

Determinants of response to CAR T cell therapy in a multicenter, multi-trial cohort analysis of patients with lymphoma

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Variable	ZUMA-1 (N = 225)	ZUMA-5 FL (N = 124)	ZUMA-5 MZL (N = 28)	ZUMA-7 (N = 166)	ZUMA-12 (N = 37)	Overall (N = 580)
Age						
Median age (range)	59 (19-85)	59.5 (34-79)	64 (43-77)	59 (21-80)	60 (23-86)	60 (19-86)
Male						
n(%)	143 (64)	73 (59)	13 (46)	104 (63)	25 (68)	358 (62)
Race, n(%)						
White	190 (84)	115 (93)	25 (89)	136 (82)	30 (81)	496 (86)
Black or African	8 (4)	4 (3)	2 (7)	9 (5)	1 (3)	24 (4)
Hispanic or Latino	26 (12)	6 (5)	3 (11)	8 (5)	2 (5)	45 (8)
Asian	3 (1)	2 (2)	0 (0)	9 (5)	1 (3)	15 (3)
Disease stage, n(%)						
I or II	57 (25)	18 (15)	2 (7)	38 (29)	1 (3)	116 (20)
III or IV	167 (74)	106 (85)	26 (93)	128 (77)	36 (97)	463 (80)
ECOG						
0	104 (46)	78 (63)	15 (54)	91 (55)	15 (41)	303 (52)
1	121 (54)	46 (37)	13 (46)	75 (45)	22 (59)	277 (48)
Study Prognostic Score ^a, n(%)						
Low	126 (56)	70 (56)	8 (29)	94 (57)	6 (16)	304 (52)
High	99 (44)	54 (44)	18 (64)	72 (43)	31 (84)	274 (47)
Prior lines of therapy						
Low (≤1)	6 (3)	3 (2)	0 (0)	166 (100)	37 (100)	212 (37)
Mid (2-3)	150 (67)	74 (60)	18 (64)	0 (0)	0 (0)	242 (42)
High (4-10)	69 (31)	46 (37)	10 (36)	0 (0)	0 (0)	125 (22)
Disease type						
DLBCL	156 (69)	0 (0)	0 (0)	99 (60)	0 (0)	255 (44)
Other (PMBCL, tFL, HGBCL, FL, MZL, etc.)	69 (31)	124 (100)	28 (100)	67 (40)	37 (100)	325 (56)
Previous ASCT						
n(%)	172 (76)	30 (24)	4 (14)	0 (0)	0 (0)	96 (17)
CD19 positivity, n(%)						
Negative	16 (7)	9 (7)	0 (0)	12 (7)	6 (16)	43 (7)
Positive	141 (63)	96 (77)	19 (68)	134 (81)	24 (65)	414 (71)
Refractory subgroup ^b						
Primary refractory	6 (3)			121 (73)		
Refractory to 2nd or greater line therapy	155 (69)					
Relapsed to 2nd or greater line therapy	15 (7)					
Relapse post ASCT	49 (22)					
Relapse ≤ 6 months of first-line therapy				26 (16)		
Relapse > 6 and ≤ 12 months of first-line therapy				19 (11)		
Refractory		84 (68)	22 (79)			
Relapsed		40 (32)	6 (21)			
Tumor burden by SPD ^c						
Median (range)	2971 (116-39658)	2790.145 (155.53-20264)	2034 (266-12327)	2508 (181-22892)	2707 (230-26124)	2768.3 (116-39658)
Naïve-like T cells (% of viable CD3+ product cells)						
n	225	124	28	166	37	580
Mean (STDEV)	20.1 (14.7)	21.9 (17.2)	25.8 (19.9)	36.2 (17.2)	40.8 (18.3)	26.7 (18.2)
Median (Q1, Q3)	16.4 (8.8, 26.4)	15.4 (9.6, 29.0)	21.5 (10.9, 35.4)	32.3 (23.6, 49.5)	35.0 (28.6, 52.9)	23.1 (12.2, 37.8)
Min, Max	0.4, 76.0	0.6, 81.4	3.3, 76.1	0.1, 74.9	6.5, 80.1	0.1, 81.4
Durable response (Investigator Read)						
n(%)	73 (32)	50 (40)	15 (54)	68 (41)	27 (73)	233 (40)
Prior regimen group ^d						
Radiation	56 (25)					56 (10)
Cytotoxic Chemotherapy-Containing	225 (100)	123 (99)	28 (100)	166 (100)	37 (100)	579 (100)
Targeted or Biologic Regimens	224 (100)	123 (99)	28 (100)	166 (100)	35 (95)	576 (99)
Anti-CD20	224 (100)	123 (99)	27 (96)	166 (100)	35 (95)	575 (99)
Other Targeted or Biologic Regimens	65 (29)	74 (60)	21 (75)	3 (2)		163 (28)

^a Study Prognostic Scores are defined as follows: For ZUMA-1, ZUMA-5, and ZUMA-12, scores of 0–2 are considered low, and 3+ are high. For ZUMA-7, scores of 0–1 are low, and 2+ are high. The International Prognostic Index (IPI) score was used in ZUMA-1 and ZUMA-12. The IPI score used in ZUMA-7 is based on Second-line age-adjusted International Prognostic Index total score (IXRS). Follicular Lymphoma International Prognostic Index (FLIPI) score was used in ZUMA-5.

^b The refractory subgroups in the ZUMA trials are defined as follows: ZUMA-1 includes four categories—Primary refractory, Refractory to 2nd or greater line therapy, Relapsed to 2nd or greater line therapy, and Relapse post ASCT. ZUMA-5 categorizes patients as either Refractory or Relapsed. ZUMA-7 defines refractory subgroups based on the derived response to first-line therapy at randomization, with three categories—Primary refractory, Relapse within 6 months of first-line therapy, and Relapse between 6 and 12 months after first-line therapy. ZUMA-12 does not include refractory subgroup information.

^c Investigator determined SPD for all subjects was used when available. If unavailable, Central SPD was used.

^d One ZUMA-5 subject received previous therapy for DLBCL, not for the primary disease of FL, thus the total number of subjects in the meta-cohort for prior regimens is 579.

Supplementary Table 1. Summary of the discovery meta-cohort baseline characteristics and demographics.

ASCT, autologous stem cell transplant; ECOG, eastern cooperative oncology group; DLBCL, diffuse large B-cell lymphoma; FL, follicular lymphoma; HGBCL, high-grade B-cell lymphoma; IHC, immunohistochemistry; MZL, marginal zone lymphoma; PMBCL, primary mediastinal B-cell lymphoma; SPD, sum of the products of the diameters of target lesions; tFL, transformed follicular lymphoma.

Phenotypic Parameter	Population	Parent population (gated on 7AAD- singlets)
N. T cells	CD3+	Total cells
N. CD3- cells	CD3-	T cells
N. CD4+ T cells	CD3+CD8-	T cells
N. CD8+ T cells	CD3+CD8+	T cells
N. CM T cells	CD3+CCR7+CD45RA-	T cells
N. CCR7- T cells	CD3+CCR7-	T cells
N. EMRA T cells	CD3+CCR7-CD45RA+	T cells
N. EM T cells	CD3+CCR7-CD45RA-	T cells
N. CCR7+ T cells	CD3+CCR7+	T cells
N. N/SCM (Naive-like) T cells	CD3+CCR7+CD45RA+	T cells
% T cells	CD3+	Total cells
% CD8+ T cells	CD3+CD8+	T cells
% CM T cells	CD3+CCR7+CD45RA-	T cells
% EMRA T cells	CD3+CCR7-CD45RA+	T cells
% EM T cells	CD3+CCR7-CD45RA-	T cells
% CCR7+ T cells	CD3+CCR7+	T cells
% N/SCM (Naive-like) T cells	CD3+CCR7+CD45RA+	T cells
Ratio CD4/CD8 T cells	CD3+CD8-/CD3+CD8+	T cells

Supplementary Table 2. Axi-cel product phenotyping panel.

Axi-cel product phenotyping via flow cytometry using a 5-color (CD45RA, CCR7, CD3, CD8, Viability) panel. CM, central memory; EM, effector memory; EMRA, terminally differentiated effector memory; N/SCM, naive/memory stem cell. N indicates the number of infused cells for each population, and % indicates the proportion relative to the parent population (total viable cells for T cells, and T cells for the other populations). Parameters in green represent the number and those in orange represent the percentage within the parent population.

Variable	ZUMA-2 (N = 154)	ZUMA-6 (N = 23)	ZUMA-14 (N = 26)	Overall (N = 203)
Age				
Median age (range)	65 (38-82)	56 (43-71)	62 (38-81)	64 (38-82)
Male				
n(%)	124 (81)	13 (57)	14 (54)	151 (74)
Race, n(%)				
White	140 (91)	18 (78)	19 (73)	177 (87)
Black or African	3 (2)	0 (0)	0 (0)	3 (1)
Hispanic or Latino	16 (10)	0 (0)	4 (15)	20 (10)
Asian	1 (0)	4 (17)	3 (12)	8 (4)
Disease stage, n(%)				
I or II	22 (14)	5 (22)	5 (19)	32 (16)
III or IV	132 (86)	18 (78)	21 (81)	171 (84)
ECOG				
0	103 (67)	13 (57)	12 (46)	128 (63)
1	51 (33)	10 (43)	14 (54)	75 (37)
Study Prognostic Score ^a , n(%)				
Low		12 (52)	26 (100)	
High		11 (48)	0 (0)	
Prior lines of therapy				
Low (≤1)	69 (45)	4 (17)	5 (19)	78 (38)
Mid (2-3)	59 (38)	11 (48)	21 (81)	91 (45)
High (4-10)	26 (17)	8 (35)	0 (0)	34 (17)
Disease type				
MCL	154 (100)			
DLBCL		23 (100)	22 (85)	
Other (HGBCL, PMBCL, etc.)			4 (15)	
Previous ASCT				
n(%)	69 (45)	4 (17)	2 (8)	75 (37)
CD19 positivity, n(%)				
Negative	9 (6)	4 (17)		
Positive	113 (73)	17 (74)		
Refractory subgroup ^b				
Primary refractory		4 (17)	5 (19)	
Refractory to last MCL therapy	39 (25)			
Refractory after ASCT			2 (8)	
Relapsed post last MCL therapy	86 (56)			
Refractory to 2nd or greater line therapy		15 (65)	19 (73)	
Relapse post ASCT	29 (43)	4 (17)		
Tumor burden by SPD ^c				
Median (range)	1930 (0-58968)	2309 (180-18381.82)	2225.5 (187-14884)	2059.5 (0-58968)
Naïve-like T cells (% of viable CD3+ product cells)				
n	154	23	26	203
Mean (STDEV)	32.2 (19.1)	26.44 (22.33)	30.4 (17.5)	31.3 (19.3)
Median (Q1, Q3)	28.9 (19.0, 45.6)	19.5 (9.6, 33.4)	28.4 (20.1, 37.3)	27.7 (18.3, 44.2)
Min, Max	0.3, 80.7	4.9, 84.7	8.6, 83.0	0.3, 84.7
Durable response (Investigator Read)				
n(%)	85 (55)	7 (30)	11 (42)	103 (51)
Prior regimen group				
Radiation	16 (10)			16 (8)
Cytotoxic Chemotherapy-Containing	154 (100)	23 (100)	26 (100)	203 (100)
Targeted or Biologic Regimens	154 (100)	23 (100)	26 (100)	203 (100)
Anti-CD20	154 (100)	23 (100)	26 (100)	203 (100)
Other Targeted or Biologic Regimens	74 (48)	4 (17)	5 (19)	83 (41)

^a Study Prognostic Scores are defined as follows: scores of 0–2 are considered low, and 3+ are high. Mantle Cell Lymphoma International Prognostic Index (MIPI) was used in ZUMA-2, International Prognostic Index (IPI) in ZUMA-6, and age-adjusted IPI in ZUMA-14

^b The refractory subgroups in the ZUMA trials are defined as follows: ZUMA-2 includes three categories—Refractory to last MCL therapy, Relapsed post last MCL therapy, and Relapse post ASCT. ZUMA-6 includes three categories—Primary refractory, Refractory to 2nd or greater line therapy, and Relapse Post ASCT. ZUMA-14 includes three categories—Primary refractory, Refractory to 2nd or greater line therapy, and Refractory after ASCT.

^c Investigator determined SPD for all subjects was used when available. If unavailable, Central SPD was used.

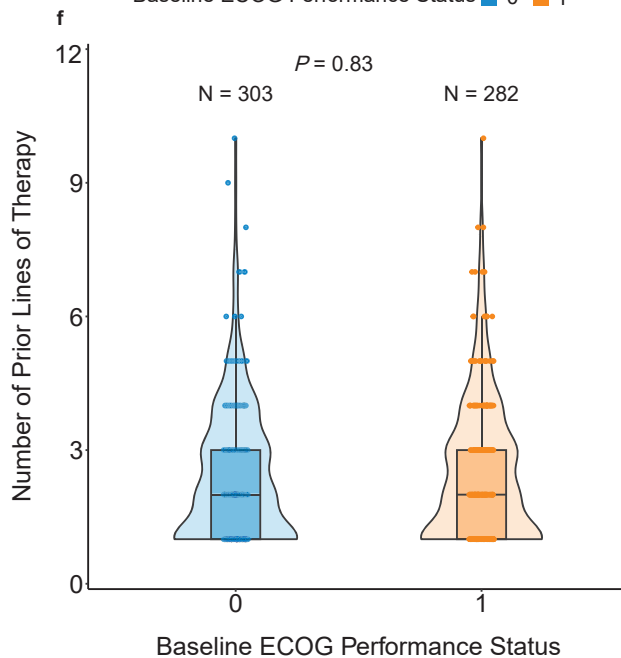
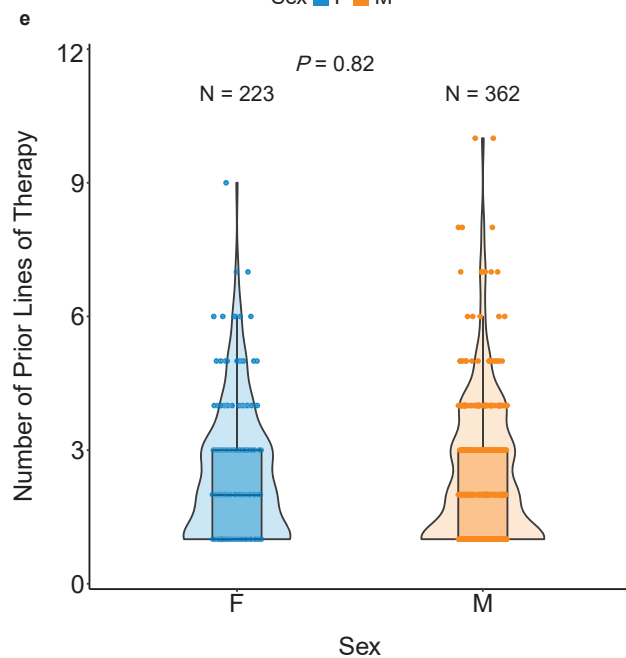
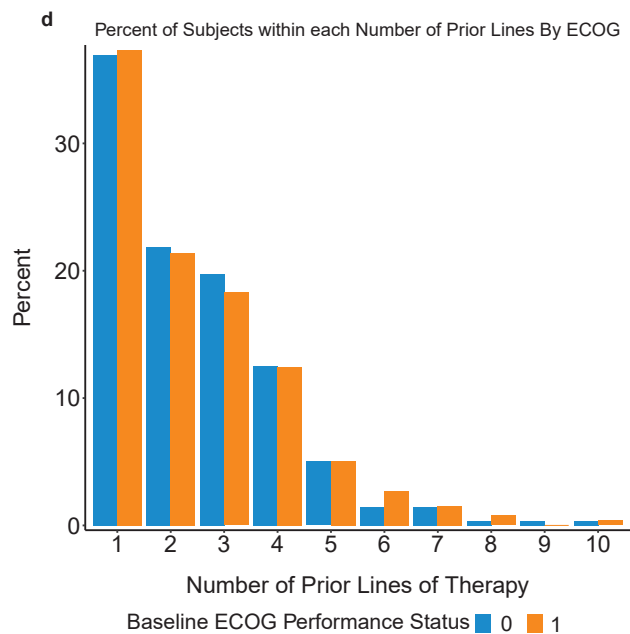
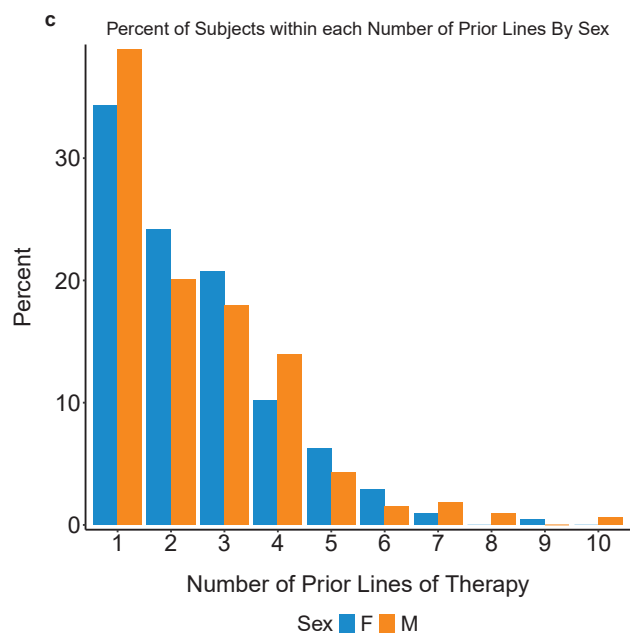
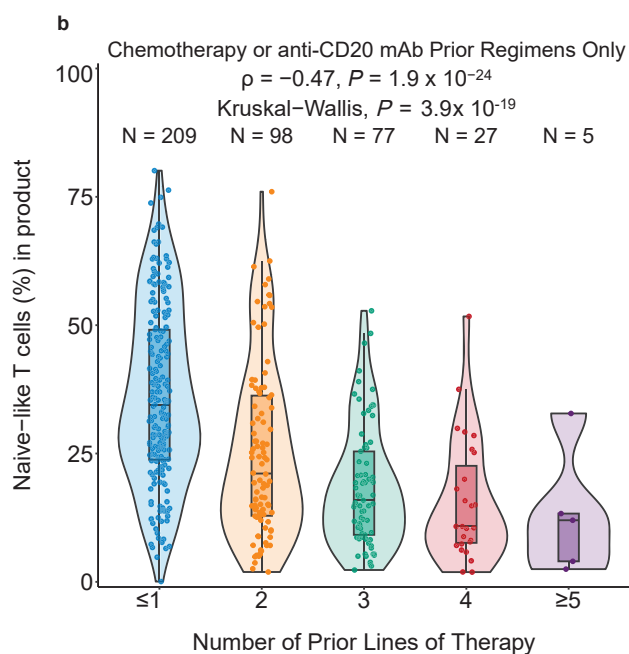
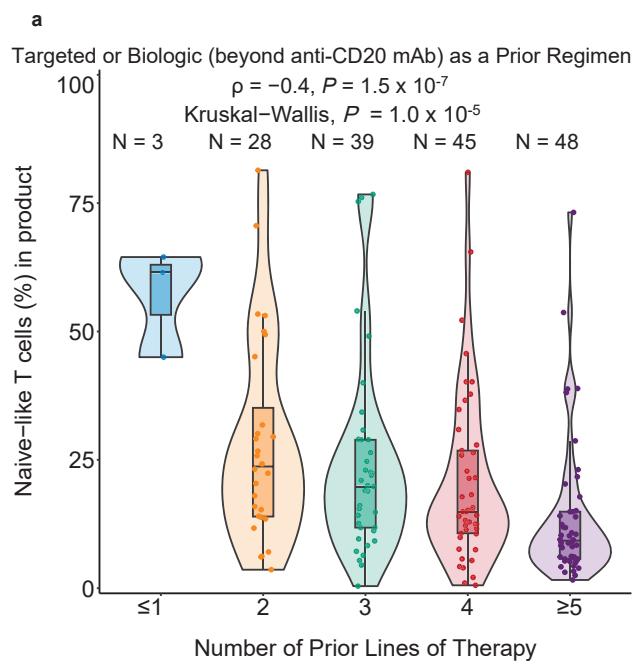
Supplementary Table 3. Summary of the validation meta-cohort baseline characteristics and demographics.

ASCT, autologous stem cell transplant; ECOG, eastern cooperative oncology group; DLBCL, diffuse large B-cell lymphoma; HGBCL, high-grade B-cell lymphoma; IHC, immunohistochemistry; MCL, mantle cell lymphoma; PMBCL, primary mediastinal B-cell lymphoma; SPD, sum of the products of the diameters of target lesions.

	Marker	Reactivity	Clone	Conjugate	Supplier
1	CD45	Human	HI30	89Y	Standard BioTools
2	HLA-DR	Cross	L243	146Nd	Biolegend
3	CD95	Human	DX2	164Dy	Standard BioTools
4	CD3	Human	UCHT1	154Sm	Standard BioTools
5	CD4	Human	SK3	174Yb	Standard BioTools
6	CD8	Human	SK1	168Er	Standard BioTools
7	CD25	Human	2A3	149Sm	Standard BioTools
8	CD127	Human	A019D5	143Nd	Standard BioTools
9	CD45RA	Human	HI100	169Tm	Standard BioTools
10	CCR7	Human	G043H7	159Tb	Standard BioTools
11	PD-1 (CD279)	Human	EH12.2H7	155Gd	Standard BioTools
12	CD19	Human	HIB19	142Nd	Standard BioTools
13	CD28	Human	CD28.2	160Gd	Standard BioTools
14	CD27	Human	L128	167Er	Standard BioTools
15	CD14	Human	M5E2	115In	Biolegend
16	CD16	Human	3G8	209Bi	Standard BioTools
17	CD56	Human	HCD56; NCAM16.2	176Yb	Standard BioTools
18	NKG2D (CD314)	Human	1D11; ON72	166Er	BD Biosciences
19	ICOS (CD278)	Human	C398.4A	148Nd	Standard BioTools
20	PD-L1 (CD274)	Human	29E.2A3	175Lu	Standard BioTools
21	Anti-CAR	Cross	Anti-Whitlow Antibody	145Nd	Kite
		Cross	1D4-C5	145Nd	Standard BioTools
22	CD29	Human	TS2/16	156Gd	Standard BioTools
23	CXCR3 (CD183)	Human	G025H7	163Dy	Standard BioTools
24	4-1BB (CD137)	Human	4B4-1	173Yb	Standard BioTools
25	OX40 (CD134)	Human	ACT35	150Nd	Standard BioTools
26	LAG-3 (CD223)	Human	11C3C65	165Ho	Standard BioTools
27	TIM-3 (CD366)	Human	F38-2E2	144Nd	Biolegend
28	CCR6 (CD196)	Human	G034H3	152Sm	Biolegend
29	CD57	Human	HCD57	172Yb	Standard BioTools
30	TIGIT	Human	MBSA43	153Eu	Standard BioTools
	Intracellular/Signaling				
31	Foxp3	Human	259D/C7; PCH101	162Dy	Standard BioTools
32	Ki67	Cross	B56	161DY	Standard BioTools
33	CTLA4(CD152)	Human	14D3	170Er	Standard BioTools
34	Granzyme	Cross	GB11	171Yb	Standard BioTools

Supplementary Table 4. CyTOF panel for ZUMA-1, ZUMA-6, ZUMA-7 product phenotyping analysis

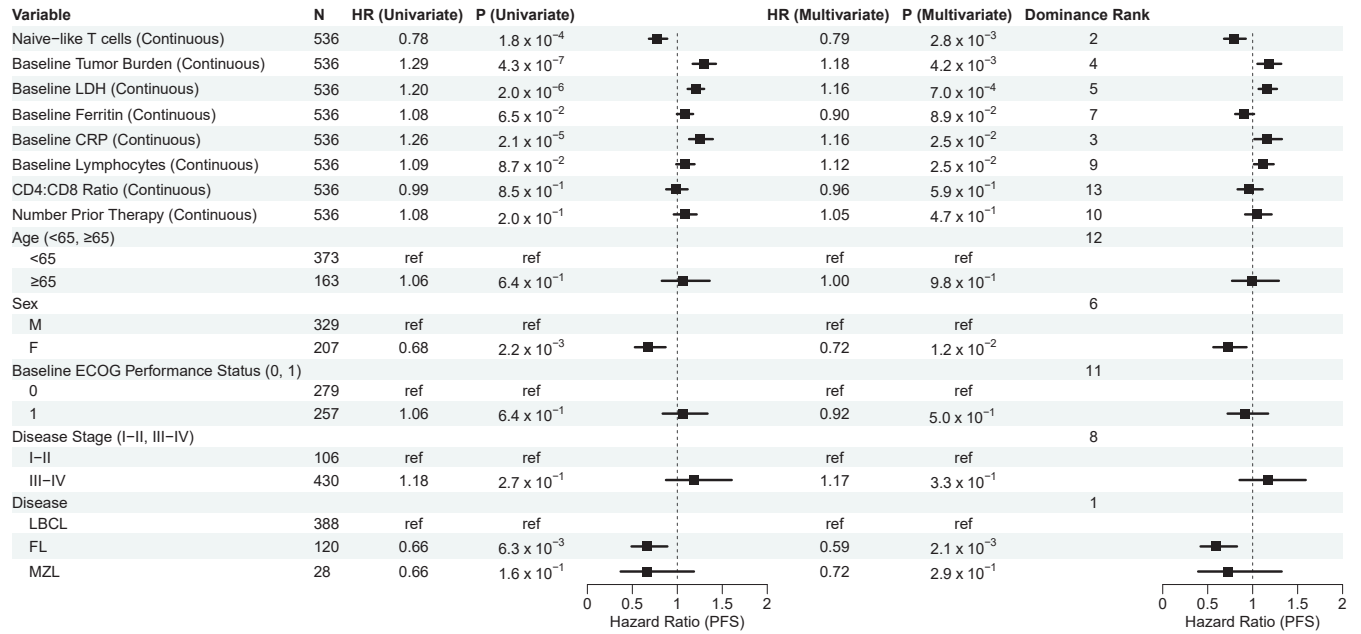
List of cytometry time-of-flight (CyTOF) markers used for product phenotyping in ZUMA-1, ZUMA-6, and ZUMA-7. For each marker the species reactivity, antibody clone, metal isotope conjugate, and supplier are provided.



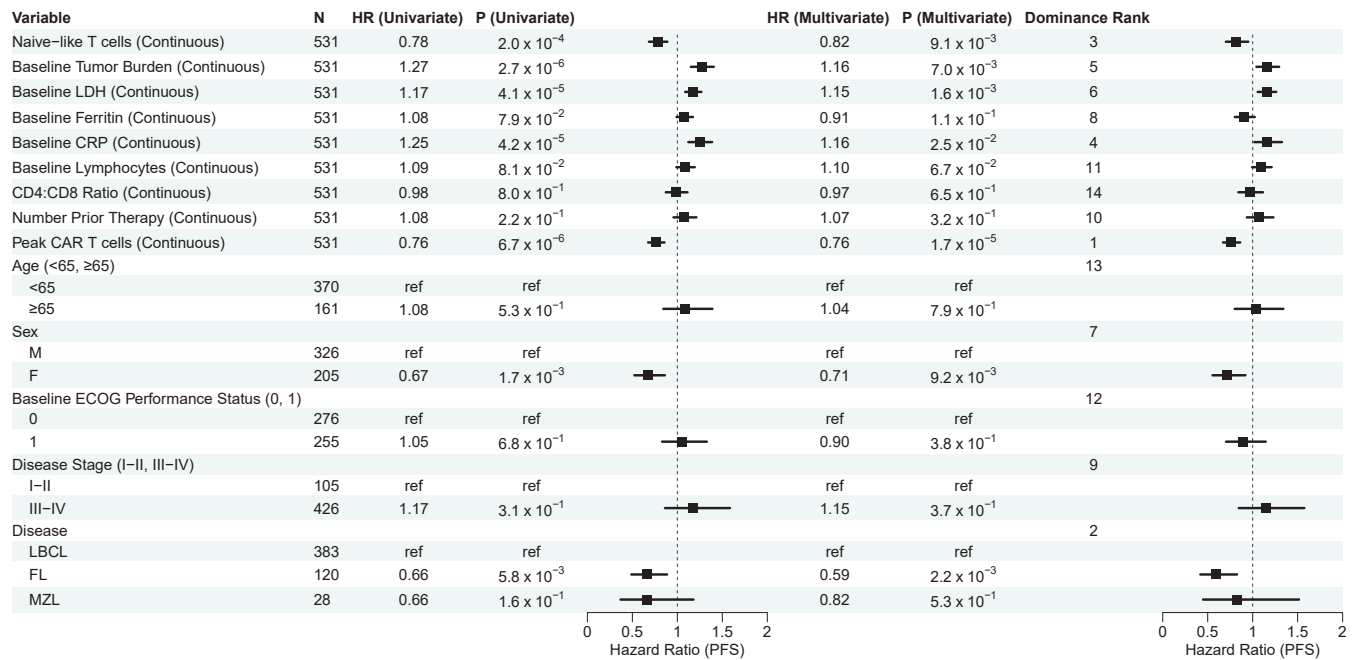
Supplementary Figure 1. Prior lines of therapy evaluated by administration of targeted or biologic regimens (beyond anti-CD20 mAb), sex, and ECOG performance status.

Kruskal-Wallis for categorical and Spearman for ordinal analysis was performed to assess the relationship between the proportion of naive-like T cells in patients who **A**) received a biological or targeted (beyond anti-CD20 mAb) regimen and patients who **B**) only received chemotherapy or anti-CD20 mAb. Prior lines of therapy were transformed as follows: ≤ 1 line = 1, 2 lines = 2, 3 lines = 3, 4 lines = 4, and ≥ 5 lines = 5. Spearman correlation coefficient (ρ) is included. The center line, box limits, and whiskers represent the median, interquartile range and $1.5 \times$ interquartile range, respectively. Histogram representation of number of prior lines of therapy by **C**) sex (male, female) and **D**) baseline ECOG performance status (0, 1). Wilcoxon rank sum test was performed to assess the statistical association between prior lines of therapy and **E**) sex (male, female) or **F**) baseline ECOG performance status (0,1). All P values are two-sided. mAb, monoclonal antibody. ECOG, eastern cooperative oncology group.

a



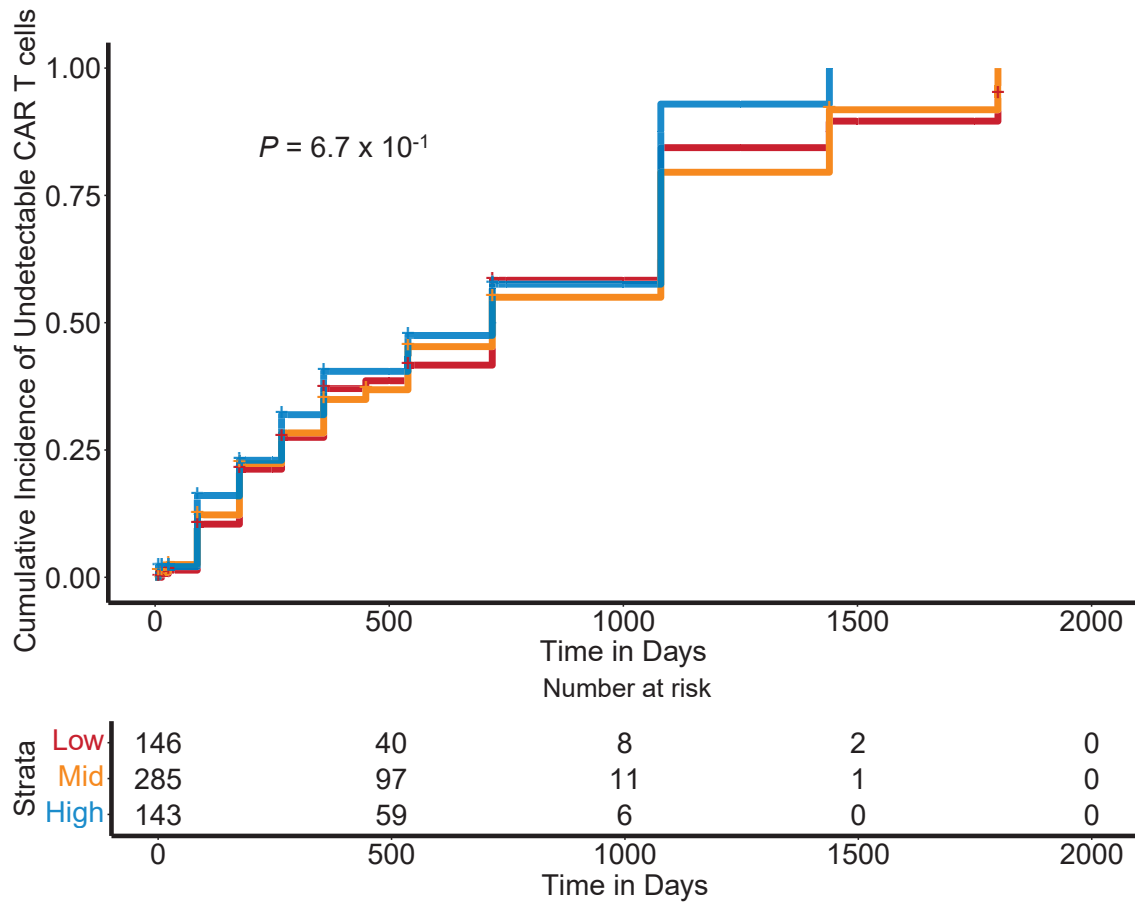
b



Supplementary Figure 2. Univariate and multivariate analysis of continuous variables associated with PFS.

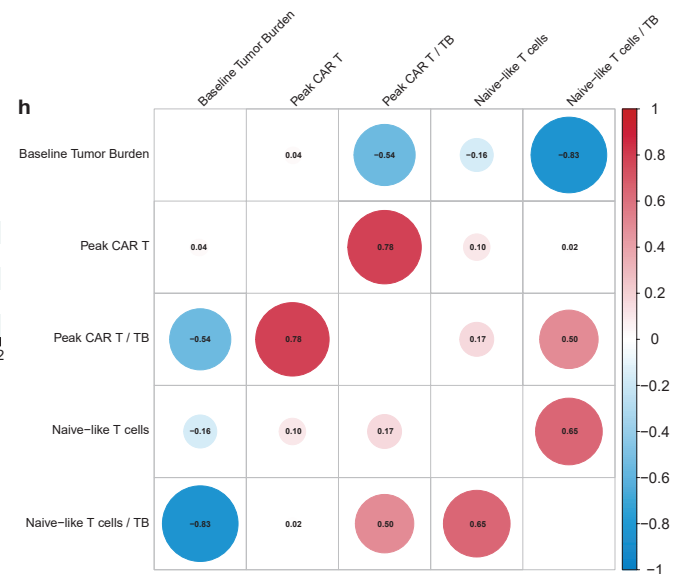
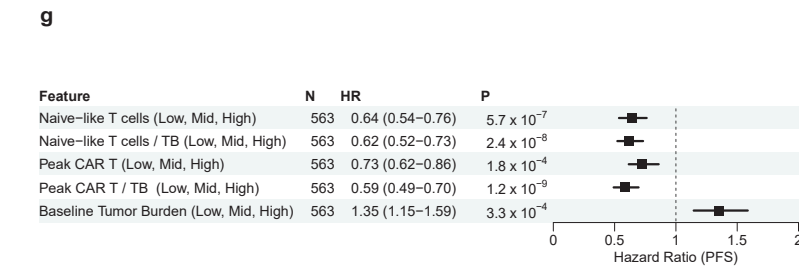
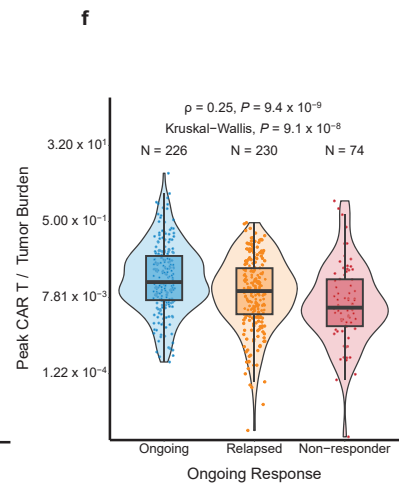
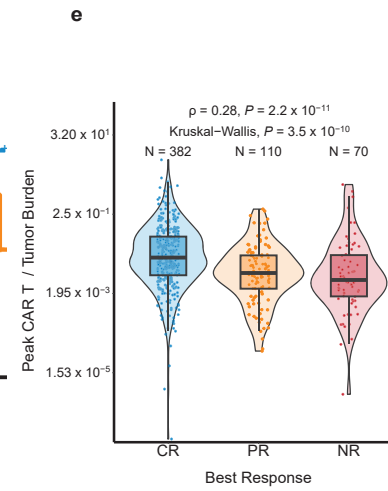
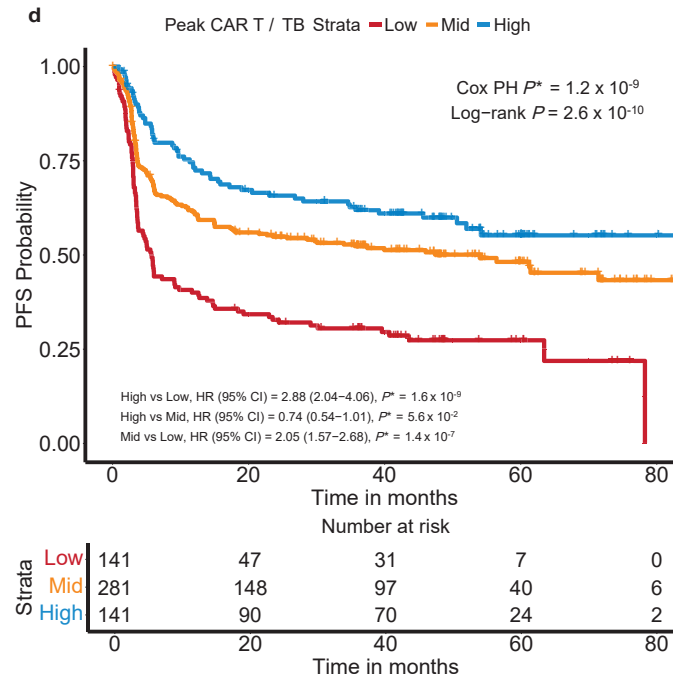
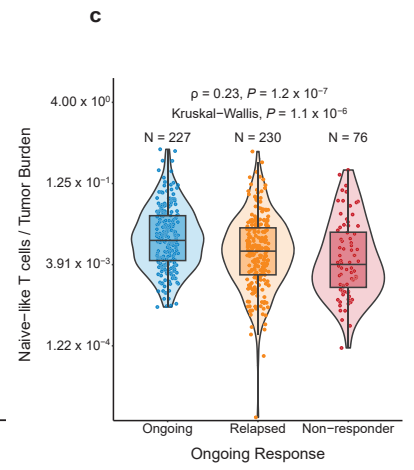
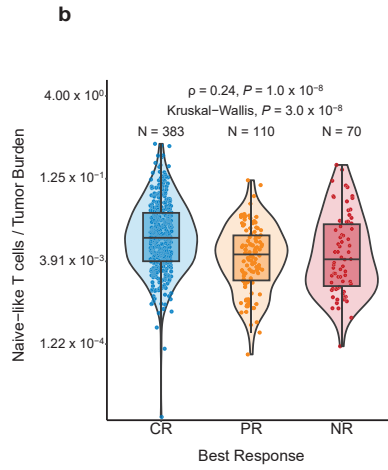
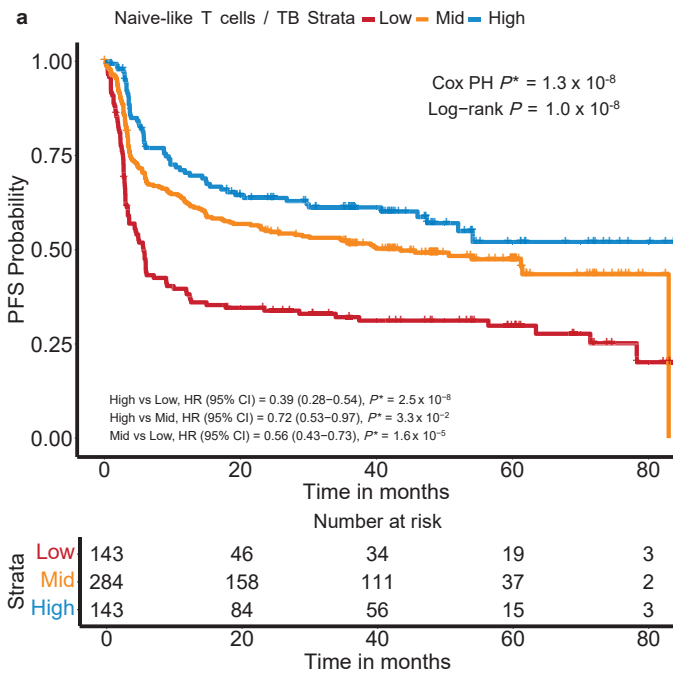
A) Forest plot showing combined PFS univariate and multivariate Cox proportional hazards regression analyses of clinico-pathologic and demographic patient characteristics, proportion of naive-like T cells in the product, baseline systemic inflammatory/prognostic serum markers (CRP, ferritin, and LDH), baseline lymphocyte count, baseline CD4:CD8 ratio, prior lines of therapy, and tumor burden (quantified as the sum of the products of the diameters of target lesions) as continuous variables. **B)** Forest plot with all variables in A and peak CAR T expansion as a continuous variable. Age, sex, ECOG performance status, disease stage, and disease are included as categorial features. Dominance ranking from multivariate analysis is provided. CRP, C-reactive protein; ECOG, eastern cooperative oncology group; FL, follicular lymphoma; LBCL, large B cell lymphoma; LDH, lactate dehydrogenase; MZL, marginal zone lymphoma; PFS, progression free survival.

Naive-like T cells (%) in product Strata Low Mid High



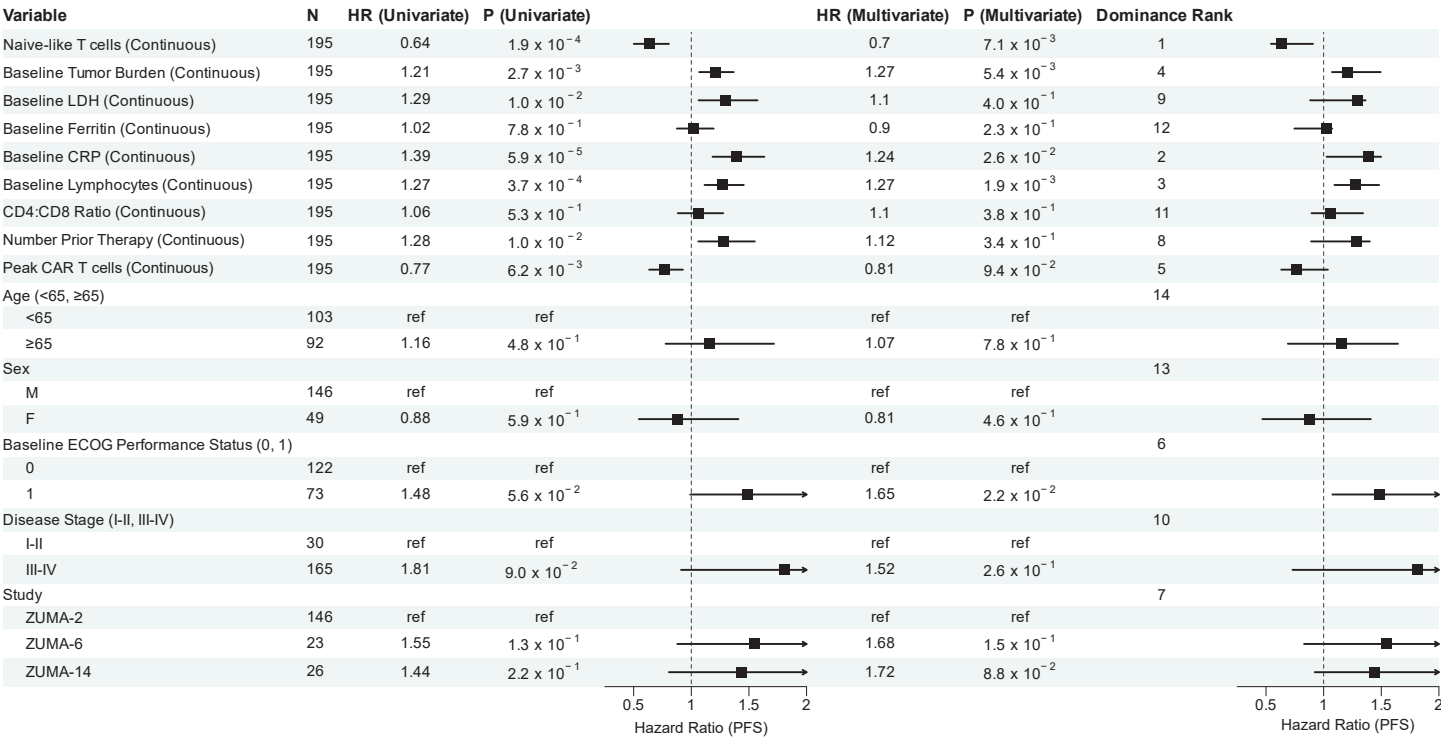
Supplementary Figure 3. Cumulative incidence analysis identifies no significant differences between CAR T cell undetectability by naive-like T cell strata

Cumulative incidence analysis of CAR T cell undetectability from baseline (day 0) to day 2000 by naive-like T cell groups (*Low* = ≤ 25 th percentile; *Mid* = 25th–75th percentile, *High* = > 75 th percentile), with log-rank P value reported.



Supplementary Figure 4. The ratio of naive-like T cells and peak CAR T expansion to tumor burden associates with efficacy .

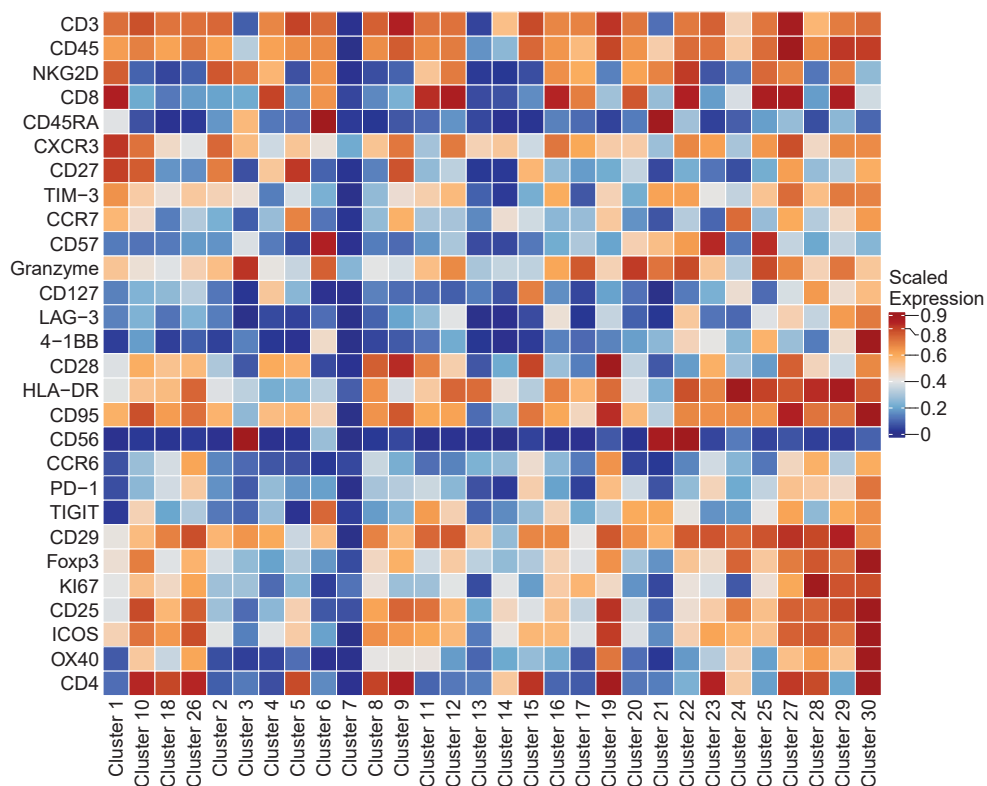
A) Kaplan-Meier PFS analysis was used to evaluate the naive-like T cells / TB ratio, with the ratio converted into categorical variables (*Low* = $\leq 25^{\text{th}}$ percentile; *Mid* = 25th–75th percentile, *High* = $> 75^{\text{th}}$ percentile). The log-rank for categorical comparisons and Cox proportional hazards P value for ordinal (*Low* = 1, *Mid* = 2, *High* = 3) is provided, with study included as a covariate (top right). P values, HRs, and 95% CIs are reported for pairwise comparisons between strata, utilizing Cox proportional hazards modeling with study as cohort included as a covariate in the model (bottom left). Naive-like T cells / TB in product grouped by **B)** best response and **C)** ongoing response status. P values are from Kruskal-Wallis test for categorical comparisons and Spearman correlation for ordinal associations, with response status treated as follows: Non-responder (NR) = 1, Partial response (PR) = 2, and Complete response (CR) = 3 and Non-responder = 1, Relapsed = 2, and Ongoing = 3. Spearman correlation coefficient (ρ) is included. The center line, box limits, and whiskers represent the median, interquartile range, and $1.5 \times$ interquartile range, respectively. **D)** Kaplan-Meier PFS analysis was used to evaluate the peak CAR T / TB ratio, with the ratio converted into categorical variables (*Low*, *Mid*, *High*). The log-rank P value for categorical comparisons and Cox proportional hazards P value for ordinal (*Low* = 1, *Mid* = 2, *High* = 3) is provided, with study included as a covariate (top right). P values, HRs, and 95% CIs are reported for pairwise comparisons between strata, utilizing Cox proportional hazards modeling with study as cohort included as a covariate in the model (bottom left). Peak CAR T / TB grouped by **E)** best response and **F)** ongoing response status. P values are from Kruskal-Wallis test for categorical comparisons and Spearman correlation for ordinal associations, with response status treated as follows: Non-responder (NR) = 1, Partial response (PR) = 2, and Complete response (CR) = 3 and Non-responder = 1, Relapsed = 2, and Ongoing = 3. Spearman correlation coefficient (ρ) is included. The center line, box limits, and whiskers represent the median, interquartile range, and $1.5 \times$ interquartile range, respectively. **G)** Forest plot representation of univariate PFS Cox proportional hazards regression analysis of naive-like T cells, peak CAR T cells, baseline tumor burden, and tumor burden normalized metrics of naive-like T cells and peak CAR T cells. These variables were converted to ordinal variables of *Low* ($\leq 25^{\text{th}}$ percentile), *Mid* (25th–75th percentile), and *High* ($> 75^{\text{th}}$ percentile) and study was included in the model. P values, HRs, and 95% CIs for each feature are reported. **H)** Spearman correlation heatmap for the pairwise comparison of each feature in Supplementary Fig. 4G against each other in the 563 patients included. The Spearman correlation coefficient (ρ) is provided for each pairwise comparison with the color capturing the directionality of correlation (positive correlation coefficient in red and negative correlation in blue), and the circle size capturing the absolute value of the correlation coefficient. All P values are two-sided. CI, confidence interval; HR, hazard ratios; PFS, progression-free survival; SPD, sum of the products of the diameters of target lesions; TB, tumor burden (quantified as SPD).



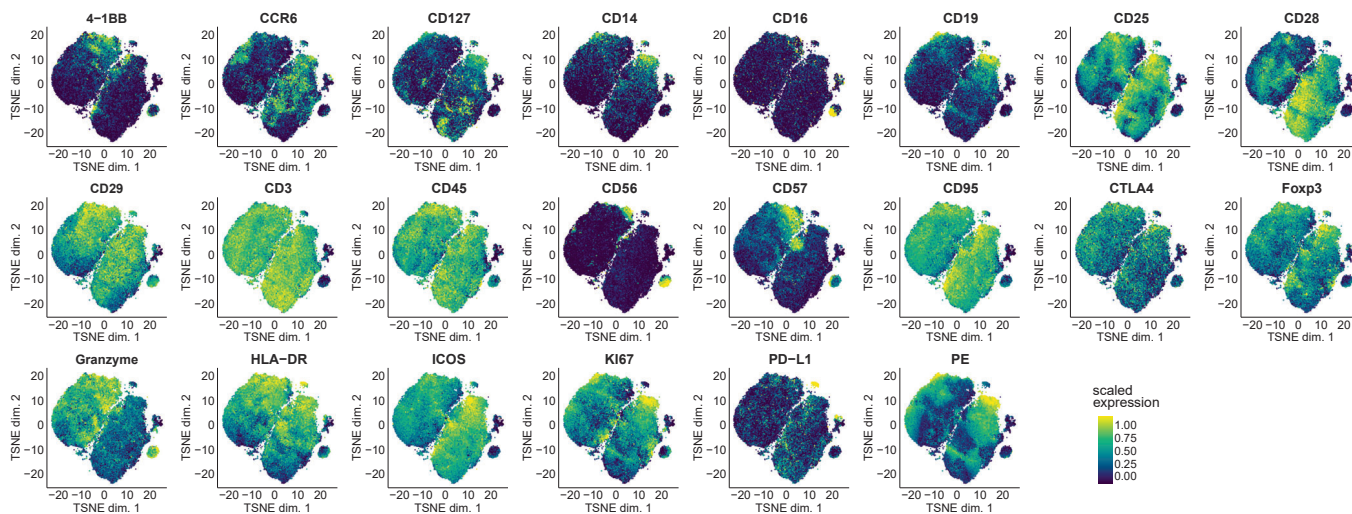
Supplementary Figure 5. Univariate and multivariate analysis of continuous variables associated with PFS in the validation meta-cohort.

Forest plot showing combined PFS univariate and multivariate Cox proportional hazards regression analyses in the validation meta-cohort of clinico-pathologic and demographic patient characteristics, proportion of naive-like T cells in the product, baseline systemic inflammatory/prognostic serum markers (CRP, ferritin, and LDH), baseline lymphocyte count, baseline CD4:CD8 ratio, prior lines of therapy, tumor burden (quantified as the sum of the products of the diameters of target lesions (SPD)), and peak CAR T expansion as continuous variables. Age, sex, ECOG performance status, disease stage, and study are included as categorial features. Dominance ranking from multivariate analysis is provided. CRP, C-reactive protein; ECOG, eastern cooperative oncology group; LDH, lactate dehydrogenase; PFS, progression free survival; SPD, sum of the products of the diameters of target lesions.

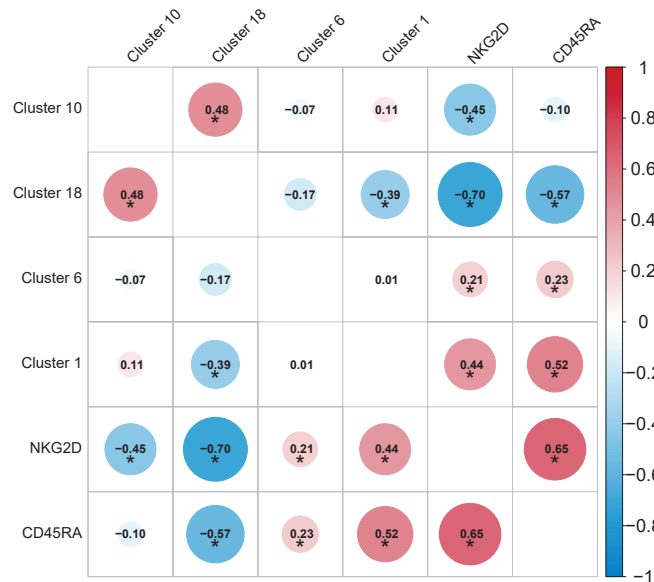
a



b

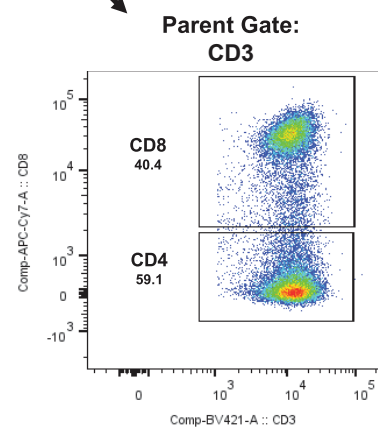
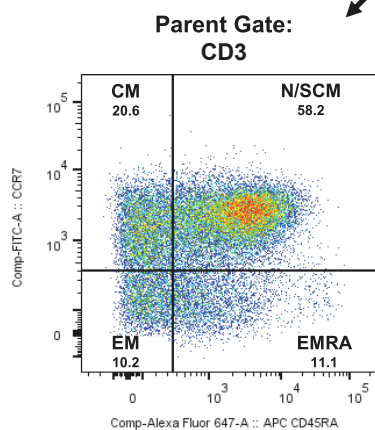
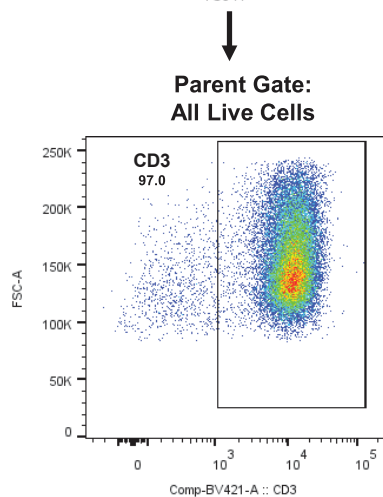
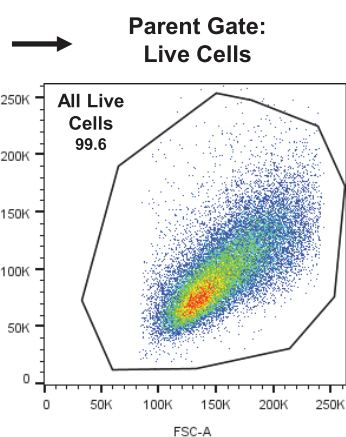
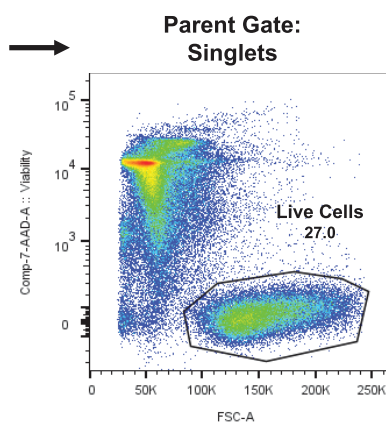
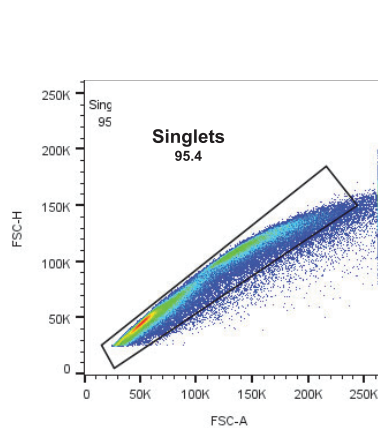


c



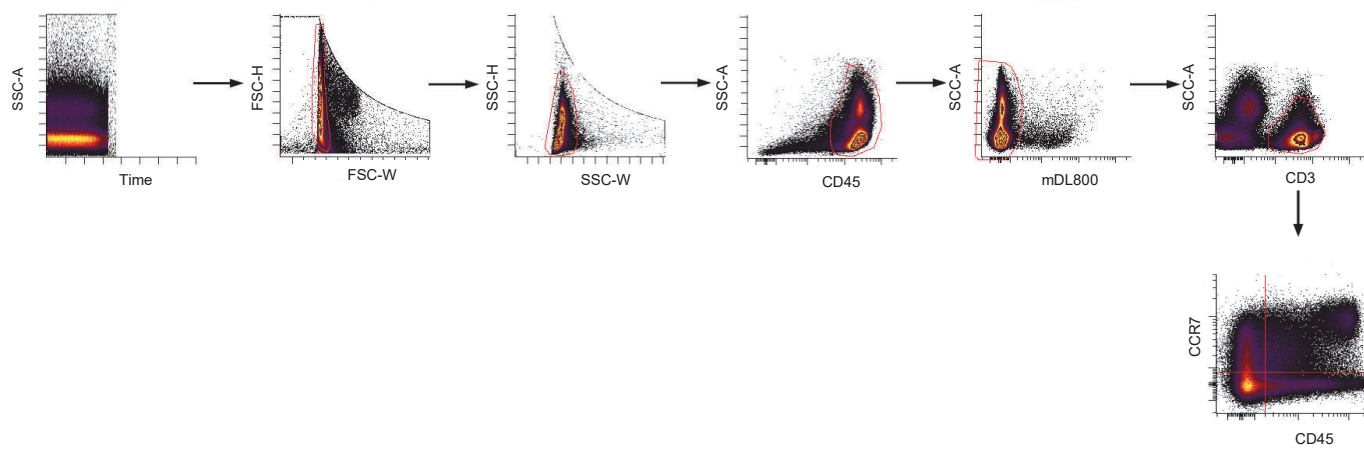
Supplementary Figure 6. Product marker expression via CyTOF characterization.

A) Heatmap of median marker intensity for single markers included in Fig. 6C across all clusters, with median marker intensity scaled across all 30 clusters and ordered by directional log₁₀ P value from panel Fig. 6C except for CD3 and CD45 which provided at the top for reference. **B)** t-SNE plots showing scaled expression of single markers included in Fig. 6C analysis that are not represented in Fig. 6F. **C)** Spearman correlation heatmap for the pairwise comparison of each significant feature in the elastic net model from Fig. 6E. The Spearman correlation coefficient (ρ) is provided for each pairwise comparison with the color capturing the directionality of correlation (positive correlation coefficient in red and negative correlation in blue), and the circle size capturing the absolute value of the correlation coefficient. The asterisk (*) captures P values less than 0.05. All P values are two-sided. t-SNE, t-Distributed Stochastic Neighbor Embedding.



Supplementary Figure 7. Gating strategy used to derive T cell phenotypes for product.

Singlets/Live Cells/Total Live Cells/CD3⁺ cells were gated to identify T cells. Further subsets were identified by CD8, CCR7 and CD45RA markers. CM, central memory; EM, effector memory; EMRA, terminally differentiated effector memory; N/SCM, naïve/memory stem cell.



Supplementary Figure 8. Gating strategy used to derive T cell phenotypes for apheresis.

Immunophenotypic subsets in apheresis were calculated for all T cells, based on CCR7 and CD45RA, employing a validated assay at Cell Carta.