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HXB2_K03455.1/1-856     1 MRVK---EKYQHLWRWGWRWGTMLLGMLMICSATEKLWVTVYYGVPVWKEATTT 51
108051_005/1-869        1 MRVKGIRRNYQHL----WRGVTLLLGILMICSVAGNLWVTVYYGVPVWKEATTT 50
108051-006/1-876        1 MRVKGIRRNYQHL----WRGATLLLGILMICSVAGNLWVTVYYGVPVWKEATTT 50

HXB2_K03455.1/1-856    52 LFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLVNVTENFNMWKNDMVEQMH 105
108051_005/1-869       51 LFCASDAKAYDTEVHNVWATHACVPTDPNPQELALENVTENFNMWENDMVEQMH 104
108051-006/1-876       51 LFCASDAKAYDTEVHNVWATHACVPTDPNPQELALENVTENFNMWENDMVEQMH 104

HXB2_K03455.1/1-856   106 EDIISLWDQSLKPCVKLTPLCVSLKCTDLKNDTNTNSSSGRM-IMEKGEIKNCS 158
108051_005/1-869      105 EDIISLWDQSLKPCVKLTPLCVTLNCTDAEVTGKTNTTIGEWEKVKEGEMKNCS 158
108051-006/1-876      105 EDIISLWDQSLKPCVKLTPLCVTLNCTDAEVTRKTNTTSGDWEKVKKGEIKNCS 158

HXB2_K03455.1/1-856   159 FNISTSIRGKVQKEYAFFYKLDIIPIDNDTTS--------------YKLTSCNT 198
108051_005/1-869      159 FD-AINTKNKVQKQYALFDTLDVVPIDDDNNS--------NSNYSDFRLTKCDT 203
108051-006/1-876      159 FD-AINTKNKVQKQYALFDTLNVVSIDDDNNSNNNSNNNNNTNYSDFRLTKCDT 211

HXB2_K03455.1/1-856   199 SVITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGIR 252
108051_005/1-869      204 SVIRQACPKVSFEPIPIHYCAPAGFAILKCNETDFNGTGLCNNVSTVQCTHGIR 257
108051-006/1-876      212 SVIRQACPKVSFEPIPIHYCAPAGFAILKCNETDFNGTGLCNNVSTVQCTHGIR 265

HXB2_K03455.1/1-856   253 PVVSTQLLLNGSLAEEEVVIRSVNFTDNAKTIIVQLNTSVEINCTRPNNNTRKR 306
108051_005/1-869      258 PVVSTQLLLNGSLAEEGVVLRSKDFKENTKIIIVQLNKAVNITCTRPNNNTRKG 311
108051-006/1-876      266 PVVSTQLLLNGSLAEKGVVLRSKDFKENTKIIIVQLNKAVNITCTRPNNNTRKG 319

HXB2_K03455.1/1-856   307 IRIQRGPGRAFVTIGKIGNMRQAHCNISRAKWNNTLKQIASKLREQFGNNKTII 360
108051_005/1-869      312 VHM--GPGGALFATDVIGDIRKAHCNITREEWNNTLKQIVLKLKEKFENKTKIV 363
108051-006/1-876      320 VHM--GPGGALFATDVIGDIRKAHCNITREEWNNTLKQIVLKLKEKFENKTKIV 371

HXB2_K03455.1/1-856   361 FKQSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTI 414
108051_005/1-869      364 FTNSSGGDPEVTMHTFNCGGEFFYCNTTELFSSTW-NITGDSIGNITGEYTLNI 416
108051-006/1-876      372 FTNSSGGDPEVTMHTFNCGGEFFYCNTTELFSSTW-NITGDSIGNITGE-SLNI 423

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108051_005/1-869      417 TLPCRIKQIINMWQGVGKAMYAPPISGQIRCISNITGLLLTRDGGGNNTENDNN 470
108051-006/1-876      424 TLPCRIKQIINMWQGVGKAMYAPPISGQIRCISNITGLLLTRDGGDNNTENDNN 477

HXB2_K03455.1/1-856   465 SEIFRPGGGDMRDNWRSELYKYKVVKIEPLGVAPTKAKRRVVQREKRAVGIGAL 518
108051_005/1-869      471 TEIFRPWGGDMRDNWRSELYKYKVVKLEPLGLAPTKAKRRVVQREKRAIGVGAM 524
108051-006/1-876      478 TEIFRPWGGDMRDNWRSELYKYKVVKLEPLGLAPTKAKRRVVQREKRAIGVGAM 531

HXB2_K03455.1/1-856   519 FLGFLGAAGSTMGAASMTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWG 572
108051_005/1-869      525 FLGFLGAAGSTMGAASLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWG 578
108051-006/1-876      532 FLGFLGAAGSTMGAASLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWG 585

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108051_005/1-869      579 IKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTTVPWNDSWGYSWSNRTNKSL 632
108051-006/1-876      586 IKQLQARVLAVERYLKDQQLLGIWGCSGKLICTTTVPWNDSWGYSWSNRTNKSL 639

HXB2_K03455.1/1-856   620 EQIWNHTTWMEWDREINNYTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF 673
108051_005/1-869      633 EEIWDNLTWREWEREIDNYTDLIYNLIEKSQNQQEKNEQELLALDKWANLWNWF 686
108051-006/1-876      640 EEIWDNLTWREWEREIDNYTDLIYNLIEKSQNQQEKNEQELLALDKWANLWNWF 693

HXB2_K03455.1/1-856   674 NITNWLWYIKLFIMIVGGLVGLRIVFAVLSIVNRVRQGYSPLSFQTHLPTPRGP 727
108051_005/1-869      687 DITNWLWYIRIFIMIVGGLIGLRIVFAVLSIVRRVRQGYSPLSFQTLLPVPRGP 740
108051-006/1-876      694 DITNWLWYIRIFIMIVGGLIGLRIVFAVLSIVRRVRQGYSPLSFQTLLPVPRGP 747

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108051_005/1-869      741 DRPEGTEKEGGEQDRGRSVRLVDGFLALFWDDLRSLCLFLYHRLRDLLLIVTRI 794
108051-006/1-876      748 DRPEGIEEEGGEQDRGRSVRLVDGFLALFWDDLRSLCLFLYHRLRDLLLIVTRI 801

HXB2_K03455.1/1-856   782 VELLGRRGWEALKYWWNLLQYWSQELKNSAVSLLNATAIAVAEGTDRVIEVVQG 835
108051_005/1-869      795 VGVLGHRGWEILKYWWSLIQYWSQELKNSAVSLLNATAITVAEGTDRVIEIVRR 848
108051-006/1-876      802 VGVLGHRGWEILKYWWSLIQYWSQELKNSAVSLLNATAITVAEGTDRVIEIRQR 855

HXB2_K03455.1/1-856   836 ACRAIRHIPRRIRQGLERILL                                  856
108051_005/1-869      849 VFRGVLHIPRRIRQGLERALL                                  869
108051-006/1-876      856 VFRGVLHIPRRIRQGLERALL                                  876
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Figure S1. MAFFT alignment of HBX2 reference sequence and 108051 clones 005 and 006 (accession numbers K03455.1, HM769943 and HM769944 respectively).

Table S1. Effect of antibody and peptide inhibitors of α4β7 binding on the neutralization of viruses with envelopes from subject 108051

Viruses/ Clones [a]	IC50 (μg/mL antibody, μM peptide) of indicated MAb or fusion inhibitor [b]					
	Z23	Act-1 MAb	CWLDVC	Act-1 + CWLDVC	α4/CD49d MAb	α4/CD49d + CWLDVC
108051_005 wtR	<100	>20	14	>20	>20	>20
108051_006 wtS	**2298**	>20	12	>20	>20	>20
108051_005_D179N	**3758**	>20	12	>20	>20	>20
JRCSF	**422**	>20	19	>20	>20	>20
NL43	**3042**	>20	13	>20	>20	>20
aMLV	<100	>20	12	>20	>20	>20

[a] wtR, indicates wild type resistant; wtS, indicates wild type sensitive. MAbs Act-1 and CD49d are known to react with the α4β7and α4 chain of VLA4, respectively. CWLDVC is a synthetic peptide known to inhibit α4β7 binding. The CWLDVC peptide used at a 10μM concentration was known to inhibit gp120 binding to α4β7 in control experiments using the RPMI8866, α4β7-expressing cell line (65).

[b] Values in bold represent neutralization titers that are at least 3 times greater than those observed against the negative control (aMLV).

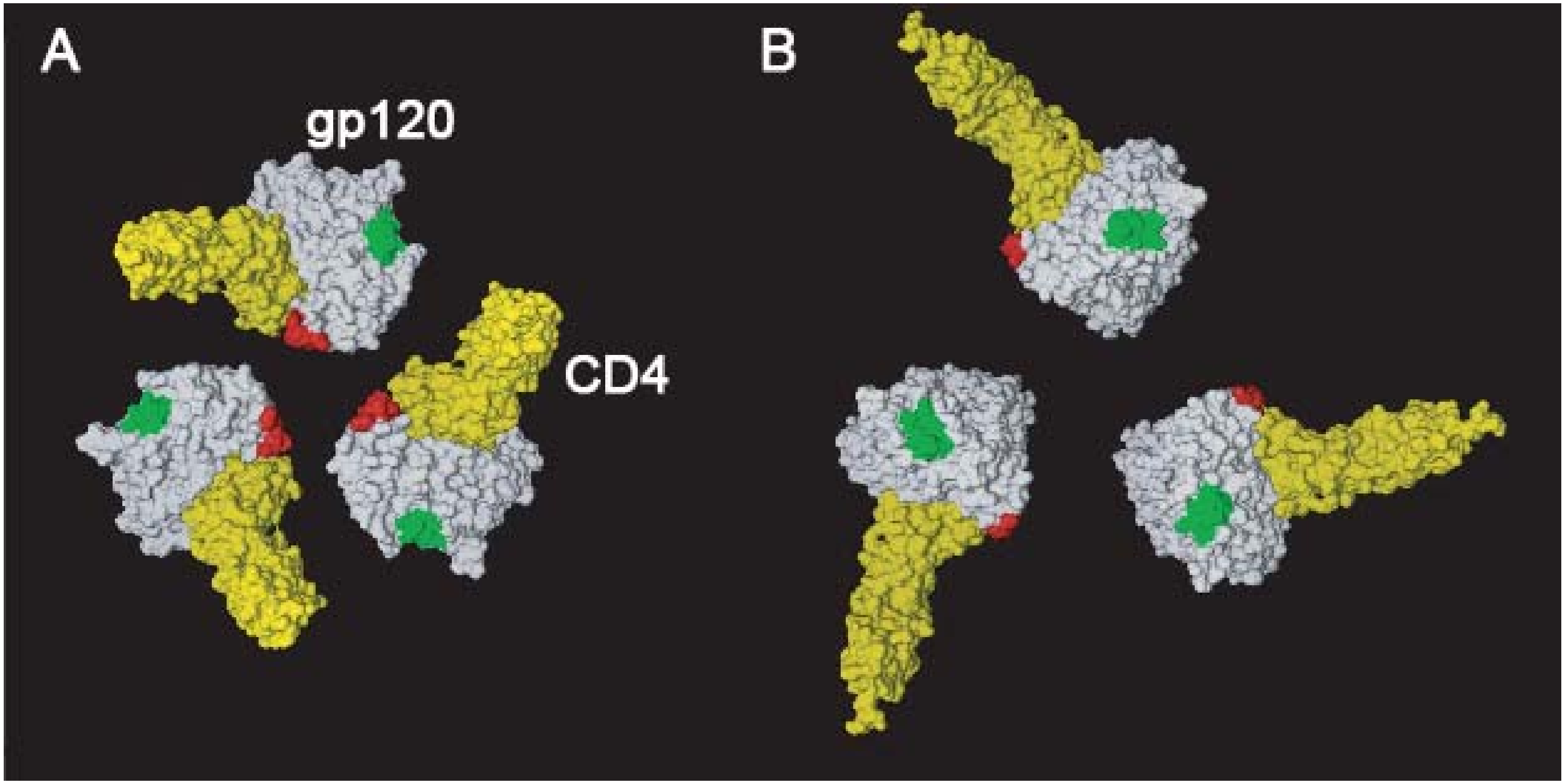

Figure S2. Conformational changes that affect the V2 domain in HIV envelope trimer before and after CD4 binding. Figure represents the orientation of gp120 monomers before (A) and after (B) a conformational change triggered by the binding of CD4. Gray, indicates gp120 monomers; yellow, indicates CD4; red, indicates the V2 domain stem; green, indicates the V3 domain stem. Following CD4 engagement, the monomers rotate and change position with respect to the central axis of symmetry. The distance between the V2 stems increases, and the V3 stems become positioned at the top. Data taken from Liu et al. (41).