



Figure S1: Frequencies of CD8⁺ T cell responses in HSV-seropositive asymptomatic individuals: Schematic representation showing the relative location within HSV-1 VP11/12 of the potential CD8⁺ T cell epitopes studied. (A) Sequence of HSV-1 (strain 17) VP11/12 regions carrying potential HLA A*0201 (HLA- A*0201)-restricted T cell epitopes (amino acid in bold) were predicted using computer-assisted algorithms based on known HLA/peptide/TCR interactions, as described in *Materials and Methods*. (B) The amino acid sequence, in a single letter code, and the peptide positions based on the 716-aa sequence of VP11/12 are shown. The high-affinity immunodominant epitopes identified in this study are shown in bold.

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Comparative analysis of the sequences of HSV-1 immuno-dominant CD8⁺ T cell VP11/12 epitopes between the strains of HSV-1, HSV-2 and across other human herpes viruses

Virus Strain (Accession number)	VP11/12 ₆₆₋₇₄ ^a	VP11/12 ₂₂₀₋₂₂₈ ^a	VP11/12 ₇₀₂₋₇₁₀ ^a
HSV-1			
Strain 17(P10230)	FLTCTDRSV	RLNELLAYV	ALSALLTKL
Strain F (P08314)	FLTCTDRSV	RLNELLAYV	ALSALLTKL
Strain RH2 (LON6A1)	FLTCTDRSV	RLNELLAYV	ALSALLTKL
HSV-2			
Strain HG52 (P89466)	FLTGADRSV	RLSELLAYV	ALSALLTKL
Strain 186 (I6U4Y7)	FLTGADRSV	RLSELLAYV	ALSALLTKL
VZV			
Strain Dumas (P09264)	FLDVVDARV	RVQEIAAYT	AASKRYTPL
Strain V-Oka (Q4JQW3)	FLDVVDARV	RVQEIAAYT	AASKRYTPL
CMV			
Strain AD169 (P16783)	LLTCVMRGY	GITSLITCV	LVTALKAKR
Strain Merlin (F5HA93)	LLTCVMRGY	EDNELVTAL	GITSLITCV

^a The identical amino acids between HSV-1, HSV-2 and across other human herpes viruses are bolded.

Table S1: Comparative analysis of the sequences of HSV-1 VP11/12 CD8⁺ T cell epitopes between the strains of HSV-1 and HSV-2 and across other human herpes viruses. The amino acid residues that are conserved across other human herpesviruses are shown in bold.