



Supplemental Figure 1

Supplemental Figure 1. Control TCR BV measurements in HIV-1-uninfected persons. PBMC from eight healthy HIV-1-seronegative donors were stimulated with the HIV-1 Gag peptide SLYNTVATL, an immunodominant A*02-restricted epitope and subjected to quantitative spectratyping as described in Figure 1. The changes in individual BV family peaks are plotted for all eight persons. Across the 1640 data points (205 peaks x 8 subjects), the mean change was 0.00 ± 0.26 units (one standard deviation).

Subject	Epitope	Location	HLA	ELISpot SFC/10 ⁶
00009	IKLEPVHGVY	Pol 464-472 (RT)	B*15	776
	ALVEICTEMEK	Pol 188-198 (RT)	A*03	147
	KVYLAWVPA	Pol 685-693 (RT)	A*03	53
	RIRTWKSLVK	Vif 17-26	A*03	429
00011	YISGKADGW	Vif 30-38	A*11	2360
	ISGKAKGWF	Vif 31-39	B*57	2120
	ISPRTLNAW	Gag 147-155 (p24)	B*57	1510
	TSTLQEQIGW	Gag 240-249 (p24)	B*57	600
	HTQGYFPDWQ	Nef 116-125	B*57	240
00016	RLRPGGKKKY	Gag 20-29 (p17)	A*03	945
	RRQDILDWY	Nef 105-115	C*07	915
	TERQANFL	Gag 427-434 (p7/p1)	B*40	605
	KELYPLASL	Gag 481-489 (p6)	B*40	815
	LEKHGAITS	Nef 37-45	B*40	210
	KEKGGLEGL	Nef 92-100	B*40	1120
00031	ILKEPVHGV	Pol 464-472 (RT)	A*02	200
	SLYNTVATL	Gag 77-85 (p17)	A*02	176
	RLISCNTSV	Env 192-200 (gp120)	A*02	176
00036	ISPRTLNAW	Gag 147-155 (p24)	B*57	619
	SLYNTVATL	Gag 77-85 (p17)	A*02	531
	IVLPEKDSW	Pol 399-407 (RT)	B*57	231
	VLEWRFDSDR	Nef 180-188	A*02	296
	KAFSPEVIPMF	Gag 162-172 (p24)	B*57	477
	TSTLQEQIGW	Gag 240-249 (p24)	B*57	462
00048	GLNKIVRMY	Gag 269-277 (p24)	B*15	1720
00049	GHQAAMQMLKE	Gag 193-203 (p24)	A*02	1255
00052	YFPDWQNYT	Nef 120-128	B*57	714
	QASQEVKNW	Gag 308-316 (p24)	B*57	703
	AVRHFPRIW	Vpr 30-38	B*57	249
	TSTLQEQIGW	Gag 240-249 (p24)	B*57	595
	PIVLPEKDSW	Pol 398-407 (RT)	B*57	350
	KAFSPEVIPMF	Gag 162-172 (p24)	B*57	1195
00068	HTQGYFPDWQ	Nef 116-125	B*57	570
	YFPDWQNYT	Nef 120-128	B*57	1000
	ISPRTLNAW	Gag 147-155 (p24)	B*57	585
	KAFSPEVIPMF	Gag 162-172 (p24)	B*57	265
	QASQEVKNW	Gag 308-316 (p24)	B*57	470
	KIATESIVIW	Pol 529-538 (RT)	B*57	260
00069	AIIRILQQL	Vpr 59-67	A*02	510
	SLYNTVATL	Gag 77-85 (p17)	A*02	280
	PLTFGWCYKL	Nef 136-145	A*02	40
	RIRQGLERI	Env 846-854 (gp 41)	A*02	265
00071	SVPLRPMTYK	Nef 73-82	C*04	985
	ISPRTLNAW	Gag 147-155 (p24)	B*57	85
	PIVLPEKDSW	Pol 398-407 (RT)	B*57	69
	RLRPGGKKK	Gag 20-28 (p17)	A*03	231
00072	KIRLRPGGK	Gag 18-26 (p17)	A*03	388
	RLRPGGKKKY	Gag 20-29 (p17)	A*03	1356

Supplemental Table 1. HIV-1-specific CTL responses studied.

<u>TCR BV Family</u>	<u>Primer Sequence</u>	<u>TRBV Genes Included</u>
BV02 (Vβ-22)	GCAGAAAGTCGAGTTTCTGG	BV2
BV03 (Vβ-09)	CCTAAATCTCCAGACAAAGC	BV3-1
BV04 (Vβ-07)	GCTTCTCACCTGAATGCCCC	BV4-1, BV4-2, BV4-3
BV05a (Vβ-05A)	TCAGTGAGACACAGAGAAAC	BV5-1
BV05b (Vβ-05B)	TGTGTCCTGGTACCAACAGG	BV5-3, BV5-4, BV5-5, BV5-6, BV5-7, BV5-8
BV06a (Vβ-13A)	CGACAAGACCCAGGCATGGG	BV6-1, BV6-3, BV6-5, BV6-6, BV6-7, BV6-8, BV6-9
BV06b (Vβ-13B)	AGACAAGATCTAGGACTGGG	BV6-4
BV07 (Vβ-06)	CTCAGGTGTGATCCAATTTTC	BV7-1, BV7-2, BV7-3, BV7-4, BV7-6, BV7-8, BV7-9
BV09 (Vβ-01)	CGCACAACAGTTCCTGACT	BV9
BV10 (Vβ-12)	CATGGGCTGAGGCTGATC	BV10-1, BV10-2, BV10-3
BV11 (Vβ-21)	TCACAGTTGCCTAAGGATCG	BV11-1, BV11-2, BV11-3
BV12 (Vβ-08)	TCTGGTACAGACAGACCATG	BV12-3, BV12-4, BV12-5
BV13 (Vβ-23)	GCAGGGTCCAGGTCAGGACCCCA	BV13
BV14 (Vβ-16)	AGTCTAAACAGGATGAGTCCG	BV14
BV15 (Vβ-24)	ACAATGAAGCAGACCCCCT	BV15
BV18 (Vβ-18)	GAGTCAGGAATGCCAAAGGA	BV18
BV19 (Vβ-17)	GGAGATATAGCTGAAGGGTA	BV19
BV20 (Vβ-02)	TCAACCATGCAAGCCTGA	BV20-1
BV24 (Vβ-15)	GTGTCTCTCGACAGGCACAG	BV24-1
BV25 (Vβ-11)	TCAACAGTCTCCAGAATAAGGACG	BV25-1
BV27 (Vβ-14)	GTCTCTCGAAAAGAGAAGAG	BV27
BV28 (Vβ-03)	GTCTCTAGAGAGAAGAAGGAGCGC	BV28
BV29 (Vβ-04)	GAGGCCACATATGAGAGTGG	BV29-1
BV30 (Vβ-20)	CAGCTCTGAGGTGCCCCAGA	BV30

Supplemental Table 2. TCR BV families, primers, and genes. The BV families, family-specific forward primers, and gene coverage of each family are listed. IMGT Database nomenclature is followed (family names in parentheses reflect the old serologic-based nomenclature for reference).

PCR Reaction	TCR BV Forward Primer	TCR Constant Reverse Primer and Dye	Run Group
1	BV09	5' FAM-CTTCTGATGGCTCAAACAC-3'	Group 1
2	BV18		
3	BV20	5' VIC-CTTCTGATGGCTCAAACAC-3'	
4	BV29		
5	BV28	5' NED-CTTCTGATGGCTCAAACAC-3'	
6	BV06a		
7	BV05a	5' FAM-CTTCTGATGGCTCAAACAC-3'	Group 2
8	BV05b		
9	BV15	5' VIC-CTTCTGATGGCTCAAACAC-3'	
10	BV27		
11	BV04	5' NED-CTTCTGATGGCTCAAACAC-3'	
12	BV02		
13	BV03	5' FAM-CTTCTGATGGCTCAAACAC-3'	Group 3
14	BV14		
15	BV25	5' VIC-CTTCTGATGGCTCAAACAC-3'	
16	BV10		
17	BV24	5' NED-CTTCTGATGGCTCAAACAC-3'	
18	BV06b		
19	BV19	5' FAM-CTTCTGATGGCTCAAACAC-3'	Group 4
20	BV07		
21	BV30	5' VIC-CTTCTGATGGCTCAAACAC-3'	
22	BV12		
23	BV11	5' NED-CTTCTGATGGCTCAAACAC-3'	
24	BV13		

Supplemental Table 3. Primer and Dye Combinations Utilized for Spectratyping. PCR amplifications were performed for each of the 24 listed primer combinations. The resulting PCR products were combined into the four indicated run groups for fragment analysis by capillary electrophoresis.

Subject	Epitope	Protein	HLA	BV	Peak#	Peak Expansion	CDR3 Sequence
00009	ALVEICTEMEK	Pol 188-198	A*03	BV04	6	6.1	ASSQALLGLTYEQYFG
				BV28	5	5.9	ASSXRTGSNEKLFFG
	IKLEPVHGVY	Pol 464-473	B*15	BV20	8	12.7	SATPGLAGVSAYEQYFG
				BV11	6	11.4	ASSSRTSGRAGEQFFG
				BV28	6	3.7	ASSSLAQGTYNQFFG
	KVYLAWVPA	Pol 685-693	A*03	BV07	3	4.3	ASSLEGAYEQYFG
				BV13	7	3.1	ASSFIGRETQYFG
	RIRTWKSLVK	Vif 17-26	A*03	BV18	3	8.4	ASSPXDAYEQYFG
				BV28	6	6.0	X
	00011	HTQGYFPDWQ	Nef 116-125	B*57	BV04	5	49.3
ISGKAKGWF		Vif 31-39	B*57	BV03	4	11.4	ASSQVNREETQYFG
				BV07	3	4.5	ASSLIEHGMFFG
ISPRTLNAW		Gag 147-155	B*57	BV11	7	27.1	ASSVTGAFTSNYGYTFG
				BV04	5	10.0	ASSQDPTANQPQHF
				BV07	4	6.6	ASSLGXGMKTQYFG
TSTLQEQIGW		Gag 240-249	B*57	BV10	1	4.1	SSQTSATLITGANVLTFFG
				BV05a	1	8.9	X
				BV20	2	14.4	X
YISGKADGW		Vif 30-38	A*11	BV25	6	6.4	SARGEGQAKNIQYFG
				BV11	4	18.8	ASSLQGGDTEAFFG
				BV27	7	11.7	ASSLGEVAGRRETQYFG
				BV03	4	10.2	ASSAVGGPGELFFG
				BV09	4	3.7	X
				BV09	8	3.2	ASSPPDYQAVSSDQYFG
00016	KEKGGLEGL	Nef 92-100	B*40	BV07	6	156.1	ASSLVSEGARYEQYFG
				BV06a	4	18.7	ASKEGTVNTEAFFG
				BV20	3	6.5	SASTLSNEQFFG
				BV05b	5	3.8	ASSSGDRSNSPLHFG
	KELYPLASL	Gag 481-489	B*40	BV04	5	49.3	ASSQDKSSWEPQHF
				BV07	4	3.5	X
				BV09	5	3.6	X
	LEKHGAITS	Nef 37-45	B*40	BV14	3	3.1	ASSVVANTEAFFG
	RLRPGGKCKY	Gag 20-29	A*03	BV14	3	4.9	ASSLDRAVEQYFG
				BV05b	4	320.2	ASSLDRNTGELFFG
	RRQDILDWY	Nef 105-115	C*07	BV09	3	4.5	X
				BV19	1	19.8	ASSFGSEAFFG
				BV07	4	13.2	ASSLAGLGQPQHF
	TERQANFL	Gag 427-434	B*40	BV28	6	4.7	X
				BV04	5	122.8	ASSQDKSSWEPQHF
BV07				4	23.5	X	
BV02				6	8.7	ASSLVXEGARYEQYFG	
00031	ILKEPVHGV	Pol 464-473	A*02	BV07	4	62.9	ASSLFTSGDTQYFG
				BV12	3	31.6	ASSWEISDGYTFG
				BV28	6	5.1	ASSFLAGANTGELFFG
				BV20	5	3.1	SATPGLAGVSAYEQYFG
	RLISCNTSV	Env 192-200	A*02	BV12	3	5.0	ASSWEISDGYTFG
00036	ISPRTLNAW	Gag 147-155	B*57	BV02	6	53.7	ASSERRGLAQEQYFG
				BV07	3	4.6	X
				BV27	7	3.4	X
	IVLPEKDSW	Pol 399-407	B*57	BV04	6	4.2	X
				BV04	5	6.7	X
	KAFSPEVPMF	Gag 162-172	B*57	BV19	2	26.0	ASSGGSYGYTFG
				BV11	1	21.2	ASSISYEQYFG
				BV18	2	3.0	FLCQWGDGETQYFG
	TSTLQEQIGW	Gag 240-249	B*57	BV11	1	10.0	ASSISYEQYFG
BV19				2	5.0	ASSGGSYGYTFG	
BV05a				2	3.4	X	
00048	GLNKIVRMY	Gag 269-277	B*15	BV11	4	25.2	ASSLDSGFLEQYFG
				BV29	2	4.4	SVEGRGGYTFG

00049	GHQAAMQMLKE	Gag 193-203	A*02	BV29	4	114.1	SVGPRQGGEQYFG
				BV07	3	44.8	ASSLGQGETQYFG
				BV20	4	31.9	SAPSLTTETQYFG
				BV27	2	31.9	ASSLGTGEAFFG
				BV06a	2	4.8	X
00052	AVRHFPRIW	Vpr 30-38	B*57	BV06a	4	3.2	ASSDFTGNAAEAFGG
	KAFSPEVIPMF	Gag 162-172	B*57	BV19	1	127.3	ASSGSYGYTFG
					2	21.6	X
				BV06a	2	4.9	ASTGVTYGYTFG
	QASQEVKNW	Gag 308-316	B*57	BV25	4	4.6	ASSGSGTYGYTFG
				BV19	1	18.8	ASSGSYGYTFG
				BV07	5	4.2	X
	TSTLQEQIGW	Gag 240-249	B*57	BV06a	2	3.8	X
				BV19	1	17.2	ASSGSYGYTFG
	YFPDWQNYT	Nef 120-128	B*57	BV19	1	12.5	ASSGSYGYTFG
BV11				3	5.6	ASSLGDQREGIFG	
BV07				5	3.6	X	
00068	HTQGYFPDWQ	Nef 116-125	B*57	BV07	5	24.2	ASSLGQGAVAEAFGG
				2	5.9	X	
			BV19	1	7.2	ASTGTYGYTFG	
	ISPRTLNAW	Gag 147-155	B*57	BV09	5	5.5	X
	KIATESIVIW	Pol 529-538	B*57	BV05a	5	12.6	ASSFNGETGELFFG
00069	QASQEVKNW	Gag 308-316	B*57	BV12	4	5.2	ASRSIDSYNEOFFG
	YFPDWQNYT	Nef 120-128	B*57	BV07	5	7.5	ASSLGQGAVAEAFGG
	AIIIRILQQL	Vpr 59-67	A*02	BV06a	6	5.2	ASSARGAWSQETQYFG
00071	PLTFGWYKYL	Nef 136-145	A*02	BV03	4	3.4	ASSRTVXEETQYFG
	SLYNTVATL	Gag 77-85	A*02	BV04	5	9.6	ASSQDIGVGYGYTFG
00071	ISPRTLNAW	Gag 147-155	B*57	BV07	4	34.0	ASSXXGWTNEQFFG
	PIVLPEKDSW	Pol 398-407	B*57	BV07	3	15.1	ASSRRQESSPLHFG
				BV05b	1	3.4	ASSNTGELFFG
	RLRPGGKKK	Gag 20-28	A*03	BV05b	4	78.6	ASSGGWGTDTQYFG
				BV04	4	14.1	X
				BV13	6	6.4	ASSSPGLSTRDEQYFG
	SVPLRPMTYK	Nef 73-82	C*04	BV06a	5	62.2	ASSYSRFGNTIYFG
				1	5.4	X	
BV05b				2	5.3	ASSIAGFEQYFG	
00072	KIRLRPGGK	Gag 18-26	A*03	BV11	4	3.8	ASSLWTXXNEQFFG
				BV13	4	5.1	ASSLVSGGDTQYFG
	RLRPGGKKKY	Gag 20-29	A*03	BV05b	4	33.5	X
					5	32.2	X
			BV09	5	4.9	ASSYAEGWKYEQYFG	

Supplemental Table 4. TCR sequences derived from bulk spectratyping PCR products. TCR sequences

were evaluated by direct analysis of the uncloned BV RT-PCR products as shown in Figure 2, for families where there was an expansion of ≥ 3 relative concentration units after epitope stimulation of PBMC.