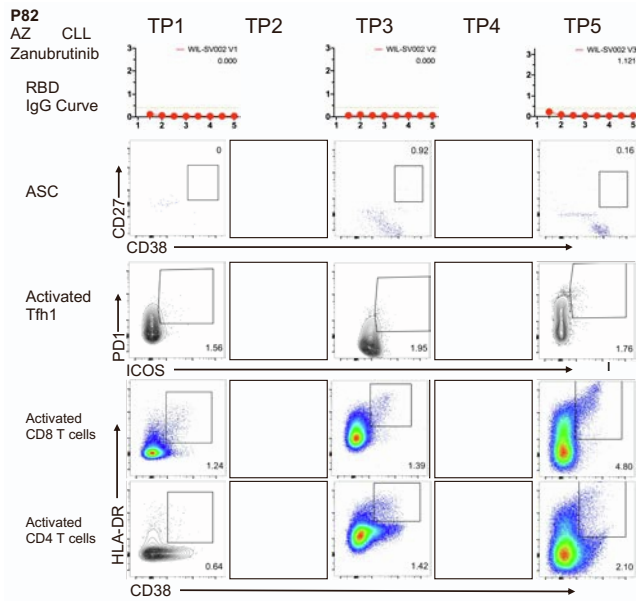
RBD
IgG Curve

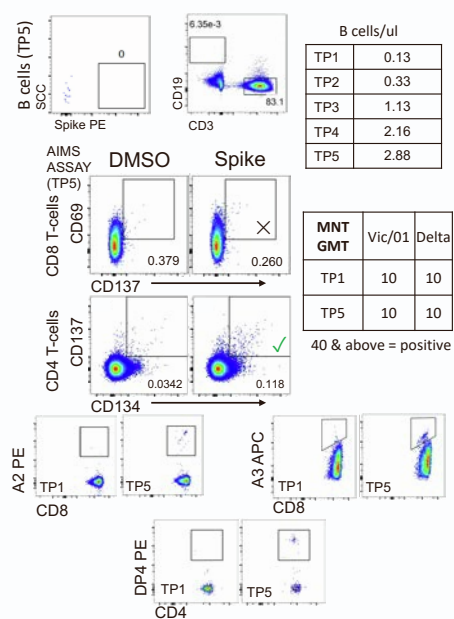
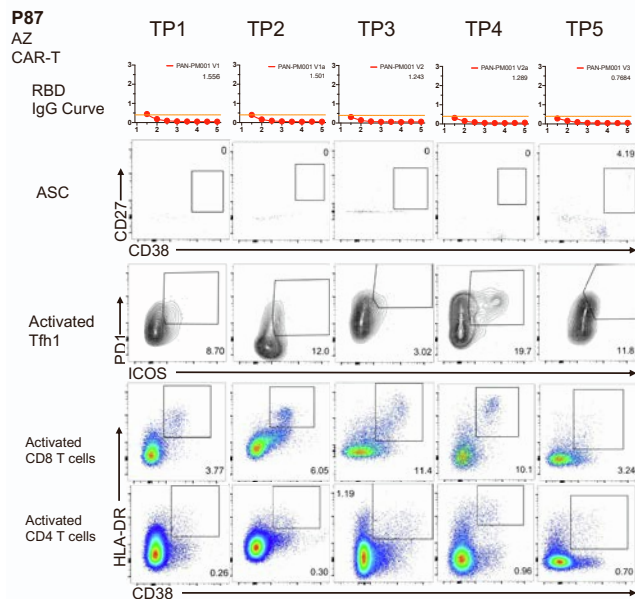
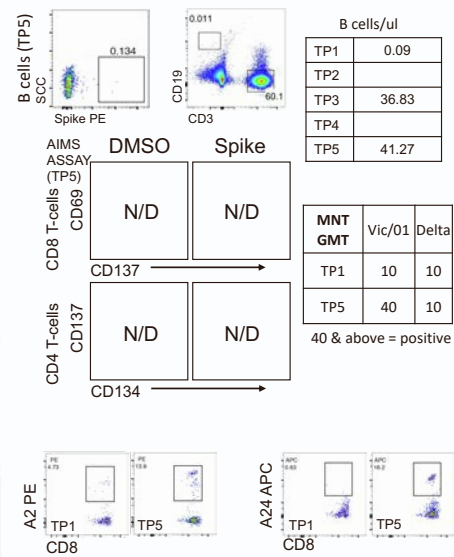
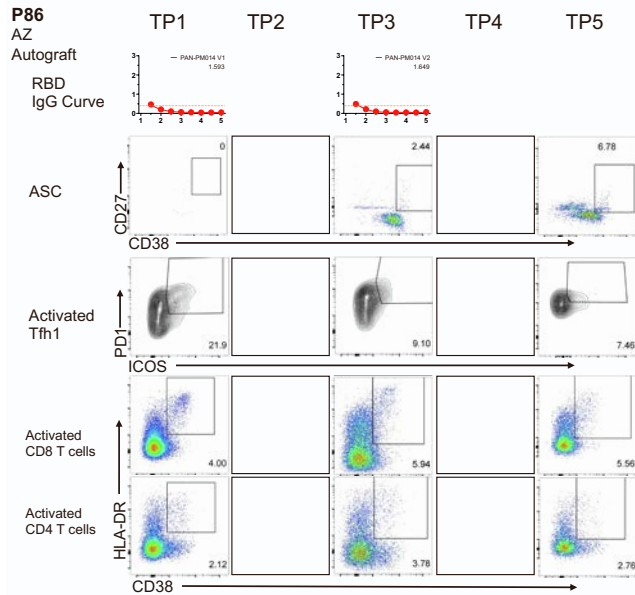
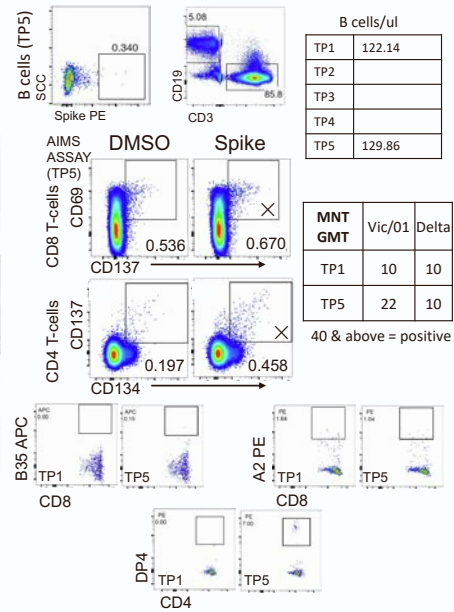
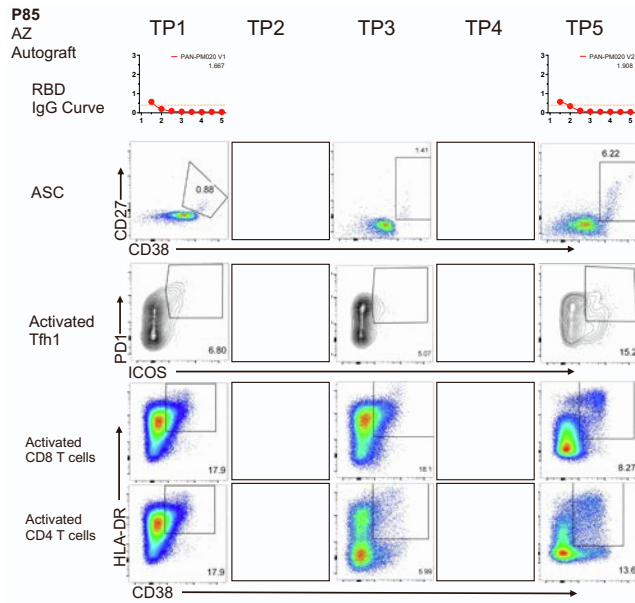


B cells/ul	
TP1	13478.11
TP2	12834.28
TP3	8714.72
TP4	9134.31
TP5	11136.65

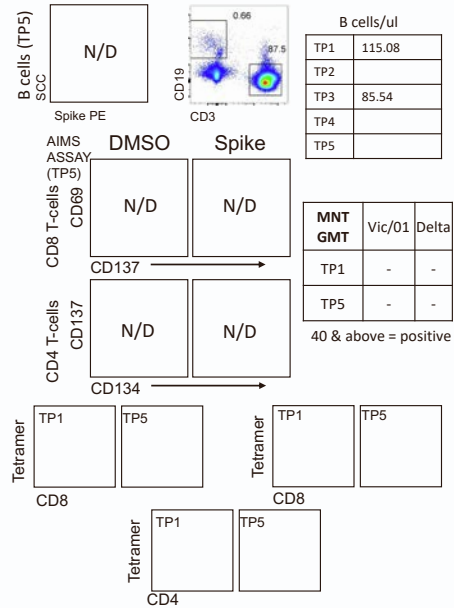
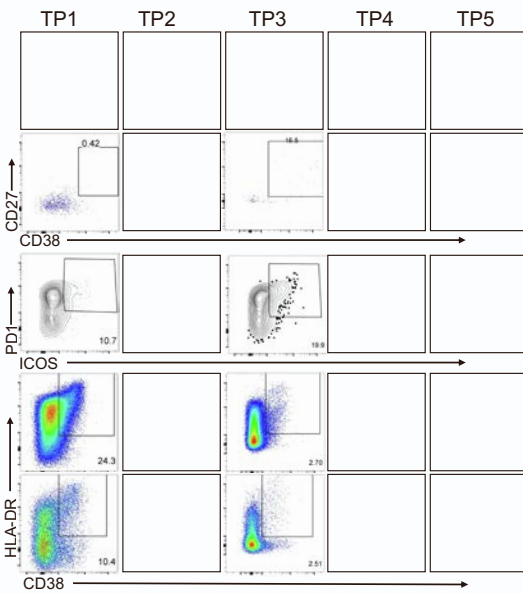
MNT GMT	Vic/01 Delta	
	TP1	10
TP5	45	10

40 & above = positive

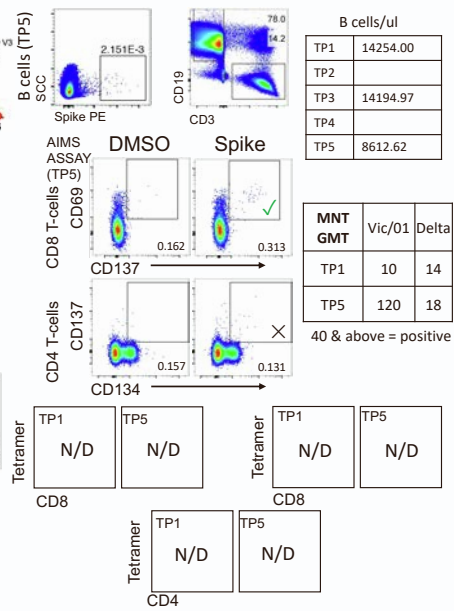
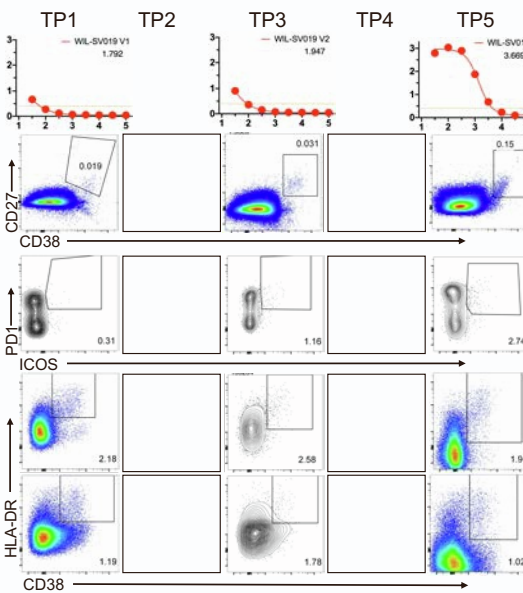




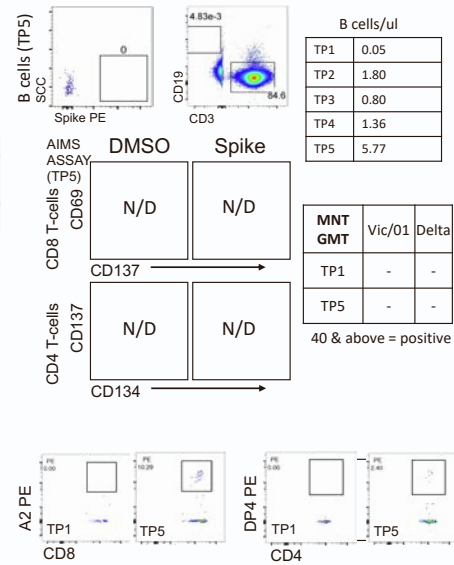
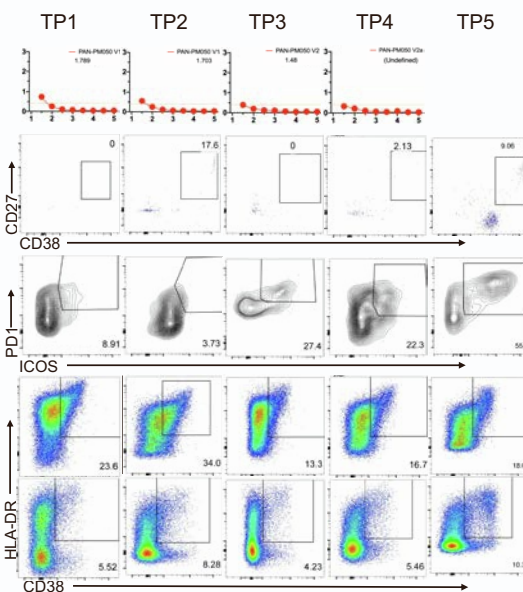
P88
Moderna
Autograft/
Myeloma



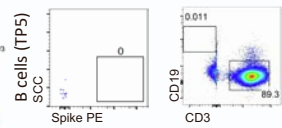
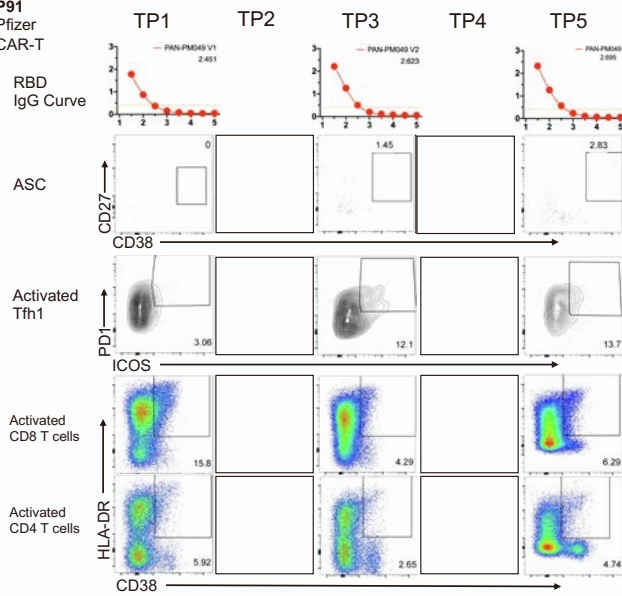
P89
AZ
CLL



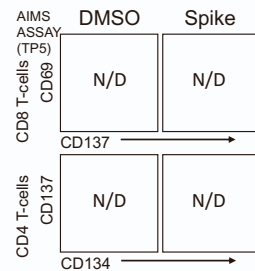
P90
Pfizer
CAR-T



P91
Pfizer
CAR-T

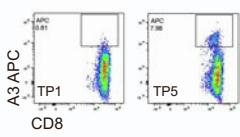


B cells/ul	
TP1	-
TP2	-
TP3	0.65
TP4	-
TP5	0.75

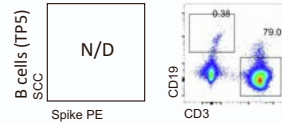
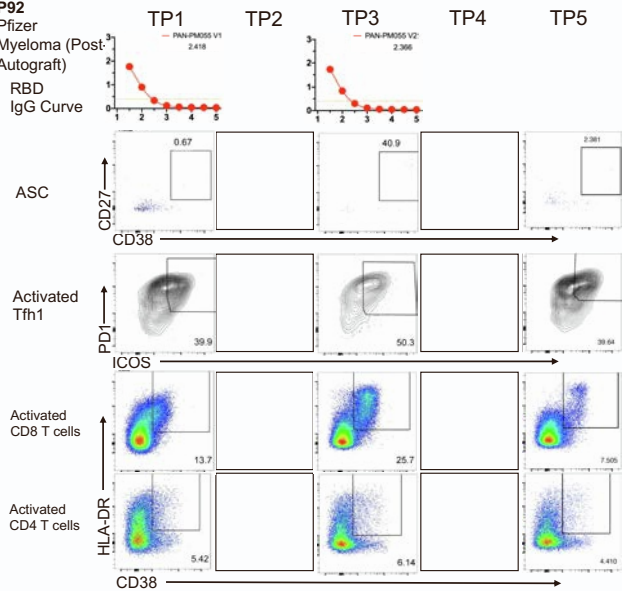


MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	14
TP5	10	10

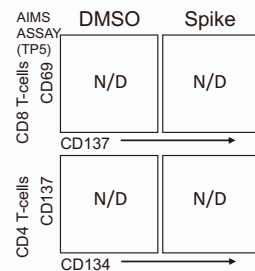
40 & above = positive



P92
Pfizer
Myeloma (Post Autograft)

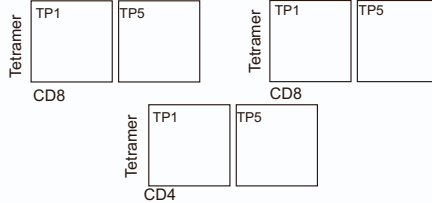


B cells/ul	
TP1	5.83
TP2	-
TP3	0.24
TP4	-
TP5	-

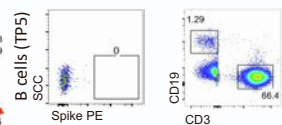
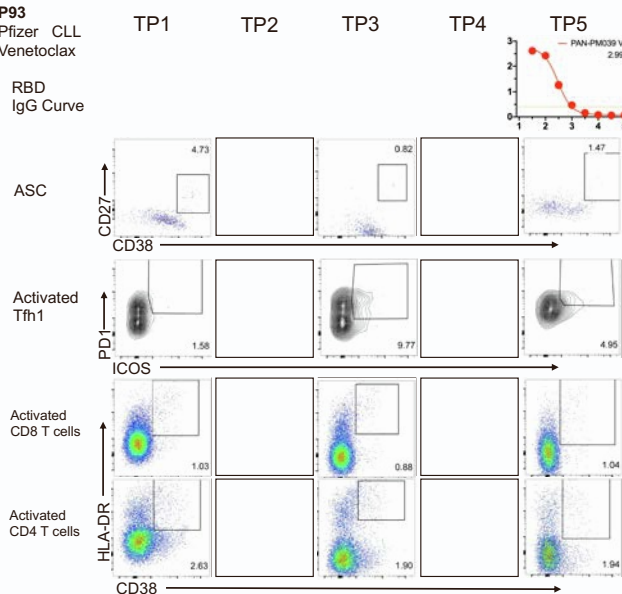


MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	-	-
TP5	-	-

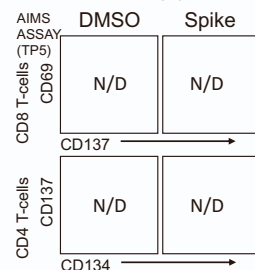
40 & above = positive



P93
Pfizer CLL
Venetoclax



B cells/ul	
TP1	8.21
TP2	-
TP3	7.92
TP4	-
TP5	8.45



MNT GMT	Vic/01 Delta	
	Vic/01	Delta
TP1	10	10
TP5	10	10

40 & above = positive

