

Supplemental Table 1: T1D Patient Information.

T1D Subject	Age	Duration of disease (days)	C-peptide*
K743T1D	33	387	D
K685T1D	18	713	NA
K276T1D	10	883	NA
K787T1D	41	140	D
K807T1D	19	468	NA
K814T1D	47	541	D
K843T1D	12	383	D
K847T1D	26	161	D
K151T1D	16	1653	NA
K180T1D	15	2482	NA
K877T1D	27	270	D
K878T1D	12	240	D
K899T1D	25	70	D
K278T1D	59	8472	ND
K454T1D	27	5110	NA

*random serum C-peptide was obtained within 6 months of the cellular assay.

D: detectable at >0.05 ng/mL; ND: not detectable at limit of detection = 0.05 ng/mL; NA: not measured

Supplemental Table 2: Frequency of epitopes identified from oligoclones

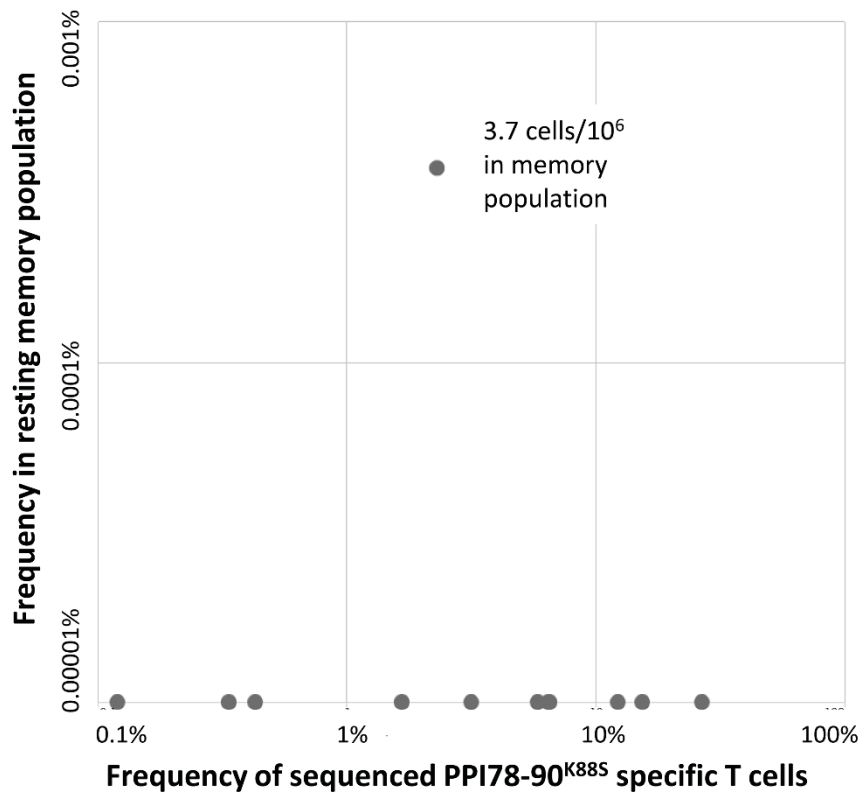
T1D Subject	# of oligo-clones generated	Name of Peptide	# of oligo-clones positive
K787T1D	4 oligo-clones generated from 41 CD38+ cells	PPI78-90 ^{K88S}	4
		GADp15	3
		GADp45	1
		GADp47	1
		GADp48	1
		GADp55	1
		Zn8Tp28	1
		ZnT8p36	1
		Igp39	1
		ChgA: NEI	
K276T1D	5 oligo-clones from 53 CD38+ cells	PPI78-90 ^{K88S}	5
		GADp23	1
		ZnT8p28	2
		Igp31	1
		ChgA: NEI	
K743T1D	6 oligo-clones generated from 62 CD38+ cells	PPI78-90 ^{K88S}	6
		GADp28	1
		GADp29	1
		GADp32	1
		GADp34	1
		GADp35	1
		ZnT8p28	4
		Igp23	1
ChgA: NEI			
K877T1D	1 oligo-clone from 4 CD38+ cells	GADp70	1
K877T1D	4 oligo-clones from 40 resting memory cells	PPI78-90 ^{K88S}	3
		GADp10	1
		GADp11	1
		ZnT8p28	1
		IGRP: NEI	
ChgA: NEI			

NEI: no epitope identified

Supplemental Table 3: Top 10 TCR Vbeta VDJ sequences of PPI₇₈₋₉₀^{K88S} specific T cells isolated from CD45RO+CD38+ oligoclones.

Nucleotide	Amino Acid	TCRB V region	TCRB D region	TCRB J region	Frequency
TGTGCCAGCAGCCCCAGG GTACTACGGGAAACACCAT ATATTTT	CASSPQGT GNTIYF	V07-09	D01-01*01	J01-03*01	26.9%
TGTGCCAGCTCACCTAAAA TGTATGAGCAGTTCTTC	CASSPKMY EQFF	V18-01*01	D02-01	J02-01*01	15.4%
TGTGCCAGCAGCTTGGGCC GGGCCGGGGCGGGGAATCA GCCCCAGCATTTT	CASSLGRA GAGNQPQH F	V07-08*01	D02-01*01	J01-05*01	12.2%
TGTGCCAGCAGCTCCCCGA GGTCTCCAGCGGGGGGGCG GTACAATGAGCAGTTCTTC	CASSPRSP AGGRYNEQ FF	V09-01	D02-01*01	J02-01*01	6.5%
TGTGCCAGCAGCGCGGCTG CTAGCGGGGGGCCAGTCAG GGTCACAGATACGCAGTAT TTT	CASSAAAS GGPVRVTD TQYF	V05-04*01	D02-01*01	J02-03*01	6.5%
TGTGCCAGCAGCTTTTGGGA CGGGGGGGAATCAGCCCCA GCATTTT	CASSFWTG GNQPQHF	V07-09	D02-01*01	J01-05*01	5.9%
TGTGCCAGCAGCCTAGACA GAATTAATGAAAAACTGTT TTTT	CASSLDRIN EKLFF	V11-02*02	D01-01*01	J01-04*01	3.2%
<i>TGTGCCAGCAGTTACGGAAT AGGGAGGGCAGATACGCAGT ATTTT</i>	<i>CASSYGIGRA DTQYF</i>	<i>V06-06</i>	<i>D02-01*02</i>	<i>J02-03*01</i>	2.3%
TGTGCCAGCAGCTTCGGGA CGGGGAGAAGGGATGGCTA CACCTTC	CASSFGTGR RDGYTF	V07-09	unresolved	J01-02*01	1.7%
TGTGCCAGCAGCTTGCAGG GAACGGCTGGAAACACCAT ATATTTT	CASSLQGT AGNTIYF	V07-09	D01-01*01	J01-03*01	0.4%

Italic indicates this sequence is also detected in the memory population of T cells with a frequency of $3.7/10^6$.



Supplemental Figure 1. Determining *in vivo* proliferation and persistence of PPI₇₈₋₉₀^{K88S} specific T cells.

PPI₇₈₋₉₀^{K88S}-specific T cells identified by CD154 epitope mapping from subject K276T1D were enriched and selected and TCR Vbeta chains sequenced. Plot includes top 10 T cells with unique rearranged CDR3 region according to the frequency of their sequence reads. X-axis: T Cell frequency in resting memory. Y-axis: Frequency from TCR Vbeta sequencing of memory (CD45RO+) T cells obtained 4 months after CD154 epitope mapping assay. One identical rearranged CDR3 region with high counts was identified in the memory fraction of PBMC.