

Supplemental Table 1: Summary of TRBV sequencing data from patient CD8+ T cells

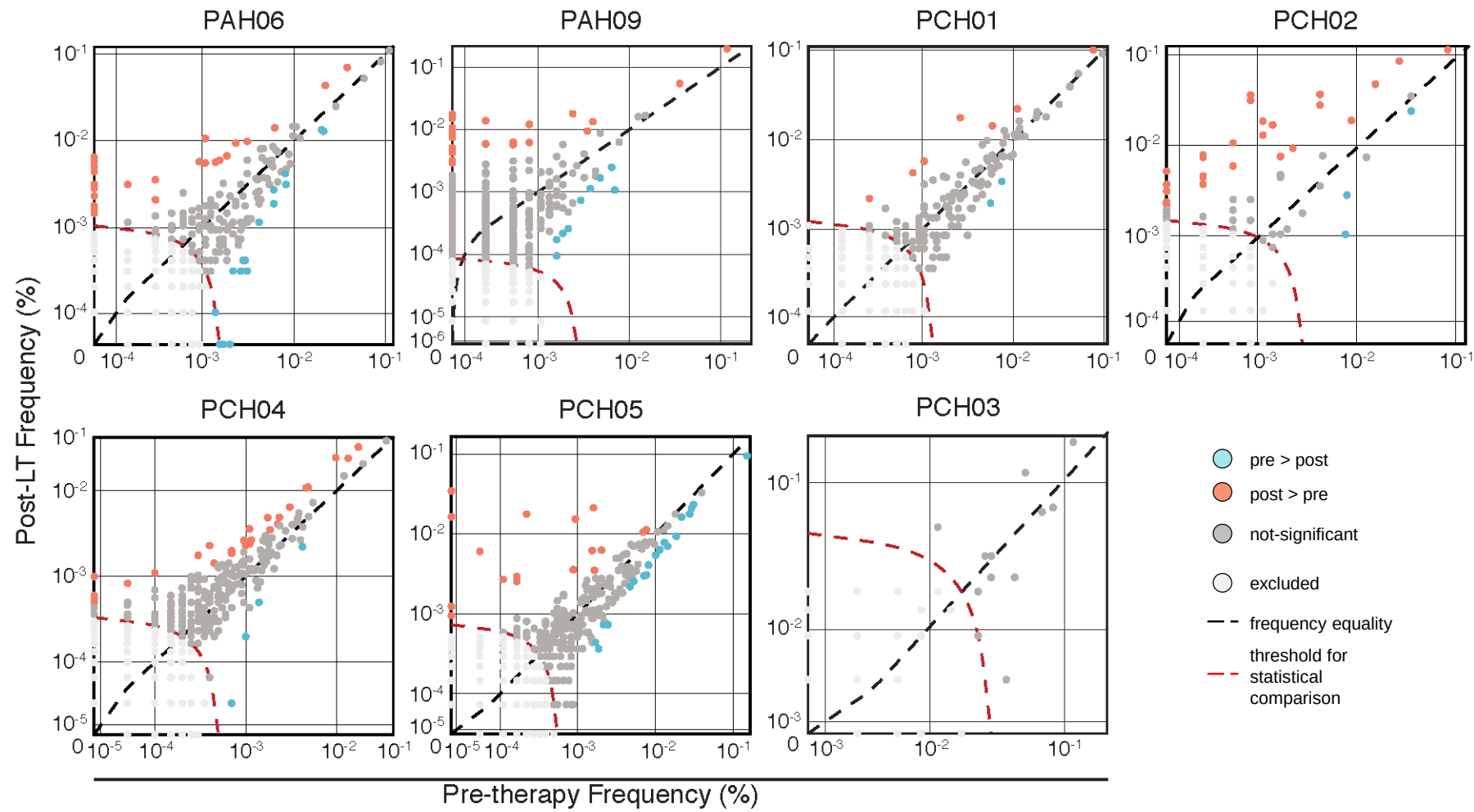
Patient	Timepoint	Total templates	Productive templates	Fraction productive	Total rearrangements	Productive rearrangements
PCH01	Pre-Therapy	8582	7607	0.886	1890	1544
	Post-ST	9611	8187	0.852	1675	1344
PCH02	Pre-Therapy	4781	3486	0.729	2695	2178
	Post-ST	22762	15073	0.662	5030	4027
	Post-LT	9869	6786	0.688	2795	2212
PCH04	Pre-Therapy	25737	20174	0.784	16854	13380
	Post-ST	41345	32356	0.783	23873	19037
	Post-LT	39390	30346	0.770	19893	15835
PCH05	Pre-Therapy	21755	18300	0.841	3910	2896
	Post-ST	68091	56218	0.826	10104	7597
	Post-LT	17471	13656	0.782	4007	2953
PCH06	Pre-Therapy	30888	25092	0.812	3637	2969
	Post-ST	58012	49849	0.859	5451	4532
	Post-LT	72322	61325	0.848	5838	4886
PAH06	Pre-Therapy	7126	6455	0.906	1692	1358
	Post-ST	61366	55491	0.904	7354	6044
	Post-LT	10793	9567	0.886	1940	1525
PAH08	Pre-Therapy	84801	71361	0.842	70345	59772
	Post-ST	64309	51584	0.802	29360	24582
	Post-LT	184126	146898	0.798	25492	21393
PAH09	Pre-Therapy	4726	3774	0.799	3392	2604
	Post-ST	1440	1200	0.833	806	615
	Post-LT	133023	115947	0.872	31246	25227

Supplemental Table 3: Summary of TRBV sequencing data from cell therapy products

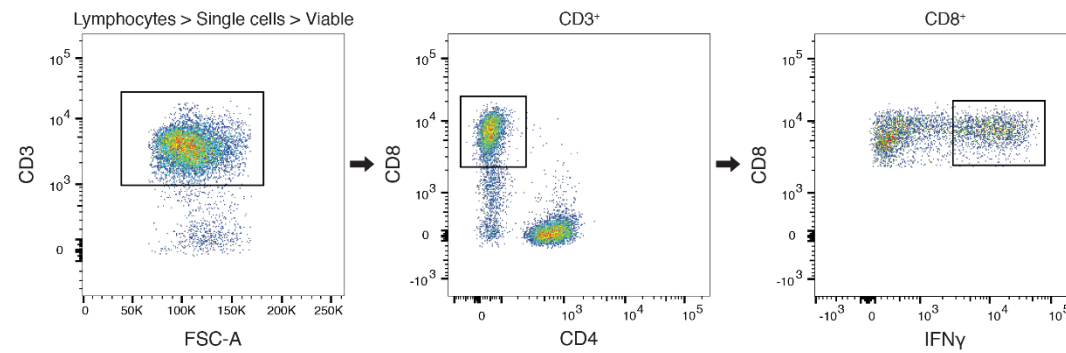
Patient	Total templates	Productive templates	Fraction productive	Total rearrangements	Productive rearrangements
PCH01	4718	4637	0.983	199	131
PCH02	523	410	0.784	175	119
PCH04	8547	6034	0.706	542	336
PCH05	6903	6261	0.907	311	194
PCH06	53022	44986	0.848	473	320
PAH06	3595	3446	0.959	294	209
PAH08	2839	2306	0.812	1012	798
PAH09	19103	15401	0.806	1860	1357

Supplemental Table 4: List of CMV epitopes used in this study

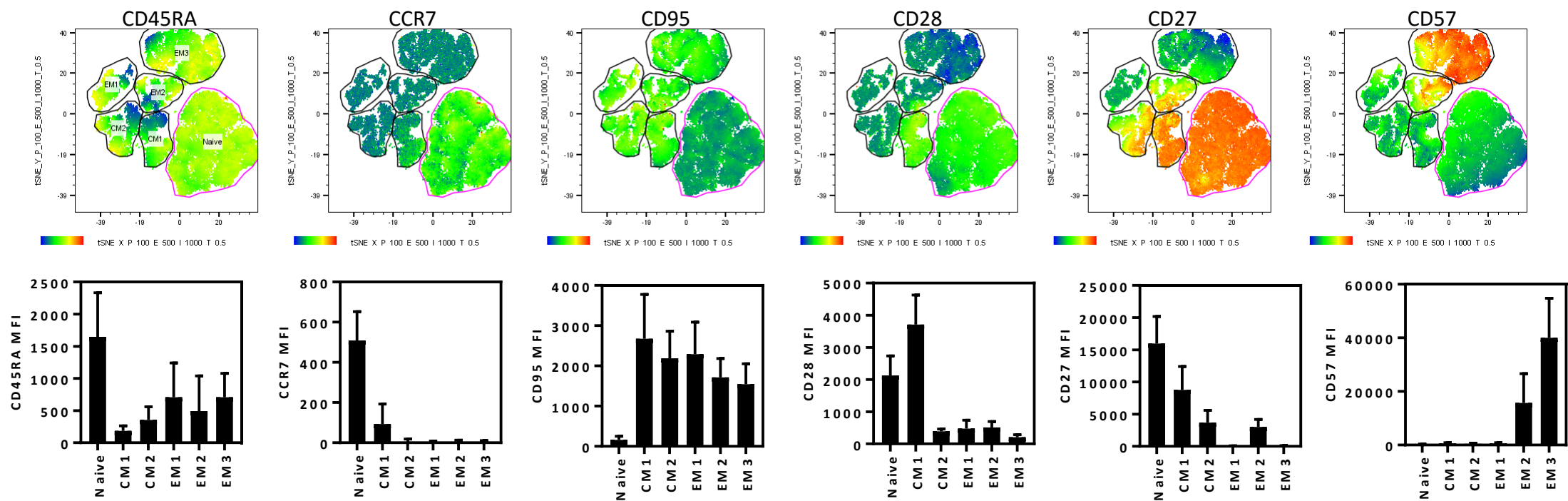
Peptide Sequence	Code	Antigen	HLA Restriction
VTEHDTLLY	VTE	pp50	A*01:01
YSEHPTFTSQY	YSEH	pp65	A*01:01
NLVPMVATV	NLV	pp65	A*02:01
VLEETSVML	VLE	IE-1	A*02:01
TPRVTGGGAM	TPR	pp65	B*07:02
RIPHERNGFTVL	RPH	pp65	B*07:02
ELKRKMIYM	ELK	IE-1	B*08:01
QIKVRVDMV	QIK	IE-1	B*08:01
HERNGFTVL	HER	pp65	B*40:01
TRATKMQVI	TRA	pp65	C*06:02
YAYIYTTYL	YAY	gB	B*41:01
CRVLCCYVL	CRV	pp65	C*07:02
KARAKKDELR	KAR	IE-1	A*31:01



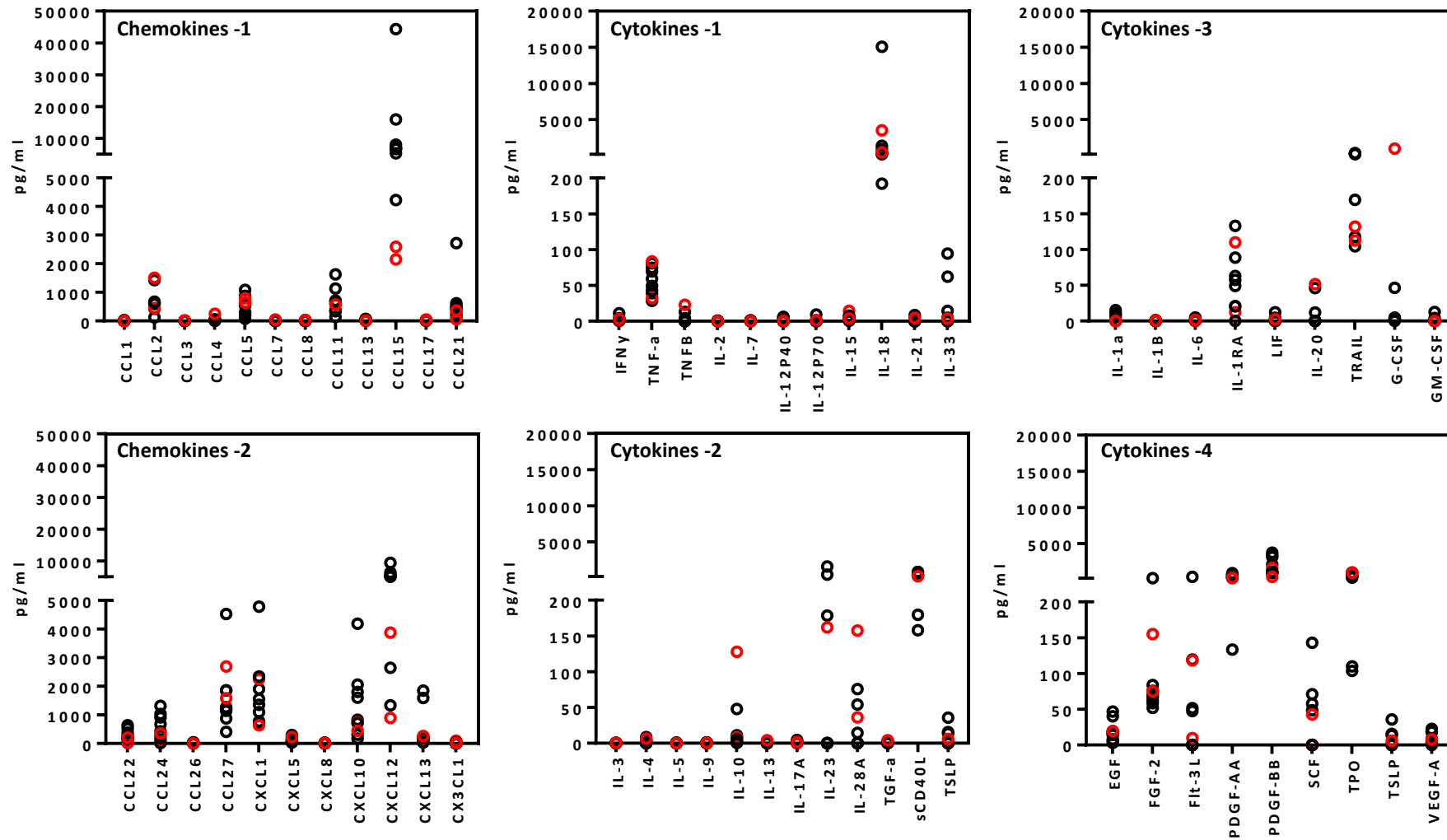
Supplemental Figure 1: Significant changes in the frequency of patient CD8+ T-cell clonotypes following adoptive cellular therapy were determined using the immunoSEQ platform. Significance was assessed in CDR3 sequences with a minimum of five reads. Data compares the frequency of T cell clonotypes prior to infusion and long-term post-therapy.



Supplemental Figure 2: Representative analysis of the flow cytometric strategy used to isolate CMV-specific CD8⁺ T cells from the cell therapy product is shown. These products were stimulated with the CMV peptide pool used to initially generate the cell therapies, and specific CD8⁺ T cells were isolated using an IFN- γ capture protocol.



Supplemental Figure 3: tSNE analysis was prepared as outlined in the Methods section and Figure 6. Top panels display representative analysis of the mean fluorescence intensity of each marker in the defined memory populations. Bottom panels represent the mean fluorescence intensity and standard deviation for each marker.



Supplemental Figure 4: Cytokine and chemokine profile in the peripheral blood of patients prior to ACT. Plasma samples prior to the first infusion were assessed for cytokine expression using the Human Cytokine/Chemokine 65-Plex Panel from Even Technologies. Data represents values from individual patients in pg/mL. The non-responding patients are represented by red symbols.