

Supplementary Materials for

Massive clonal expansion of polycytotoxic skin and blood CD8⁺ T cells in patients with toxic epidermal necrolysis

Axel Patrice Villani, Aurore Rozieres, Benoît Bensaid, Klara Kristin Eriksson, Amandine Mosnier, Floriane Albert, Virginie Mutez, Océane Brassard, Tugba Baysal, Mathilde Tardieu, Omran Allatif, Floriane Fusil, Thibault Andrieu, Denis Jullien, Valérie Dubois, Catherine Giannoli, Henri Gruffat, Marc Pallardy, François-Loïc Cosset, Audrey Nosbaum, Osami Kanagawa, Janet L. Maryanski, Daniel Yerly, Jean-François Nicolas, Marc Vocanson*

*Corresponding author. Email: marc.vocanson@inserm.fr

Published 19 March 2021, *Sci. Adv.* 7, eabe0013 (2021)
DOI: 10.1126/sciadv.abe0013

This PDF file includes:

Tables S1 to S12
Figs. S1 to S17

Biological investigations				
	CyTOF	TCRV β	TCR sequencing	TCR transfectant stimulation assay
TEN-1		D0	-	-
TEN-2	-	D0	D0*	-
TEN-3	D0	D0	D0	D2
TEN-4	D0	D0	D0	-
TEN-5		D0	D0	-
TEN-6	-	D0	D0	-
TEN-7	D1	D0	D1	D2
TEN-8	-	D0	D1	-
TEN-9	D1	D0	D1	-
TEN-10	D0	D2	D0	D0 & D2
TEN-11	-	D0	D2	-
TEN-12	-	-	D0	-
TEN-13	-	D0	D2	-
TEN-14	-	-	D1*	-
TEN-15	D1	D1	D1	D1
TEN-16	-	-	D1	-
TEN-17	D0	-	-	-
TEN-18	D0 [‡]	-	-	-
MPE-1	-	-	D1	-
MPE-2	-	-	D1	-
MPE-3	-	D1	D1	-
MPE-4	-	D1	D1	-
MPE-5	-	D1	D1	-
MPE-6	-	-	D1	-
MPE-7	-	D1	D1	-
MPE-8	-	D1	-	-
MPE-9	D1	-	-	-
MPE-10	D1	-	-	-
MPE-11	D1	-	-	-
MPE-12	D1	-	-	-
MPE-13	D2	-	-	-
MPE-14	D1	-	-	-

Table S1. Sampling days and subsequent biological analysis.

Table describes the days at which samples were collected after patient's arrival to the hospital (all from day 0 to day 2), as well as the corresponding biological investigations performed on these samples.

*Blister and PBMC samples for TCR sequencing were collected as indicated in the table, except for TEN-2 and TEN-14, for which PBMC samples were performed at 1 day of interval.

[‡]For patient TEN-18, the cytotoxic but not the lineage phenotype was excluded from the analysis due to a technical problem.

Antibodies and panel information				
Isotope Channel	Antibody/reagent name	Clone	Source	Category
191/193 Ir	DNA		Miltenyi	Cells isolation
194Pt	Viability		Miltenyi	Viability
89Y	CD45	HI30	Fluidigm	Lineage
142Nd	CD19	LT19	Miltenyi	Lineage
144Nd	TCR V α 14-J α 18	6B11	Miltenyi	Lineage
145Nd	CD11c	M54-27G12	Miltenyi	Lineage
148Nd	CD14	TUK4	Miltenyi	Lineage
150Nd	CD11b	M1/70.15.11.5	Miltenyi	Lineage
153Eu	CD45RA	T6D11	Miltenyi	Lineage
155Gd	CD8 β	SID18BEE	Miltenyi	Lineage
158Gd	CCR7(CD197)	FR11-11EB	Miltenyi	Lineage
159Tb	TCR V α 7.2	REA179	Miltenyi	Lineage
164Dy	CD4	VIT4	Miltenyi	Lineage
166Er	NKp46	9 E2	Miltenyi	Lineage
168Er	TCR $\alpha\beta$	BW242/412	Miltenyi	Lineage
169Tm	CD8 α	BW135/80	Miltenyi	Lineage
175Lu	TCR $\gamma\delta$	11F2	Miltenyi	Lineage
141Pr	CD56	HCD56	Miltenyi	Lineage/Activation
146Nd	CD107a	H4A3	Miltenyi	Activation
152Sm	CD27	M-T271	Miltenyi	Activation
163Di	CD57	HCD57	Miltenyi	Activation
167Er	CD38	REA572	Miltenyi	Activation
170Er	CD137	4B4-1	Miltenyi	Activation
171Yb	Annexin A1	74/3	Miltenyi	Activation
172Yb	CD253	RIK2.1	Miltenyi	Activation
174Yb	CD226	DX11	Miltenyi	Activation
147Sm	PERF	delta G9	Miltenyi	Cytotoxicity
149Sm	GzmB	REA226	Miltenyi	Cytotoxicity
151Eu	GzmA	REA162	Miltenyi	Cytotoxicity
161Dy	CD255	CARL-1	Miltenyi	Cytotoxicity
162Dy	GNLY	AF3138	Miltenyi	Cytotoxicity
154Sm	V-beta 13.2	H132	Beckman Coulter	TCR
156Gd	V-beta 7.2	ZIZOU4	Beckman Coulter	TCR
160Gd	V-beta 21.3	IG125	Beckman Coulter	TCR

Table S2. Antibodies and panel information.

A

Patient ID	Total templates	Productive templates	Productive fraction	Productive rearrangements	Productive clonality	TRB accounting for >0.5% total	
						N TRB sequences	Cum% of TRB repertoire
TEN-2	15156	12345	0.81	10051	0.03	1	3.65
TEN-3	9911	9083	0.92	2612	0.55	2	63.40
TEN-4	7602	5904	0.78	2261	0.17	16	29.97
TEN-5	951	718	0.76	452	0.06	18	22.98
TEN-6	27148	24951	0.92	2568	0.61	9	77.04
TEN-7	135218	109695	0.81	32357	0.17	7	14.26
TEN-8	91287	73280	0.80	56653	0.03	2	1.70
TEN-9	24344	23321	0.96	1745	0.69	6	85.44
TEN-10	115687	111243	0.96	4319	0.87	2	89.60
TEN-11	7408	5691	0.77	836	0.36	24	70.64
TEN-12	16159	12809	0.79	8121	0.09	5	11.66
TEN-13	2564	2163	0.84	1134	0.21	9	33.24
TEN-14	37,685	30113	0.80	18898	0.04	0	0
TEN-15	51687	30309	0.58	2111	0.59	11	69.94
TEN-16	15801	12384	0.78	4962	0.13	10	13.64
MPE-1	64906	53041	0.81	19223	0.08	2	1.70
MPE-2	211797	170222	0.80	68346	0.07	0	0
MPE-3	45946	36899	0.80	14225	0.09	2	2.39
MPE-4	7087	5775	0.81	2757	0.09	17	14.61
MPE-5	10537	8457	0.80	5139	0.06	8	6.83
MPE-6	5114	4280	0.84	2364	0.15	4	20.68
MPE-7	48944	39474	0.81	20772	0.07	3	2.38

B

Patient ID	Total templates	Productive templates	Productive fraction	Productive rearrangements	Productive clonality	TRB accounting for >0.5% total	
						N TRB sequences	Cum% of TCB repertoire
TEN-2	42212	33656	0.80	26806	0.02	1	0.65
TEN-3	25349	21559	0.85	12802	0.12	11	16.70
TEN-4	22380	16933	0.76	6559	0.16	9	18.68
TEN-5	97423	77785	0.80	38437	0.15	16	17.01
TEN-6	45198	36165	0.80	24135	0.11	11	16.86
TEN-7	68825	50224	0.73	21623	0.22	10	29.79
TEN-8	18785	15003	0.80	13198	0.01	1	0.55
TEN-9	857	676	0.79	471	0.06	14	22.63
TEN-10	5087	4021	0.79	3170	0.04	4	5.65
TEN-11	19359	15443	0.80	9465	0.08	4	8.01
TEN-12	108801	87610	0.81	71003	0.02	1	0.86
TEN-13	97529	80175	0.82	57810	0.03	1	0.81
TEN-14	20670	17286	0.84	11424	0.01	4	22.5
TEN-15	29410	24394	0.83	15989	0.1	6	15.21
TEN-16	61236	47672	0.78	19237	0.27	11	33.27
MPE-3	23185	18627	0.80	10726	0.12	11	15.74
MPE-4	6152	4815	0.78	4176	0.02	3	4.38
MPE-5	11093	8560	0.77	6762	0.06	5	10.68
MPE-6	80269	65498	0.82	50441	0.02	2	1.31
MPE-7	31855	25294	0.79	17336	0.04	2	1.54

Table S3: Raw parameters of TRBV repertoire analysis.

Genomic DNA extracted from blister and skin (**A**) or PBMC (**B**) samples from 15 TEN and 7 MPE patients were used for survey level deep sequencing of the TCR β -chain, using ImmunoSEQTM platform. Data were analyzed using ImmunoSEQTM analyser toolset. Table describes raw parameters of TCR repertoire analysis.

Total template: the sum of templates for all rearrangements in the sample. Productive templates: the sum of templates for all productive rearrangements in the sample. Fraction productive: the fraction of productive templates among all templates. Productive rearrangement: the count of unique rearrangements in the sample that are in-frame and do not contain a stop codon. Productive rearrangements can produce a functional protein receptor. Productive clonality: a statistic for how much of the repertoire is made of up of expanded clones. Number and cumulative percentage of TRBV sequences, representing > 0.5% of total TRBV repertoire.

	MPE (n=7)	TEN (n=15)	Healthy donors (n=44)
Mean productive clonality	0.053	0.092	0.099
Standard Deviation	0.039	0.065	0.056
Standard Error of Mean	0.018	0.017	0.008
t-test (vs healthy donors)	ns	ns	

Table S4: Comparison of productive clonality in PBMC samples from TEN, MPE patients and healthy donors.

ns. Student t test (two-tailed).

Patient	V family	TRBV	TRBD	TRBJ	Templates	Amino-acid	CDR3 rearrangement	Productive frequency	Respective anti-Vβ mAb	% Vβ+ cells among CD3+CD8+ T cells as determined by FACs analysis
TEN-2	TRBV09	TRBV09-01	TRBD02-01*01	TRBJ02-01*01	450	CASSVDLSGNEQFF	CTGAGCTCTCGAGCTGGGGGACTCAGCTTGTATTTCTGTGCCAGCAGCTAGATCTGCGGGGAATGAGCAGTCTTCGGGGCCA	3.64	Vb 1	27.00
	TRBV06	TRBV06-06	unresolved	TRBJ02-01*01	28	CASSYVLEQFF	CTCAGGCTGGAGTGGCTCCCTCCCAAGACATCTGTGTACTTCTGTGCCAGCAGTCAATCACTGATGAGCAGTCTTCGGGGCCA	0.23	Vb 13.6	2.55
	TRBV02	TRBV02-01*01	TRBD02-01*01	TRBJ02-07*01	21	CASSLQAGLVSYEQYF	TCCAAAGCTGGAGGACTCAGCCATGTACTCTGTGCCAGCAGTGAACAACCTAGCGGGGGTCTCTACGAGCAGTACTCGGGGGCC	1.17	Vb 2.6	5.75
	TRBV06	TRBV06-05*01	unresolved	TRBJ01-02*01	19	CASSQRDGYGYTF	AGGCTGTGTGGCTCTCCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGCAAAAGGGCAGGATGATGCTACACCTCTGGTTCG	0.15	Vb 13.1	na
TRBV06	TRBV06-05*01	TRBD01-01*01	TRBJ02-05*01	19	CASSYANTYQEQYF	CTGTGGCTGCTCCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTGAACAACCTAGCGGGGGAGTCTTCGGGGCCA	0.15	Vb 13.1	13.7	
TEN-3	TRBV11	TRBV11-02*02	unresolved	TRBJ02-01*01	5621	CASSPFRDSYNEQFF	CAGCCTCAAGGCTTGGAGCTGGCGCTGTATCTGTGCCAGCAGCCCTTCGGTACTCTCAATGAGCAGTCTTCGGGGCCA	61.88	Vb 21.3	57.00
	TRBV19	TRBV19-01	TRBD01-01*01	TRBJ01-05*01	138	CATLDKRYSNQPHF	GTGACATCGCCGCAAAAAGACCCAGCAGCTTCTGTCTGTGCCACTTGGACAGATATAGCAATCAGCCCGCAGCTTTGGTGTAT	1.52	Vb 17.7	1.02
	TRBV19	TRBV19-01	TRBD02-01*02	TRBJ01-02*01	39	CASSEGSYGYTF	CTCAGCTGTACATCGGCCAAAAGAACCCGACGCTTCTATCTCTGTGCCAGTAGTGGGGCAGCTATGGTCAACCTCTGGTTCG	0.43	Vb 17	na
	TRBV09	TRBV09-01	unresolved	TRBJ02-01*01	17	CASSVSGTNSNEQFF	AGCTCTGTGGAGCTGGGGGACTCAGCTTGTATTTCTGTGCCAGCAGTGTCCAGCGACAGTACCAATGACCAATCTTCGGGGCCA	0.19	Vb 1	3.61
TRBV06	TRBV06-01*01	unresolved	TRBJ02-02*01	16	CASSEARGSGELFF	GAGTGGCTGCTCCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTGAACAACCTAGCGGGGGAGTCTTCGGGGCCA	0.18	na	na	
TEN-4	TRBV05	TRBV05-06*01	TRBD02-01	TRBJ02-01*01	348	CASSPSENEQFF	AATGTGACGCTTGTGTGGGGGACTCGCCCTGTACTCTGTGCCAGCAGTCTTCTAGCGAAATAGCAGTCTTCGGGGCCA	5.89	Vb 5.2	2.75
	TRBV28	TRBV28-01*01	TRBD02-01	TRBJ02-07*01	248	CASLGTSSYEQYF	ATTCCTGAGTCCGCGACCAACAGACATCTATGTACTCTGTGCCAGCAGTCTTCTAGCGAAATAGCAGTCTTCGGGGCCA	4.20	Vb 3	24.2
	TRBV30	TRBV30-01*01	TRBD01-01*01	TRBJ02-07*01	185	CAGQAREQYF	TTCACTGTAGTATGAAGCTCTCTCTGAGTACTCTGGTCTTATCTCTGTGCCAGCGGGGGCGGAGCAGTACTCGGGCC	3.13	Vb 20	1.56
	TRBV29	TRBV29-01*01	unresolved	TRBJ02-03*01	180	CSVLQTDQYF	TCACTGTGAGCAATGAGCCTTGAAGCAGCAGTATATCTGTGCCAGCAGTCTTCAACTACAGATACCGAGTATTTGGCCCA	3.05	Vb 4	3.33
TRBV14	TRBV14-01*01	TRBD01-01*01	TRBJ02-07*01	167	CASSPLTSGSEQYF	CAGCCTCGAAGACTGGAGTCTGGAGTATTTCTGTGCCAGCAGCCATCTTTCAGGGAGCGCGGAGCAGTACTCGGGCCG	2.83	Vb 16	3.62	
TEN-5	TRBV15	TRBV15-01*01	TRBD02-01*01	TRBJ02-05*01	49	CATSRDVAAGGTOYF	CGCTCACAGGCTGGGGGACGACCTGTACTCTGTGCCAGCAGTGAAGTGGTGGGGGGGCGGAGCAGTCTTCGGGGCCA	6.82	na	na
	TRBV14	TRBV14-01*01	na	TRBJ02-07*01	18	CASSHLQAGGGEQYF	CAGCCTCGAAGACTGGAGTGTGGAGTATTTCTGTGCCAGCAGCCTTGGCCAGGGTGGGGGGGAGCAGTACTCGGGCC	2.51	Vb 16	1.88
	TRBV06	TRBV06-05*01	TRBD02-01*01	TRBJ02-02*01	12	CASSPTNGDGYTF	CTGTGGCTGCTCCCTCCAGACATCTGTGTACTCTGTGCCAGCAGTCCGACGAACAGGGGGGGTGGTCACTCTGGTTCG	1.67	Vb 13.1	0.94
	TRBV10	TRBV10-03*01	na	TRBJ01-02*01	11	CAISGAANYGYTF	CTGGAGTCCGCTACAGCTCCAGACATCTGTGTACTCTGTGCCAGTCTGAGGCTCAGCCCACTATGGTACACCTCGGTTCG	1.53	Vb 12	1.7
TRBV04	TRBV04-03*01	TRBD02-01	TRBJ01-04*01	10	CASSQDLSYKELFF	CACACCTCGCAGCAGAAAGCTGGCCCTGTACTCTGTGCCAGCAGCAGCAAGTCTCGGACTGATAAAAACTGTTTTGGAG	1.59	Vb 7.2	9.15	
TEN-6	TRBV21	TRBV21-01*01	TRBD01-01*01	TRBJ01-04*01	8509	CASSDRGRNTKELFF	TCGACGGAGTCAAGGAGACAGCAGTATTTCTGTGCCAGCAGCAGGAGGAGGAGTCAATGAAAACTGTTTTGGAGT	34.10	na	na
	TRBV28	TRBV28-01*01	unresolved	TRBJ01-04*01	8503	CASSGPNKELFF	CAGAGTCCGCGCAGCAACACAGACATCTGTACTCTGTGCCAGTGTGGGGGGCTAATGAAAACTGTTTTGGAGT	34.08	Vb 3	48.1
	TRBV18	TRBV18-01*01	TRBD01-01*01	TRBJ01-02*01	695	CASSPQGRSYGYTF	CAGCAGGATCGGAGGAGTCTGGCAGCTTATTTCTGTGCCAGCAGCAGGAGGAGGAGTCAATGGTCACTCTGGTTCG	2.79	Vb 18	3.26
	TRBV06	TRBV06-04	TRBD02-01	TRBJ01-02*01	508	CASSLEPGDSVYGYTF	CTCTGTACTCTCAGACATCTGTGTACTCTGTGCCAGCAGTGAAGCTGGGACTCGGTCTATGGTCACTCGGTTCG	2.04	na	na
TRBV03	unresolved	TRBD01-01*01	TRBJ01-03*01	297	CASSQERGRDITF	ATCAATCCCTGGAGCTTGGTACTCTGTGTACTCTGTGCCAGCAGCAGAAAGGGGAGGGACACCATATTTGGAGAG	4.19	Vb 9	3.56	
TEN-7	TRBV02	TRBV02-01*01	TRBD02-01*01	TRBJ02-07*01	5168	CASSEVWAGASSYEQYF	ACAAGTGTGAGGACTCAGCCATGTACTCTGTGCCAGCAGTGAAGTGGTGGGGGGTACTCTAGCAGCAGTACTTCGGGGCC	1.71	Vb 22	2.46
	TRBV05	TRBV05-05*01	TRBD01-01*01	TRBJ01-01*01	3889	CASSLNDRSNTAEFF	CGCTTGTGTGGGGGACTCGCCCTGTACTCTGTGCCAGCAGTGAAGAGGAGGAGTCAATGAAAACTGTTTTGGAGT	3.55	Vb 5.3	9.6
	TRBV06	unresolved	TRBD02-01*02	TRBJ02-01*01	3588	CASSPTSSNEQFF	GAGTGGCTGCTCCCTCCAAACATCTGTGTACTCTGTGCCAGCAGCCGACTAGCGGGAGTGAATGAGCAGTCTTCGGGGCCA	3.27	Vb 13.1; Vb 13.2; Vb 13.6	3.25
	TRBV06	TRBV06-05*01	TRBD02-01*01	TRBJ01-02*01	1168	CASSLGGEGYTF	CTCAGGCTGTGGCTGCTCCCTCCAGACATCTGTGTACTCTGTGCCAGCAGTCTGGGGGAGGAGGCTACACCTCGGTTCG	1.06	Vb 13.1	4.39
TRBV04	TRBV04-01*01	TRBD02-01	TRBJ02-07*01	652	CASSQDELEQYF	TTCTCACTCAAGCCTCGCAGCAGAAGACTCAGCCCTGTACTCTGTGCCAGCAGCAGGAGTGAAGTCTGAGCAGTACTTCGGGGCC	0.59	Vb 7.1	1.25	
TEN-8	TRBV11	TRBV11-03*01	TRBD01-01*01	TRBJ01-05*01	775	CASSNPTGGHNSNPQHF	GAGCTGGGAGCTCGCCCTGTACTCTGTGCCAGCAGCAACCCAGGGGAGGAGGAGTCAATGAAAACTGTTTTGGAGT	1.06	na	na
	TRBV27	TRBV27-01*01	TRBD01-01*01	TRBJ02-03*01	471	CASRGTPTDQYF	CTGATCTGTGGAGTCCGCAACCCAGCAGCTCTGTACTCTGTGCCAGCAGGCGGAGTACGCGAGTATTTGGGGCCA	0.64	Vb 14	1.2
	TRBV04	TRBV04-03*01	na	TRBJ02-02*01	289	CASSPQGGTGELEFF	ACCTCTGAGCAGGAGAGACTCGCCCTGTACTCTGTGCCAGCAGCAAGGAGGGGGGAGCAGCCGGGAGCTGTTTTGGAGAA	0.39	Vb 7.2	5.76
	TRBV27	TRBV27-01*01	TRBD02-01	TRBJ02-07*01	197	CASSFTSYEQYF	GTATCTGTGGAGTCCGCAACCCAGCAGCTCTGTACTCTGTGCCAGTCTACTAGCTCTACAGCAGTACTTCGGGGCC	0.27	Vb 14	1.2
TRBV04	TRBV04-03*01	TRBD01-01*01	TRBJ01-05*01	123	CASSQAGSNQPHF	ACCTCTGAGCAGGAGACTCGCCCTGTACTCTGTGCCAGCAGCAAGTGGAGTCAATGAAAACTGTTTTGGAGT	0.47	Vb 7.2	5.76	
TEN-9	TRBV02	TRBV02-01*01	TRBD02-01*02	TRBJ01-05*01	10334	CASSDVRGTSNPQHF	TCACAAGCTGGAGGACTCAGCCCTGTACTCTGTGCCAGCAGTGAAGTGGGGGAGTCAATGAAAACTGTTTTGGAGT	41.31	na	35.9
	TRBV06	TRBV06-01*06	TRBD01-01*01	TRBJ01-01*01	7373	CASSVPRDNTAEFF	CGTCTCCCTCCAAACATCTGTGTACTCTGTGCCAGTCTCTCGATCGAGGAGTCAATGAAAACTGTTTTGGAGAA	31.62	Vb 13.1; Vb 13.2; Vb 13.6	42.26
	TRBV21	TRBV21-01*01	TRBD01-01*01	TRBJ01-01*01	763	CASSKHPLNTEAFF	CAGTCCAGGACTGAGGAGCAGCAGCTGTACTCTGTGCCAGCAGCAACCCAGGGTAAACACTGAAGCTTCTGGAGCA	3.27	na	na
	TRBV29	TRBV29-01*01	TRBD02-01*01	TRBJ01-02*01	737	CSVHSFGASGYTF	TDGAGCAACATGAGCCTGAAGCAGCAGCAATATCTGTGCCAGTCTTCACTTCTGGGGGGAGGAGTGGTCACTCGGTTCG	3.16	Vb 4	5.86
TRBV24	TRBV24	na	TRBJ02-01*01	590	CATSPDPADDEFF	CTAGAGTCCGCTCCCAACAGCAGCTTCTACTCTGTGCCAGCAGCCCGCCGCTGATGAGCAGTCTTCGGGGCCA	2.53	na	na	
TEN-10	TRBV28	TRBV28-01*01	TRBD02-01*01	TRBJ01-04*01	99110	CASSFGPNKELFF	CTGGAGTCCGCGCAGCAACACAGACATCTGTACTCTGTGCCAGCAGTTCGGGGGGCTAATGAAAACTGTTTTGGAGT	89.09	Vb 3	na
	TRBV28	TRBV28-01*01	na	TRBJ02-02*01	566	CASSPNSNTELEFF	CTGGAGTCCGCGCAGCAACACAGACATCTGTACTCTGTGCCAGCAGCCGCGGAGGAGGAGTCAATGAAAACTGTTTTGGAGAA	0.51	Vb 7.2	93.9
	TRBV04	TRBV04-03*01	TRBD01-01*01	TRBJ02-07*01	376	CASSQDLPVEYEQYF	ACCTCTGAGCAGGAGACTCGCCCTGTACTCTGTGCCAGCAGCAAGTCTGGGGGGTGAAGTACGAGCAGTACTCGGGCC	0.34	Vb 7.2	0.88
	TRBV07	TRBV07-03*03	TRBD02-01	TRBJ02-02*01	374	RASSFTGTGASLEFF	CAGCAGAGCAGGGGACTCAGCCGCTGTACTCTGTGCCAGCAGTCTCAGCGGACTGGGGCTCTGGGAGCTGTTTTGGAGAA	0.34	na	na
TRBV19	TRBV19-01	na	TRBJ02-05*01	238	CASSIRGGETQYF	CTGTACTGTGGCCCAAAGAACCCAGCAGCTTCTACTCTGTGCCAGTATAGGGGGGGGAGACCCAGTACTCGGGGCC	0.21	Vb 17	3.18	
TEN-11	TRBV12	TRBV12	TRBD01-01*01	TRBJ02-05*01	760	CASSLQEQYF	CTGAAGACTCAGCCTCAGAACCCAGGACTCAGCTGTGTACTCTGTGCCAGCAGTTCGGAGGAGGAGCAGTACTCGGGCCA	13.35	na	na
	TRBV05	TRBV05-01*01	unknown	TRBJ01-02*01	706	CASSLDDSGFYGYTF	AGCACCTTGGAGTGGGGGACTCGCCCTTACTTTTGGCCAGCAGTCTGGACAGCAGGATTTATGGTCAACCTTCGGTTCG	12.41	Vb 5.1	11.9
	TRBV04	TRBV04-01*01	unknown	TRBJ01-01*01	379	CASSQDTEAFF	TTCTCTACAGCCCTCGACGCAAGAGACTCAGCCCTGTACTCTGTGCCAGCAGCAAGGGGAGCAGTGAAGCTTCTGGAGCA	6.66	Vb 7.1	6.04
	TRBV24	TRBV24	TRBD02-01*02	TRBJ02-01*01	316	CATEREWNEQFF	CTCCTAGACTCTGCCATCCCAACAGCAGCTTCTACTCTGTGCCAGCAGGAGTGGGGAAATGAGCAGTCTTCGGGGCCA	5.55	na	na
TRBV05	TRBV05-06*01	unknown	TRBJ01-05*01	194	CASSLGYQPQHF	CTGAATGAAAGCCTTGTGTGGGGGACTCGCCCTCTACTCTGTGCCAGCAGTTCGGGCTACAGCCAGCAGTTCGGTGTAT	3.41	Vb 5.2	0.086	
TEN-12	TRBV27	TRBV27-01*01	na	TRBJ01-02*01	997	CASSYGAADGYTF	CTGGAGTCCGCGCAGCAACACAGCAGCTCTGTACTCTGTGCCAGCAGTTCGGGGGGTGGGATGGTCAACCTTCGGTTCG	7.78	Vb 14	nd
	TRBV04	TRBV04-01*01	TRBD02-01*01	TRBJ02-02*01	187	CASLTSSTGELFF	CAGCCCTCGCAGCAGGAGACTCAGCCCTGTACTCTGTGCCAGCAGCCTTACGCGGGGGTCCAGCGGGAGCTTTTTGGAGAA	1.46	Vb 7.1	na
	TRBV07	TRBV07-08*01	TRBD01-01*01	TRBJ02-07*01	130	CASSLQJAYEQYF	AAGATCAGCGCACACAGCAGGAGGACTCGCCCTGTACTCTGTGCCAGCAGTTCAGCCAGGCTACGAGCAGTACTTCGGGGCC	1.01	na	na
	TRBV05	TRBV05-04*01	TRBD02-01*01	TRBJ02-07*01	107	CASSLGRGGSYEQYF	AAGCCTTGGAGCTGGAGCAGTGGCCCTGTACTCTGTGCCAGCAGTGGTGGGGGGGCTCTACGAGCAGTACTTCGGGGCC	0.84	na	na
TRBV04	TRBV04-01*01	TRBD01-01*01	TRBJ01-02*01	73	CASSPRHQINRYGYTF	CGCTTCGAGCAGGAGACTCAGCCCTGTACTCTGTGCCAGCAGCCAGCAGGGGTTAATGAGTCACTTCGGTTCG	0.57	Vb 7.1	nd	
TEN-13	TRBV04	TRBV04-01*01	TRBD01-01*01	TRBJ01-02*01	565	CASSQDLSGTGYTF	CGCTTCGAGCAGGAGACTCAGCCCTGTACTCTGTGCCAGCAGCAAGTATGAGTCAAGGCTGGTCACTTCGGTTCG	26.11	Vb 1	18.1
	TRBV28	TRBV28-01*01	TRBD02-01*02	TRBJ02-01*01	42	CASSHFLPAGLEQFF	TCGCGCAGCAACCAACAGACATCTATGTACTCTGTGCCAGCAGTCTTCGGGAGTACGCGGGAGGAGGAGCAGTCTTCGGGGCCA	1.94	Vb 7.1	8.84
	TRBV24	TRBV24	TRBD02-01	TRBJ01-02*01	22	CATSDIDNYGYTF	TCCTAGACTTGCATCCCAACAGCAGCTTCTACTCTGTGCCAGCAGTATGATAGTAACTATGGTCACTTCGGTTCG	1.02	na	na
	TRBV11	TRBV11-03*01	TRBD02-01	TRBJ01-01*01	21	CASSVLAIEAFF	AAGATCAGCCTGAGAGCTGGGGACTCGCCCTGTACTCTGTGCCAGCAGTAAATTTAGCAAGGAACTCTTCGGAGCA	0.97	na	na
TRBV04	TRBV04-03*01	TRBD01-01*01	TRBJ01-02*01	19	CASSPNTGYSYTF	CTACACCTCTCAGCCAGGAGACTCGCCCTGTACTCTGTGCCAGCAGTTCACACAGGGGCTCTGCTCACTTCGGTTCG	0.88	Vb 7.2	0.59	
TEN-14	TRBV07	TRBV07-03*01	TRBD01-01*01	TRBJ01-01*01	139	CASSWTEIEAFF	AAGATCAGCAGCAGCAGGCGGGGGACTCAGCCCTGTACTCTGTGCCAGCAGTTCGAGGAGGAGCAGTGAAGCTTCTTCGGAGAA	0.46	na	na
	TRBV10	TRBV10-03*01	unknown	TRBJ01-01*01	95	CAISESGALNTEAFF	TGCGTCCAGCTCCCAAGACATCTGTGTACTCTGTGCCAGTCTGAGTGGGGGAGGAGGAGTGAAGCTTCTTCGGAGCA	0.32	Vb 12	na
	TRBV29	TRBV29-01*01	unknown	TRBJ02-02*01	94	CSVSGANTGELFF	ACTGTGAGCAACATGAGCCTGAAGCAGCAGCAATATCTGTGCCAGTCTGGGGGAGGAGGAGGAGTTCGGGGGGTTCGGAGAA	0.31	Vb 4	na
	TRBV27	TRBV27-01*01	TRBD01-01*01	TRBJ01-05*01	80	CASSLRTGHYQPHF	GAGTCCGCGCCCAACAGCAGCTTCTACTCTGTGCCAGGATTTAGGACGGGAGCAGTCAAGCCAGCAGTTCGGTGTAT	0.27	Vb 14	na
TEN-15	TRBV27	TRBV27-01*01	TRBD02-01*01	TRBJ02-01*01	12643	CASSLAGLGEQFF	CTGGAGTCCGCGCAGCAACACAGCAGCTCTGTACTCTGTGCCAGCAGTTCAGGGGGGGTGGTGGAGCAGTCTTCGGGGCCA	41.71	Vb 14	27.2
	TRBV18	TRBV18-01*01	TRBD01-01*01	TRBJ01-05*01	3635	CASSGRRDQPHF	AGGATCAGCAGGAGTGTGCGAGGAGTTCGCGAGCTTACTCTGTGCCAGCAGTTCGGGGGGGAGGAGTCAAGCTTCGGTGTAT	11.99	Vb 18	0.65
	TRBV06	TRBV06-05*01	unknown	TRBJ02-03*01	3463	CASSPSSDQYF	AGGCTGTCTGGCTCTCCCTCCAGACATCTGTACTCTGTGCCAGCAGTTCGGGGGGTGGAGTATTTGGGGCCA	11.43	Vb 13.1	16.4
	TRBV20	TRBV20-01*01	TRBD02-01	TRBJ01-02*01	1893	CASLPGYGYTF	ACTCTGACAGTGGAGCAGTCCCTCTGAGAGCAGCAGTCTACTCTGTGCCAGTCTTCGGTCTTCGGTCTTCGGGGCC	6.25	Vb 2	4.72
TRBV20	TRBV20-01*01	TRBD01-01*01	TRBJ01-05*01	648	CSAGRRDRDQPHF	ACAGTGCAGGAGTCCCTCTGAGAGCAGCAGTCTACTCTGTGCCAGCAGGAGGAGGAGTCAAGCCAGCAGTTCGGTGTAT	1.40	Vb 2	4.72	
TEN-16	TRBV09	TRBV09-01	TRBD01-01*01	TRBJ01-02*01	648	CASSGRTASYGYTF	CTGAGCTCTGTGGAGTGGGGGACTCAGCTTGTATTTCTGTGCCAGCAGGCGGAGCAGCAAGTATGGTCACTTCGGTTCG	5.23	Vb 1	na
	TRBV10	TRBV10-03*01	TRBD01-01*01	TRBJ01-05*01	422	CAISGTDSNPQHF	CTGGAGTCCGCTACAGCTCCCAAGCAGTCTGTACTCTGTGCCAGCAGGAGGAGTGAAGTCAAGCCAGCAGTTCGGTGTAT	3.41	Vb 12	na
	TRBV29	TRBV29-01*01	TRBD02-01*02	TRBJ02-01*01	213	CSATYLAGVHNEQFF	AGCAACATGAGCCTGAGGACAGCAGATATATCTGTGCCAGCAGTTCAGGCGGAGTTCACATGAGCAGTCTTCGGGGCCA	1.82	Vb 4	na
	TRBV12	TRBV12	TRBD01-01*01	TRBJ01-01*01	100	CASSPNDGQDEAFF	CAGCCCTCAAGAACCCAGGACTCAGCTGTACTCTGTGCCAGCAGTTCGAAGTCAAGCAGGAGGAGTGAAGCTTCTTCGGAGCA	0.71	Vb 8	na
TRBV30	TRBV30-01	TRBD01-01*01	TRBJ01-02*01	87	CAWMLISEKRYLNYGYTF	AGTACTCTGGCTCTACTCTGTGCCAGTGGCTCAATTCGAGAAATACAGGGGGCTCAACTGAGTCACTTCGGTTCG	0.70	Vb 20	na	

Table S5: Productive frequency of the 5 most common TCR- β clonotypes found in blister TEN samples, and comparison to the frequency of respective TCR V β chains detected by FACS.

Genomic DNA extracted from blister TEN samples were used for survey level deep sequencing of the TCR β chain, using ImmunoSEQ™ platform. TRBV repertoire data were compared to the frequency of respective TCR V β + cells detected among CD3+CD8+ T cells by FACS. Of note, the anti-V β mAb nomenclature is distinct from the corresponding TRBV nomenclature. Information for Vb family, TRBV, TRBD, TRBJ, template number, amino acid and CDR3 rearrangement are also provided.

V β family: the identified V Gene Family that contributed to a specific rearrangement. TRBV: a concise string identifying the most specific V Gene family, gene or allele identified during annotation. TRBD: a concise string identifying the most specific D Gene family, gene or allele identified during annotation. TRBJ: a concise string identifying the most specific J Gene family, gene or allele identified during annotation. Templates: the total number of templates for a specific rearrangement in the sample. CDR3 rearrangement: a particular nucleotide sequence generated through V(D)J recombination. Only productive rearrangements are shown. Productive rearrangements are in-frame, do not contain a stop codon and can produce a functional protein receptor. Productive frequency: the frequency of a specific « productive rearrangement » among all productive rearrangements within a sample, calculated as the templates for a specific rearrangement divided by the sum of productive templates for a sample.

Patient	Locus	Sorting Strategy	V family	TRAV/TRBV	TRAJ/TRBJ	Templates	Amino-acid	CDR3 rearrangement	Productive Frequency
TEN-9	TRA	BLISTERS - CD8+Vβ22+	TRAV19	TRAV19-01*01	TRAJ30-01*01	1022	CALSVVMNRDDKIIF	CTCACAAAGTCGTGGACTCAGCAGTATACTTCTGTGCTCTGAGTGTGTATATGAACAGAGATGACAAGATCATCTTTGGAAAA	51,93
			TRAV19	TRAV19-01*01	TRAJ29-01*01	951	CALSEAWGNTPLVF	AGCCTCACAAAGTCGTGGACTCAGCAGTATACTTCTGTGCTCTGAGTGAGGCGTGGGGAAACACACCTCTTGTCTTTGGAAAG	47,88
			TRAV16	TRAV12-02	TRAJ54-01*01	2	CALRGAAGNKLTF	ATTTGCTCAAGAGGAAGACTCAGCCATGATTACTGTGCTCTAAGGGCCCCGCTGCAGGCAACAAGCTAACCTTTGGAGGA	0,08
			TRAV12	TRAV17-01*01	TRAJ06-01*01	1	CAVTSQGAQKLVF	CAGAGACTCCCAGCCAGTATTAGCCACCTACCTCTGTGCCGTGACTAGCCAGGGAGCCAGAAAGCTGTTATTTGGCCAA	0,05
			TRAV17	TRAV16-01*01	TRAJ17-01*01	1	CATDAGAGGSYPTF	TTCCGGGACAGCAGACACTGCTTCTTACTTCTGTGCTACGGACGCGGGGACAGGAGGAAGCTACATACCTACATTTGGAAGA	0,03
TEN-9	TRA	BLISTERS - CD8+Vβ13.2+	TRAV19	TRAV19-01*01	TRAJ30-01*01	128	CALSVVMNRDDKIIF	CTCACAAAGTCGTGGACTCAGCAGTATACTTCTGTGCTCTGAGTGTGTATATGAACAGAGATGACAAGATCATCTTTGGAAAA	49,41
			TRAV19	TRAV19-01*01	TRAJ29-01*01	112	CALSEAWGNTPLVF	AGCCTCACAAAGTCGTGGACTCAGCAGTATACTTCTGTGCTCTGAGTGAGGCGTGGGGAAACACACCTCTTGTCTTTGGAAAG	42,88
			TRAV26	TRAV26-02	TRAJ34-01*01	4	CILLNTDKLIF	GATCCTGCACCGTGTCTACTTGAGAGATGCTGTGTACTACTGCTCCTCAACACCCGCAAGCTCATCTTTGGGACT	1,7
			TRAV17	TRAV17-01*01	TRAJ06-01*01	3	CATDAGAGGSYPTF	TTCCGGGACAGCAGACACTGCTTCTTACTTCTGTGCTACGGACGCGGGGACAGGAGGAAGCTACATACCTACATTTGGAAGA	1,25
			TRAV19	TRAV19-01*01	TRAJ54-01*01	2	CALRPVTPQGAQKLVF	ACAAGTCGTGGACTCAGCAGTATACTTCTGTGCTCTGCGCCCGTTACCCTCAGGGAGCCAGAAGCTGGTATTTGGCCAA	0,57
TEN-9	TRB	BLISTERS - CD8+Vβ22+	TRBV02	TRBV02-01*01	TRBJ01-05*01	136	CASSDVGRSNQPQHF	TCCACAAAGTCGGAGGACTCAGCCATGACTTCTGTGCCAGCAGTGTATGTTGGGGAGAACTAGCAATCAGCCCCAGCATTTTGGTGAT	56,43
			TRBV06	TRBV06	TRBJ01-01*01	77	CASSYSDPRDMNTEAFF	GCTGCTCCCTCCCAACATCTGTGACTTCTGTGCCAGCAGTACTCCGATCCGAGGGACATGAACACTGAAGCTTTCTTTGGACAA	31,9
			TRBV03	TRBV03	TRBJ02-02*01	1	CASSTRRSGLTGELFF	TCCTGGAGCTTGGTACTCTGCTGTGATTTCTGTGCCAGCAGCAGAGACGTTACGGCTTGACCGGGAGCTGTTTTTGGAGAA	0,0041
			TRBV09	TRBV09-01	TRBJ01-04*01	1	CASSPRQATNEKLVF	AGCTCTCGAGCTGGGGACTCAGCTTTGATTTCTGTGCCAGCAGCCGAGACAGGCAACTAATGAAAACTGTTTTTGGCAGT	0,0041
			TRBV25	TRBV25-01*01	TRBJ02-06*01	1	CASSYTGQSRANLVTF	TCTGCCAGGCCCTCACATACCTCTCAGTACTCTGTGCCAGCAGTTACACGGGCAAAAGTCCGGCCCAACGTCCTGACTTCCGGGGCC	0,0041
TEN-9	TRB	BLISTERS - CD8+Vβ13.2+	TRBV02	TRBV02-01*01	TRBJ01-05*01	1231	CASSDVGRSNQPQHF	TCCACAAAGTCGGAGGACTCAGCCATGACTTCTGTGCCAGCAGTGTATGTTGGGGAGAACTAGCAATCAGCCCCAGCATTTTGGTGAT	59,4
			TRBV06	TRBV06	TRBJ01-01*01	810	CASSYSDPRDMNTEAFF	GCTGCTCCCTCCCAACATCTGTGACTTCTGTGCCAGCAGTACTCCGATCCGAGGGACATGAACACTGAAGCTTTCTTTGGACAA	39,1
			TRBV02	TRBV02-01*01	TRBJ01-05*01	2	CASSDVGRSNQPQHF	GTCCACAAGTCGGAGGACTCAGCCATGACTTCTGTGCCAGCAGTGTATGTTGGGGAGAACTAGCAATCAGCCCCAGCATTTTGGTGAT	9,65E-04
			TRBV06	TRBV06	TRBJ01-01*01	2	CASSYSDPRDMNTEAFF	GGCTGCTCCCTCCCAACATCTGTGACTTCTGTGCCAGCAGTACTCCGATCCGAGGGACATGAACACTGAAGCTTTCTTTGGACAA	9,65E-04
			TRBV22	TRBV22-01*01	TRBJ01-02*01	2	CPGRALGKRRTYGYTF	TTGGCCACACCAGCCAAACAGCTTTGACTTCTGTCTGGGAGGGCCCTCGGAAAGCGAAAGACCTATGGCTACACCTTCGGTTCG	9,65E-04

Table S6. The two dominant TCRVβ cells isolated from TEN-9 blisters represent a single clone, which has rearranged 2 functional TRBV genes, as well as 2 functional TRAV genes.

Dominant CD8+TCRVβ13.2+ and CD8+TCRVβ22+ cells were isolated from blister cells of patient TEN-9. Genomic DNA was extracted and used for survey level deep sequencing of the TCRα-chain and TCRβ-chain, using ImmunoSEQ™ platform. Information for Vβ/Vα family, TRB/AV, TRB/AD, TRB/AJ, amino acid and CDR3 rearrangement and productive frequency are provided.

CD8+TCRVβ13.2+ and CD8+TCRVβ22+ cells (expressed at similar percentages in skin lesions (**Figure 3**)) were associated with the same pair of overexpressed Vα chains (TCRVA19-01*01) but with distinct TRAJ segments (respectively TRAJ30-01*01 and TRAJ29-01*01). In parallel to the 2 TRAV genes, 2 functional TRBV genes (TRBV02-01*01 and TRBV06) were also detected, indicating that CD8+TCRVβ13.2+ and CD8+TCRVβ22+ cells were derived from the same unusual T cell clone.

Patient	V family	TRBV	TRBD	TRBJ	Templates	Amino-acid	CDR3 rearrangement	Productive frequency	Respective anti-Vβ mAb	% Vβ+ cells among CD3+CD8+ T cells as determined by FACs analysis
MPE-1	TRBV05	TRBV05-06*01	unresolved	TRBJ01-01*01	499	CASSWVQLMNTAEFF	AACGCTCTGTGCTGGGGGACTCGGCCCTCTATCTGTGCGCAGCAGTGGGTCCAGTAAATGAACACTGAAGCTTTCTTGGACAA	3.65	Vb 1	na
	TRBV04	TRBV04-01*01	unresolved	TRBJ01-02*01	404	CASSQDRSYGYVTF	CACGCCCTGACGCCAGAAAGACTCAGCCTGTATCTGTGCGCAGCAGCAAGATCGGGGAGTACTATGGCTACACCTTCGGTTCG	0.23	Vb 13.6	na
	TRBV03	unresolved	TRBD01-01*01	TRBJ01-04*01	253	CASSLQSGQINEKLF	TCCTGGAGCTTGGTACTCTGCTGTATTTCTGTGCGCAGCAGCAATATCTGTGACAGATTAAATGAAAACTGTTTTTGGCAGT	0.17	Vb 22	na
	TRBV07	TRBV07-06*01	TRBD01-01*01	TRBJ02-02*01	246	CASSLVQAGALYFF	ATCCAGCCACAGAGCAGCGGGACTCGGCCATGTATGCTGTGCCAGCAGCTTAGTACAGGGGGCCGGGGAGCTGTTTTGGAGAA	0.15	Vb 13.1	na
	TRBV09	TRBV09-01	TRBD01-01*01	TRBJ02-07*01	232	CASSVGHSTSYEQYF	AGCTCTGTGAGCTGGGGGACTCAGCTTGTATTTCTGTGCGCAGCAGCTAGGGCCAGCAGCTCTACAGCAGACTCTCGGGCCG	0.15	Vb 13.1	na
MPE-2	TRBV27	TRBV27-01*01	TRBD02-01	TRBJ01-06*01	660	CASPAGDYNSPLHF	GAGTCGCCACGCCCAACAGCAGCTCTGTACTCTGTGCGCAGCAGCCCGGGGGGACTAATACCCCTCCACTTTGGGAAC	0.39	Vb 14	na
	TRBV04	TRBV04-03*01	TRBD01-01*01	TRBJ02-02*01	654	CASSPTRGYAGELFF	CACACCCTGCAGCCAGAAAGACTCGGCCCTGTATCTGTGCGCAGCAGCCCGAGGGGATATGCCGGGAGCTGTTTTGGAGAA	0.38	Vb 7.2	na
	TRBV11	TRBV11-02*02	TRBD01-01*01	TRBJ01-02*01	452	CASSTAGTYGAYTF	ATCCAGCCTGCAAAAGTTGAGGACTCGGCCGTGTATCTGTGCGCAGCAGCAGCGGGGACAGGGTATGGCTACACCTTCGGTTCG	0.27	Vb 21.3	na
	TRBV03	unresolved	TRBD01-01*01	TRBJ01-02*01	399	CASSQGLKVQATNYGYTF	GAGCTTGGTACTCTGCTGTATTTCTGTGCGCAGCAGCAAGTTTTAAAGTAGGGGAACTAACTATGGCTACACCTTCGGTTCG	0.23	unknown	na
	TRBV02	TRBV02-01*01	TRBD02-01*01	TRBJ01-02*01	334	CASSEARSGYGYTF	ATCCGGTCCCAAAGCTGGAGGACTCAGCCATGACTCTGTGCGCAGCAGTGAAGCGGGGAAAGCTATGGCTACACCTTCGGTTCG	0.20	Vb 22	na
MPE-3	TRBV05	TRBV05-04*01	TRBD01-01*01	TRBJ01-02*01	547	CASSLQWADYGYTF	GTGAACGCTTGGAGCTGGAGCAGCTCGGCCCTGTATCTGTGCGCAGCAGCTTGGGGTGGCTGACTATGGCTACACCTTCGGTTCG	1.48	unknown	na
	TRBV04	TRBV04-01*01	unknown	TRBJ01-02*01	334	CASSRSEAPNYGYTF	CACGCCCTGACGCCAGAAAGACTCAGCCTGTATCTGTGCGCAGCAGCTAGAGCGGGCCCTAAGCTATGGCTACACCTTCGGTTCG	0.90	Vb 7.1	6.36
	TRBV07	TRBV07-02*01	TRBD02-01	TRBJ01-02*01	175	CASSLSLYGYTF	ACTCTGAGCATCAAGCCACAGCAGGAGCAGCTCGGCCGTGTATCTGTGCGCAGCAGCTTAAAGCTTGGCTACACCTTCGGTTCG	0.47	unknown	na
	TRBV07	TRBV07-09	TRBD01-01*01	TRBJ01-02*01	137	CASSPQGARIGYGYTF	ACAGAGAGGGGGACTCGGCCATGTATCTGTGCGCAGCAGCCACACAGGGGGCCGGGGGATCTATGGCTACACCTTCGGTTCG	0.37	unknown	na
	TRBV20	TRBV20	unknown	TRBJ02-02*01	136	CSARRQNTGELFF	GTGACAGTGGCCATCTGAAGCAGCAGCTTACATCTGCAGTGTAGACCGGGCAGAACACCGGGGAGCTTTTTGGAGAA	0.37	unknown	na
MPE-4	TRBV24	TRBV24	unknown	TRBJ02-04*01	106	CATSGPMLIANKIQYF	TCTGCCATCCCCAACAGCAGCTCTTACTTCTGTGCGCAGCAGTGGCCCAATGTTAAGCCAAACACTTCACTTCGGGCC	1.84	unknown	na
	TRBV30	TRBV30-01*01	unknown	TRBJ01-01*01	90	CAWSVLRRRDPAFF	TCTAAAGACTCTTCTCAGTACTGCTGGCTCTATCTGTGCGCAGCAGTACTGAGCAGCAGACTGATGCTTTCTTGGACAA	1.56	Vb 20	6.07
	TRBV09	TRBV09-01	unknown	TRBJ01-01*01	89	CASSEWTVSEAFF	AACCTGAGCTCTGGAGCTGGGGGACTCAAGCTTGTATTTCTGTGCGCAGCAGGAGTGGCAGTAAGCGAAGCTTTTGGACAA	1.54	Vb 1	12.5
	TRBV05	TRBV05-04*01	TRBD02-01	TRBJ02-03*01	77	CASSPQGLAIPGDTQYF	TTGGAGCTGAGCAGCTCGGCCCTGTATCTGTGCGCAGCAGCCCGGGGCTAGGCTACAGGGGATACGAGTATTTGGCCCA	1.33	unknown	na
	TRBV19	TRBV19-01	TRBD02-01	TRBJ02-07*01	57	CATHASSYEQYF	ACTGTGACATCGGCCCAAAAGAACCCGACAGCTTCTATCTGTGCGCAGCAGTCAAGTCTCACGAGCAGTACTTCGGGGCCG	0.99	Vb 17	12.2
MPE-5	TRBV02	TRBV02-01*01	TRBD01-01*01	TRBJ01-05*01	162	CASSPLRQGIASSNQPHF	CTGGAGGACTGACCCATGTACTCTGTGCGCAGCAGTCCCCTTAGCAGGGCAGTCCCTTAGCAATCAGCCAGCATTGGGTGAT	1.92	Vb 22	5.68
	TRBV19	TRBV19-01	TRBD02-01*02	TRBJ02-03*01	73	CASSIGLAGLTDQYF	TCGGCCAAAGAACCCGACAGCTTTCTATCTGTGCGCAGTATAGGCTAGCGGACTCAGAGATACGAGTATTTGGCCCA	0.86	Vb 17	5.07
	TRBV09	TRBV09-01	TRBD02-01	TRBJ02-01*01	71	CASSVDPPSPGRNEAFF	CTGGAGCTGGGGGACTCAGCTTTGTATTTCTGTGCGCAGCAGCTAGTCCAGGGCTAGCGGGGCTAATGAGCAGTCTTCGGGCCA	0.84	Vb 1	2.1
	TRBV07	TRBV07-06*01	TRBD02-01	TRBJ01-02*01	69	CASSLGEYGYTF	ACGATCAGCGCAGAGCAGCGGGGACTCGGCCATGTATGCTGTGCGCAGCAGCTTAGCGGAGTACTATGGCTACACCTTCGGTTCG	0.82	unknown	na
	TRBV02	TRBV02-01*01	unknown	TRBJ01-03*01	64	CASSPMGISGNITYF	CGGTCCAAAGCTGGAGGACTCAGCAGTACTCTGTGCGCAGCAGTCCATCGGGGATCTCTGAAACACCATATATTTGGAGAG	0.76	Vb 22	5.68
MPE-6	TRBV07	TRBV07-03*01	TRBD02-01*02	TRBJ01-03*01	771	CASTRKAGGSGNTYF	ACAGAGCGGGGGGACTCAGCCGTGTATCTGTGCGCAGCAGCTCCGAAAGGGGGAGGGTCTGGAACACCATATATTTGGAGAG	18.01	unknown	na
	TRBV28	TRBV28-01*01	TRBD01-01*01	TRBJ01-01*01	68	CASSVFRGTGAETFF	TCGCAGCAGCAACCAAGCAGTATGATCTGTGCGCAGCAGTTCGGTGTTCAGGACAGGGGCCACTGAAGCTTTCTTGGACAA	1.59	Vb 3	na
	TRBV25	TRBV25-01*01	TRBD02-01*01	TRBJ01-01*01	24	CASSTRPSNTEAFF	CTGGAGTCTGCAGGCCCTCACATACGTCTCAGTACTCTGTGCGCAGCAGCAGCGGGGCTGAACACTGAAGCTTTCTTGGACAA	0.56	Vb 11	na
	TRBV07	TRBV07-09	TRBD02-01*02	TRBJ02-01*01	22	CASSLALLRVDVYNEQYF	GAGCAGGGGGACTCGGCCATGTATCTGTGCGCAGCAGCTTAGCTTTCCGGGGGATGTCTACAATGAGCAGTCTTCGGGCCA	0.51	unknown	na
	TRBV09	TRBV09-01	TRBD02-01	TRBJ01-05*01	21	CASSEDGGLNVPQHF	AGCTCTGTGAGCTGGGGGACTCAGCTTGTATTTCTGTGCGCAGCAGCGAGGACGGGGGACTGAATCAGCCCCAGCATTTTGGTGTAT	0.49	Vb 1	na
MPE-7	TRBV06	TRBV06-01*01	TRBD02-01*01	TRBJ01-03*01	489	CASSAFLTGSYF	AGGCTGGAGTGGCTCTCCCTCCAGCAGACTCTGTACTCTGTGCGCAGCAGTTCATTTACGGGGTCCATATATTTGGAGAG	1.24	unknown	na
	TRBV03	TRBV03	TRBD02-01	TRBJ02-02*01	243	CASNQGRTRGELFF	ATCAATCCCTGGAGCTTGGTACTCTGTGATTTCTGTGCGCAGCAACCAAGGACTCGCACGGGGAGCTGTTTTGGAGAA	0.62	unknown	na
	TRBV15	TRBV15-01*01	TRBD01-01*01	TRBJ01-01*01	207	CATSRDRQEAFF	CTTGACCTCCGCTCACCAGGCTCGGGGACGACGACCTATACCTGTGTGCGCAGCAGAGATCGACAGGAACTTTCTTGGACAA	0.52	unknown	na
	TRBV05	TRBV05-03	TRBD01-01*01	TRBJ01-03*01	171	CARRRGRISGNTYF	AGTGCTTGGAGCTGGGGGACTCGGCCCTGTATCTGTGCGCAGAGCAGGGGAAATAGGCTGGAACACCATATATTTGGAGAG	0.43	unknown	na
	TRBV11	TRBV11-03*01	TRBD02-01*02	TRBJ02-07*01	132	CASSLLEAYEQYF	AAGATCCAGCTGCAGAGCTGGGGACTCGGCCGTATCTGTGCGCAGCAGTCAACGGAGGCTCAGAGCAGTACTTCGGGGCCG	0.33	unknown	na

Table S7: Comparison of the productive frequency of the 5 most common TCR-β clonotypes found in skin MPE samples, and the frequency of respective TCR-Vβ chains detected by FACs.

Genomic DNA extracted from skin MPE samples was used for survey level deep sequencing of the TCRβ-chain, using ImmunoSEQ™ platform. The TRBV repertoire and TCR-Vβ FACS analysis is described in the footnotes of Table S5.

Patient	V family	TRBV	TRBD	TRBJ	Templates	Amino-acid	CDR3 rearrangement	Productive frequency	Respective anti-Vβ mAb	% Vβ+ cells among CD3+CD8+ T cells as determined by FACs analysis
TEN-2	TRBV06	TRBV06-06	na	TRBJ02-01*01	218	CASSYSIHQEKF	CTCAGGCTGGAGTTGGCTGCTCCCTCCAGACATCTGTGACTTCTGTGCCAGCAGTTCATCAATGAGCAGTCTTCGGGCCA	0.65	Vb 13.6	na
	TRBV09	TRBV09-01	TRBD02-01*01	TRBJ02-01*01	144	CASSVDSLQNEQFF	CTGAGCTCTGCGAGCTGGGGGACTCAGCTTGTATTTCTGTGCCAGCAGTAACTGTCCGGGGAATGAGCAGTCTTCGGGCCA	0.43	Vb 1	na
	TRBV06	TRBV06-05*01	TRBD01-01*01	TRBJ02-05*01	117	CASSYANTGWETQYF	CTGTCCGCTGCTCCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTACGACAAATAGGTTGGGAGACCCAGTACTTCGGGCCA	0.35	Vb 13.1	na
	TRBV05	TRBV05-01*01	na	TRBJ02-02*01	99	CASSLYTEGELFF	ATGAATGTGAGCAGCTGGAGCTGGGGGACTCGCCCTTATTTCTGTGCCAGCAGCTGTACACCGGGGAGCTGTTTTGGAGAA	0.29	Vb 5.1	na
	TRBV06	TRBV06-05*01	TRBD01-01*01	TRBJ01-02*01	94	CASSYSGGQVGYTF	CTGTCCGCTGCTCCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTACTTCGGGAGGGGACTTGTGTACACTTCGGGCCA	0.28	Vb 13.1	na
TEN-3	TRBV11	TRBV11-02*02	na	TRBJ02-01*01	1094	CASSPRDSYNEQFF	CAGCCTCGAAGCTTGAGGACTCGGCCGTGTATCTGTGCCAGCAGCCCTTCGTTACTTCAATAGCAGTCTTCGGGCCA	5.07	Vb 23.3	6.54
	TRBV27	TRBV27-01*01	TRBD01-01*01	TRBJ02-07*01	553	CASSLQCGARTTFLYEQYF	CCCAACAGACCTCTGTACTTCTGTGCCAGCAGTCTTACAGGGGGGGGGGAGAGATTTCTGTGCCAGTACTTCGGGCCA	2.57	Vb 14	7.88
	TRBV09	TRBV09-01	na	TRBJ02-01*01	420	CASSVQTSNEQFF	AGCTGCTGGAGCTGCTCAGCTTGTATTTCTGTGCCAGCAGTACGACAAATGAGCAGTACTTCGGGCCA	1.95	Vb 1	3.89
	TRBV28	TRBV28-01*01	TRBD02-01	TRBJ01-01*01	243	CASRDSGTEAFF	ATTTCTGGAGTCCGCGACCAACAGACATCTGTACTTCTGTGCCAGCAGTCTTCGGGAGAACTGAAGCTTCTTTGGACAA	1.12	Vb 3	na
	TRBV07	TRBV07-02*01	TRBD02-01*02	TRBJ02-01*01	233	CASSVWGSNNNEQFF	CGCACAGCAGGAGGAGACTCGGCCGTGTATCTGTGCCAGCAGCTGGTGGGGGGGAGTAAACAATGAGCAGTCTTCGGGCCA	1.08	na	na
TEN-4	TRBV19	TRBV19-01	TRBD02-01*02	TRBJ02-05*01	1374	CASSVGGTEQYF	GTGACTTCGGCCAAAGAACCCGACAGCTTCTATCTGTGCCAGTAACTGTGGAGGAGGGAGACCCAGTACTTCGGGCCA	8.11	Vb 17	10.5
	TRBV27	TRBV27-01*01	TRBD01-01*01	TRBJ01-05*01	845	CASSLGGARTAGDPQYHF	AGCCCAACAGCAGCTCTGTACTTCTGTGCCAGCAGTAAAGAGCAGCAGGAGGAGCTGACGCTGACGACTTTGGTGTAT	4.99	Vb 14	3.17
	TRBV07	TRBV07-03*01	TRBD01-01*01	TRBJ02-01*01	265	CASSLGGDQYNEQFF	CGCACAGGCGGGGGGACTCAGCGCTGTATCTGTGCCAGCAGCTTCTGGGACAGGGGAGTACAATGAGCAGTCTTCGGGCCA	1.56	na	na
	TRBV07	TRBV07-02*01	TRBD01-01*01	TRBJ02-07*01	176	CASSFWHPYEQYF	ACGATCCAGGCGCACAGCAGGAGGACTCGGCCGTATCTGTGCCAGCAGCTTCTGGCCACTCAGAGCAGTCTTCGGGCCA	1.04	na	na
	TRBV06	TRBV06-05*01	TRBD02-01*01	TRBJ02-01*01	123	CASSLAPGYNEQFF	CTGCTGTCCGCTCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTAAAGGGGGGCTACAATGAGCAGTCTTCGGGCCA	0.73	Vb 13.1	0.27
TEN-5	TRBV13	TRBV13-01*01	TRBD01-01*01	TRBJ01-02*01	1951	CASSLSTGGWLDGYTF	TCCTTGGAGCTGGGGGACTCAGCCCTGTACTTCTGTGCCAGCAGCTAAAGTACAGGGGGCTGTTAGTGGTCACTTCGGGCCA	2.18	Vb 23	3.6
	TRBV15	TRBV15-01*01	TRBD02-01*01	TRBJ02-05*01	1776	CATSRDVAAGGTQYF	CGCTCACCAGGCTGGGGGACGACGCTGACTGTGTGCCAGCAGCTAAAGTGGGGGGGGGGGAGCCTGACTTCGGGCCA	2.28	na	na
	TRBV28	TRBV28-01*01	TRBD01-01*01	TRBJ02-02*01	1701	CASSPPGDRNTGELFF	TCGCGCAGCACCAACAGACATCTGTACTTCTGTGCCAGCAGCCCGGGGAGCAGAAACCCGGGAGCTGTTTTGGAGAA	2.19	Vb 3	5.43
	TRBV06	TRBV06-05*01	TRBD02-01*01	TRBJ02-01*01	916	CASSYLAGASYNEQFF	TCGGCTCTCCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTAAAGGGGGGCTTCTACAATGAGCAGTCTTCGGGCCA	1.18	Vb 13.1	2.34
	TRBV27	TRBV27-01*01	na	TRBJ02-02*01	779	CASSFPEGTGELFF	GAGTCCGCGCCCAACAGCAGCTCTGTACTTCTGTGCCAGCAGTCTTCCGCAAGGGGAGCGGGGAGCTGTTTTGGAGAA	1.00	Vb 14	2.26
TEN-6	TRBV07	TRBV07-02*01	na	TRBJ01-02*01	1748	CASSLRENYEQYF	CAGCTCAGGCGCACAGCAGGAGGACTCGGCCGTGTACTTCTGTGCCAGCAGCTCAGGGGAGAACTAGTCACTTCGGGCCA	4.83	na	na
	TRBV18	TRBV18-01*01	TRBD01-01*01	TRBJ01-02*01	905	CASSPQGSRYGYTF	CACGATGTGTCGAGGAGATTCGGCAGCTTCTGTGCCAGCAGCTCAGGGGAGGAAAGCTAGTCACTTCGGGCCA	2.50	Vb 18	3.07
	TRBV19	TRBV19-01	TRBD01-01*01	TRBJ02-01*01	769	CASRMGPSNEQFF	ACTGTGACTTCGGCCCAAGAACCCGACGCTTCTATCTGTGCCAGTAAAGTGGGGGGGCTGAATGAGCAGTCTTCGGGCCA	2.13	Vb 17	6.78
	TRBV30	TRBV30-01*01	TRBD01-01*01	TRBJ01-02*01	754	CAWSSGTGASYGYTF	AAGAAGCTCTTCTCAGTACTTGTGCTTCTATCTGTGCCAGCAGGGGGGAGCCGCTTATGGTCACTTCGGGCCA	2.08	Vb 20	1.63
	TRBV27	TRBV27-01*01	na	TRBJ02-02*01	398	CASRRPNTGELFF	GAGTCCGCGCCCAACAGCAGCTCTGTACTTCTGTGCCAGCAGGAGGCGGGGAGCAGAACCCGGGAGCTGTTTTGGAGAA	1.10	Vb 14	0.74
TEN-7	TRBV06	TRBV06	TRBD02-01*02	TRBJ02-01*01	5623	CASSPTSGSSNEQFF	GAGTCCGCTGCTCCTCCAAACATCTGTGTACTTCTGTGCCAGCAGCCGACTAGCGGGGAGTAAATGAGCAGTCTTCGGGCCA	11.20	Vb 13.1; Vb 13.2; Vb 13.6	na
	TRBV02	TRBV02-01*01	TRBD02-01*01	TRBJ02-07*01	4141	CASSEVAGASYEQYF	ACAAGCTGCGAGGACTCAGCAGTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTCACTTCAGCAGTACTTCGGGCCA	8.25	Vb 22	4.83
	TRBV20	TRBV20-01*01	TRBD02-01*01	TRBJ02-07*01	1526	CASSLQCGARTTFLYEQYF	AGCTGCTGGAGCTGCTCAGCTTGTATTTCTGTGCCAGCAGTACGACAAATGAGCAGTACTTCGGGCCA	3.04	na	na
	TRBV06	TRBV06-01*01	TRBD01-01*01	TRBJ02-02*01	997	CASSELLWDRISKEELFF	CGCTCCCTCCAGACATCTGTACTTCTGTGCCAGCAGTAAATTTATGGGAGAGAAATCCGCAAGGAGCTGTTTTGGAGAA	1.99	na	na
	TRBV05	TRBV05-05*01	TRBD01-01*01	TRBJ01-01*01	646	CASSLNDRSNTAEFF	GACTTGTTCGGGGGACTCGGCCGTGTACTTCTGTGCCAGCAGCTTGAACAGGACGATGGAACCTGAAGCTTCTTTGGACAA	1.29	Vb 5.3	2.74
TEN-8	TRBV11	TRBV11-03*01	TRBD01-01*01	TRBJ01-05*01	82	CASSNPTGGQHSNQPHF	CAGCTTTGGGACTCGCCGCTGTACTTCTGTGCCAGCAGCAACCCGAGCAGGGGAGTAAAGTCAATGAGCAGTCTTCGGGCCA	0.55	na	na
	TRBV27	TRBV27-01*01	TRBD01-01*01	TRBJ02-03*01	47	CASFSTYSYEQYF	CTGATCTTGGAGTCCGCCACCCCAACGACCTCTGTACTTCTGTGCCAGCAGCAGGCGCAGATACGAGTATTTGGGCCA	0.31	Vb 14	0.97
	TRBV04	TRBV04-03*01	na	TRBJ02-02*01	27	CASRYRNHQEYF	ACCTGCGAGCAGAAAGACTCGGCCGTGTACTTCTGTGCCAGCAGCAAGAAAGAGGGGGGAGCAGCCGGGAGCTGTTTTGGAGAA	0.18	Vb 7.2	1.29
	TRBV27	TRBV27-01*01	TRBD02-01	TRBJ02-07*01	25	CASSQDAGSTNQPHF	CTGATCTTGGAGTCCGCCACCCCAACGACCTCTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGCTTCTTCGGGCCA	0.17	Vb 14	0.97
	TRBV04	TRBV04-03*01	TRBD01-01*01	TRBJ01-05*01	20	CASRTGPDQYF	CAGCTCAGCAGAAAGACTCGGCCGTGTACTTCTGTGCCAGCAGCAAGGTCAGGATCAGCAATCAGCCAGCTTTGGGAT	0.13	Vb 7.2	1.29
TEN-9	TRBV29	TRBV29-01*01	TRBD02-01*01	TRBJ01-02*01	23	CVSHSFGSAGYTF	GTGACCAACTGAGCCCTGAAGCAGCAGCATATCTGTGCCAGCTTCTTCCTTTCGGGGGGGCAAGTGGCTCACTTCGGGCCA	3.40	Vb 4	0.14
	TRBV21	TRBV21-01*01	TRBD01-01*01	TRBJ01-01*01	22	CASSKHPGLNTEAFF	CAGTCCAGGAGTCAGGGGACACAGCACTGTACTTCTGTGCCAGCAGCAACACCCAGGTTAAACACTGAAGCTTCTTTGGACAA	3.25	na	na
	TRBV06	TRBV06	TRBD01-01*01	TRBJ01-01*01	18	CASSYSDPRDMNTEAFF	CGTCTCCTCCAAACATCTGTGTACTTCTGTGCCAGCAGTACTCCAGTCCGAGGAGCAATGAACCTGAAGCTTCTTTGGACAA	2.66	na	na
	TRBV24	TRBV24	na	TRBJ02-01*01	17	CASSPDPDADEQYF	CTAGAGTCTGCATCCCAACACAGACAGCTTCTTACTTCTGTGCCAGCAGCCGACCCCGGCTGATGAGCAGTCTTCGGGCCA	2.51	na	na
	TRBV02	TRBV02-01*01	TRBD02-01*02	TRBJ01-05*01	15	CASSDVGRTSNQPHF	TCACAAGCTGTGAGGACTCAGCAGTGTACTTCTGTGCCAGCAGTAAAGTGGGGGAACTAGCAATCAGCCAGCTTTGGGAT	2.22	Vb 22	2.49
TEN-10	TRBV28	TRBV28-01*01	TRBD02-01*01	TRBJ01-04*01	87	CASSFSGPNEKLF	CTGGAGTCCGCGACCAACAGCAGATCTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGTAAAGTGAACCTGTTTTGGGACT	2.16	Vb 3	0.17
	TRBV06	TRBV06	TRBD01-01*01	TRBJ02-02*01	81	CASSYQVATGELFF	GAGTCCGCTCCTCCCAACATCTGTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGGAGCTGTTTTGGAGAA	2.01	Vb 14	na
	TRBV27	TRBV27-01*01	TRBD02-01*01	TRBJ01-01*01	32	CASNLGGVTEAFF	CTGGAGTCCGCGCCCAACAGCAGCTTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGGAGCTGTTTTGGACAA	0.80	na	0.11
	TRBV04	TRBV04-03*01	TRBD01-01*01	TRBJ02-07*01	27	CASSQDLPEYEQYF	ACCTGCGAGCAGAAAGACTCGGCCGTGTACTTCTGTGCCAGCAGCAAGATGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGAGAA	0.67	Vb 7.2	0.34
	TRBV24	TRBV24	TRBD01-01*01	TRBJ02-07*01	20	CATKDLRGPASEQYF	GAGTCTGCATCCCAACAGCAGCTTCTTACTTCTGTGCCAGCAGTAAAGTGGGGGGGCTTCTCAGAGCAGTACTTCGGGCCA	0.50	na	na
TEN-11	TRBV28	TRBV28-01*01	TRBD02-01	TRBJ02-01*01	800	CASSLTSVSYNEQFF	TCGGCAGCAGCAACAGACATCTATGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	5.18	Vb 3	14.9
	TRBV07	TRBV07-06*01	na	TRBJ02-03*01	258	CASSLWVSDTYQYF	ATTCAGCGCACAGACAGCAGGGGACTCGCCAGTATCTGTGCCAGCAGCTTATGGGTGAGCAGCAGATACGACAGTACTTCGGGCCA	1.67	na	0.021
	TRBV27	TRBV27-01*01	TRBD02-01	TRBJ02-07*01	100	CASSLWPLNTEQYF	GATGCTCCGAGCCCAACAGCAGCTTGTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.65	Vb 14	na
	TRBV10	TRBV10-02*01	na	TRBJ02-05*01	79	CASSVYEQYF	CTCACTTGGAGTCACTCCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.51	Vb 12	0.51
	TRBV19	TRBV19-01	TRBD02-01	TRBJ01-01*01	74	CASSPWPMLNTEAFF	TCGGCCCAAGAAAGCCAGCAGCTTCTACTTCTGTGCCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.48	Vb 17	3.55
TEN-12	TRBV27	TRBV27-01*01	na	TRBJ01-02*01	755	CASSYHGAADGYTF	CTGGAGTCCGCGCCCAACAGCAGCTTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.86	Vb 14	nd
	TRBV03	TRBV03	TRBD01-01*01	TRBJ01-01*01	186	CASSPDKNTEAFF	ATCAATTCCTGGAGCTTGGTGACTGTGTACTTCTGTGCCAGCAGCCGATGACAAAGAACTGAAGCTTCTTTGGACAA	0.21	na	nd
	TRBV14	TRBV14-01*01	TRBD02-01*01	TRBJ02-01*01	166	CASSQLAGAYNEQFF	CAGCTTCGAGAAGTGGAGTCTGGAGTATTTCTGTGCCAGCAGCAACTAGCGGGGGGCTACAATGAGCAGTCTTCGGGCCA	0.19	Vb 16	nd
	TRBV05	TRBV05-04*01	TRBD02-01*01	TRBJ02-07*01	154	CASSLGGVSYEQYF	AAGCTCTTGGAGCTGGAGCAGTCCGCTGTACTTCTGTGCCAGCAGCTTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.18	na	nd
	TRBV07	TRBV07-08*01	TRBD01-01*01	TRBJ02-07*01	151	CASSLQYAEQYF	AAGACTCAGGCGCACAGCAGGAGGACTCGGCCGTGTACTTCTGTGCCAGCAGCTAGCCAGGCTCAGCAGCAGTACTTCGGGCCA	0.17	na	nd
TEN-13	TRBV28	TRBV28-01*01	TRBD02-01	TRBJ02-01*01	646	CASSLITRNEQYF	CTGGAGTCCGCGACCAACAGCAGATCTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.81	Vb 3	8.17
	TRBV11	TRBV11-03*01	TRBD02-01	TRBJ01-01*01	349	CASSVSLATEAFF	AAGATCAGCTGCAGAGACTGGGAGCTCGGCCGTGTACTTCTGTGCCAGCAGCTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.44	na	na
	TRBV06	TRBV06-01*01	TRBD02-01*01	TRBJ01-05*01	201	CASSWSSGGNQPHF	GAGTCCGCTCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.25	na	na
	TRBV05	TRBV05-01*01	na	TRBJ02-02*01	172	CASSFDGGDGEELFF	CTGAGCACTTGGAGTGGGGGACTCGGCCCTTCTTCTGTGCCAGCAGCTTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.18	Vb 5.1	5.03
	TRBV06	TRBV06-05*01	TRBD02-01*02	TRBJ02-01*01	146	CASSYTGGRAYNEQYF	TCGGCTCCTCCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.21	Vb 13.1	4.02
TEN-14	TRBV06	TRBV06-05*01	TRBD02-01*01	TRBJ02-05*01	97	CASSFVGGGRETQYF	TCGGCTCCTCCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.37	Vb 13.1	na
	TRBV07	TRBV07-03*01	TRBD01-01*01	TRBJ01-01*01	87	CASSWTEATEAFF	AAGATCAGCGCACAGCAGGGGGGACTCAGCCGTGTACTTCTGTGCCAGCAGCTGACAGAGAACTGAAGCTTCTTTGGACAA	0.20	na	na
	TRBV07	TRBV07-08*01	unknown	TRBJ01-05*01	79	CASPLWQPHF	ACTCTGAAGACTCAGCGCACACAGCAGGAGGACTCGGCCGTGTACTTCTGTGCCAGCAGCTTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.24	na	na
	TRBV05	TRBV05-06*01	unknown	TRBJ02-01*01	50	CASSWGINEOFF	CTGAATGTAAAGCCTTGTGCTGGGGGACTCGGCCCTTACTTCTGTGCCAGCAGCTGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.15	Vb 5.2	na
	TRBV29	TRBV29-01*01	TRBD01-01*01	TRBJ02-02*01	47	CVSANTGTEQYF	ACTGTGAGCAAGTGAAGCTGAAGCAGCAGATATCTCTGCGAGCTTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	0.14	Vb 4	na
TEN-15	TRBV06	TRBV06-05*01	unknown	TRBJ02-03*01	1504	CASSFSGDTEQYF	AGGCTGTGCTCGGCTCCTCCAGACATCTGTGTACTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	6.17	Vb 13.1	48
	TRBV21	TRBV21-01*01	unknown	TRBJ01-01*01	877	CASSWNGTEAFF	TTGAGACTCAGCTCAGGAGTCAAGGGGACACAGCAGTATTTCTGTGCCAGCAGCTTGGGGGAGCAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	3.60	na	na
	TRBV12	TRBV12	unknown	TRBJ01-05*01	721	CASSVWDRISKEELFF	ATTCAGCGCACAGACAGCAGGGGACTCGCCAGTATCTGTGCCAGCAGCTTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	2.96	Vb 8	13.8
	TRBV07	TRBV07-09	TRBD02-01*01	TRBJ02-07*01	250	CASFTDRATYEQYF	CAGCCGACAGAGAGGGGGGACTCGCCAGTATCTGTGTACTTCTGTGCCAGCAGCTGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	1.02	na	na
	TRBV12	TRBV12	unknown	TRBJ01-04*01	234	CASSPWSYNEKELFF	ATCCAGCCTCAAGAACAGGGGACTGAGTGTACTTCTGTGCCAGCAGCTGGAATTTCAATGAAAAACTGTTTTGGGCCA	0.96	Vb 8	13.8
TEN-16	TRBV19	TRBV19-01	TRBD01-01*01	TRBJ02-02*01	6434	CASSKVTQPELFF	GTGACTTCGGCCAAAGAACCCGACAGCTTCTACTTCTGTGCCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGAGAA	13.50	Vb 17	na
	TRBV12	TRBV12	TRBD01-01*01	TRBJ01-01*01	6380	CASSPNDGQDEAFF	CAGCCTCCAGAACCCAGGAGCTGTGTACTTCTGTGCCAGCAGCTGGAATGAGCAGCAGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGACAA	13.38	Vb 8	na
	TRBV10	TRBV10-01	TRBD02-01*02	TRBJ02-03*01	1119	CASSDSSQPIPEYF	CTGGAGTCTGCTCCTCCAGACATCTGTATATTTCTGTGCCAGCAGTAAAGTGGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGACAA	2.25	Vb 12	na
	TRBV02	TRBV02-01*01	TRBD01-01*01	TRBJ02-07*01	682	CASSRTGGIYEQYF	ATCCGCTCCAAAGCTGGAGGACTCAGCAGTGTACTTCTGTGCCAGCAGCTGCAAGGGGGGAGTAAAGTGGGGGGGAGCTGTTTTGGGCCA	1.43	Vb 22	na
	TRBV07	TRBV07-06*01	TRBD02-01*01	TRBJ01-04*01	485					

Genomic DNA extracted from PBMC TEN samples was used for survey level deep sequencing of the TCR β -chain, using ImmunoSEQTM platform. The TRBV repertoire and TCR-V β FACS analysis is described in the footnotes of Table S5.

Patient	V family	TRBV	TRBD	TRBJ	Templates	Amino-acid	CDR3 rearrangement	Productive frequency	Respective anti-Vβ mAb	% Vβ+ cells among CD3+CD8+ T cells as determined by FACS analysis
MPE-3	TRBV05	TRBV05-04*01	TRBD01-01*01	TRBJ01-02*01	621	CASSLGVADYGYTF	GTGAACGCTTGGAGCTGGACGACTGGCCCTGTATCTCTGTGCCAGCAGCTTGGGGTGGGCTGACTATGGCTACACCTTCGGTTCG	3.33	unknown	na
	TRBV05	TRBV05-06*01	TRBD01-01*01	TRBJ01-04*01	391	CASSDRYRAEKLF	GTGAACGCTTGTGCTGGGGGACTGGCCCTATCTCTGTGCCAGCAGCAGATACAGGGCCGAAAACTGTTTTTGGCAGT	2.10	Vb 5.2	0.81
	TRBV04	TRBV04-03*01	TRBD02-01*02	TRBJ02-01*01	386	CASSPSGGRLSNEQFF	CTGCAGCCAGAAAGACTGGCCCTGTATCTCTGTGCCAGCAGCCATCTGGGGAGGGGGGACTCTCCAATGAGCAGTCTTCGGGCCA	2.07	Vb 7.2	0
	TRBV15	TRBV15-01*01	TRBD02-01*02	TRBJ02-05*01	377	CATSRTGRWETQYF	ATCCGCTCACCAGGCTGGGGGACGACGACCTGTACCTGTGTGCCACCAGCCGACGGGGAGGTGGGAGACCAGTACTTCGGGCCA	2.02	unknown	na
	TRBV11	TRBV11-02*02	TRBD01-01*01	TRBJ02-07*01	354	CASSSRDRGYEQYF	ATCCAGCCCTCAAAAGCTTGGAGACTCGGCCCTGTATCTCTGTGCCAGCAGCTCCCGGGACAGGGGGCTACGAGCAGTACTTCGGGCCG	1.90	Vb 21.3	3.94
MPE-4	TRBV07	TRBV07-09	TRBD01-01*01	TRBJ01-02*01	101	CASSLAGTGHGYTF	ATCCAGCCACAGACGAGGGGACTCGGCCATGTATCTCTGTGCCAGCAGCTTAGCGGGACAGATATGGCTACACCTTCGGTTCG	2.10	unknown	na
	TRBV06	TRBV06	TRBD01-01*01	TRBJ01-02*01	59	CASSPTGSLGYTYF	TCCGCTGCTCCTCCAGACATGTGTACTGTGTGCCAGCAGTCCCGGACAGGCTCTTGGCTATGGCTACACTTCGGTTCG	1.23	unknown	na
	TRBV07	TRBV07-09	unknown	TRBJ01-03*01	51	CASSLTVLLGNTIYF	ACAGAGCAGGGGGACTGGCCATGTATCTCTGTGCCAGCAGCTCACTACAGTACTCTCGGGGAAACACCATATATTTGGAGAG	1.06	unknown	na
	TRBV05	TRBV05-04*01	TRBD02-01	TRBJ02-01*01	19	CASSLTGLEQFF	CTGAATGTGAACGCTTGGAGCTGGAGCAGCTGGCCCTGTATCTCTGTGCCAGCAGCTTGGGGACTTTGGAGCAGTCTTCGGGCCA	0.39	unknown	na
	TRBV07	TRBV07-02*01	TRBD02-01*01	TRBJ01-02*01	13	CASSPTGGGNGYTF	ATCCAGCCACAGCAGGAGACTCGGCCGTGTATCTCTGTGCCAGCAGCTCCCGGGGGCGGGAATGGCTACACCTTCGGTTCG	0.27	unknown	na
MPE-5	TRBV04	TRBV04-01*01	unknown	TRBJ02-01*01	283	CASSLIDGEEQFF	CTTCACTACAGCCCTCGACGCAAGACTCAGCCCTGTATCTCTGTGCCAGCAGCTACTGGACGGAGAGCAGTCTTCGGGCCA	3.31	Vb 7.1	2.81
	TRBV10	TRBV10-03*01	TRBD01-01*01	TRBJ02-07*01	281	CAISEGGAGTGSSEQYF	TCCGCTACAGCTCCCGAAGCATCTGTGACTCTGTGCCATCAGTGAGGGGGGCGCGGACAGGCTCCGAGCAGTACTTCGGGCCG	3.28	Vb 12	7.74
	TRBV20	TRBV20	TRBD02-01*02	TRBJ02-01*01	155	CSARDLELVGWNQYF	ACCAGTGGCCATCCTGAAGACAGCAGCTTCACTCTGTGCCAGCTAGAGATCTCAGGATTTGGGTGAATGAGCAGTCTTCGGGCCA	1.81	unknown	na
	TRBV07	TRBV07-09	unknown	TRBJ01-01*01	127	CASVPLSGNTEAFF	ATCCAGCCACAGAGCAGGGGACTCGGCCATGTATCTCTGTGCCAGCAGCTCCCTGTGCCGCAACACTGAGCAGTCTTCGGGCCA	1.48	unknown	na
	TRBV07	TRBV07-02*01	TRBD01-01*01	TRBJ02-07*01	68	CATRPGPTRPSPSYEQYF	CAGCAGGAGGACTCGGCCGTGTATCTCTGTGCCAGCAGCCCGGGCCGACGAGGGGGCGGAGCTCTACGAGCAGTACTTCGGGCCG	0.79	unknown	na
MPE-6	TRBV03	TRBV03	TRBD02-01	TRBJ02-01*01	447	CASRGSYSNEQFF	ATCAATCCCTGGAGCTTGGTACTCTGTGTATTTCTGTGCCAGCAGGGGGAGCGCTCTACAATGAGCAGTCTTCGGGCCA	0.68	unknown	na
	TRBV28	TRBV28-01*01	TRBD01-01*01	TRBJ01-01*01	410	CASSVFRTGATEAFF	TCCGCGACCAACAGACATCTGTACTCTGTGCCAGCAGTTCGGTGTTCAGGACAGGGGCCACTGAAGCTTCTTCGGGCCA	0.63	Vb 3	na
	TRBV07	TRBV07-09	TRBD01-01*01	TRBJ01-04*01	75	CASSPASGTEGKLF	CGCAGAGCAGGGGGACTCGCCATGTATCTCTGTGCCAGCAGCCCGCTCCGGACAGAGGGTGAACAACTGTTTTGGCAGT	0.11	unknown	na
	TRBV28	TRBV28-01*01	TRBD02-01*02	TRBJ02-07*01	74	CASSLGGVAYEQYF	CTGAGTCCGACAGCAACACAGACATCTGTACTCTGTGCCAGCAGTTAGGAGGGTGGCTCAGCAGCAGTACTTCGGGCCG	0.11	Vb 3	na
	TRBV05	TRBV05-01*01	TRBD01-01*01	TRBJ01-02*01	64	CASSRTGYVGYTF	AATGTGAGCACCTTGGAGCTGGGGGACTCGCCCTTATCTTTCGGCCAGCAGCCGGACAGCAGCTATTATGGCTACACCTTCGGTTCG	0.10	Vb 5.1	na
MPE-7	TRBV30	TRBV30-01*01	unknown	TRBJ01-01*01	249	CAWSLENTEAFF	CTGAGTCTAAGAAGCTCCTCTCAGTACTGGCTTCTATCTCTGTGCCCTGGAGTTGGAGAACACTGAAGCTTCTTCGGGCCA	0.98	Vb 20	6.42
	TRBV03	TRBV03	unknown	TRBJ01-06*01	140	CASSSGNGNSPLHF	ATCAATCCCTGGAGCTTGGTACTCTGTGTATTTCTGTGCCAGCAGCTCCGGCAATGGGAATTCACCCCTCCACTTCGGGAAAC	0.55	unknown	na
	TRBV09	TRBV09-01	TRBD01-01*01	TRBJ02-02*01	125	CASSRRRRRAGNPNTGELFF	CTGGGGGACTCAGCTTTGATTTCTGTGTGCCAGCAGCCCGAAGACGTGACGGGAATCCGAACACCGGGGAGCTGTTTTGGAGAA	0.49	Vb 1	2.72
	TRBV12	TRBV12	TRBD01-01*01	TRBJ02-07*01	121	CASSFGTNYEQYF	ATCCAGCCCTCAGAAACCAGGGACTCAGCTGTGTATCTCTGTGCCAGCAGTTTGGTGGGACAAATTCAGAGCAGTACTTCGGGCCG	0.48	unknown	na
	TRBV15	TRBV15-01*01	TRBD01-01*01	TRBJ01-01*01	99	CATSRDRQEAFF	CTTGACTCCCTCACCAGCCCTGGGGGAGCGAGCAGTACTGTGTGCCAGCAGCAGATGACAGGAACTTCTTCGGGCCA	0.39	unknown	na

Table S9: Comparison of the productive frequency of the 5 most common TCR-β clonotypes found in PBMC MPE samples, and the frequency of respective TCR-Vβ chains detected by FACS.

Genomic DNA extracted from PBMC MPE samples were used for survey level deep sequencing of the TCRβ-chain, using ImmunoSEQ™ platform. The TRBV repertoire and TCR-Vβ FACS analysis is described in the footnotes of Table S5.

Patient	Sorted Vβ	V family	TRAV	TRAJ	Templates	Amino-acid	CDR3 rearrangement	Productive Frequency
TEN-3	Vβ21.3	TRAV25	TRAV25-01*01	TRAJ43-01*01	13167	CANNMRF	CAGCTCCCTGCACATCACAGCCACCCAGACTACAGATGTAGGAACCTACTTCTGTGCCAACAATGACATGCGCTTTGGAGCA	87.6
		TRAV25	TRAV25-01*01	TRAJ43-01*01	1309	CANNMRF	CAGTTCCCTGCACATCACAGCCACCCAGACTACAGATGTAGGAACCTACTTCTGTGCCAACAATGACATGCGCTTTGGAGCA	8.5
		TRAV19	TRAV19-01*01	TRAJ17-01*01	55	CALSEAHPRGKAAGNKLTF	GGACTCAGCAGTATACTTCTGTGCTCTGAGTGAGGCGCATCCCCGGTAAAGCTCAGGCAACAAGCTAACTTTGGAGGA	0.4
		TRAV39	TRAV39-01*01	TRAJ27-01*01	32	CAVVRPNAGKSTF	CACAGCTGCCGTGCATGACCTCTCTGCCACCTACTTCTGTGCCGTGGTGCAGCCCAATGCAGGCAAAATCAACCTTTGGGGAT	0.1
		TRAV20	TRAV20-01	TRAJ42-01*01	10	CAVQVLYGGSQNLIF	TAAACCTGAAGACTCAGCCACTTATCTGTGCTGTGCAGTCTTATATGGAGGAAGCCAAAGGAAATCTCATCTTTGGAAAA	0.07
TEN-7	Vβ13.2	TRAV13	TRAV13-01	TRAJ39-01*01	284	CADNAGNMLTF	GCACATCACAGAGACCCAACCTGAAGACTCGGCTGTACTTCTGTGCCGATAATGCAGGCAACATGCTCACCTTTGGAGGG	86.95
		TRAV14	TRAV14-01	TRAJ53-01*01	24	CAMREGQSGGSNYKLTF	ACTGGGGGACTCAGCAATGATTTCTGTGCAATGAGAGAGGGCCAGAGTGGAGGTAGCAACTATAAACTGACATTTGGAAAA	7.52
		TRAV29	TRAV29-01	TRAJ52-01*01	4	CAANSYGVKLF	CATTGTGCCCTCCAGCCTGGAGACTCTGCAGTGTACTTCTGTGCAGCAAATAGCGGCTATGGAAAAGCTGACATTTGGACAA	1.62
		TRAV39	TRAV39-01*01	TRAJ45-01*01	2	CAVPPGGADGLTF	AGCTGCCGTGCATGACCTCTGCCACCTACTTCTGTGCCGTCCCCCAGGAGGAGGTGCTGACGGACTCACCTTTGGCAA	0.93
		TRAV12	TRAV12-01	TRAJ50-01*01	2	CVVLYDKVIF	CCTGCTCATCAGAGACTCCAAGCTCAGTGATTCAGCCACCTACCTCTGTGTGTTCTCTACGACAAGGTGATATTTGGGCCA	0.66
TEN-10	Vβ3	TRAV27	TRAV27-01*01	TRAJ26-01*01	170295	CAGDDNYGQNFVF	CACTGCAGCCCGCTGGTGATACAGGCTCTACCTCTGTGCAGGGGACGATAACTATGGTCAGAATTTGTCTTTGGTCCC	89.84
		TRAV21	TRAV21-01	TRAJ20-01*01	817	CAVVRPNKYLSF	CATTGCAGCTTCTCAGCCTGGTGACTCAGCCACCTACTCTGTGCTGTGAGGCCAAACGACTACAAGCTCAGCTTTGGAGCC	0.43
		TRDV02	TRDV02-01	TRDJ01-01*01	752	CACDPVSWETGDQDKLIF	AGATGAAGGGTCTTACTACTGTGCTGTGCCCTGTTCTTCCGGAGACTGGGGATCAAACCGATAAACTCATCTTTGGAAAA	0.39
		TRAV21	TRAV21-01	TRAJ47-01*01	544	CAVKELYGNKLVF	AGCTTCTCAGCCTGGTGACTCAGCCACCTACTCTGTGCTGTGAAGGAATTGGAATATGGAACAACCTGGTCTTTGGCGCA	0.29
		TRAV21	TRAV21-01	TRAJ49-01*01	436	CAVRPFTGNQFYF	AGCTTCTCAGCCTGGTGACTCAGCCACCTACTCTGTGCTGTGAGGCCAACTTACCAGGTAACCAAGTTCTATTTGGGACA	0.22
TEN-15	Vβ14	TRAV39	TRAV39-01*01	TRAJ40-01*01	2732	CAVDIVGKYIF	CATCACAGCTGCCGTGCATGACCTCTCTGCCACCTACTTCTGTGCCGTGGACATTTGTTGCTACAAATACATCTTTGGAAAC	96.08
		TRAV24	TRAV24-01*01	TRAJ22-01*01	32	CASLSGSARQLTF	CAAAGGATCCAGCCTGAAGACTCAGCCACATACCTCTGTGCTCTCTTTCTGTTCTGCAAGGCAACTGACCTTTGGATCT	1.23
		TRAV12	TRAV12-01	TRAJ41-01*01	11	CVVRDSGYALNF	CATCAGAGACTCCAAGCTCAGTGATTCAGCCACCTACTCTGTGTTGGTGAGGGATTCCGGGTATGCACTCAACTTCGGCAAA	0.42
		TRAV26	TRAV26-01	TRAJ37-01	9	CIGGFRVCTQL	GATCTGCCCCAGCTACGCTGAGAGACACTGCTGTACTATTGCATCGGCGGATCCGGGTATGCACTCAACTTCGGCAA	0.38
		TRAV19	TRAV19-01*01	TRAJ18-01*01	6	CAPDRGSLGRLYF	AGCCTCACAAGTCGTGGACTCAGCAGTACTTCTGTGCTCCGACAGAGGCTCAACCTGGGGAGGCTACTTTGGAAGA	0.19

Table S10: Identification of the main TCR-α chains expressed by dominant TCR-Vβ+ cells.

Dominant CD8+TCR-Vβ+ cells were FACS sorted from the blister or PBMC samples of patients TEN-3, -7, -10 and -15. Genomic DNA was extracted and used for survey level deep sequencing of the TCRα-chain, using ImmunoSEQ™ platform. Information for Vα family, TRAV, TRAJ, template number, amino acid and CDR3 rearrangement and productive frequency are provided, as described in Table S5.

Patient	Sorted V β	V family	TRAV	TRAJ	Templates	CDR3 rearrangement	Unproductive TCR α chain Frequency
TEN-3	V β 21.3	TRAV23	TRAV23-01	TRAJ37-01	14520	AAGCAGTTCTCATTGCATATCATGGATTCCCAGCCTGGAGACTCAGCCACCTAGGAACACAGGCAAATAATCTTTGGGCAA	47
		TRAV23	TRAV23-01	TRAJ37-01	164	AAGCACCTCTCATTGCATATCATGGATTCCCAGCCTGGAGACTCAGCCACCTAGGAACACAGGCAAATAATCTTTGGGCAA	0.6
TEN-7	V β 13.2	TRAV35	TRAV35-01	TRAJ27-01*01	3	TTCTGAATATCTCAGCATCCATACCTAGTGATGTAGGCATCTACTTCTGTGCTGGGCAGGGCCAAATCAACCTTTGGGGAT	1.2
		TRAV01	TRAV01-01	TRAJ30-01*01	3	TTCTACAGGAGCTCCAGATGAAAGACTCTGCCTTACTTCTGCGCTGTGAGAGGGGGCCGGGCAAGATCATCTTTGGAAAA	1.1
TEN-10	V β 3	TRAV36	TRAV36-01	TRAJ40-01*01	94386	ACAGCCACCCAGACCGGAGACTCGGCCGTCTACCTCTGTGCTGTGGAGTGCCTCAGGAACCTACAAATACATCTTTGGAACA	31.5
		TRAV25	TRAV25-01*01	TRAJ30-01*01	672	ACAGCTCCCTGCACATCACAGCCACCCAGACTACAGATGTAGGAACCTCCTGAACAGAGATGACAAGATCATCTTTGGAAAA	0.2
TEN-15	V β 14	TRAV27	TRAV27-01*01	TRAJ26-01*01	170295	CACTGCAGCCCAGCCTGGTGATACAGGCCTCTACCTCTGTGACAGGGGACGATAACTATGGTCAGAATTTGTCTTTGGTCCC	50.2
		TRDV02	TRDV02-01	TRDJ01-01*01	752	AGATGAAGGGTCTTACTACTGTGCCTGTGACCTGTTTCTGGGAGACTGGGGATCAAACCGATAAATCATCTTTGGAAAA	0.4

Table S11. Main unproductive TCR- α chains found in dominant TCR-V β + cells.

Dominant CD8+TCR-V β + cells from the blister or PBMC samples of patients TEN-3, -7, -10 and -15 were FACS sorted and analysed as described in Table S10. Information for nature and frequency of unproductive TCR- α chains are provided.

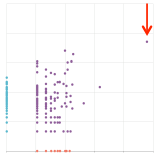
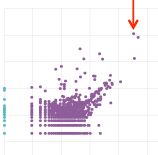
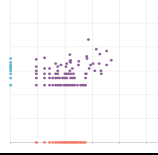
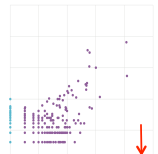
	Target clone	Dominant clonotypes obtained through V β sorting				TCR transfectant ID	
		Chains	V family	TCR(A/B)V	TCR(A/B)J		Rearrangement
TEN-3		β	TRBV11	TRBV11-02*02	TRBJ02-01*01	CAGCCTGCAAAGCTTGAGGACTCGGCCGTGTATCTCTGTGCCAGCAGCCCTCCGTGACTCTACAATGAGCAGTTCTTCGGGCCA	C1
		α	TRAV25	TRAV25-01*01	TRAJ43-01*01	CAGCTCCCTGCACATCACAGCCACCCAGACTACAGATGTAGGAACCTACTTCTGTGCCAACCAATGACATGCGCTTTGGAGCA	
TEN-7		β	TRBV06	TRBV06	TRBJ02-01*01	GAGTCGGCTGCTCCCTCCCAACATCTGTGTACTTCTGTGCCAGCAGCCGACTAGCGGGAGTAGTAATGAGCAGTTCTTCGGGCCA	C2
		α	TRAV13	TRAV13-01	TRAJ39-01*01	GCACATCACAGAGACCAACCTGAAGACTCGGCTGTACTTCTGTGCCGATAATGCAGGCAACATGCTCACCTTTGGAGGG	
TEN-10		β	TRBV28	TRBV28-01*01	TRBJ01-04*01	CTGGAGTCGCCAGCACCAACCAGACATCTGTACTCTGTGCCAGCAGTTTCGGGGGCTAATGAAAACTGTTTTTGGCAGT	C3
		α	TRAV27	TRAV27-01*01	TRAJ26-01*01	AGCCTCACAAAGTCGTGGACTCAGCAGTACTTCTGTGCTCTGAGTGAGGCGTGGGAAACACACCTTGTCTTTGGAAG	
TEN-15		β	TRBV27	TRBV27-01*01	TRBJ02-01*01	CTGGAGTCGCCAGCCCCAACAGACCTCTGTACTTCTGTGCCAGCAGCTAGCGGGGGGCTGGGTGAGCAGTTCTTCGGGCCA	C4
		α	TRAV39	TRAV39-01*01	TRAJ40-01*01	CATCACAGCTGCCGTGCATGACCTCTGTGCCACTACTTCTGTGCCGTGGACATTGTGGCTACAAAATACATCTTTGGAACA	

Table S12. Paired TCR α and TCR β sequences used to generate Skw3 transductants.

Table shows minimal information (V β /V α family, TRB/AV, TRB/AD, TRB/AJ, CDR3 rearrangement) for the TCR α and TCR β chain rearrangement CDR3 sequences that were transduced in Skw3 cells to test drug-specificity of dominant TCR clonotypes from patients TEN-3, -7, -10 and -15. The targeted top clone in paired blister/PBMC heat map scatters is shown, as well as respective transfectant ID.

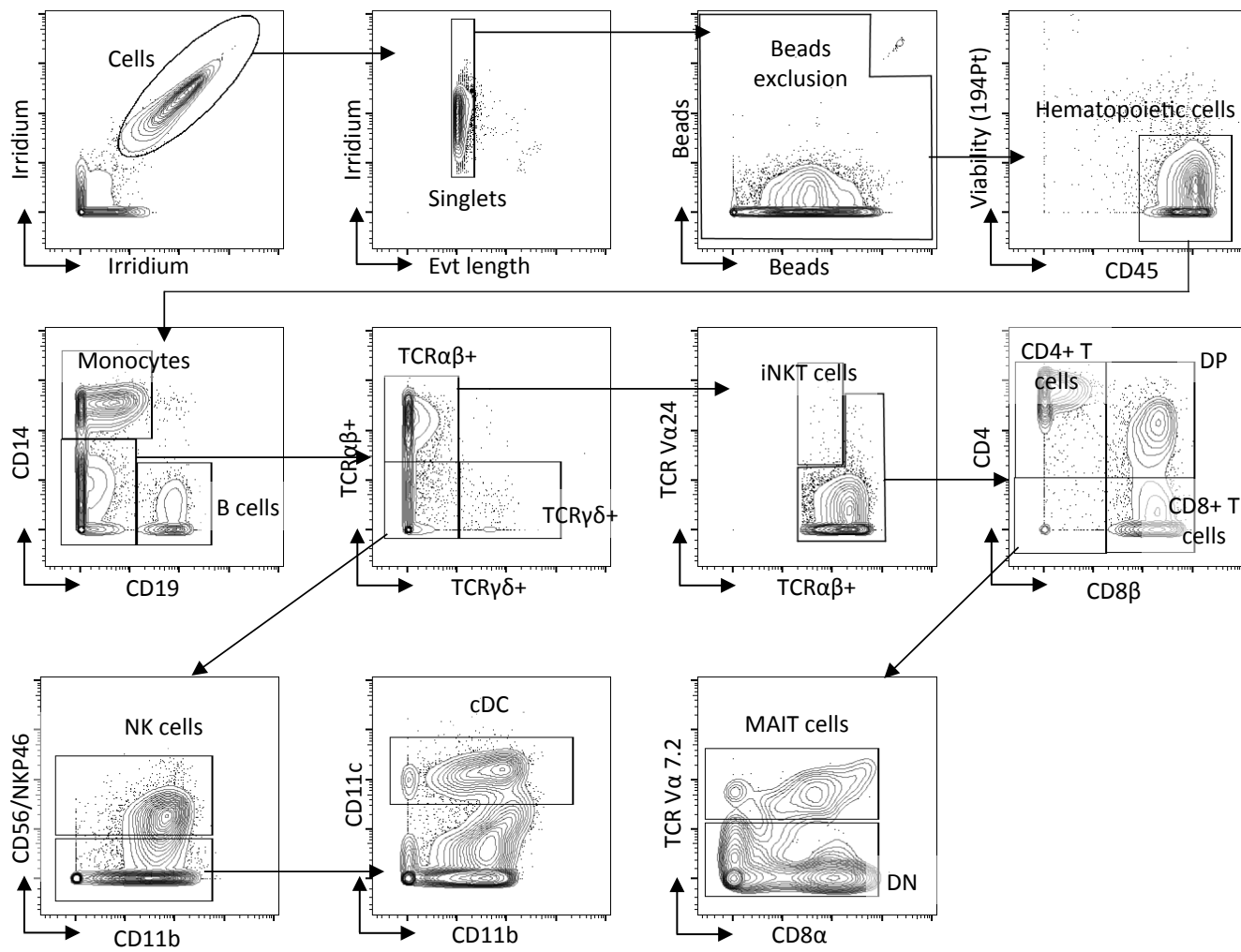


Figure S1

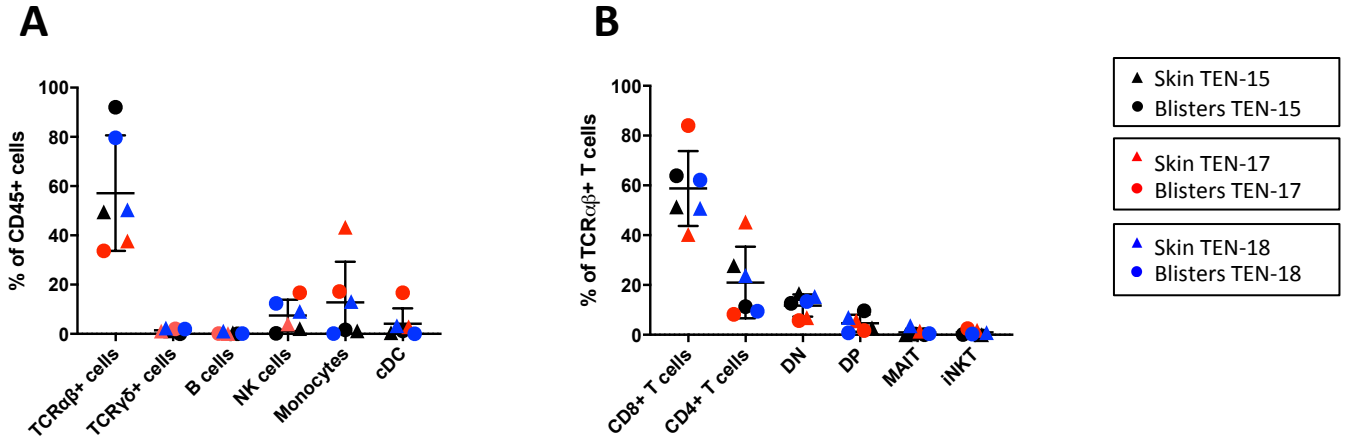


Figure S2

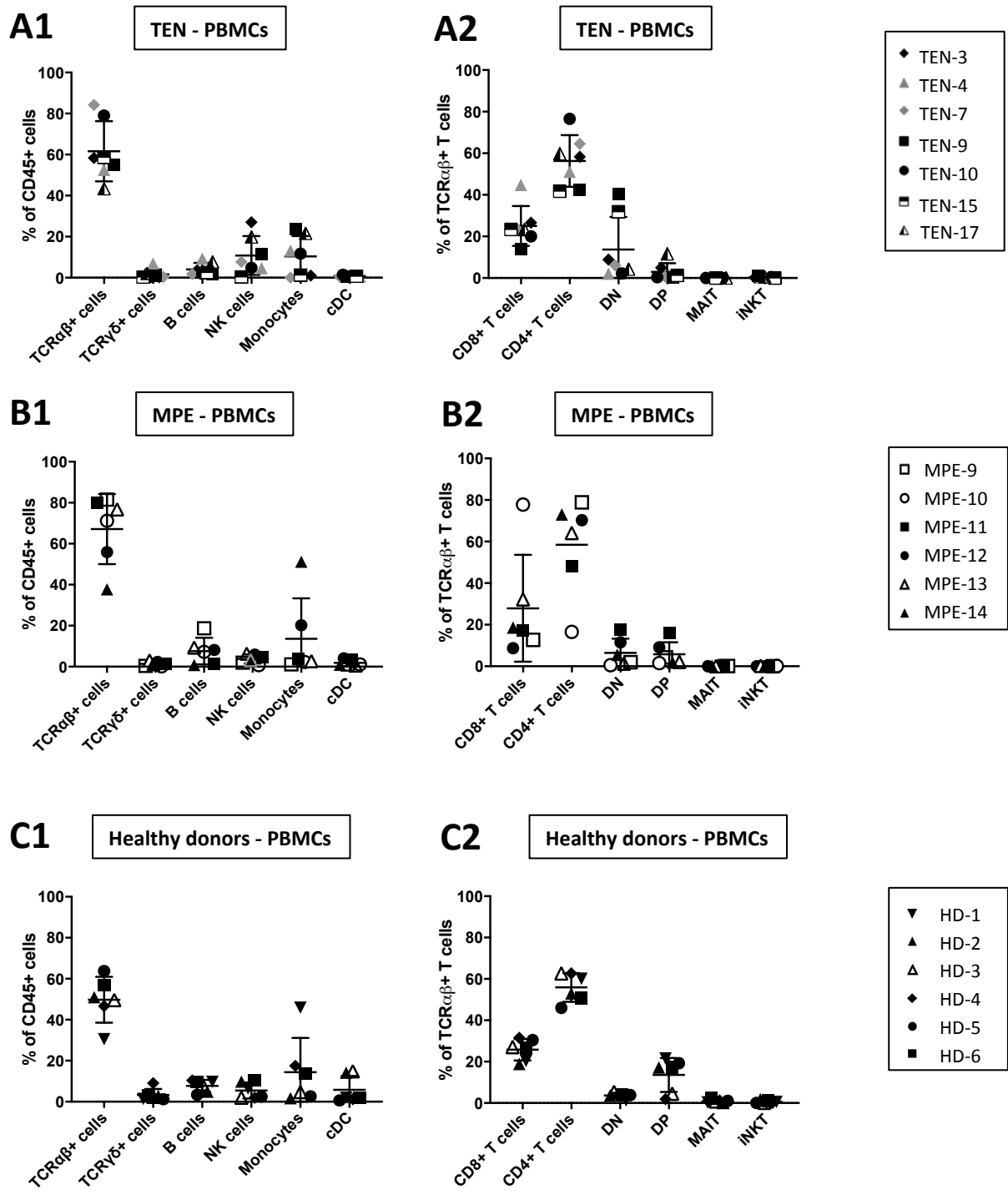


Figure S3

**Concatenated CD8 + T cells
TEN-MPE-Healthy donors
Skin/Blisters and PBMCs**

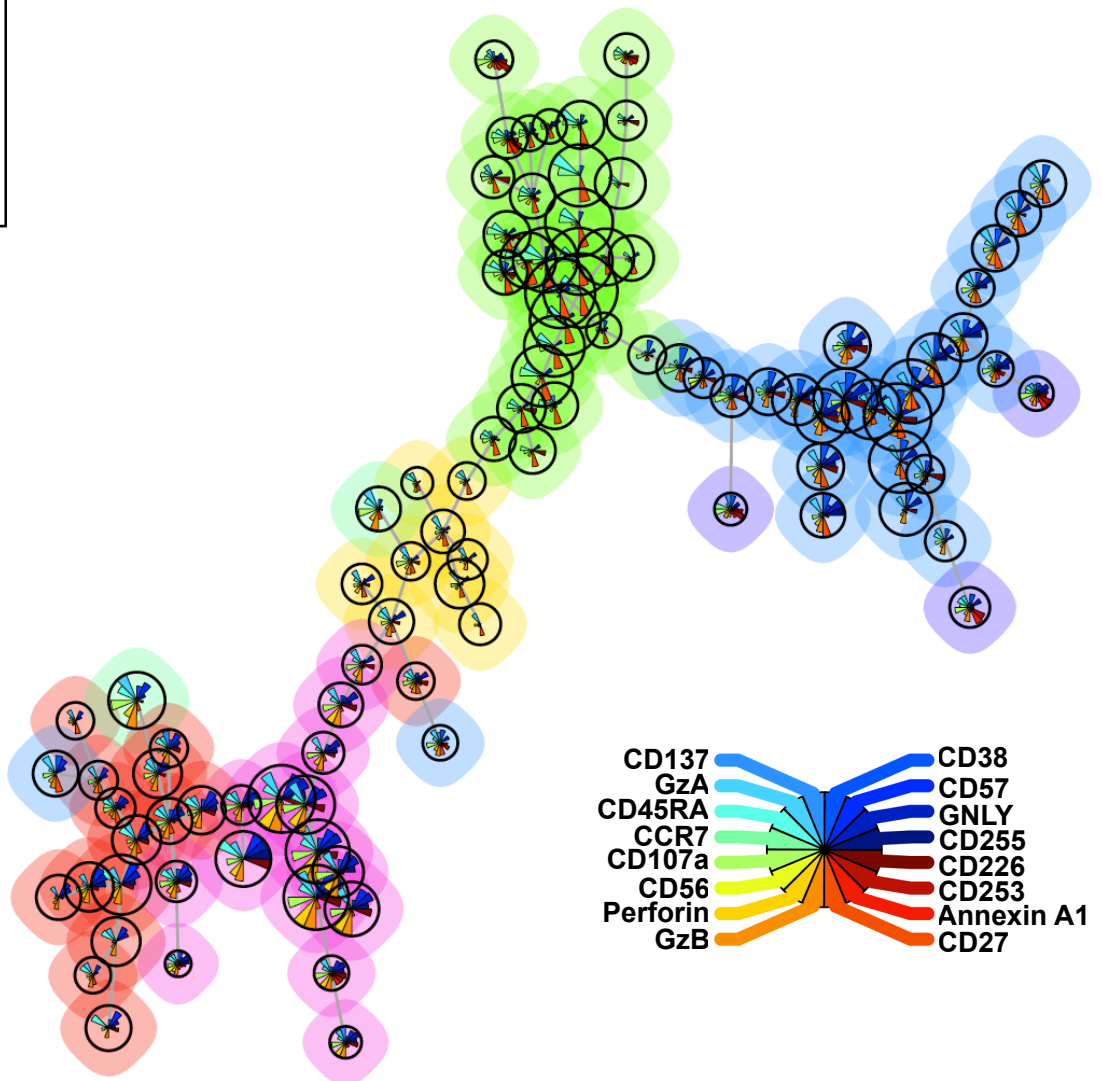


Figure S4

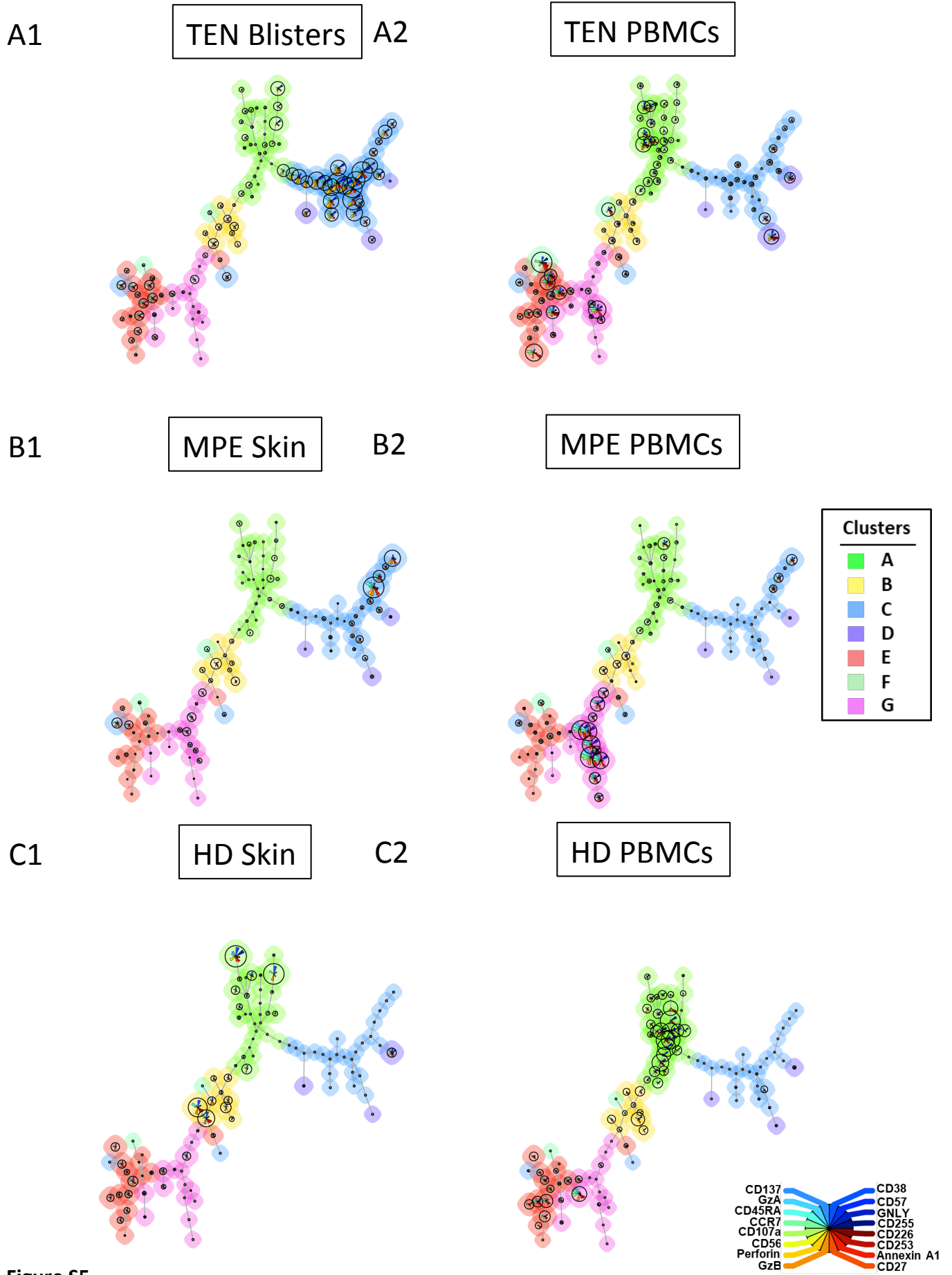


Figure S5

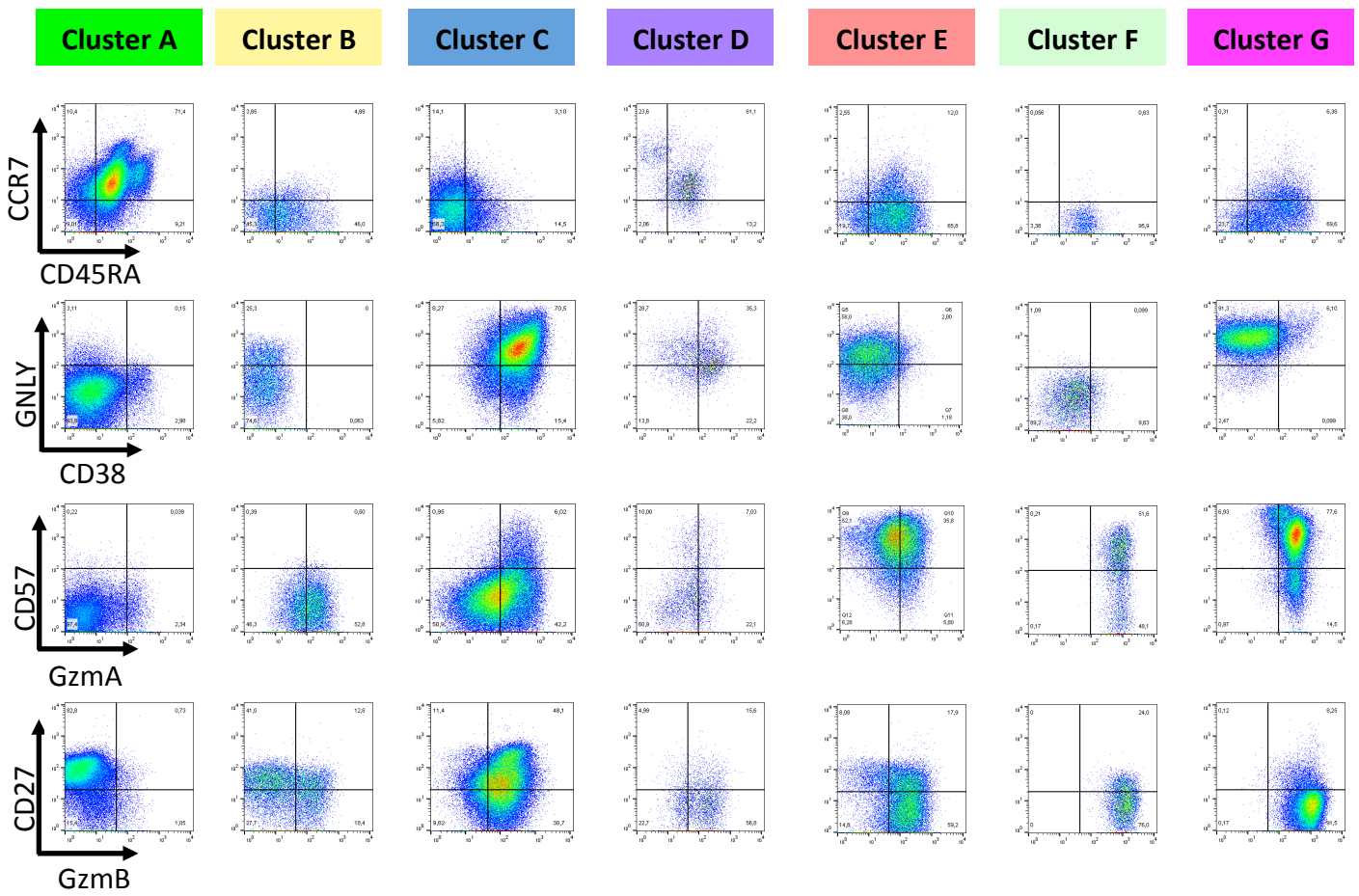


Figure S6

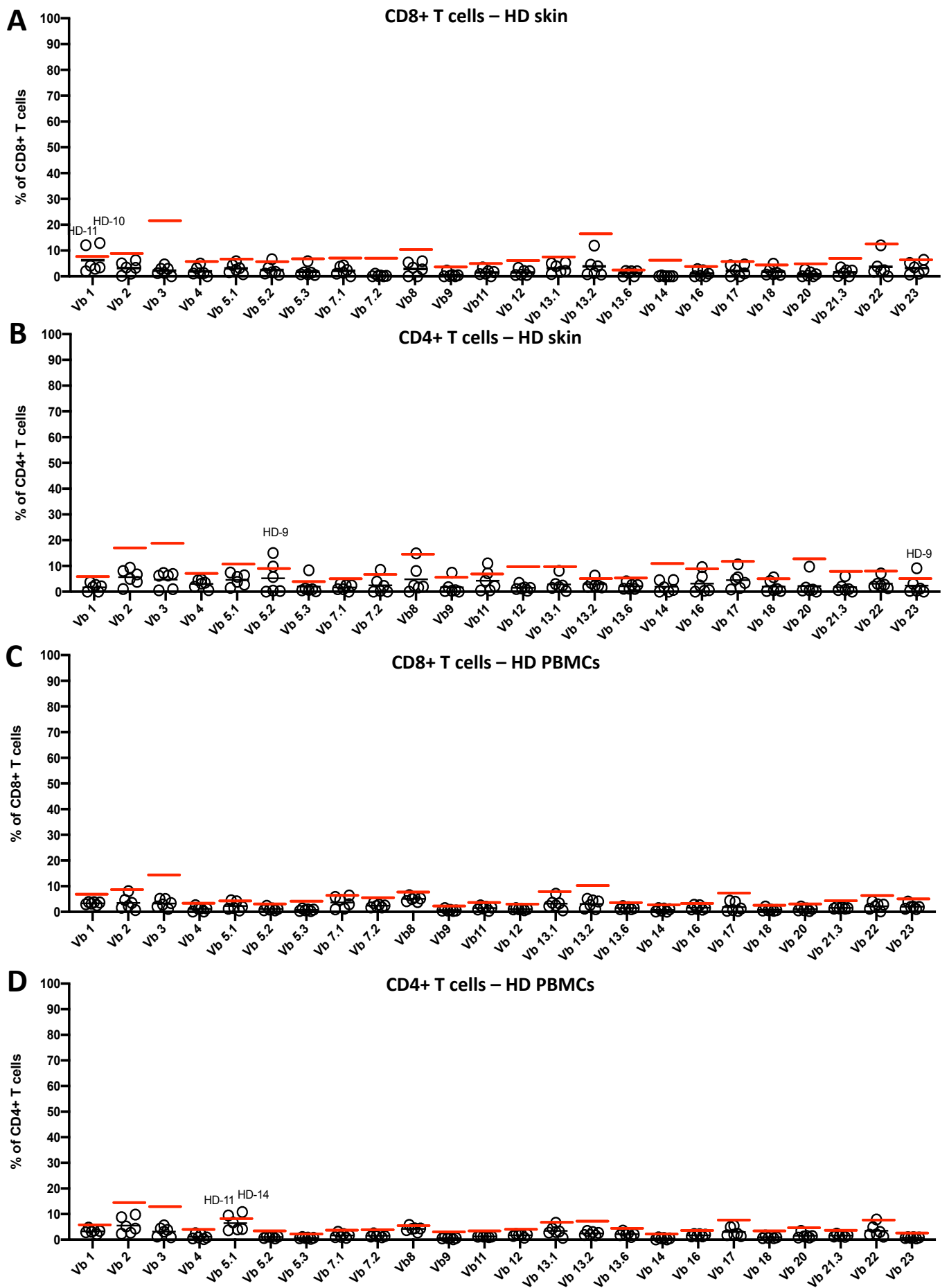


Figure S7

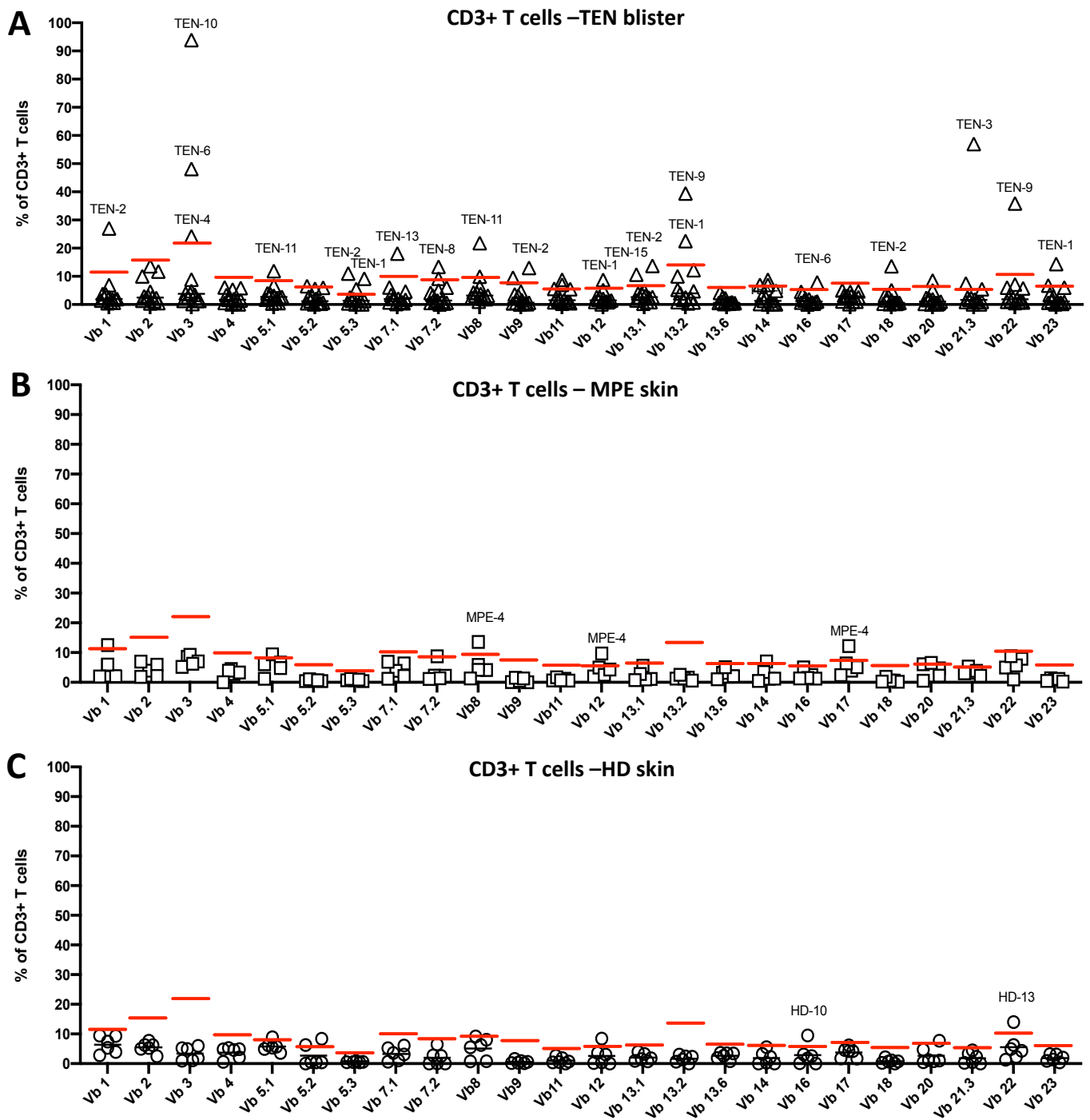


Figure S8

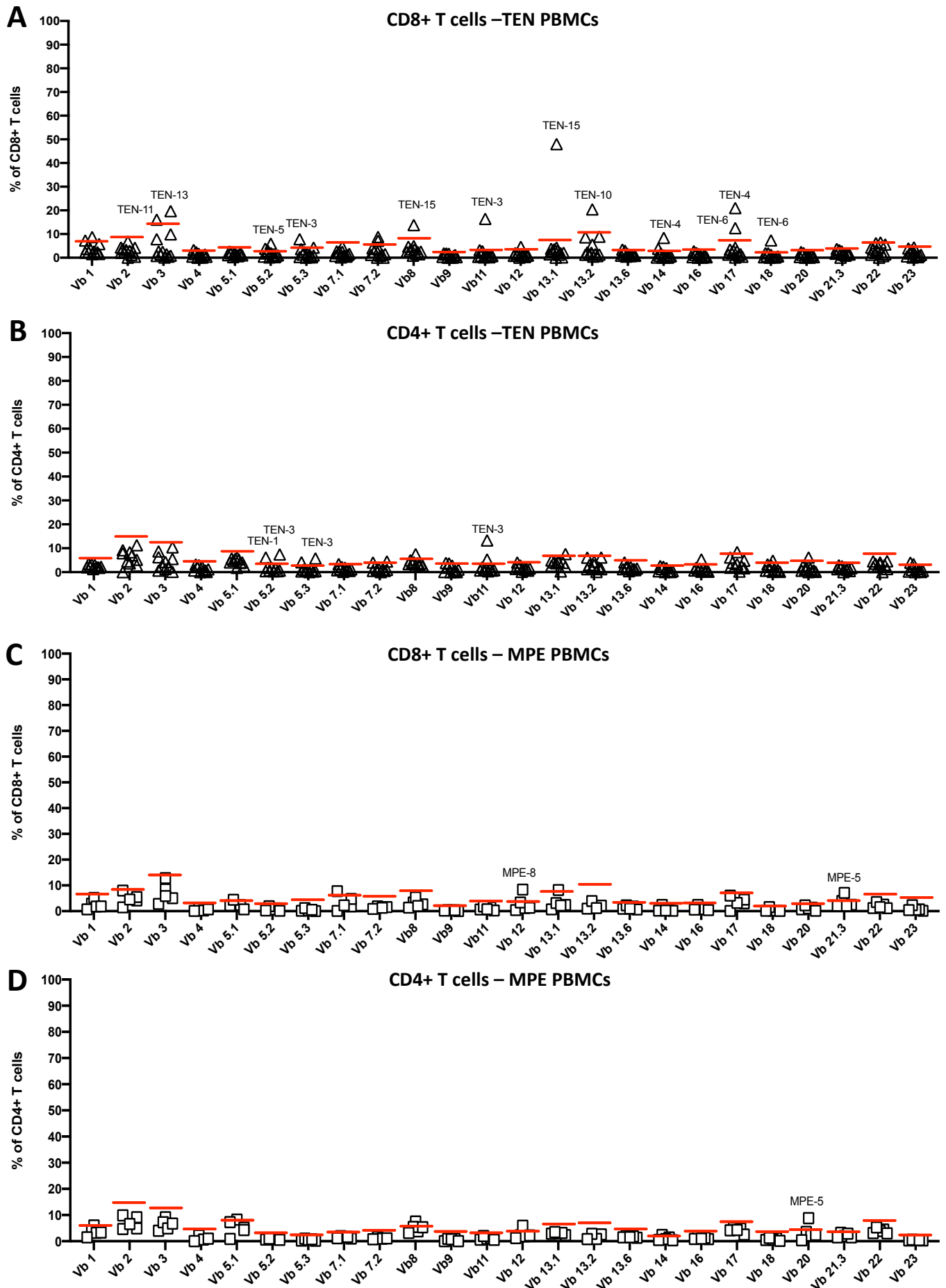


Figure S9

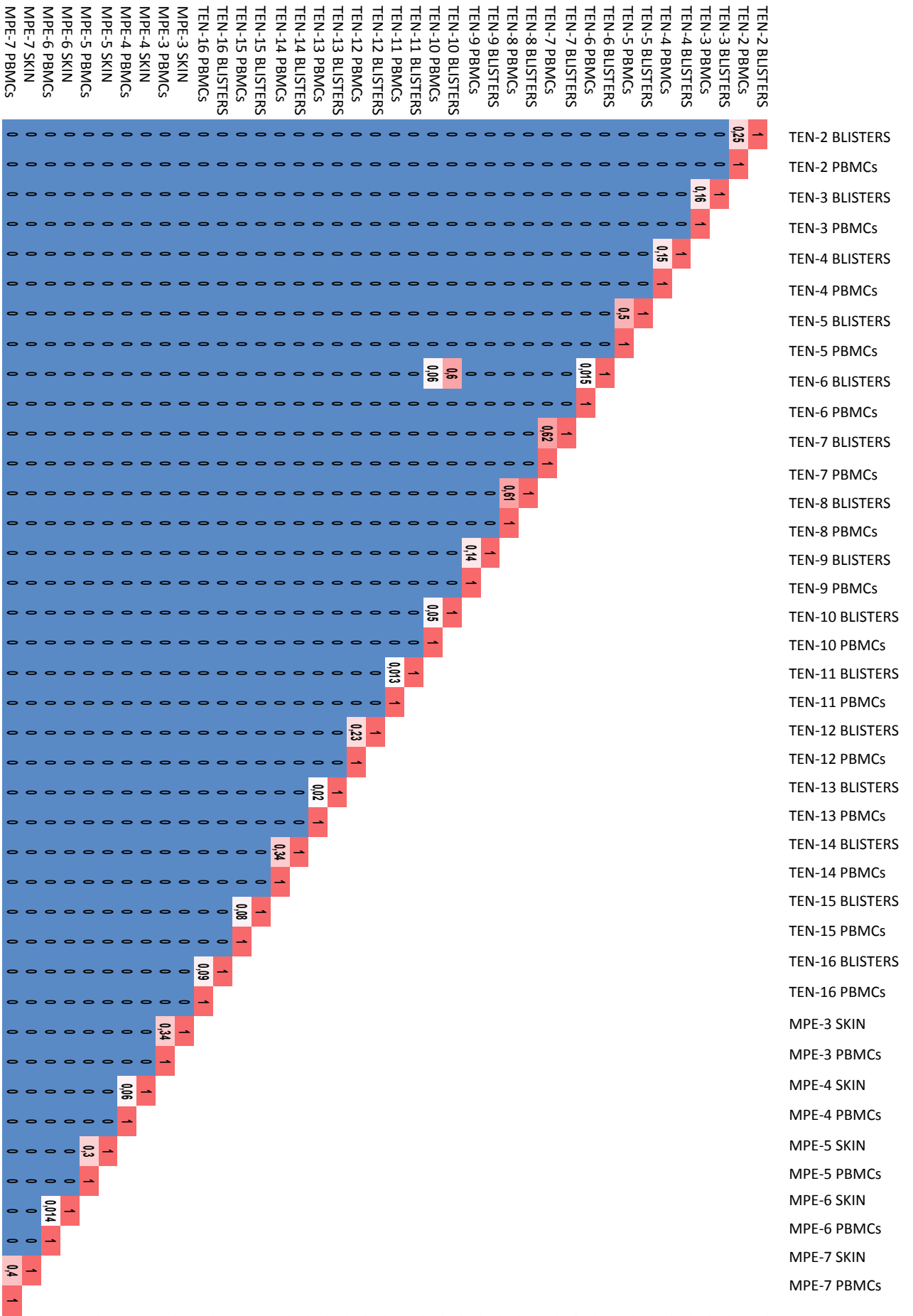


Figure S11

TEN

MPE

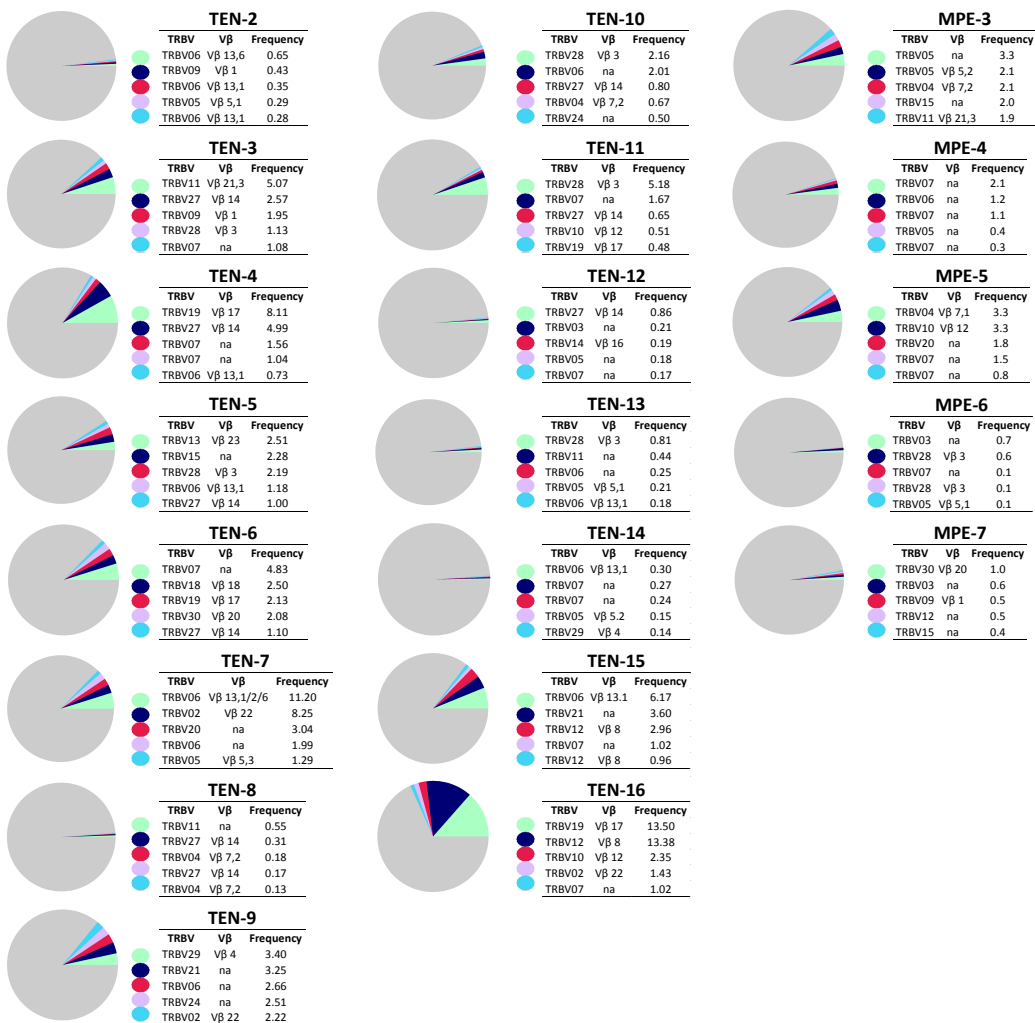


Figure S12

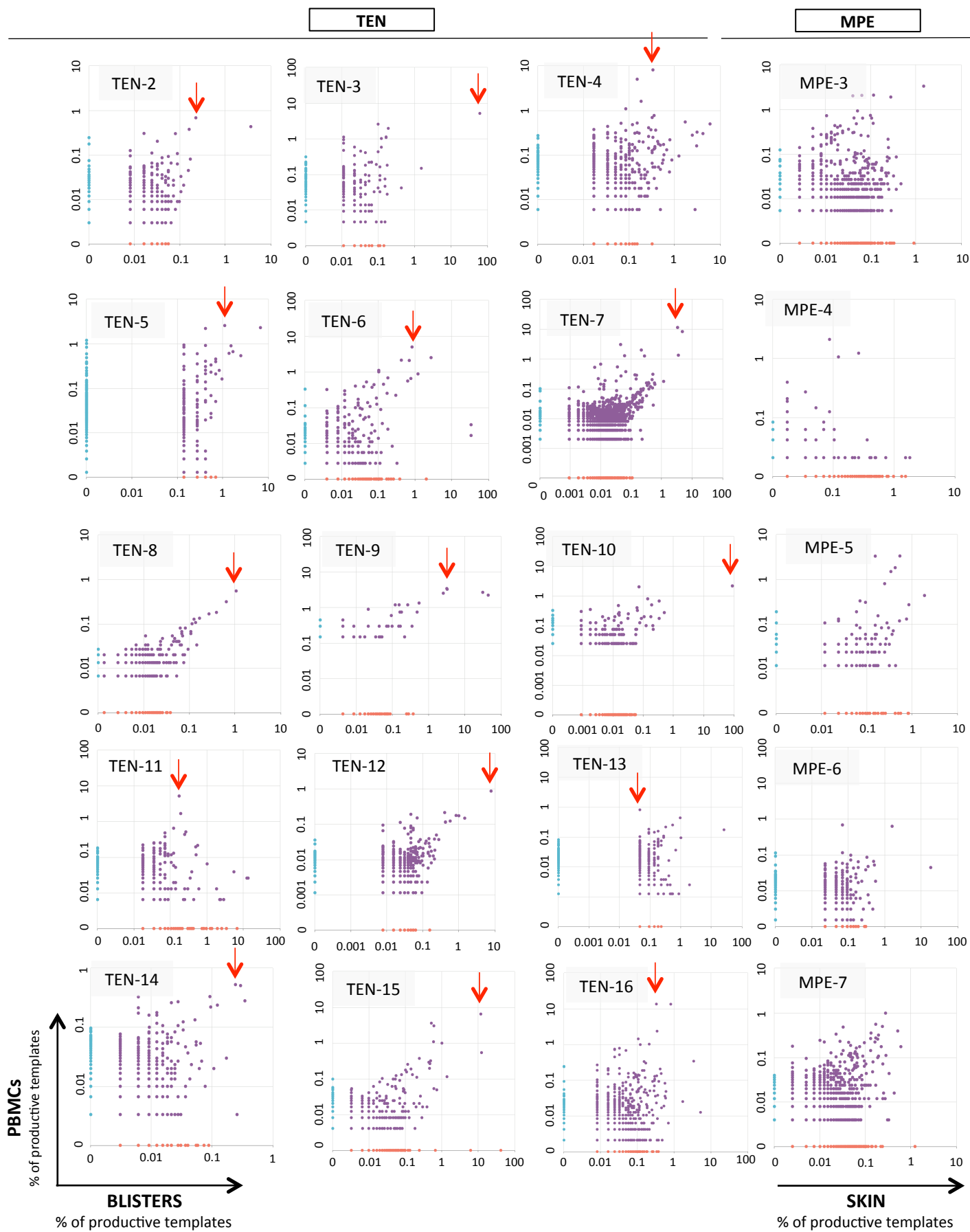


Figure S13

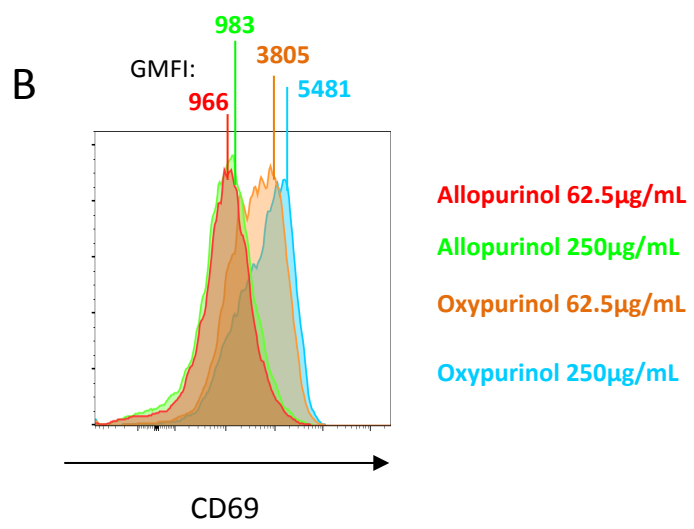
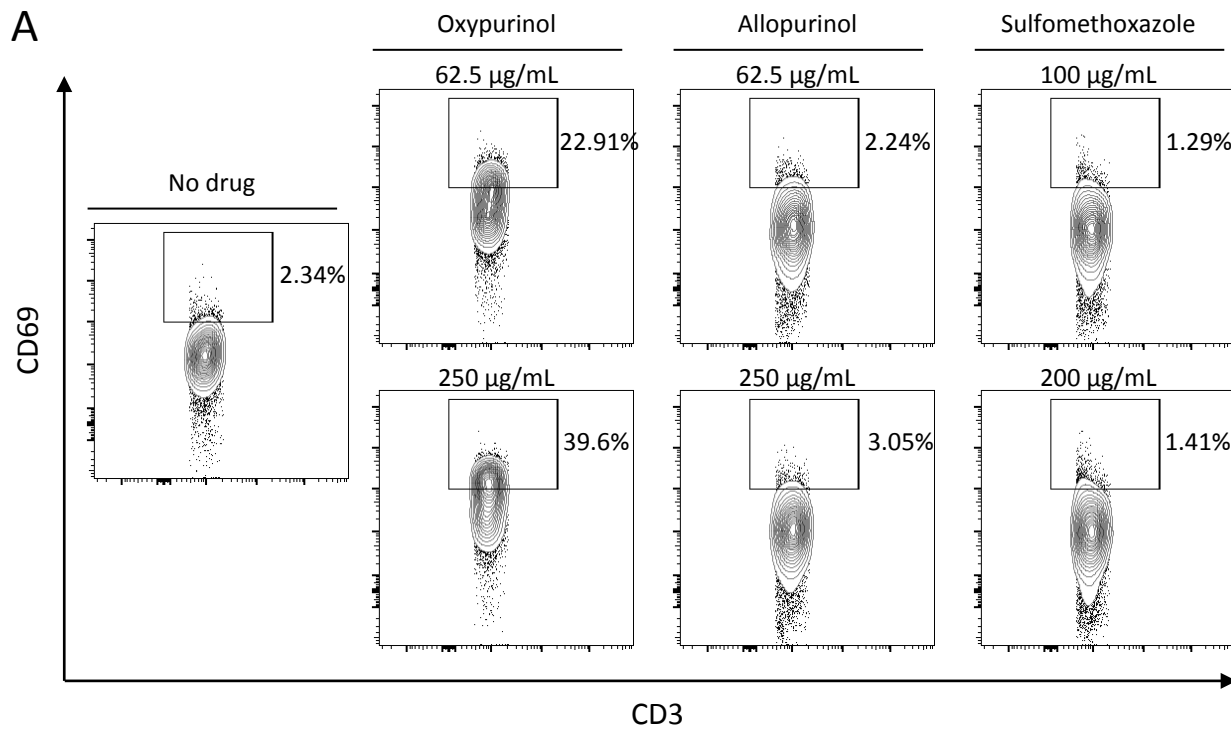


Figure S14

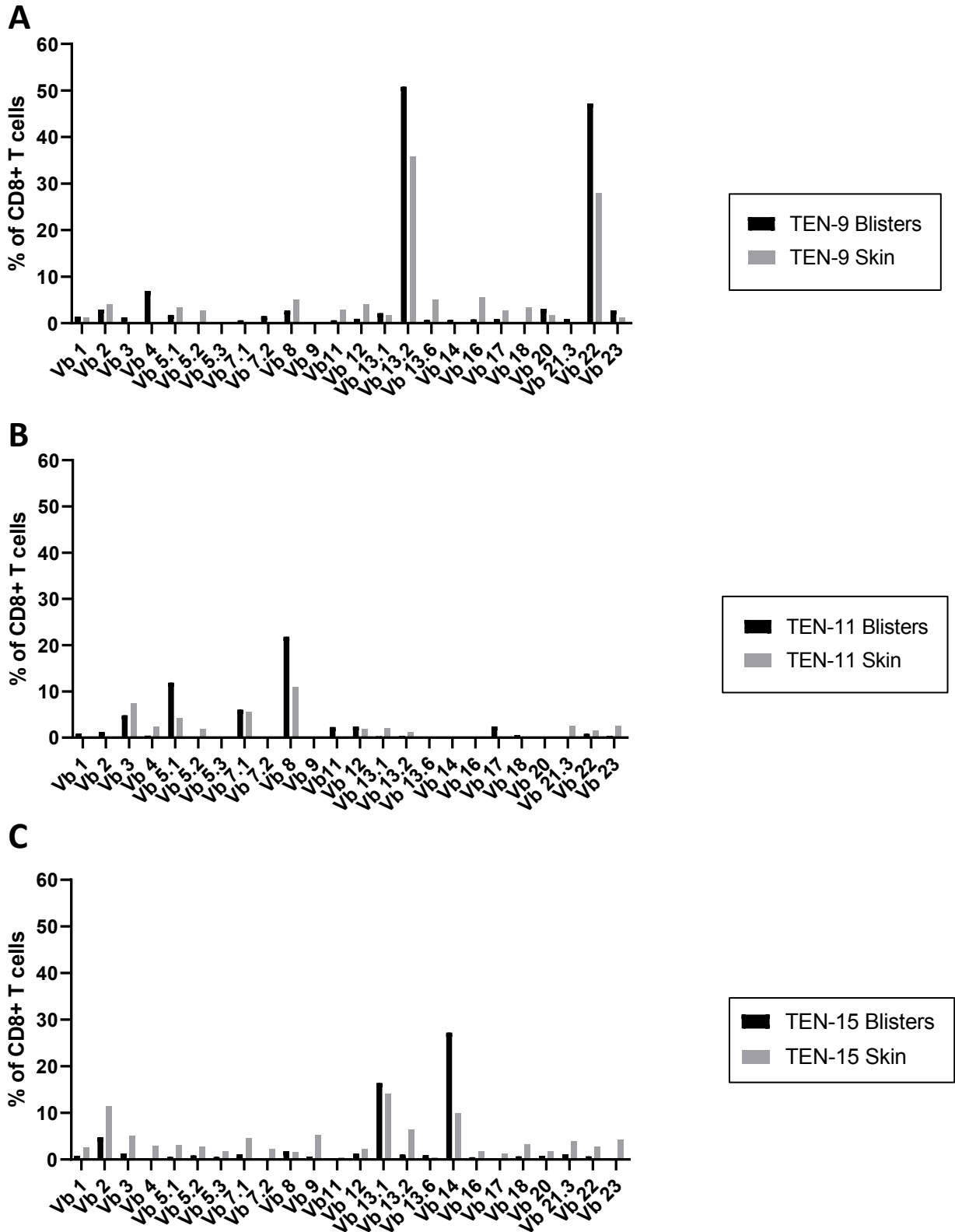


Figure S15

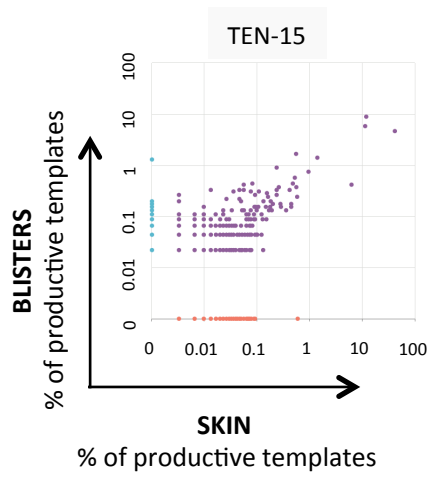
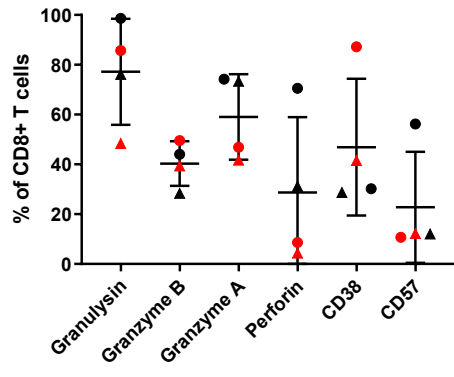
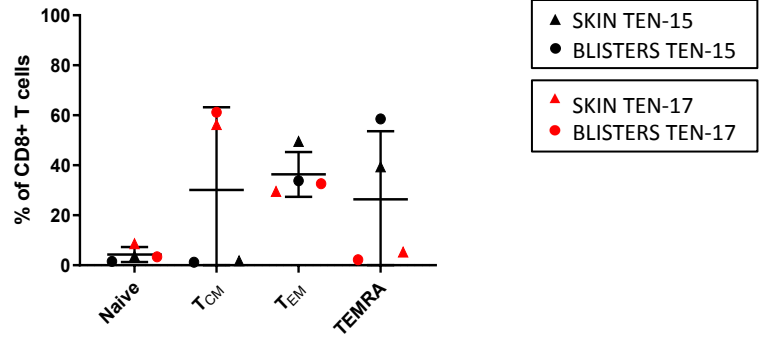


Figure S16

A**B****Figure S17**

Supplementary Figure legends

Figure S1. Lineage gating strategy used for supervised analysis of mass cytometry data.

Representative example of the gating strategy used to identify leucocyte lineages and T cell subpopulations in the blister, skin and PBMC samples from TEN, MPE and healthy donors. Cells were detected using iridium staining, and doublets and beads were excluded. Live (cisplatin negative (194 Pt)) CD45⁺ hematopoietic cells were then progressively subcategorized into different subpopulations: monocytes (CD14⁺), B cells (CD19⁺), conventional T cells (TCR $\alpha\beta$ ⁺), gamma delta T cells (TCR $\gamma\delta$ ⁺), NK cells (TCR $\alpha\beta$ -TCR $\gamma\delta$ -CD56⁺), conventional dendritic cells (cDC, CD11c+TCR $\alpha\beta$ -TCR $\gamma\delta$ -CD56⁻), invariant natural killer cells (iNKT, TCR $\alpha\beta^{\text{int}}$ TCRV α 24⁺) (53), CD4⁺ T cells (TCR $\alpha\beta$ +CD4⁺), CD8⁺ T cells (TCR $\alpha\beta$ +CD8 β ⁺), double positives (DP, TCR $\alpha\beta$ +CD4+CD8 β ⁺), double negatives (DN, TCR $\alpha\beta$ +CD4-CD8 β -TCRV α 7.2⁻) and MAIT cells (TCR $\alpha\beta$ +CD4-CD8 β -CD8 α \pm TCRV α 7.2⁺) (54).

Figure S2. Immunophenotyping of leucocytes present in TEN blisters and in adjacent skin samples.

The leucocytes isolated from different bullae or adjacent non-bullous inflammatory skin from 3 subjects with TEN (black, red or blue symbols) were analyzed by mass cytometry. Scatter plots depict percentages of conventional TCR $\alpha\beta$ ⁺ lymphocytes, gamma delta T cells, B lymphocytes, NK cells, monocytes or conventional dendritic cells in hematopoietic CD45⁺ cells (A) and percentages of CD8⁺, CD4⁺, double negative and double positive T cell subsets, as well as iNKT and MAIT cells in gated TCR $\alpha\beta$ ⁺ population (B). Mean frequencies \pm SD are also indicated.

Figure S3: Immunophenotyping of PBMCs from TEN, MPE and healthy donors.

The PBMCs from 7 TEN patients (A), 6 MPE patients (B) and 6 healthy donors (C) were analyzed by mass cytometry. Scatter plots depict percentages of conventional TCR $\alpha\beta$ ⁺ lymphocytes, gamma delta T cells, B lymphocytes, NK cells, monocytes or conventional dendritic cells in hematopoietic CD45⁺ cells (A1-C1), and percentages of CD8⁺, CD4⁺, double negative and double positive T cell subsets, as well as iNKT and MAIT cells in gated TCR $\alpha\beta$ ⁺ population (A2-C2). Mean frequencies \pm SD are also shown. The frequencies of each subset in TEN and MPE samples compared to healthy donor samples were not statistically different.

Figure S4: Minimal spanning tree magnification. All samples - Skin and PBMC of TEN, MEP and healthy donors.

High-dimensional cell analysis using FlowSOM was conducted, as in Figure 2, on concatenated CD8⁺ T cell data (300 cells/sample) obtained from both blister, skin and PBMC samples from TEN and MPE patients and healthy donors (as reported in Table S1). Minimal spanning tree

(with 100 nodes) and automatically subcategorized clusters (clusters A, B, C, D, E, F, G) are depicted. Each node includes phenotypically similar cells and the size of the node indicates the number of cell events. At the center of each node is represented a star chart. Each coloured star branch corresponds to the specific markers (CD45RA, CCR7, granzyme B (GzB), gA (GzA), granulysin (GNLY), perforin, CD27, CD38, CD56, CD57, CD107a, CD137, CD226, CD253, CD255, annexin A1) used for phenotypic comparison. The height of each star branch indicates the mean intensity: if the part reaches the border of the circle, the cells have a high expression for the marker.

Figure S5: Minimal spanning trees obtained after FlowSOM analysis of concatenated CD8+ T cell data from TEN, MPE and healthy donor samples. High-dimensional cell analysis using FlowSOM was conducted on concatenated CD8+ T cell data (300 cells/sample) from either blister, skin or PBMC samples from subjects with TEN (**A**), with MPE (**B**) and from healthy donors (**C**), as reported in **Table S1**.

Figure S6. FACS illustrations of the seven FlowSOM CD8+ T cell clusters. The 7 FlowSOM clusters (A-G) identified by high-dimensional analysis in Figure 2 were displayed for standard FACS plots visualization, using CCR7, CD45RA, granulysin (GNLY), CD38, CD57, granzyme A (GzA), CD27 and granzyme B (GzB) markers.

Figure S7: TCR V β repertoire usage in CD8+ and CD4+ T cell subsets isolated from the skin and PBMCs of healthy donors. The leucocytes isolated from the skin (**A & B**) and PBMCs (**C & D**) of 12 (HD-9 to HD-20) healthy donors were analysed by flow cytometry. Histograms depict percentages of the 24 TCR V β chains in gated CD8+ (**A & C**) and CD4+ (**B & D**) T cell subsets, using the IOTest[®] Beta Mark TCR V β

Repertoire Kit. Each round symbol represents a different subject. The red bar illustrates the threshold value from which TCR V β chains were considered as highly expanded (using Tukey's rule for the detection of outliers, i.e. $Q3 + 1.5 \times IQR$).

Figure S8: TCR V β repertoire usage in CD3+ T cells isolated from the skin of TEN, MPE and healthy individuals. The leucocytes isolated from the blister fluids of 13 subjects with TEN (**A**), the lesional skin of 5 subjects with MPE (**B**) and the healthy skin of 6 donors (**C**) were analysed by flow cytometry, as in **Figure 3**. Each symbol (triangles for TEN, squares for MPE, rounds for healthy donors) represents a different subject. The red bar illustrates the threshold value from which TCR V β chains

were considered as highly expanded (using Tukey's rule for the detection of outliers, i.e. $Q3 + 1.5 \times IQR$).

Figure S9: TCR V β repertoire usage in CD8+ and CD4+ T cell subsets isolated from PBMCs of TEN and MPE patients. PBMCs from 13 subjects with TEN (A & B) and 5 subjects with MPE (C & D) were analysed by flow cytometry. Histograms depict percentages of 24 TCR V β chains in gated CD8+ (A & C) and CD4+ (B & D) T cell subsets, using the IOTest[®] Beta Mark TCR V β Repertoire Kit. Each symbol (triangles for TEN, squares for MPE) represents a different subject. The red bar illustrates the threshold value from which TCR V β chains were considered as highly expanded (using Tukey's rule for the detection of outliers, i.e. $Q3 + 1.5 \times IQR$).

TEN-2 (both CD8 and CD4+ T cells; not done) and TEN-15 (CD4+ T cells; technical issue) data are not depicted in the scatter plots.

Figure S10: Clonotype nucleotide sequence overlap between blister and PBMC samples from TEN and MPE patients. Morisita-Horn similarity index heatmap depicts overlap metrics (provided by ImmunoSEQ Analyzer V.3.0) for each possible pair-wise percent sharing between all pairs of TEN and MPE samples. This was computed by averaging across the two ratios of shared sequencing reads for each sample. Blue squares illustrate low (<1%) or no reads sharing between samples, white being intermediate and red being the highest level of sharing. Figures at the center of each square indicate percent sharing.

Figure S11: Clonotype amino acid overlap between blister and PBMC samples from TEN and MPE patients. Morisita-Horn similarity index heatmap depicts overlap metrics (provided by ImmunoSEQ Analyzer V.3.0) for each possible pair-wise percent sharing between all pairs of TEN and MPE samples. This was computed by averaging across the two ratios of shared sequencing reads for each sample. Blue squares illustrate low (<1%) or no reads sharing between samples, white being intermediate and red being the highest level of sharing. Figures at the center of each square indicate percent sharing.

Figure S12: Frequency and TRBV usage of the highly expanded TCR β clonotypes in PBMC samples. The leucocytes isolated from the PBMCs of 15 subjects with TEN and 5 subjects with MPE were evaluated using HTS of the TCR. Pie charts illustrate frequencies of the 5 most expanded TCR β clonotypes (measured as % of unique CDR3 sequence among all productive rearrangements within a sample). Colours indicate the respective TRBV usage of each TCR β clonotypes. Grey indicates the

remaining clonotypes found in the same sample. TCR β chain amino acid sequences are also provided. Cross-reference for the corresponding anti-V β mAb nomenclature is also provided.

Figure S13: Frequency of the most expanded TCR β clonotypes in the blood and the blisters or skin of TEN and MPE patients. Comparison of TCR β -chain CDR3 sequences in paired blister, skin and PBMC samples. Each dot of the heat map scatters represent one clone and the percentage of total productive templates of this given clone in skin and PBMC samples of TEN or MPE patients. Clones uniquely found in skin samples are located on the x-axis in red, clones uniquely present in PBMCs are located on the y-axis in blue; and clones found in both samples are in violet. Most expanded clones in the blood are shown with an arrow (such clones were used for correlation calculations in Figure 6).

Figure S14: FACS plot illustration of drug-induced activation of TCR $\alpha\beta$ Skw3 transductants. Skw3 cell lines engineered for the expression of TCRs bearing V α and V β chains from the top clone found in patient TEN-3 were stimulated *in vitro* with EBV-transformed B cells in presence of graded doses of different drugs (oxypurinol, allopurinol and sulfamethoxazole), or left unpulsed (no drug). Contour plots represent the percentage of CD69 expression in CD3+Skw3 transductants (A). Histograms represent the geometric mean fluorescence intensity (GMFI) of CD69 marker. Each color represents a different stimulatory condition. The GMFI values are listed above each histogram (B).

Figure S15: TCR V β repertoire usage in T cell subsets isolated from blister and adjacent skin samples of patients TEN-9, -11 and -15. The leucocytes isolated from the blister and adjacent skin samples of 3 subjects with TEN (TEN-9, TEN-11 and TEN-15) were analyzed by flow cytometry. Histograms depict percentages of 24 TCR V β chains in gated CD8+ T cell subsets, using the IOTest[®] Beta Mark TCR V β Repertoire Kit.

Figure S16: Frequency of the most expanded TCR β clonotypes in paired blister and adjacent skin samples of patient TEN-15. Comparison of TCR β -chain CDR3 sequences in paired blister and adjacent skin samples. Each dot of the heat map scatters represents one clone and the percentage of total productive templates of this given clone in respective sample. Clones uniquely found in adjacent skin sample are located on the x-axis in red, clones uniquely present in blister sample are located on the y-axis in blue; and clones found in both samples are in violet.

Figure S17: Immunophenotyping of leucocytes present in TEN blisters and adjacent skin samples.

The leucocytes isolated from the blister (dots) and adjacent skin (triangles) samples of 2 subjects with TEN (TEN-15 in black and TEN-17 in red) were analyzed by mass cytometry. Scatter plots depict percentages \pm SD of Granulysin, Granzyme B, Granzyme A, Perforin, CD38 and CD57 markers in total CD8⁺ T cells (**A**). Frequencies \pm SD of naïve (CD45RA+CCR7⁺), central memory T cells (T_{CM}; CD45RA-CCR7⁺), effector memory T cells (T_{EM}; CD45RA-CCR7⁻) and effector memory T cells expressing CD45RA (T_{EMRA}; CD45RA+CCR7⁻) in total CD8⁺ T cells are also shown (**B**).