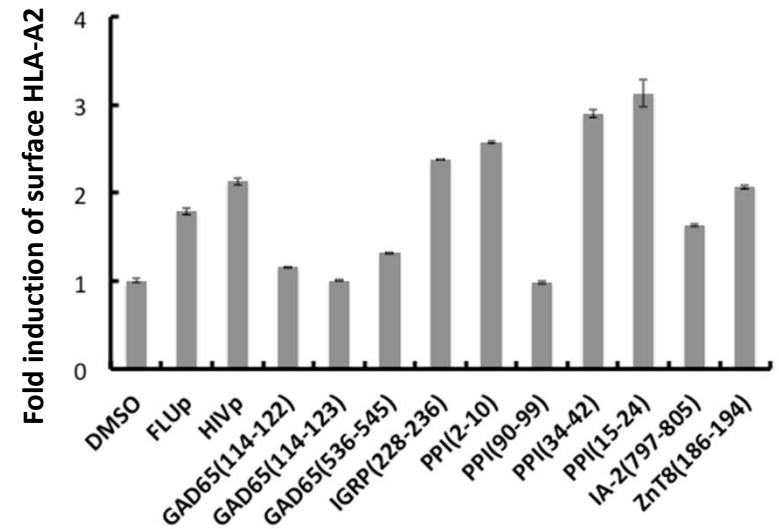


A.

HLA-A2 associated peptide	Sequence
<u>GAD(114-122)</u>	<u>VMNILLQYV</u>
<u>GAD(114-123)</u>	<u>VMNILLQYVV</u>
<u>GAD(536-545)</u>	<u>RMMEYGTMTV</u>
<u>PPI(2-10)</u>	<u>ALWMRLLPL</u>
<u>PPI(15-24)</u>	<u>ALWGPDAAA</u>
<u>PPI(34-42)</u>	<u>HLVEALYLV</u>
<u>PPI(90-99)</u>	<u>GIVEQCCTSI</u>
<u>IGRP(228-236)</u>	<u>LNIDLLWSV</u>
<u>IA-2(797-805)</u>	<u>MVWESGCTV</u>
<u>ZnT8(186-194)</u>	<u>VAANIVLTV</u>
<u>EBV BMLF-1(280-288)</u>	<u>GLCTLVAML</u>
<u>Influenza M1(58-66)</u>	<u>GILGFVFTL</u>
<u>HIV-1 p17 Gag(77-85)</u>	<u>SLYNTVATL</u>

B.

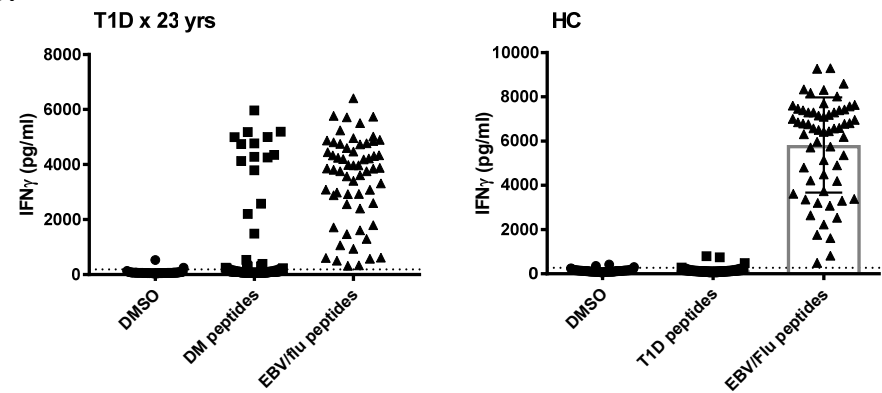


Supplemental Figure 1: Peptides used in this study A Peptide sequences. B Stability of HLA-A2 with diabetes antigen peptides in a T2 assay. The fold induction of HLA-A2 was measured by flow cytometry for each the designated peptides.

A.

Fraction	Peptide	Exp. 1	Exp. 2	p-value
CD45RO+	EBVp+FLUp	21/33	22/34	1.00
CD45RA+	EBVp+FLUp	5/58	2/40	0.70

B.

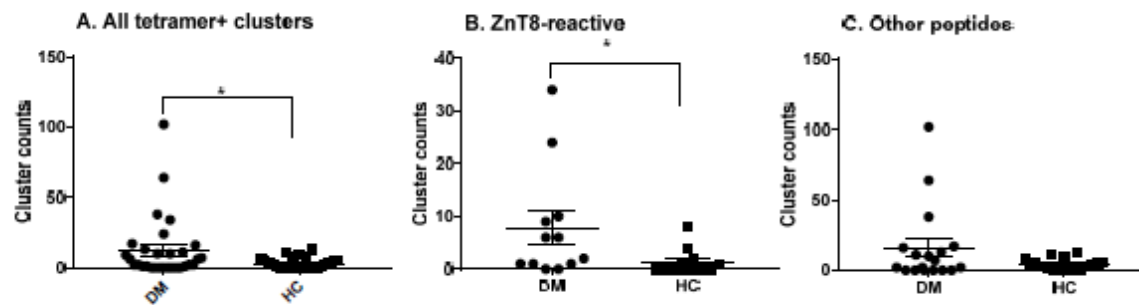


Supplemental Figure 2: Library performance: A. Reproducibility of libraries to EBV/FLU peptides. CD8<sup>+</sup> T cell libraries were prepared from the same healthy donor in 2 independent experiments. Positive wells/total wells are shown in the table after stimulation with indicated peptides. Frequency of positive wells were compared using Fisher's exact test. There was no significant difference on each condition between the experiments ( $p=0.70-1.00$ ). B. Examples of results from libraries from a patient with T1D for 23 years and a HC subject. Each symbol represents a library well.

A.

Isotope	Marker
141Pr	CCR6
142Nd	CD19
144Nd	CCR5
145Nd	CD4
146Nd	CD8a
147Sm	Tetramer-147
148Nd	CD28
149Sm	CD25
151Eu	CD5
152Sm	BCL2
153Eu	CCR4
154Gd	CXCR5
155Gd	CD27
156Gd	CXCR3
158Gd	CD3
159Tb	CD57
160Gd	T-bet
161Dy	CTLA4
162Dy	FoxP3
164Dy	CD45RO
165Ho	Tetramer-165
166Er	Tetramer-166
167Er	Tetramer-167
168Er	CD127
169Tm	CD45RA
170Yb	CCR7
171Yb	CD45-171
174Yb	CD69
175Lu	PD-1
176Yb	Perforin
191Ir+193Ir	DNA
195Pt	Cell-ID™ cisplatin
198Pt	CD45-198

B.



Supplemental Figure 3 CyTOF analysis: A. Antibodies and probes used for CyTOF analysis. B. Frequency of clusters of tetramer+ cells by CyTOF from the SAUCIE analysis. \*p<0.05 by Mann-Whitney

Amino Acid	TCRVbeta	sum (%)	T1D63				T1D69		T1D116	
			#1	#16	#60	#81	#2	#4	#3	#23
<b>CASSLGVGIGGYGYTF</b>	TCRBV27-01*01	95.4	4.7	55.5	2.4	32.7	0	0	0	0
CASRVAGGPEETQYF	TCRBV28-01*01	22.4	0	0	0	0	0	22.4	0	0
CASSEAGGNEQYF	TCRBV02-01*01	19.5	0	0	0	0	0	0	0	19.5
CASSQVQGPGYGYTF	TCRBV14-01*01	17.8	0	0	0	0	17.8	0	0	0
<b>CATYSSSYEQYF</b>	TCRBV27-01*01	14.4	0	0	0	0	0.1	14.3	0	0
CASSITGEDTQYF	TCRBV28-01*01	8.3	0	0	0	0	0	0	0	8.3
CASSLVGWGDEQFF	TCRBV07-03*01	8.1	0	0	0	0	0	0	0	8.1
CASSLGGPEQYF	TCRBV07-02*01	7.0	0	0	0	0	0	0	7.0	0
<b>CASSLSSAYNEQFF</b>	TCRBV27-01*01	6.8	0	0	0	0	5.4	1.4	0	0
CASSQALSGDYGTYF	TCRBV04-02*01	5.9	0	0	0	0	0	5.9	0	0
CASRWGSDQPQHF	TCRBV19-01	5.2	0	0	0	0	0	0	0	5.2
CASSSSRFGLEQYF	TCRBV05-04*01	5.1	0	0	0	0	5.1	0	0	0
CASSNSWGEGQQFF	TCRBV07-08*01	4.8	0	0	0	4.8	0	0	0	0
CASSVASSTQGDGYTF	TCRBV09-01	4.3	0	0	0	0	4.3	0	0	0
CASSLRREIGPEAFF	TCRBV28-01*01	4.2	0	0	0	0	0	0	0	4.2
CASSLGQDDSGNTIYF	TCRBV07-06*01	4.0	4.0	0	0	0	0	0	0	0
CASKQTGGNSPLHF	TCRBV19-01	3.7	0	0	0	0	0	0	0	3.7
CASSVRASGNTIYF	TCRBV09-01	3.6	0	0	0	3.6	0	0	0	0
CASSWTVNEQFF	TCRBV19-01	3.3	0	0	0	0	0	0	0	3.3
CSAPPVGGQYTEAFF	TCRBV20	3.0	0	0	0	0	0	0	3.0	0

Supplemental Table 1: TCR CDR sequences in positive wells from 3 individuals with T1D. Each column identifies a patient and the subcolumns identify a positive well. Sequences that were present at a frequency of at least 0.05% are displayed. The Vbeta sequence is shown. Bolded sequences are those found in more than 1 well. The sum represents the proportion of the total sequences represented by the identified sequences.