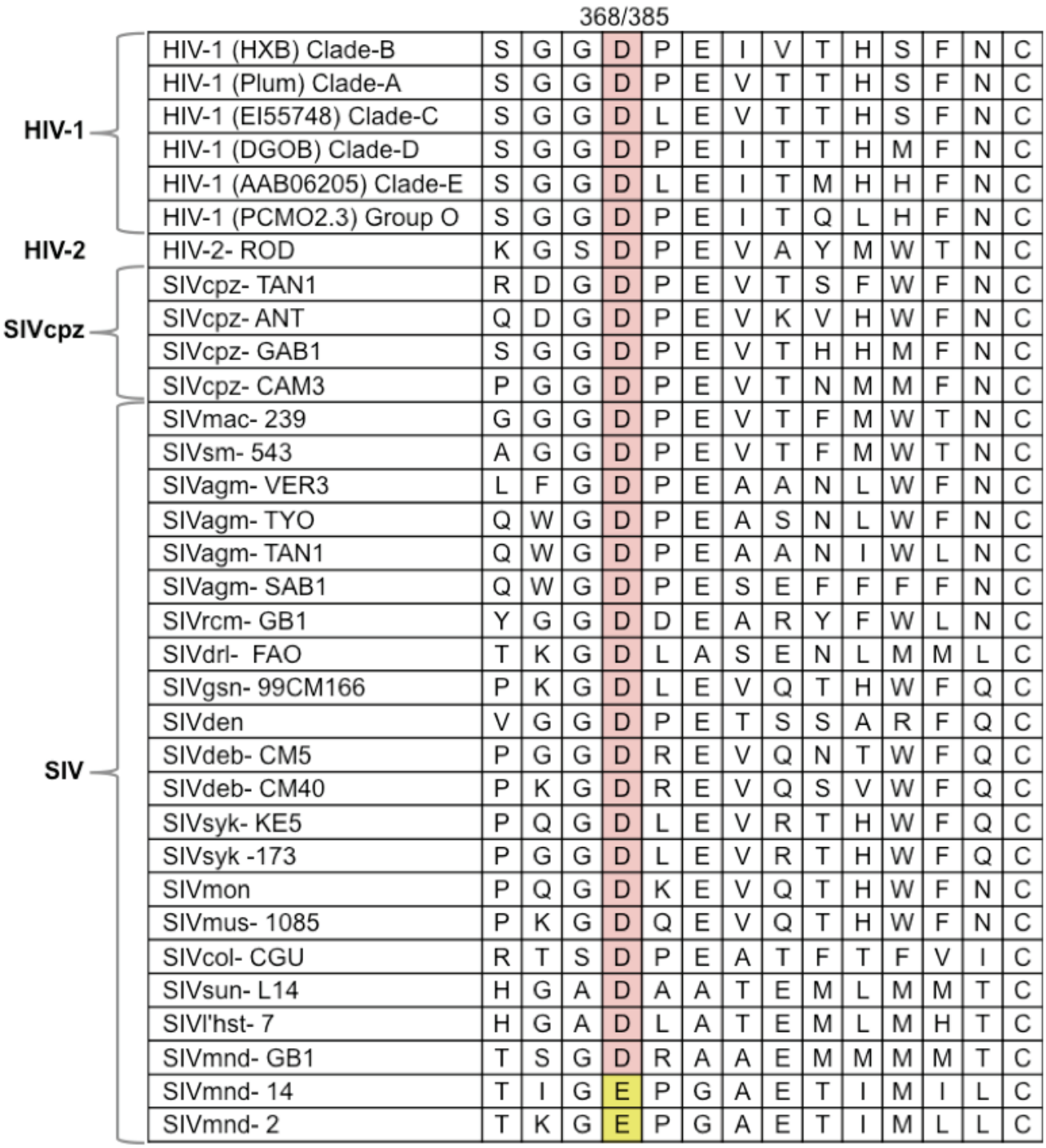
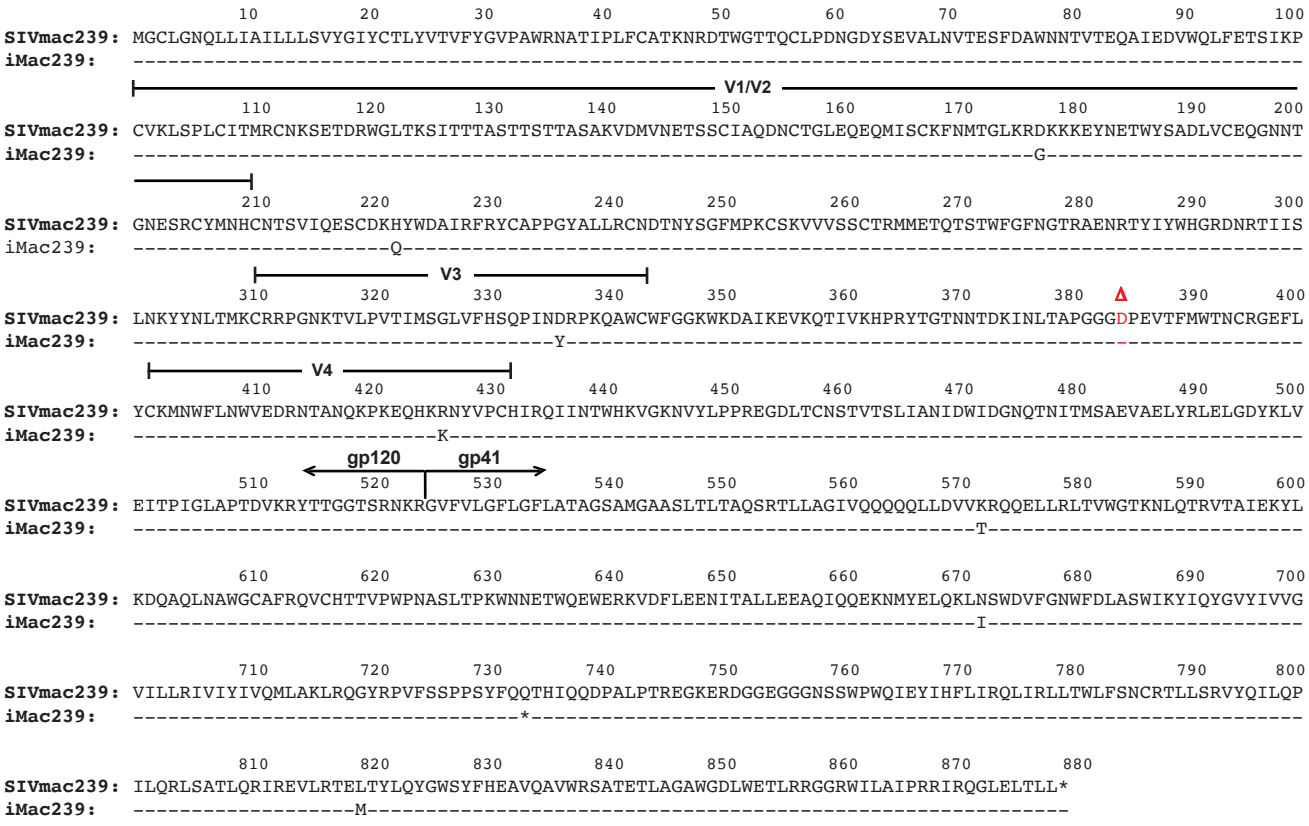
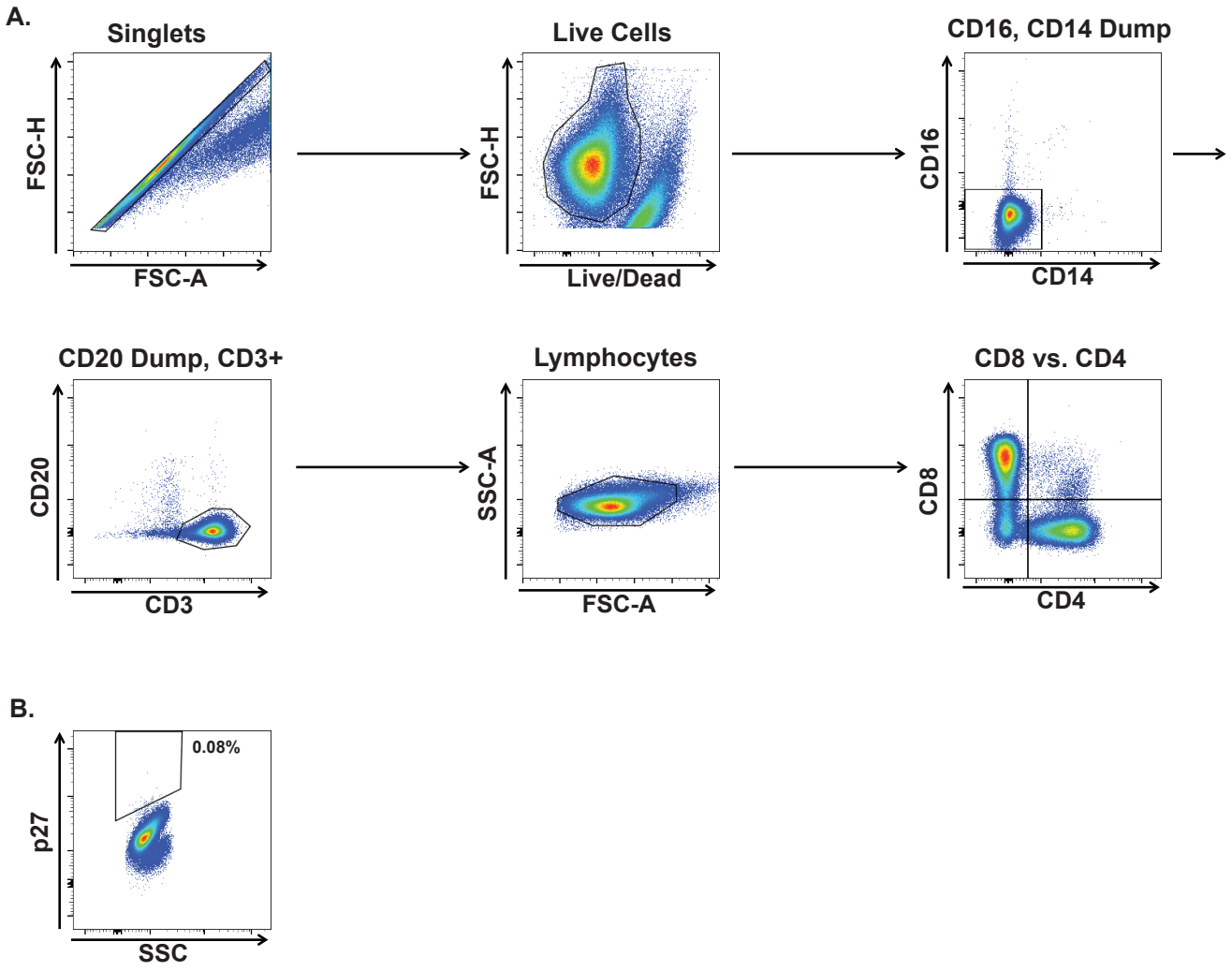


Supplemental Figure 1: Amino acid sequence alignment of HIV-1, HIV-2, and SIV gp120. Shown is a region that for HIV-1 contributes to the CD4 binding site. Aspartic acid-368 for HIV-1, which is critical for CD4 binding (i.e., D-385 for SIVmac239), is highlighted and is highly conserved with the only exception being two SIVmnd isolates.



Supplemental Figure 2: Alignment of Env sequences for SIVmac239 and iMac239 are shown. Variable loops and the cleavage site for gp120 and gp41 are indicated. Stop codons are denoted by asterisks (*). A stop codon at position 734 in the gp41 cytoplasmic tail, acquired as expected (76) during in vitro passaging of iMac239 in human T cell lines and present in the p8cl18 env clone, was repaired to create the iMac239 Env. The red delta (Δ) symbol at position 385 denotes the site of mutagenesis to remove D385 within the CD4 binding site.



Supplemental Figure 3: The flow cytometry gating strategy is shown for analysis of SIV-infected PBMCs. Monoclonal antibodies included those reactive with CD3, CD4, CD8, CD20, CD14, CD16 and SIV p27 Gag. **(A)** Gating strategy is shown for CD4+ and CD8+ T cells. Shown are cytograms for uninfected cells. **(B)** A representative cytogram of uninfected cells is shown to demonstrate negligible staining for p27 Gag.