

Supplementary Table S1. HIV-1 protein regions targeted by T cells and by CD3neg cell subsets

Cell Subsets	n ^a	Gag	Pol	Nef	Reg ^b	Env
HIV-infected mothers						
CD3pos subsets						
CD8 T cells						
Median (Range) ^c	79	0.43 (0-5.50)	0.27 (0-2.71)	0.39 (0-3.09)	0.19 (0-3.0)	0.20 (0-3.16)
No. (%) ^d		64 (81)	60 (75.9)	65 (82.3)	54 (68.4)	52 (65.8)
CD4 T cells						
Median (Range)	79	0 (0-0.73)	0 (0-0.5)	0 (0-0.37)	0 (0-1.48)	0 (0-3.78)
No. (%)		25 (31.6)	17 (21.5)	14 (17.7)	23 (29.1)	32 (40.5)
CD3neg subsets						
CD3neg						
Median (Range)	79	0 (0-3.44)	0 (0-6.14)	0 (0-1.25)	0 (0-18.66)	1.64 (0-18.58)
No. (%)		0	1 (1.3)	0	16 (20.3)	25 (31.6)
CD3-CD8+						
Median (Range)	79	0 (0-5.36)	0 (0-6.74)	0 (0-3.07)	0.23 (0-30.72)	2.79 (0-19.72)
No. (%)		0	2 (2.5)	0	17 (21.5)	34 (43)
CD3-CD8-						
Median (Range)	79	0 (0-2.40)	0.04 (0-6.14)	0 (0-1.78)	0.01 (0-18.91)	1.22 (0-18.29)
No. (%)		0	0	0	12 (15.2)	21 (26.6)
NK ^{+e}						
Median (Range)	50	0 (0-4.79)	0 (0-3.80)	0 (0-6.27)	0.58 (0-33.86)	2.01 (0-15.63)
No. (%)		0	0	0	11 (22)	18 (36)
NK+CD8+						
Median (Range)	50	0 (0-5.02)	0 (0-3.06)	0 (0-3.84)	0.21 (0-26.76)	1.63 (0-15.20)
No. (%)		0	0	0	10 (20)	18 (36)
NK+CD8-						
Median (Range)	50	0 (0-5.10)	0.28 (0-5.01)	0 (0-3.53)	0.72 (0-36.72)	2.30 (0-18.62)
No. (%)		0	0	0	11 (22)	17 (34)
Infants born to HIV-infected mothers						
CD3pos subsets						
CD8 T cells ^f						
Median (Range)	76	0 (0-6.72)	0 (0-0.28)	0 (0-1.81)	0 (0-1.58)	0 (0-0.75)
No. (%)		8 (9.9)	4 (4.9)	10 (12.3)	8 (9.9)	6 (7.4)
CD4 T cells ^f						
Median (Range)	76	0 (0-0.41)	0 (0-0.99)	0 (0-0.41)	0 (0-0.54)	0 (0-0.39)
No. (%)		2 (2.5)	0	4 (4.9)	2 (2.5)	3 (3.7)
CD3neg subsets						
CD3neg						
Median (Range)	76	0.02 (0-2.31)	0 (0-1.39)	0 (0-2.34)	0 (0-2.85)	0.05 (0-9.70)
No. (%)		0	0	0	0	7 (9.2)
CD3-CD8+						
Median (Range)	76	0 (0-4.20)	0 (0-3.88)	0 (0-7.89)	0 (0-9.81)	0.21 (0-23.44)
No. (%)		0	1 (1.3)	1 (1.3)	4 (5.3)	12 (15.8)
CD3-CD8-						
Median (Range)	76	0 (0-1.84)	0 (0-1.46)	0 (0-0.94)	0.02 (0-1.96)	0.04 (0-5.62)
No. (%)		0	0	0	0	3 (3.9)
NK ^{+e}						
Median (Range)	52	0.14 (0-1.45)	0.17 (0-2.07)	0.27 (0-4.16)	0.05 (0-7.49)	0.08 (0-20.85)
No. (%)		0	0	1 (1.9)	3 (5.8)	6 (11.5)
NK+CD8+						
Median (Range)	52	0 (0-1.65)	0 (0-1.53)	0 (0-5.44)	0.01 (0-9.06)	0.22 (0-24.68)
No. (%)		0	0	1 (1.9)	3 (5.8)	6 (11.5)
NK+CD8-						
Median (Range)	52	0 (0-2.03)	0 (0-1.15)	0.09 (0-3.80)	0.48 (0-6.57)	1.57 (0-19.52)
No. (%)		0	0	1 (1.9)	2 (3.8)	6 (11.5)

^aTotal sample numbers tested for each cell subset

^bReg region peptides (Tat, Rev, Vif, Vpu, Vpr) are combined

^cMedian of percentage of cell subset expressing IFN- γ (after background subtraction); range of these responses in parentheses

^dNumber of HIV-specific CD3neg responders with frequency in parentheses, positive responders are shown in bold

^eNK+ used throughout indicates CD3-CD56+

^fInfants with detectable HIV-specific CD4 or CD8 T cell responses were all HIV-1 infected

Note: CD3neg cell subset responses are considered positive if values >3% and at least 2-fold greater than background (after background subtraction from the unstimulated control); CD4 and CD8 T cell responses are considered positive if >0.1% following subtraction of background.

Where top range values are >3% for CD3neg responses but indicate that no individuals are positive for responses in that subset, these were because of high background levels of stimulation that then did not meet the criterion of at least 2-fold above background for the outlier individuals.

Supplementary Table S2. Percentage of CD3neg cell subsets of mothers and infants with positive responses to HIV-1 peptide pools^a

ID	Peptide pool	Mother				Infant							
		CD3- CD3-	CD3- CD8+	CD3- CD8-	NK+ NK+	NK+ CD8+	NK+ CD8-	CD3- CD3-	CD3- CD8+	CD3- CD8-	NK+ NK+	NK+ CD8+	NK+ CD8-
001	Env	8.14	10.82	7.05	ND				ND				ND
	Reg	4.67	5.07	4.62									
003	Env	3.25	4.11	-	ND				ND				ND
	Reg	8.8	10.22	7.23									
004	Env	5.92	6.87	5.78	ND				ND				ND
008	Env	18.58	19.72	18.29	ND				ND				ND
	Reg	13.18	15.92	12.39									
010	Env	8.78	13.16	9.38	ND				ND				ND
	Reg	12.98	18.06	13.98									
026	Reg	3.07	4.88	-	ND				ND				ND
027	Env	4.28	8.31	3.94	ND				ND				ND
029	Pol	-	3.21	-	ND				ND				ND
030	Env	5.74	4.24	5.84	ND				-	6.92	-		ND
	Pol	6.14	6.74	6.14					-	-	-		
031	Env	-	3.09	-	ND				4.26	8.09	-		ND
035	Env	4.7	10.56	4.33	ND				-	20.33	-		ND
038i	Env	-	4.65	-	ND				-	-	-		ND
038ii	Env	-	5.52	-	3.15	4.26	4.97		-	-	-		ND
039	Env	3.25	5.38	-	ND				-	-	-		ND
042	Env	5.16	5.55	5.7	4.92	3.29	5.2	6.21	14.89	4.06	6.33	16.05	4.48
043	Env	-	-	-	ND				-	3.05	-		ND
	Reg	-	-	-					-	3.91	-		
047	Env	4.95	9.82	3.92	6.89	7.11	7.38		-	-	-	-	-
048i	Env	11.65	17.8	9.98	ND				-	-	-		ND
	Reg	21.25	32.2	16.63					-	11.43	-		
048ii	Env	10.28	13.62	9.44	11.6	14.3	12.3	9.59	22.28	5.93	16.89	20.46	16.37
	Reg	18.22	25.04	17.4	22.6	22.7	23.9		-	9.74	-	7.49	9.06
	Nef	-	-	-	-	-	-		-	6.01	-	4.16	5.44
052	Env	-	4.12	-	ND				-	-	-		ND
	Reg	3.85	4.78	3.89					-	-	-		
053	Env	3.82	6.2	4.41	ND				-	-	-		ND
	Reg	13.28	19.05	13.86					-	-	-		
069	Env	3.24	4.44	3.86	4.28	4.84	5.51		-	-	-	-	-
071	Env	3.02	6.77	-	5.6	3.5	5.99		-	18.38	-	9.9	16.19
	Pol	-	-	-	-	-	-		-	3.88	-	-	-
155	Reg	7.5	6.51	7.49	11.77	5.97	15.44		-	3.38	-	ND	-
211	Env	-	-	-	-	-	-	3.47	22.97	-	20.85	24.68	19.52
305	Env	4.57	6.95	4.19	7.29	7.94	6.79	5.05	6.64	4.52	3.24	3.84	3.66
306	Env	-	-	-	-	-	-		-	3.91	-	3.9	-
	Reg	3.83	4.87	3.85	4.99	4.45	6.67		-	-	-	-	-
307	Env	8.72	14.66	7.54	15	11.87	14.68		-	-	-	-	-
311	Env	-	4.14	-	3.5	4.07	-		-	-	-	-	-
	Reg	-	6.27	-	5.29	5.56	3.36		-	-	-	-	-
318	Env	5.83	11.14	4.75	6.3	8.65	4.48		-	-	-	-	-
330	Env	11.19	17.12	10.32	15.63	15.2	16.39	3.69	15.04	-	11.1	12.13	10.83
425	Env	4.27	13.12	-	4.49	6.64	-		-	-	-	-	-
433	Env	4.99	5	5.27	6.09	5.03	6.24		-	-	-	-	-
	Reg	18.21	18.53	18.91	25.71	19.97	26.62		-	-	-	-	-
563	Env	12.59	11.45	13.49	14.57	12.54	18.62	3.16	23.30	-	18.56	23.29	10.04
	Reg	16.44	14.88	17.15	21.77	16.44	23.62		-	-	-	-	-
589	Env	-	4.93	4.91	5.96	5.23	6.33		-	-	-	-	-
624	Env	4.31	7.04	-	6.42	6.1	6.64		-	-	-	-	-
	Reg	4.36	6.68	-	5.91	6.05	5.51		-	-	-	-	-
649	Reg	6.28	16.41	-	11.8	18.4	5.04		-	-	-	-	-
654	Env	-	4.16	-	3.77	4.38	3.59		-	-	-	-	-
655	Env	11.28	11.96	11.61	15.24	10.41	15.48		-	3.96	-	3.46	-
658	Reg	8.03	9.69	-	9.71	11.1	10.3		-	3.62	-	4.14	4.05
671	Env	-	3.03	-	-	-	-		-	-	-	-	-
	Reg	17.32	30.72	14.52	33.86	26.76	36.72		-	-	-	-	-
773	Env	-	3.98	-	3.02	-	3.32		-	-	-	-	-
791	Env	-	5.27	-	3.79	6.65	4.27		-	-	-	-	-

^aPositive responses are indicated by values (>3% and at least 2-fold greater than background), negative responses by dashes, ND: Not determined
NK+ indicates CD3-CD56+

Supplementary Figure S1 Amino acid regions targeted by CD3-CD56+ NK cells and T cell subsets

Whole HIV-1 subtype C genome mapping was conducted according to methods described in¹ with inclusion of NK cell antibody to CD56. Details of peptides included in pools and matrices that allow determination of the peptide/s stimulating the responses are given in this same publication; example of analysis shown below.

1. Meddows-Taylor, S., Shalekoff, S., Kuhn, L., Gray, G.E. & Tiemessen, C.T. Development of a whole blood intracellular cytokine staining assay for mapping CD4(+) and CD8(+) T-cell responses across the HIV-1 genome. *J Virol Methods* **144**, 115-21 (2007).

a

Matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
Pol 1	Pol 2	Pol 3	Pol 4	Pol 5	Pol 6	Pol 7	Pol 8	Pol 9	Pol 10	Pol 11	Pol 12	Pol 13	Pol 14	Pol 15	Pol 16	Pol 17	Pol 18	Pol 19	Pol 20	Pol 21	Pol 22	Pol 23	Pol 24	
Pol 25	Pol 26	Pol 27	Pol 28	Pol 29	Pol 30	Pol 31	Pol 32	Pol 33	Pol 34	Pol 35	Pol 36	Pol 37	Pol 38	Pol 39	Pol 40	Pol 41	Pol 42	Pol 43	Pol 44	Pol 45	Pol 46	Pol 47	Pol 48	
Pol 49	Pol 50	Pol 51	Pol 52	Pol 53	Pol 54	Pol 55	Pol 56	Pol 57	Pol 58	Pol 59	Pol 60	Pol 61	Pol 62	Pol 63	Pol 64	Pol 65	Pol 66	Pol 67	Pol 68	Pol 69	Pol 70	Pol 71	Pol 72	
Pol 73	Pol 74	Pol 75	Pol 76	Pol 77	Pol 78	Pol 79	Pol 80	Pol 81	Pol 82	Pol 83	Pol 84	Pol 85	Pol 86	Pol 87	Pol 88	Pol 89	Pol 90	Pol 91	Pol 92	Rev 1	Rev 2	Rev 3	Rev 4	
Rev 5	Rev 6	Rev 7	Rev 8	Rev 9	Rev 10	Rev 11	Rev 12	Rev 13	Rev 14	Tat 1	Tat 2	Tat 3	Tat 4	Tat 5	Tat 6	Tat 7	Tat 8	Tat 9	Tat 10	Tat 11	Tat 12	Vpu 1	Vpu 2	
Vpu 3	Vpu 4	Vpu 5	Vpu 6	Vpu 7	Vpu 8	Vpu 9	Vif 1	Vif 2	Vif 3	Vif 4	Vif 5	Vif 6	Vif 7	Vif 8	Vif 9	Vif 10	Vif 11	Vif 12	Vif 13	Vif 14	Vif 15	Vif 16	Vif 17	
Vif 18	Vif 19	Vif 20	Vif 21	Vif 22	Vif 23	Vif 24	Vpr 1	Vpr 2	Vpr 3	Vpr 4	Vpr 5	Vpr 6	Vpr 7	Vpr 8	Vpr 9	Vpr 10	Vpr 11	Env 1	Env 2	Env 3	Env 4	Env 5	Env 6	
Env 7	Env 8	Env 9	Env 10	Env 11	Env 12	Env 13	Env 14	Env 15	Env 16	Env 17	Env 18	Env 19	Env 20	Env 21	Env 22	Env 23	Env 24	Env 25	Env 26	Env 27	Env 28	Env 29	Env 30	
Env 31	Env 32	Env 33	Env 34	Env 35	Env 36	Env 37	Env 38	Env 39	Env 40	Env 41	Env 42	Env 43	Env 44	Env 45	Env 46	Env 47	Env 48	Env 49	Env 50	Env 51	Env 52	Env 53	Env 54	
Env 55	Env 56	Env 57	Env 58	Env 59	Env 60	Env 61	Env 62	Env 63	Env 64	Env 65	Env 66	Env 67	Env 68	Env 69	Env 70	Env 71	Env 72	Env 73	Env 74	Env 75	Env 76	Env 77	Env 78	
Env 79	Env 80	Env 81	Env 82	Env 83	Env 84	Env 85	Env 86	Env 87	Env 88	Env 89	Env 90	Env 91	Env 92	Env 93	Env 94	Env 95	Env 96	Env 97	Env 98	Env 99	Env 100	Env 101	Env 102	
Env 103	Env 104	Env 105	Env 106	Env 107	Env 108	Env 109	Env 110	Env 111	Env 112	Env 113	Env 114	Vif 16	Vif 17											

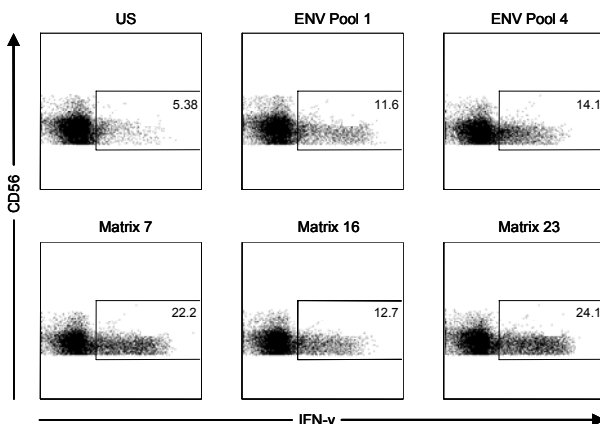
Matrix

	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48
Gag 1	Gag 2	Gag 3	Gag 4	Gag 5	Gag 6	Gag 7	Gag 8	Gag 9	Gag 10	Gag 11	Gag 12	Gag 13	Gag 14	Nef 1	Nef 2	Nef 3	Nef 4	Nef 5	Nef 6	Nef 7	Nef 8	Nef 9	Nef 10	
Gag 15	Gag 16	Gag 17	Gag 18	Gag 19	Gag 20	Gag 21	Gag 22	Gag 23	Gag 24	Gag 25	Gag 26	Gag 27	Gag 28	Nef 11	Nef 12	Nef 13	Nef 14	Nef 15	Nef 16	Nef 17	Nef 18	Nef 19	Nef 20	
Gag 29	Gag 30	Gag 31	Gag 32	Gag 33	Gag 34	Gag 35	Gag 36	Gag 37	Gag 38	Gag 39	Gag 40	Gag 41	Gag 42	Nef 21	Nef 22	Nef 23	Nef 24	Nef 25	Nef 26	Nef 27	Nef 28	Nef 29	Nef 30	
Gag 43	Gag 44	Gag 45	Gag 46	Gag 47	Gag 48	Gag 49	Gag 50	Gag 51	Gag 52	Gag 53	Gag 54	Gag 55	Gag 56	Nef 31	Nef 32	Nef 33	Nef 34	Nef 35	Nef 36	Nef 37	Nef 38	Nef 39	Nef 40	
Gag 57	Gag 58	Gag 59	Gag 60	Gag 61	Gag 62	Gag 63	Gag 64	Gag 65	Gag 66	Gag 67	Gag 68	Gag 69	Gag 70	Nef 41	Nef 42	Nef 43	Nef 44	Nef 45	Nef 46	Nef 47	Nef 48	Nef 49	Nef 50	

Pools

	1	2	3	4	5
Pol	1-24	25-48	49-72	73-92	
Rev	1-14				
Tat	1-12				
gp160	1-24	25-48	49-72	73-96	97-114
Vpu	1-9				
Vif	1-12	13-24			
Gag	1-14	15-28	29-42	43-56	57-70
Vpr	1-11				
Nef	1-10	11-20	21-30	31-40	41-50

b



Supplementary Figure S1 Identification of individual HIV-1 subtype C peptide responses using a pool and matrix screening method. Detectable CD56+ responses in Env pools 1 (peptides 1-24) and 4 (peptides 73-96) and matrices 7, 16 and 23 (a), allowed the identification of Env 13, 22, 77, 85 and 94 as the individual peptides targeted in this patient. (b) Flow cytometric plots showing unstimulated (US), and positive pool and matrix responses.

(c) Six HIV-1 infected women were recruited for the purpose of whole genome mapping of HIV-specific NK responses. Data are shown only for the two individuals who had responses to Vpu (MP002, MP006) and the one that responded to Tat (MP001), showing the coordinates of the amino acid regions targeted. Peptide-specific responses for CD4 and CD8 T cell responses are shown for these same individuals.

MP001

	Positive response		Identified peptide	Amino acid region spanned
	Pool	Matrix		
CD4 T cells	Gag 4	31	Gag 49	354-SHKARVLAEMSQANSA-370
	Env 2	11-13	Env 41, 42, 43	292-IRIGPGQAFYTNHIGDIRQAYCNISKQEWNK-323
	Env 2	16, 17	Env 46, 47	330-KKLQEHPNKTIKFNSSSGDLEI-353
	Nef 2	45	Nef 17	66-EVGFPVRPQVPLRPM-80
	Tat	11-13	Tat 1, 2, 3	1-MEPIDPNLEPWNHPGSQPNTPCNNCYCKHCSYH-33
	Tat	16, 17	Tat 6, 7	40-TKGLGISYGRKKRRRQRSTPPSSEDH-65
CD8 T cells	Gag 1	27	Gag 3	17-EKIRLRPGGKHKHYMLKHL-34
	Gag 1	34, 35	Gag 10, 11	63-QLQPALQTGTEELRSLYNTVATLY-86
	Gag 1	38	Gag 14	92-IEVRDTKEALDKIEEQNK-110
	Gag 2	27	Gag 17	118-KAAADKGKVSQNYPIV-132
	Gag 2	34, 35	Gag 24, 25	167-PMFTALSEGATPQDLNMLNTVGGH-191
	Gag 2	38	Gag 28	198-LKDTINEEAAEWDRHPV-215
	Pol 2	6, 7	Pol 30, 31	238-FWEVQLGIPHPAGLKKKSVTVLDV-262
	Pol 2	12-17	Pol 36, 37, 38, 39, 40, 41	284-PSINNETPGIRYQYNVLPQGWKGSFAIFQASMTKILEPFRAKNPEIYI-332
	Pol 4	6, 7	Pol 78, 79	590-TFYVDGAANRETKIGKAGYVTDGR-614
	Pol 4	12-17	Pol 84, 85, 86, 87, 88, 89	635-LALQDSESEVNIIVTDSQYALGIIQAQPDSESELVNIIEQLIKKERAYLSWVPAHK-691
	Env 2	6, 7	Env 36, 37	257-IRSENLNNTVKTIVHLNESIGIV-280
	Env 2	12-17	Env 42, 43, 44, 45, 46, 47	300-FYTNHIGDIRQAYCNISKQEWNKTLLEEVKRLQEHPNKTIKFNSSSGDLEI-353
	Env 4	6, 7	Env 84, 85	601-MQWDREINNYTNIYQLLEDSQI-623
	Env 4	12-17	Env 90, 91, 92, 93, 94, 95	644-WFSITNWLWYIKIFIMIVGGLIGLRIIFAVLSIVNRVRQGYSPFSQTLTPNPR-697
	Nef 2	40	Nef 12	46-SNTAHNNPDCAWLQA-60
	Nef 2	44-46	Nef 16, 17, 18	62-EEEEEVGFPVRPQVPLRPMYKA-84
	Vif 1	12-17	Vif 5, 6, 7, 8, 9, 10	33-RRANGWFYRHHYESRHPKVSSEVHIPLGEARLVIKTYWGLQTGERDWHLGHGVSIEW-89
Tat	12-17	Tat 2, 3, 4, 5, 6, 7	8-LEPWNHPGSQPNTPCNNCYCKHCSYHCLVCFQTKGLGISYGRKKRRRQRSTPPSSEDH-65	
NK+	Env 2	11, 12	Env 41, 42	292-IRIGPGQAFYTNHIGDIRQAYCNI-316
	Env 2	15-17	Env 45, 46, 47	322-NKTLEEVKRLQEHPNKTIKFNSSSGDLEI-353
	Tat	11, 12	Tat 1, 2	1-MEPIDPNLEPWNHPGSQPNTPCNNCY-26
	Tat	15-17	Tat 5, 6, 7	32-YHCLVCFQTKGLGISYGRKKRRRQRSTPPSSEDH-65

MP002

	Positive response		Identified peptide	Amino acid region spanned
	Pool	Matrix		
CD8 T cells	Gag 3	30	Gag 34	238-STLQEQIAWMTSNPPVPV-255
	Gag 3	36, 37	Gag 40, 41	285-GPKEPFRDYVDRFFKTLRAEQATQDV-310
	Env 4	23	Env 77	551-RVLAIERYLKQDQLLGLW-568
	Env 4	2	Env 80	573-KLICITNVPWNSSWSNK-589

	Nef 2	39	Nef 11	42-ALTSSNTAHNNPDCA-56
	Nef 2	48	Nef 20	78-RPMTYKAAFDSLFFL-92
NK+	Env 1	21, 23	Env 3, 5	17-GILGFWMLMICSQVGNLWVTIYYGVPVWREAK-48
	Env 1	4	Env 10	65-RNVWATHACVPTDPNPQEI-83
	Env 1	7	Env 13	87-NVTENFNMWKNMVDQMH-104
	Env 1	17	Env 23	159-VYALFYKPDIVPINESEY-176
	Env 2	21, 23	Env 27, 29	192-KVSFDPIPIHYCAPAGYAILKCNKTFNGTGPC-224
	Env 2	7	Env 37	264-NNVKTIIVHLNESIGIV-280
	Env 2	17	Env 47	338-NKTIKFNSSSGDLEI-353
	Vpu	23	Vpu 1	1-MLDLLAKVDYRLGVGALI-18
	Vpu	4	Vpu 6	43-KIDWLIKRIRERAEDSGNES-62
	Vpu	7	Vpu 9	70-STMVDMGHLRLLDVNDL-86

MP006

	Positive response		Identified peptide	Amino acid region spanned
	Pool	Matrix		
CD4 T cells	Gag 3	25-36	Gag 29- 40	206-AAEWDRLHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIAWMTSNPPVPVGDYIKRWIILGLNKIVRMYSVPSILDIK QGPKEPFRDYDRFFKTLR-302
	Gag 3	38	Gag 42	
	Env 1	19	Env 1	1-MRVRGIQRNWPQWWIWI-18
	Env 1	23, 24, 7	Env 5, 6, 7	32-NLWVTIYYGVPVWREAKTTLFCASDAKAYDR-62
	Env 1	7-10	Env 13, 14, 15, 16	87-NVTENFNMWKNMVDQMHEDIINLWDQSLKPCVKLTPL-124
	Env 1	14, 15	Env 20, 21	133-YNGSDTNDMRNCSFNTTTEIRDKKQTVY-160
	Env 1	18	Env 24	167-DIVPINESEYILHCNTSTI-186
	Nef 3	39-42, 44-48	Nef 21 -24, 26-30	82-YKAAFDSLFFLKEKGGLEGLIHSKRRQDILDWVYHTQGYFPDQWQNYTPGP-132
CD8 T cells	Gag 1	25-37	Gag 1 - 13	1-MGARASILRGKLDKWEKIRLRPGGKHYMLKHLVWASRELERFALNPGLLETSEGCKQIMKQLQPALQTGTEELRSL YNTVATLYCVHAGIEVRDTKEAL-101
	Gag 3	25-37	Gag 29- 41	206-AAEWDRLHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIAWMTSNPPVPVGDYIKRWIILGLNKIVRMYSVPSILDIK QGPKEPFRDYDRFFKTLRAEQATQDV-310
	Pol 1-4	1-24	Pol 1-92	32-711
	Env 1-5	1-24	Env 1-114	1-835
	Nef 1-5	39-48	Nef 1-50	2-207
	Vif 1, 2	1-24	Vif 1-24	1-192
	Vpr	8-18	Vpr 1-11	1-96
	Rev	1-10, 21-24	Rev 1-14	1-107
	Vpu	1-7, 23, 24	Vpu 1-9	1-86
NK+	Env 1	21, 23, 24	Env 3, 5, 6	17-GILGFWMLMICSQVGNLWVTIYYGVPVWREAKTTLFCA-54
	Env 1	11	Env 17	115-LKPCVKLTPLCVTLK-129
	Vpu	23, 24	Vpu 1, 2	1-MLDLLAKVDYRLGVGALIVALIIAIV-26

Amino acid coordinates at the start and end of each region are given according to their positions on Du179 (Env), Consensus C (Vpu, Vif, Vpr, Gag), Du151 (Nef) and Du422 (Tat, Pol, Rev) (Genbank accession numbers AY043174, consensus C of Jan 2002, AY043173 and AY043175, respectively; Los Alamos <http://www.hiv.lanl.gov>).