SUPPLEMENTARY FIGURE LEGENDS

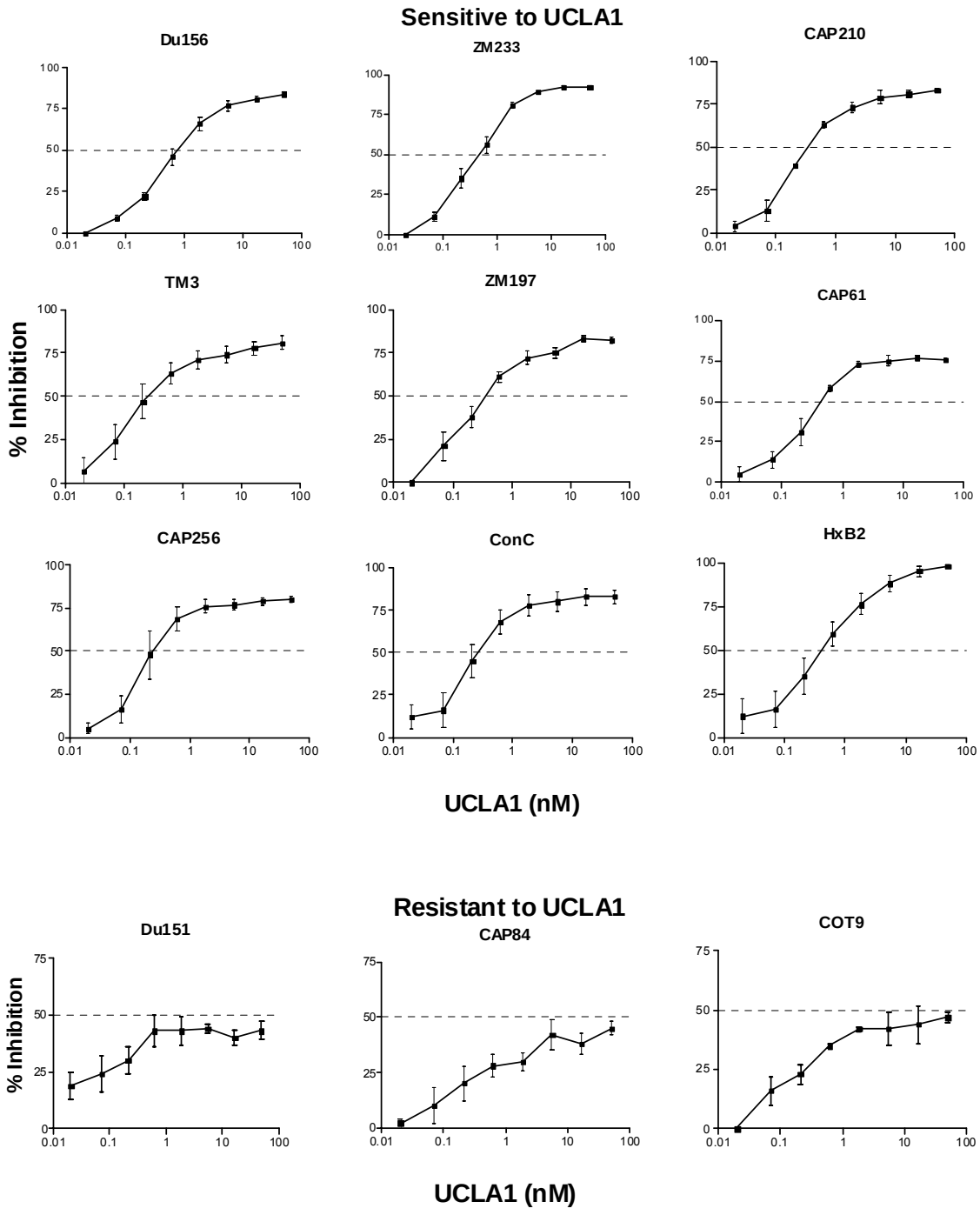
Figure S1: Representative dose-dependent neutralization graphs of HIV-1 subtype C Env-pseudotyped viruses and a subtype B HxB2 reference strain with the UCLA1 aptamer using the TZM-bl cell line. The aptamer was used at a starting concentration of 50 nM. The IC_{50} of UCLA1 is indicated with the dotted line. Nine viruses sensitive to UCLA1 and three viruses resistant to UCLA1 neutralization are shown.

Figure S2: BIAcore® sensorgrams to detect the dissociation constant (K_D) of UCLA1 aptamer from the core, ΔV1/V2 and ΔV3 truncated HIV-1 Con-C gp120, and from I420R (CoRbs) and D368R (CD4bs) mutated HIV-1 Con-C gp120. The truncated and mutated ConC glycoproteins were compared with the wildtype ConC gp120. The UCLA1 aptamer was simultaneously injected over the immobilized gp120 at 2-fold dilutions (500 nM to 8 nM).

Figure S3: The binding profile of ½ log dilutions (500 nM to 1.0 nM) of the UCLA1 aptamer over the immobilized HIV-1 Du151 gp120. The binding kinetics was performed in triplicate.

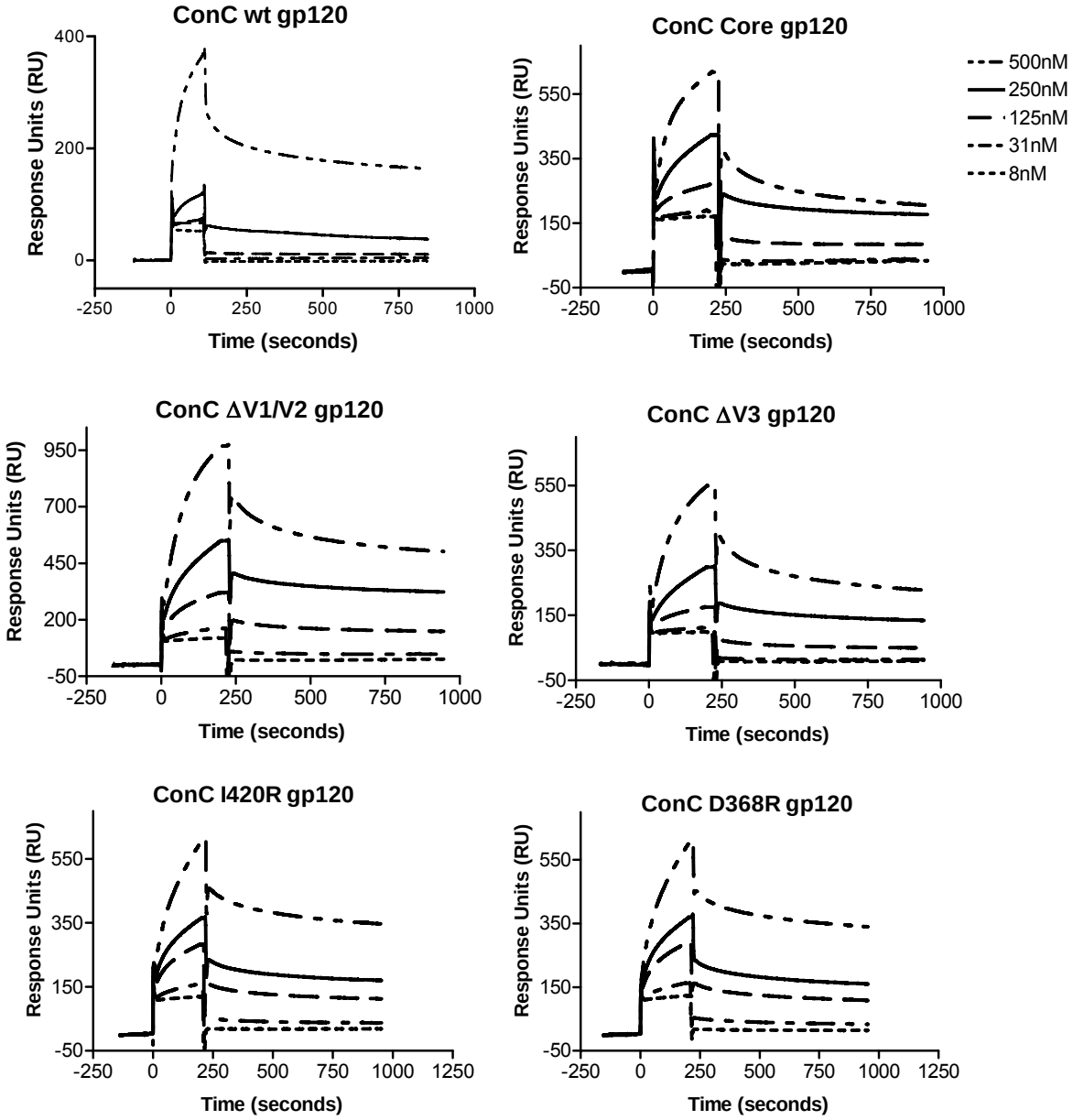
Figure S4: [A] Amino acid sequence alignment of HIV-1 gp120 of the Env-pseudotyped viruses that were tested for neutralization with UCLA1 aptamer in the TZM-bl assay. The resistant viruses, listed below the horizontal line in the alignment, were compared with viruses that were sensitive to UCLA1 neutralization including the ConC virus that was used to map the UCLA1 binding sites. The amino acid residues that were changed by site-directed mutagenesis of the ConC gp120 are numbered and their respective regions exhibited within the *env* genome. The numbering is according to the sequence of the

HxB2 (IIIB) gp120. The amino acid residues that were shown to modulate binding of UCLA1 aptamer are bolded and highlighted in grey colour. **[B]** Amino acid sequence alignment of HIV-1 gp120 of primary isolates that were tested for neutralization with UCLA1 aptamer in the PBMC assay. The viruses that were not neutralized by the aptamer are listed below the horizontal line in the sequence alignment. The amino acid residues that were changed by site-directed mutagenesis of ConC gp120 are numbered and their respective regions exhibited within the env genome. The numbering is according to the sequence of the HxB2 (IIIB) gp120. The amino acid residues that were shown to modulate binding of UCLA1 aptamer are bolded and highlighted in grey colour.

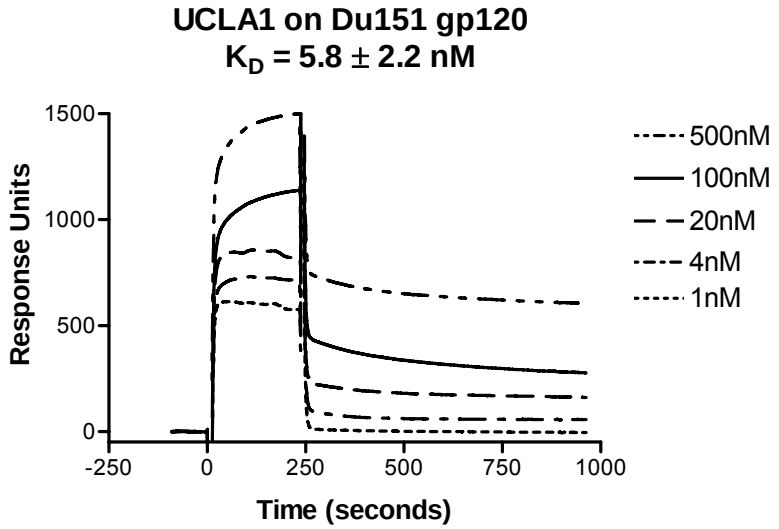


1

2 **Supplementary Figure 1.**

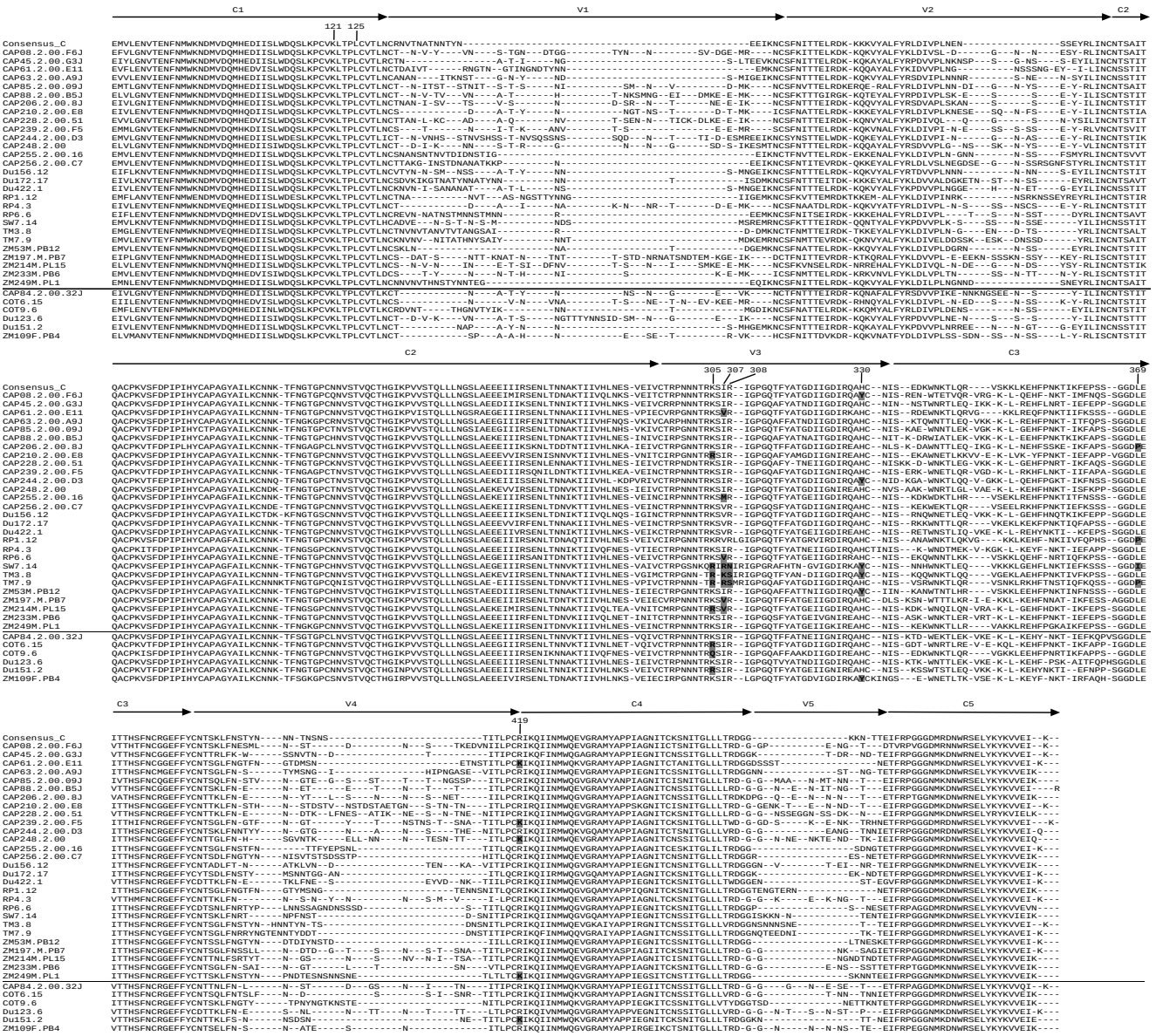


Supplementary Figure 2.

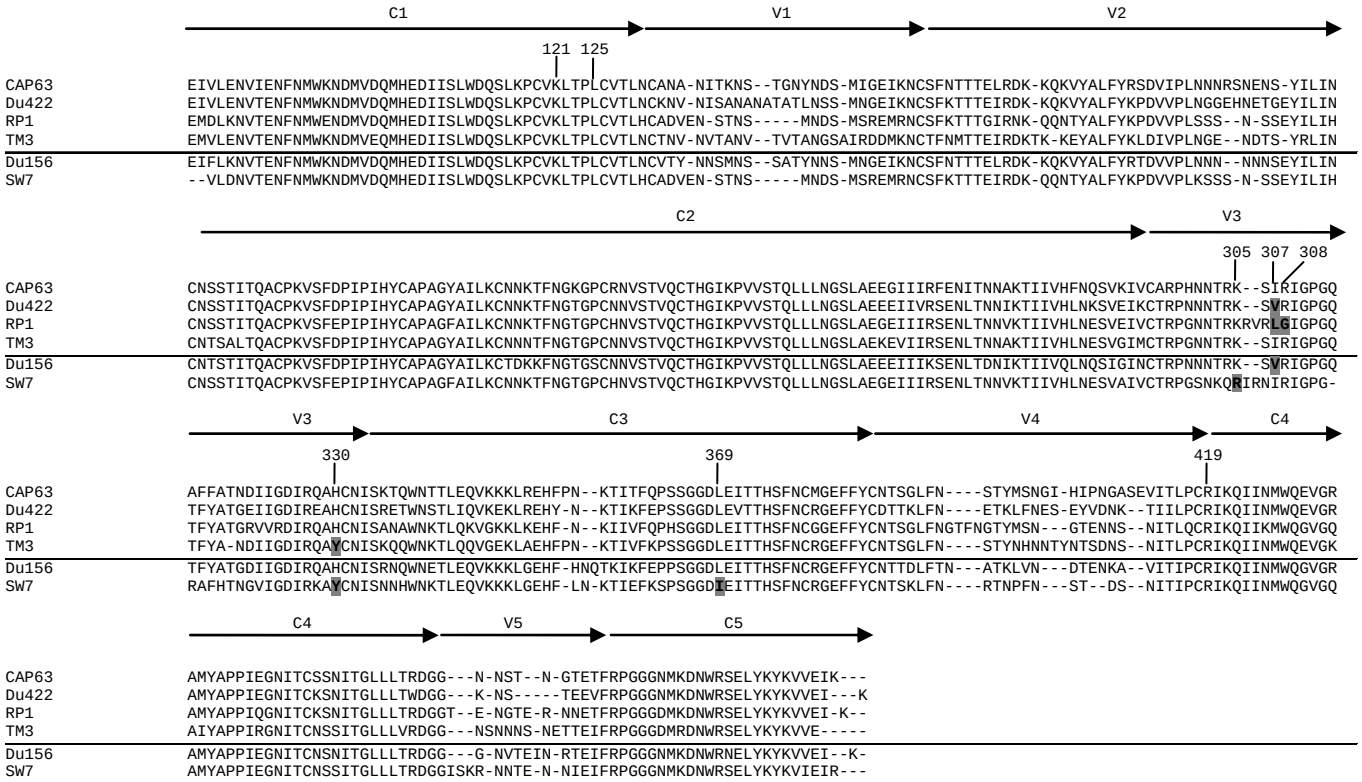


Supplementary Figure 3.

A



B



Supplementary Figure 4.