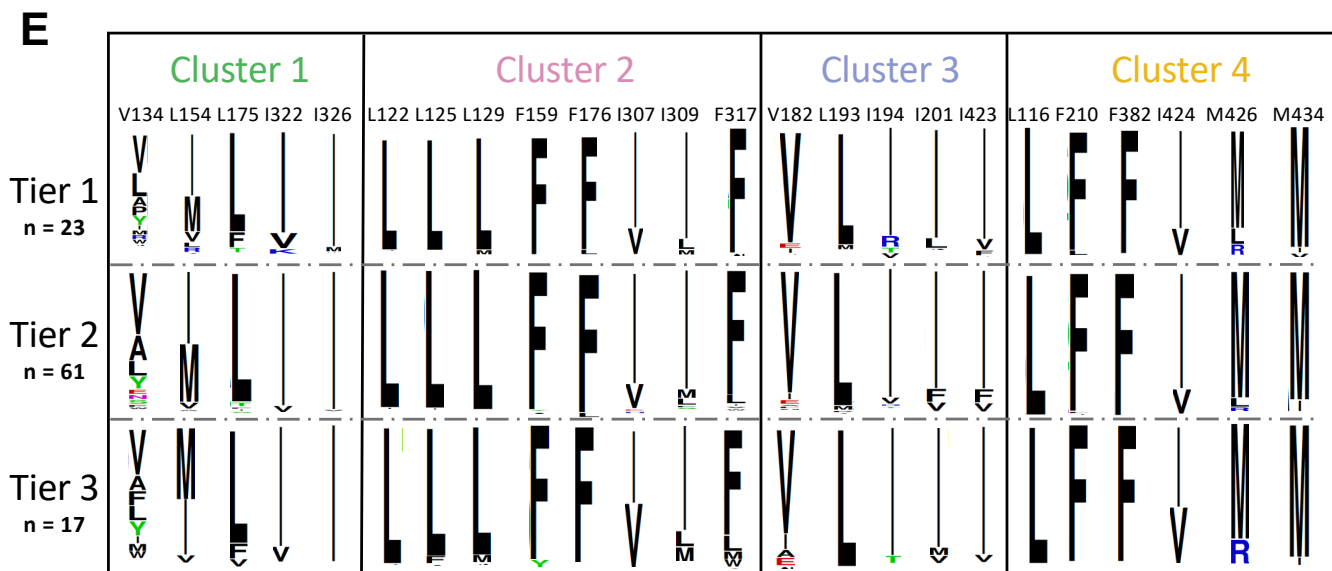
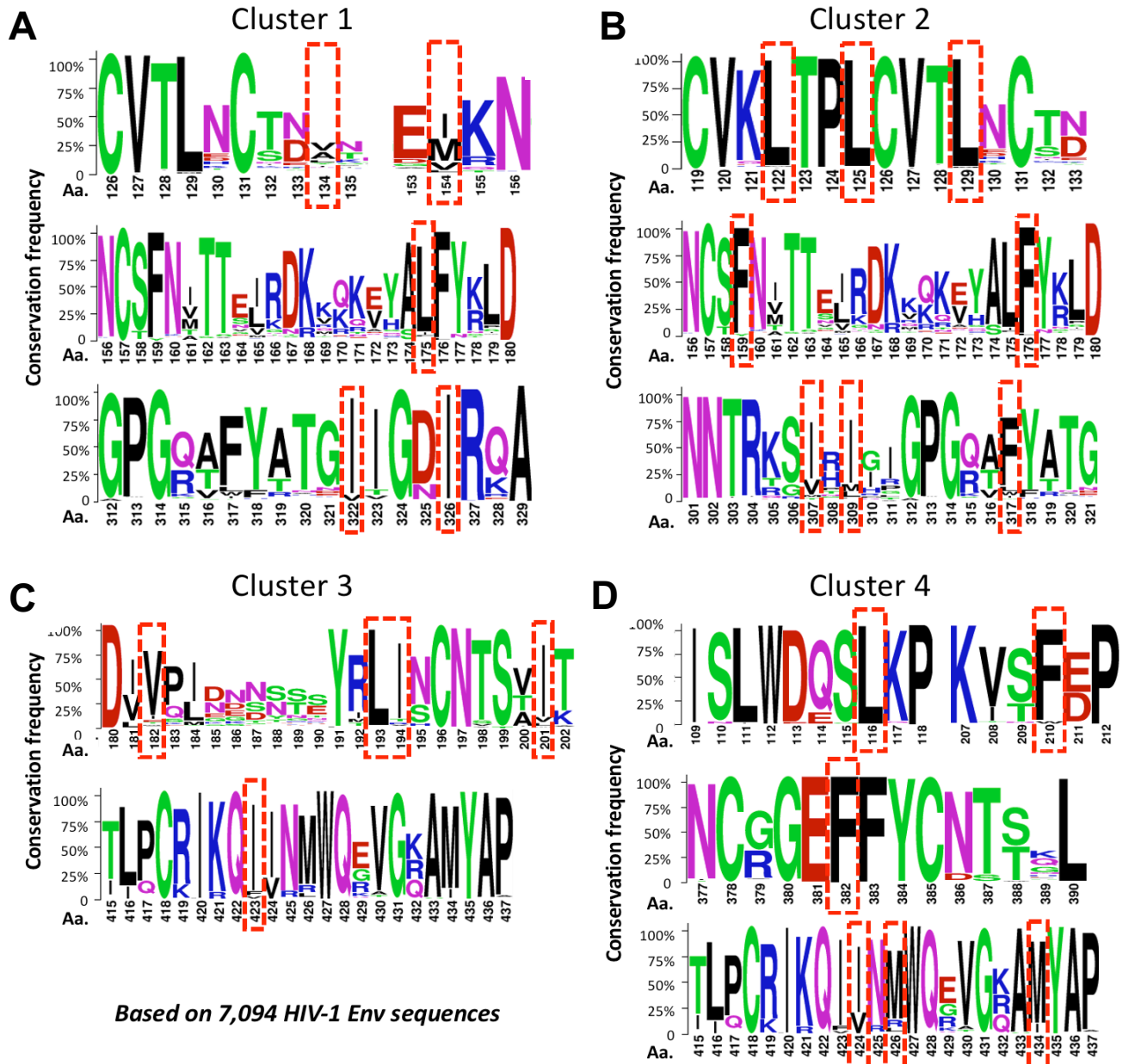


Figure S2



## Figure S2 (legend)

**FIG S2 Sequence conservation of the four apical hydrophobic clusters among global HIV-1 strains.** (A) Sequence logo representation of aa. residue conservation in hydrophobic cluster 1 (red frames) calculated from the sequence of 7,094 HIV-1 gp120 sequences deposited in the Los Alamos HIV-1 database. The degree of conservation is indicated by the height of the residue logo. (B) Aa. residue conservation in hydrophobic cluster 2. (C) Aa. residue conservation in hydrophobic cluster 3. (D) Aa. residue conservation in hydrophobic cluster 4. (E) Sequence logo representation of aa. residue conservation in the four hydrophobic clusters based on HIV-1 neutralization tiers. Selected isolates categorized in the different tiers (tier-1, n = 23; tier-2, n = 61; tier-3, n = 17) were analyzed. Numbering and alignment are according to HXB2 numbering system. HIV-1 isolates Env sequences were derived from the Los Alamos database and the tier classification was derived from Seaman et al. [33].