Supplemental 1 Information:

HLA peptide RP-HPLC separation:

Peptides were separated by reverse phase HPLC with a 4 um, 90 A, 2 x 150 mm Jupiter Proteo C12 column (Phenomenex, Torrance, CA) on a Paradigm MG4 system (Michrom Bioresources, Auburn, CA) using an CH3CN gradient as follows: 2% B for 11 min. (80 µl/min), 2-5% B in 0.02 min (80-160 µl/min), 5-40% B in 40 min (160 µl/min), and 40-80% B in 20 min (160 µl/min). Composition of solvents was as follows: Solvent A: 98% H20, 2% CH3CN, and 0.1% TFA (trifluoroacetic acid) and Solvent B: 95% CH3CN, 5% H20, and 0.08% TFA. Approximately 250 µg of total peptide was separated into 120 0.7 minute fractions with forty fractions (numbers 40-80) containing peptide. UV absorbance was monitored at 215 nm. Consecutive and identical peptide separations were performed for drug treated and untreated B*57:01 peptide-batches.

Liquid chromatography-mass spectrometry analysis

Fractions #50, 60, and 70 (at 35, 43 and 49 minutes) from untreated and abacavir-treated RP-HPLC samples were lypholized, resuspended and then analyzed with an Agilent 1260-HPLC-Chip/6520-Q-TOF mass spectrometry (MS) using a Zorbax 300SB-C18-150mm Chip. Solvent-A was 0.1% formic acid in water and solvent-B was 0.1% formic acid in 95% acetonitrile. QTOF VCap and fragmentor were 1,850 V and 175 V, respectively. The peptide mixtures were reconstituted with 25 µL of solvent-A. 0.5 µL was loaded onto the enrichment column in the chip at a flow rate of 3 µL/min in 3% B, then separated at 0.6 µL/min with a linear gradient, 3-63% B, in 60 minutes followed by 63-100%B in 10 minutes and held for 5 min additional minutes. Post run time was 10 minutes at 3% B to allow for column re-equilibration. The MS scan range was 280-3,200 *m/z* and resolution of 15,000 at 1,222 *m/z*. Selected compounds were

subjected to targeted MS/MS fragmentation using either a ramped collision energy setting with slope 3 and offset 2 (Collision Energy = slope × m/z /100 + offset), or a fixed energy of 30 V and 25 V.

Data analysis and database search

To select the peptides of interest for sequencing, all samples were analyzed in triplicate in MS only mode. The 50 most abundant compounds were extracted by using the "Find Compound by Molecular Feature" function of Agilent MassHunter Quanlitative Analysis Software (version B.03.01) with the following settings: extraction input data range restricted to 290-2,000 *m/z*; extraction of peaks with heights >= 1,000 counts for fraction 50 and 5,000 counts for fractions 60, 70 to ensure over 50 compounds been extracted from each run; isotopes groups with peak spacing ± 0.0025 *m/z* and within 7.0 ppm were allowed using an isotope model for peptides, default charge states were limited to a maximum of 15. The top 50 compounds extracted from all triplicate runs were analyzed manually based on their mass, and only those present in all 3 runs within a mass range of 600-1700 Da (a range covering all possible 9-mer peptides) and within 5 ppm error were selected to pull out common peptides or unique peptides present in the Abacavir-treated samples. The unique peptides were further narrowed down to those also absent from the all-compound list for the untreated sample extracted from any of triplicate runs using a much wider "Find Compound by Molecular Feature" setting: extraction of peaks with height >= 100 counts; no limitation in the compound filters and extraction input data range.

Targeted MS/MS data was analyzed with Agilent Spectrum Mill MS Proteomics Workbench software (version Rev A.03.03.084 SR4), searched against SwissProt HOMO SAPIENS protein database (release data 7/15/2010). The search parameters and acceptance criteria were: no digest enzyme specificity, no fixed modification(s), variable modifications of oxidized methionine and

deamidated, mass tolerance of 5 ppm for precursor and 20 ppm for fragment ions, threshold score > 6 with % Scored Peak Intensity (SPI) > 60.0. Peptide identifications were manually verified.