

**Table S5:** Conservation of capsid binding site residues across HIV-1 strains

<i>N-terminal domain binding site residues</i>		
<b>Residue</b>	<b>Conservation</b>	<b>Other residues (% observed)</b>
N53	99.4%	X(0.6%)
L56	99.4%	X(0.6%)
N57	99.4%	X(0.6%)
V59	99.4%	I(0.6%)
Q63	100%	-
M66	95.2%	L(4.8%)*
Q67	98.8%	E(1.2%)
L69	100%	-
K70	99.4%	E(0.6%)*
I73	100%	-
A105	98.8%	X(0.6%), V(0.6%)
T107	96.4%	A(1.8%), S(1.8%)
Y130	100%	-
<i>Putative C-terminal contact residues</i>		
<b>Residue</b>	<b>Conservation</b>	<b>Other residues (% observed)</b>
Y169	35%	F(65%)
L172	99.4%	I(0.6%)
R173	100%	-
Q179	99.4%	H(0.6%)
K182	100%	-

Sequence data taken from 2009 HIV-1 sequence compendium  
 (<http://www.hiv.lanl.gov/content/sequence/HIV/COMPENDIUM/2009compendium.html>) comprising  
 164 representative sequences from different viral strains

\*All from O genotype