A

MSAREPAGRR RRASTRPRAS PVADEPAGDG VGFMGYLRAV FRGDDDSELE ALEEMAGDEP PVRRRREGPR ARRRRASEAP PTSHRRASRQ RPGPDAARSQ SVRGRLDDDD EVPRGPPQAR QGGYLGPVDA RAILGRVGGS RVAPSPLFLE ELQYEEDDYP EAVGPEDGGG ARSPPKVEVL EGRVPGPELR AAFPLDRLAP QVAVWDESVR SALALGHPAG FYPCPDSAFG LSRVGVMHFA SPDNPAVFFR QTLQQGEALA WYITGDGILD LTDRRTKTSP AQAMS**FLADA VVRL**AINGWV CGTRLHAEAR GSDLDDRAAE LRRQFASLTA LRPVGAAAVP LLSAGGLVSP QSGPDAAVFR SSLGSLLYWP GVR**ALLDRDC RV**AARYAGRM TYLATGALLA RFNPDAVRC**V LTREAAFLGR VLDVL**AVMAE QTVQWLSVVV GARLHPHVHH PAFADVAREE LFR**ALPLGSP AV**VGAEHEAL GDTAARRLLA NSGLNA**VLGA AVYALHTALA TV**TLKYARAC GDAHRRRDDA AATRAILAAG LVLQ**RLLGFA DTVV**ACVTLA AFDGGFTAPE VGTYTPLRYA CVLRATQPLY ARTTPAKFWA DVRAAAEHVD LRPASSAPRA PVSGTADPAF LLKDLEPFPP APVSGGSVLG PRVRVVD**IMS QFRKLL**MGDE GAAALRAHVS GRRATGLGGP PRP

B

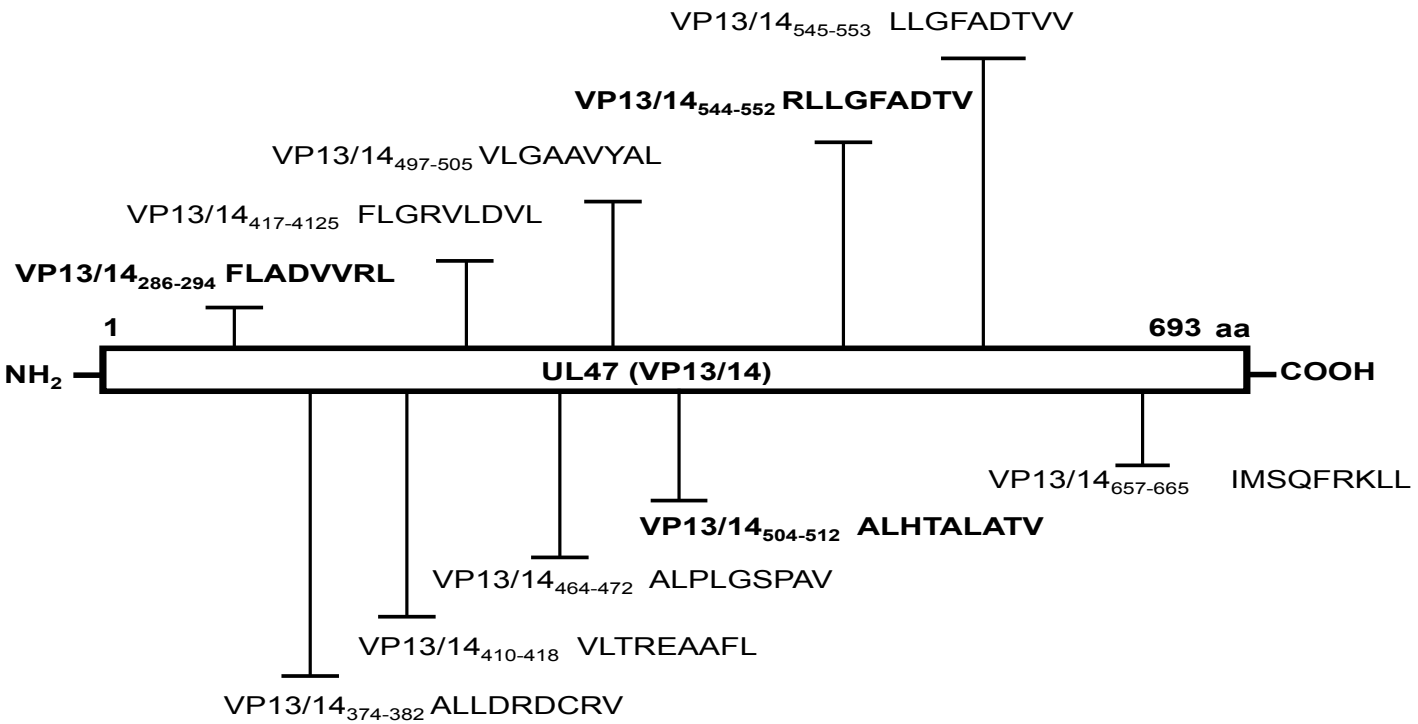

Figure S1: **Schematic representation showing the relative location within HSV-1 VP13/14 of the potential CD8+ T cell epitopes studied.** (A) Sequence of HSV-1 (strain 17) VP13/14 regions carrying potential HLA A*0201 (HLA- A*0201)–restricted T cell epitopes (amino acid in bold) were predicted using computer-assisted algorithms based on known HLA/peptide/TCR interactions. B) The amino acid sequence, in a single letter code, and the peptide positions based on the 693-aa sequence of VP13/14 are shown. The high affinity immuno-dominant epitopes identified in this study are shown in **bold**.

Srivastava *et. al.* Figure S2

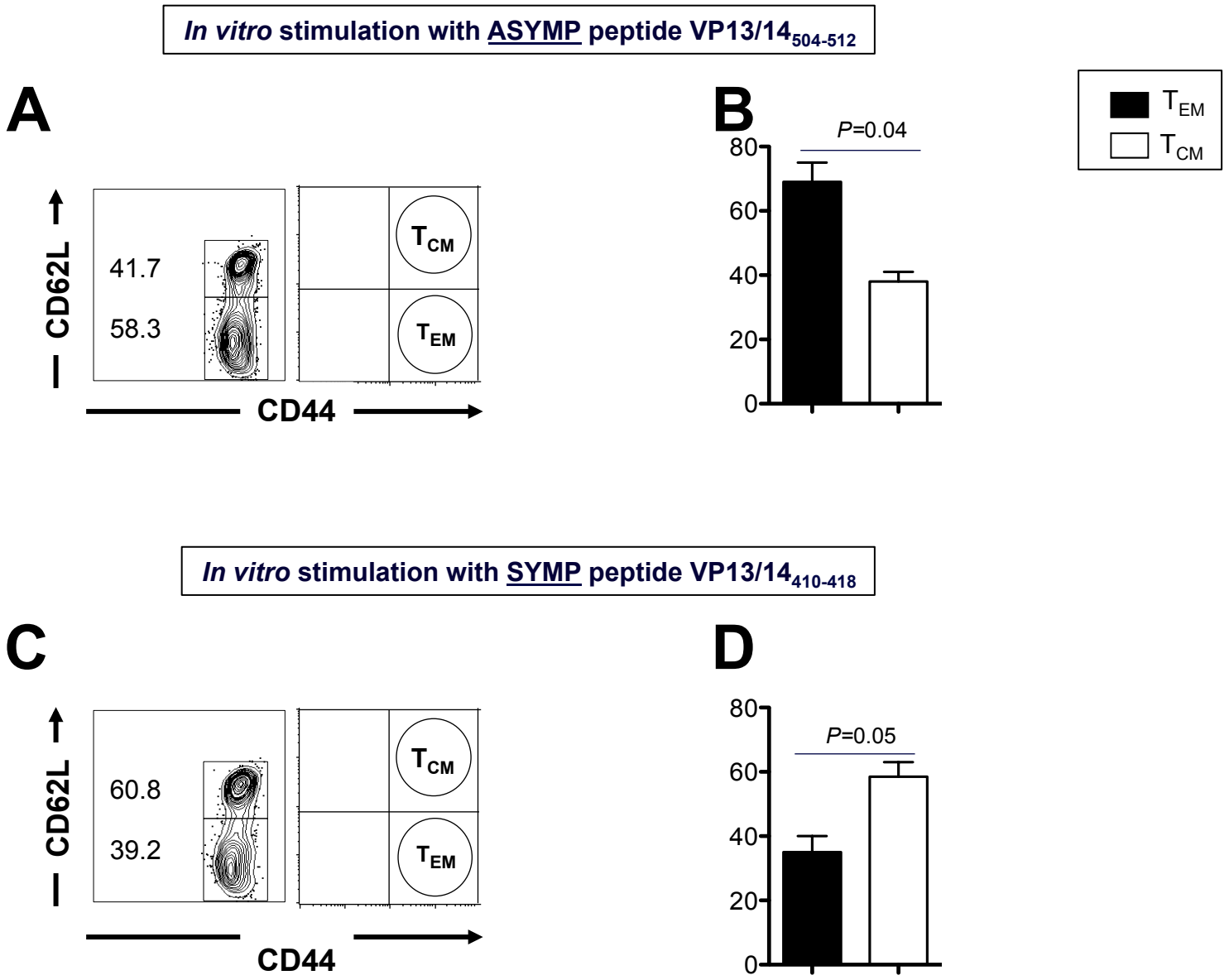

Figure S2: **More CD8$^+$ T_{EM} cells detected in cells stimulated with VP13/14 specific ASYMP epitopes compared to more CD8$^+$ T_{CM} cells detected in cells stimulated with SYMP epitopes.** We compared the T_{EM}/T_{CM} phenotypes of enriched CD8$^+$ T cells, following *in vitro* stimulation with VP13/14 specific SYMP or ASYMP peptides (**A** and **C**) Representative FACS data of the frequencies of CD44^{high}CD62L^{low}CD8$^+$ T_{EM} cells and CD44^{high}CD62L^{high}CD8$^+$ T_{CM} cells following *in vitro* stimulation with either ASYMP or SYMP peptide epitopes. (**B** and **D**) Average frequencies of CD44^{high}CD62L^{low}CD8$^+$ T_{EM} cells and CD44^{high}CD62L^{high}CD8$^+$ T_{CM} cells following *in vitro* stimulation with either ASYMP or SYMP peptide epitopes. The indicated *P* values, calculated using unpaired *t*-Test, show statistical significance between the T_{EM}/T_{CM} phenotypes.

Comparative analysis of the sequences of HSV-1 VP13/14 immuno-dominant CD8$^+$ T cell epitopes between the strains of HSV-1, HSV-2 and across other human herpes viruses

Virus Strain (Accession number)	VP13/14$_{286\text{-}294}$	VP13/14$_{504\text{-}512}$	VP13/14$_{544\text{-}552}$
HSV-1			
Strain 17(P10231)	**FLADAVVRL**[a]	**ALHTALATV**[a]	**RLLGFADTV**[a]
Strain F (P08313)	**FLADAVVRL**	**ALHTALATV**	**RLLGFADTV**
Strain RH2 (LON5H7)	**FLADAVVRL**	**ALHTALATV**	**RLLGFADTV**
HSV-2			
Strain HG52 (P89467)	**FL**V**DA**I**VR**V	**ALHTALATV**	**RLLG**L**ADTV**
VZV			
Strain DUMAS (P09263)	**FL**L**DA**A**IR**I	I**LS**T**A**ACAI	**R**V**LG**H**A**NLL
Strain V-Oka (Q4JQW4)	**FL**L**DA**A**IR**I	I**LS**T**A**ACAI	**R**V**LG**H**A**NLL
CMV			
Strain AD169 (P16784)	**FL**F**D**HRR**RL**	HR**H**R**ALA**PM	**RLL**DLTQM**V**
Strain TOWNE (B9VXL5)	**FL**F**D**HRR**RL**	HR**H**R**ALA**PM	**RLL**DLTQM**V**

[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 VP13/14 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 herpes viruses are shown in **bold**.