

Figure S1. Magnitude of HLA-B*42:01-restricted CD8+ T-cell responses. (A) Magnitude of HLA-B42:01-restricted CD8+ T-cell responses directed against 'protein-18mer peptide-optimal epitope name' OLPs in *ex vivo* IFN γ assays for HLA-B*42:01+ individuals lacking HLA-B*07:02/39:10/42:02/81:01 co-expression (n = 154). (B) Correlation between CD8+ T-cell response magnitude and % targeting frequency.

Fig S1

Fig S2

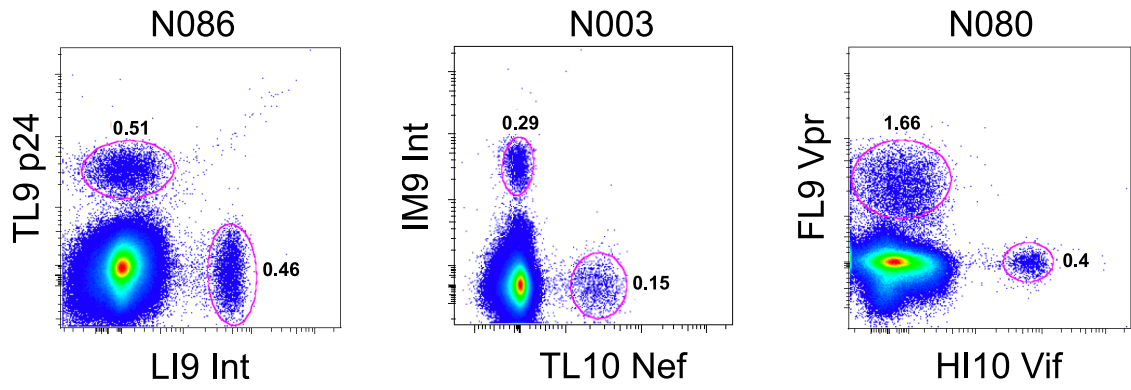


Figure S2. HLA-B*42:01 tetramer staining of epitope-specific CD8⁺ T-cell populations for TCR sequencing. Six different HLA-B*42:01 tetramers were used to sort six different HLA-B*42:01-restricted CD8⁺ T-cell populations as depicted. Representative dual stains are shown for three different donors. Plots are gated on live CD3⁺ CD8⁺ events.

Table S1. Peptide-HLA-B*42:01 binding affinity and stability.

Epitope	Sequence	Binding score K _D (nM) ^b	Binding half-life (hrs) ^c
Gag-RM9	RPGGKKHYM ^a	7.0	6.2
Gag-SV9	SPRTLNAWV ^a	2.0	2.0
Gag-TL9	TPQDLNTML	82.0	3.6
Gag-GL9	GPSHKARVL	24.0	1.9
Gag-GF9	GPKRIVKCF ^a	8.0	11.0
RT-LI11	LPQGWKGSPAI ^a	15.0	1.1
RT-SM9	SPAIFQSSM ^a	3.0	12.0
RT-YL9	YPGIKVRQL ^a	3.0	6.2
Int-LI9	LPPIVAKEI	7.0	5.0
Int-IM9	I IKDYGKQM ^a	19.0	13.5
Nef-RM9	RPQVPLRPM	3.0	22.4
Nef-TL10	TPGPGVRYPL	1.0	14.3
Vpr-FL9	FPRPWLHGL	1.0	11.6
Vif-HI10	HPKVSSEVHI ^a	38.0	17.1
Env-RI10	RPNNNTRKSI ^a	9.0	13.2
Env-IF9	I PRRIRQGF ^a	23.0	7.3

^a Novel HLA-B*42:01-restricted epitopes.

^b Mean of two experiments.

^c Mean of two experiments.

Table S2. Clonal analysis of HLA-B*42:01-restricted Gag-RM9-specific CD8⁺ T-cell populations.

Subject (ddmmyy)	Epitope	CD8 ⁺		CD4	TRBV	CDR3	TRBJ	Freq (%)
		Tet ⁺	pVL					
R014 (130907)	RM9	0.2	1177	300	10-3	CAISGGEYNQPQH	1-5	98.5
HLA-A*30:01/33:01					2	CASSDKAGTDTQY	2-3	1.5
HLA-B*42:01/57:03							count	(65)
HLA-C*17:01/18:01								
Number of cells sorted	428							

Columns show: HLA genotyping data below the subject identifier with sample date in brackets; targeted epitope; frequency of tetramer⁺ (Tet⁺) cells in the total CD8⁺ T-cell population; plasma viral load (pVL, HIV RNA copies/ml of plasma); CD4⁺ T-cell count (CD4, cells/μl blood); TRBV usage; CDR3 amino acid sequence; TRBJ usage; clonotype frequency (%).