

Supplemental Figure 1

Figure S1. Comparison of dN/dS for epitope vs. non-epitope regions. Epitope regions

were defined by a positive IFN-gamma ELISpot response of > 3times the mean

background and >40 SFC/million using HLA-matched minimal epitope peptides.

Maximum likelihood estimated for dN/dS were calculated separately for epitope and non-

epitope encoding segments of the nucleotide alignments for each subject except 01, who

did not have any significant responses to minimal epitope peptides.

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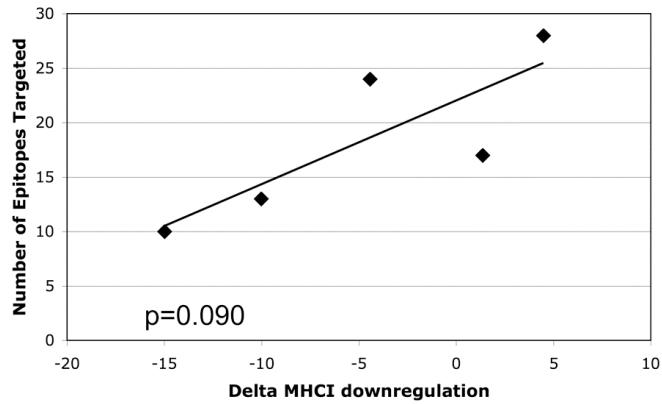
      .....|.....| .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
      5          15          25          35          45          55          65          75
CONSENSUS_  MGGKWSKRSV  VGWPTVRERM  RRA-----E  PAADGVGAVS  RDLEKHGAI  SSNTAANNAD  CAWLEAQEEE  EVGFPPVRQV
01_V2       ....X..NNX  X...A.....  ...RTTEPA.  .....A.    ...DR...L.  N.....    .....    .....
01_V5       ....X.XXXX  X..XA.X...  .XXXXTEXXX  ...X.X.A.  ...XRK..TX  X...X....  .....X.X.  .....
02_V1       ..X.C...T  G.....    .QT-----  .....    .....    .....    .....X.  .....
02_V5       ....X..XXT  G..X.....  .XT-----  .XXX...X.  X..X...X  ...X.XT.X.  .X...X.    .....
03_V1       ....X..S.  ...A.....  K.Q-----  .....A.    ...R...N.  N.....T...  .....D.    .....K...
03_V5       X.X.X..SX.  ...A.....  KAQ-----  .....A.    X...R...  N.....T...  .....D.    .....K...
04_V1       ..XXX..S.L  ..XA..X.  EQX-----  ...E.....  .....Y..V.  ...P.T..T  .....    .....
04_V5       ..S..X.S.L  ..XX..R.  EQ-----  ...E.....  .....Y..V.  ...P.T..T  .....X.    .....
05_V1       ..CX..SK.  P..XAI...  .X.EPRA--  .....A.    .....X.  ...P....  .....X.    .....X...
05_V6       ....X..SK.  P...AI...  .EPRA--  .....X..X.  .....L.  ..XXXXXXX  XXXX...D.  .....
06_V1       .XX.X..XXX  X..XXXXXX  .R-----  ...X.....  Q.X.X...  .X...T..X  .....    .....
06_V5       ....X..XXX  X...XX..X  .X-----  ...X.X...  Q...X...  .X...T..X  .....    .....

      .....|.....| .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
      85          95          105         115         125         135         145         155
CONSENSUS_  PLRPMTYKGA  LDLSHFLKEK  GGLEGLIYSQ  KRQDILDLVW  YHTQGYFPDW  QNYTPGPGIR  YPLTFGWCFK  LVPVEPEKVE
01_V2       .....F...  .....    ...D.....  KRQDILDLVW  .....    .....T.  F.....    .....D..
01_V5       .....X...  X.....    ...X..X...  ...X.....  .X.....  ...X...X.  X.....    ...X..X..
02_V1       .....    .....R...  .....    ...X.....  .N.....  .....V.  .....    .....D...
02_V5       .....X...  ...X..R.  .....X    .....    .X.....  .....V.  .....    .....DX..
03_V1       .....A.  V.M...I.  .....    R.....I    .....    .....    .....    .....L...QI.
03_V5       .....A.  V.M...I.  .....    R.....I    .....X    .....    .....    .....L...QI.
04_V1       .....QL.  H...F...XX  ...D..XH..  ...E...I  X...I...  .....    .....Y.  .....E.
04_V5       .....QL.  H...F...X  ...D..TH..  ...X...X  ...I...  .....X    .....Y.  .....EX.
05_V1       ....X..XX  X.....    .....H..  .....X    .....X...T.  .....X.  .....X...
05_V6       .....    .....H..  X.....X    .....X    .....X.  .....X.  .....X...
06_V1       .....    X..X...  ...XXX.X.X  ...X.....  .....X.  ...X.V.  .....X.  ...X.X...
06_V5       .....    X..X...  .....P    ...E...X.  .....V.  .....X    .....X.X...

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Supplemental Figure 2

Figure S2. Alignment of Nef amino acid consensus sequences. Consensus sequences for each subject were generated using all clones obtained at the first (visit 1 or 2) and last time points (visit 5 or 6) and aligned against the Clade B consensus (top line). Dots denote positions with 100% identity with the Clade B consensus among all clones, and “X” denotes a position with at least one polymorphic allele in the quasispecies population. Dashes indicate positions of insertions relative to the consensus.



Supplemental Figure 3

Figure S3. Relationship between CTL Response and Preservation of Nef-mediated MHC Class I Downregulation. The difference in MHC Class I downregulation between peak viremia and viral set point (Delta MHC CLASS I downregulation) was compared with the total CTL response measured in number of positive peptide pools. There was a trend ( $p=0.090$ ) for a positive association between number of CTL responses and preservation of MHC Class I downregulation.