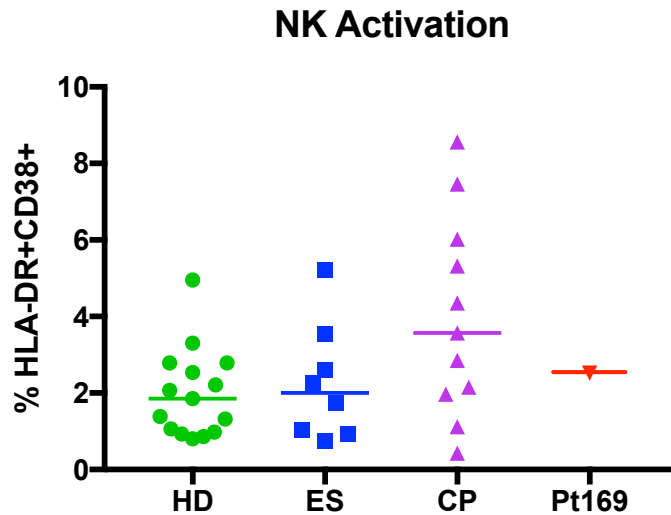
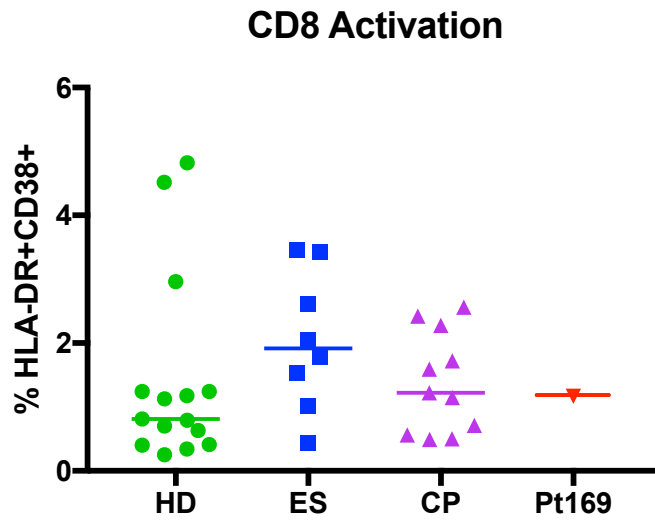
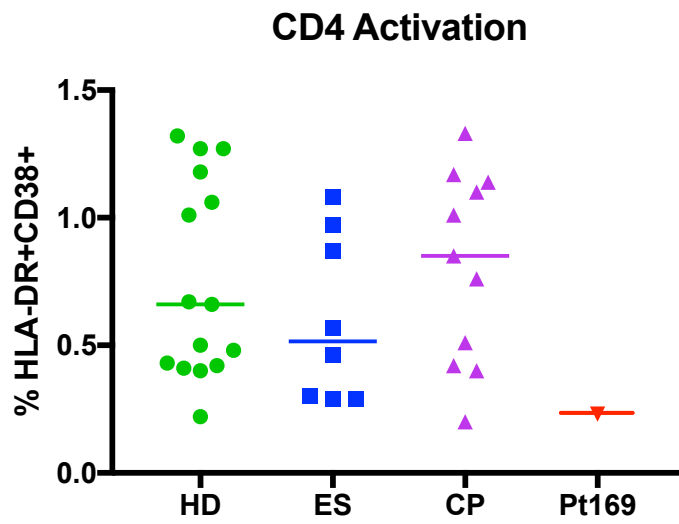


**Supplementary Figure 1. Clinical characteristics of Pt169 1999-2018**

Gray boxes indicate time when on ART. Black circles are timepoint in which virus was isolated from patient.



**Supplementary Figure 2**

Expression of activation markers on T cells and NK cells in healthy donors (HD), elite suppressors (ES), chronic progressors (CP) and Pt169

**Supplementary Table 1. Nucleotide changes in the sequences of replication competent isolates from Pt169 1999, 2010 and 2017**

Replication Competent (RC) clones	# of near full length sequences	NT changes ( $\Delta$ ) compared to 1999	NT changes ( $\Delta$ ) compared to majority clone 2017
2010-1A/1B	2	2 NT $\Delta$ LTR 18 NT <sub>del</sub> Gag 2 NT $\Delta$ Pol 1 NT $\Delta$ Vpr 2 NT $\Delta$ , 21 NT <sub>del</sub> Env 1 NT $\Delta$ Nef	2 NT $\Delta$ LTR 18 NT <sub>del</sub> Gag 2 NT $\Delta$ Pol 1 NT $\Delta$ Vpr 2 NT $\Delta$ , 21 NT <sub>del</sub> Env 1 NT $\Delta$ Nef
2010-2B	1	1 NT $\Delta$ Gag	1 NT $\Delta$ Nef 1 NT $\Delta$ Gag
2017-A (majority clone)	9	1 NT $\Delta$ Nef	NA
2017-B	1	2 NT $\Delta$ Nef	1 NT $\Delta$ Nef
2017-C	1	1 NT $\Delta$ Nef 1 NT $\Delta$ Env	1 NT $\Delta$ Env
2017-D	1	1 NT $\Delta$ Nef 1 NT $\Delta$ Gag	1 NT $\Delta$ Gag

**Supplementary Table 2. Nucleotide changes in the ES24 2017 clonal replication competent sequence compared to 2014**

Replication Competent (RC) clones	# of near full length sequences	NT changes ( $\Delta$ ) compared to 2014
2017	7	1 NT $\Delta$ Gag 1 NT $\Delta$ Env

**Supplementary Table 3. Integration Sites Pt169**

Patient	CellType	Position	GeneID	Detected	Abundance	Reads
Pt169	Tcells:CD4+	chr11-66090842	PACS1 *	U3:U5	2	204920
Pt169	Tcells:CD4+	chr11+118245719	MPZL3 *	U3	2	83918
Pt169	Tcells:CD4+	chr3+197125050	DLG1 *~	U3	2	964
Pt169	Tcells:CD4+	chr16+14219073	MKL2 *	U3:U5	1	103479
Pt169	Tcells:CD4+	chr17+32726741	MYO1D *	U5	1	1780
Pt169	Tcells:CD4+	chr16+1650101	CRAMP1 *	U5	1	1541
Pt169	Tcells:CD4+	chr1-117498637	MAN1A2 *	U3	1	214
Pt169	Tcells:CD4+	chr19-34200256	LSM14A *	U3	1	91
Pt169	Tcells:CD4+	chr4-5727077	EVC *	U3	1	57
Pt169	Tcells:CD4+	chr12+118311101	TAOK3 *	U3	1	53
Pt169	Tcells:CD4+	chr15+58131256	AQP9	U3	1	36
Pt169	Tcells:CD4+	chr3+171304517	TNIK *	U3	1	32
Pt169	Tcells:CD4+	chr22+21848473	MAPK1 *~	U5	1	6
Pt169	Tcells:CD4+	chr3-197155529	DLG1 *~	U5	1	2
Pt169	Tcells:CD4+	chr4-49040251	CWH43 *	U3	1	2
Pt169	Tcells:CD4+	chrY-6289171	FAM197Y9	U3	1	2
Pt169	Tcells:CD4+	chr11-38128576	LOC105376633	U3	1	1
Pt169	Tcells:CD4+	chr12-19713908	AEBP2	U3	1	1
Pt169	Tcells:CD4+	chr12-850073	WNK1 *	U3	1	1
Pt169	Tcells:CD4+	chr13-51510221	MIR4703	U3	1	1
Pt169	Tcells:CD4+	chr14-24470812	LOC101927045 *	U3	1	1
Pt169	Tcells:CD4+	chr18+34336630	NOL4	U3	1	1
Pt169	Tcells:CD4+	chr19+28053359	LOC101927151	U3	1	1
Pt169	Tcells:CD4+	chr22+16480471	CCT8L2	U3	1	1
Pt169	Tcells:CD4+	chr3-46992304	NBEAL2 *	U3	1	1
Pt169	Tcells:CD4+	chr3-65214462	MAG1	U3	1	1
Pt169	Tcells:CD4+	chr4-10286735	ZNF518B	U3	1	1
Pt169	Tcells:CD4+	chr4+19733685	SLIT2	U3	1	1
Pt169	Tcells:CD4+	chr6-117396395	ROS1 *~	U5	1	1
Pt169	Tcells:CD4+	chr6-62578024	KHDRBS2	U3	1	1
Pt169	Tcells:CD4+	chr7-102423034	LOC100630923 *	U3	1	1
Pt169	Tcells:CD4+	chr9+137975579	CACNA1B *	U3	1	1

**Supplementary Table 4. Integration Sites ES24**

Patient	CellType	Position	GeneID	Detected	Abundance	Reads
ES24	Tcells:CD4+	chr12+788438	WNK1 *	U3	11	50417
ES24	Tcells:CD4+	chr19-56575835	ZNF470 *	U3:U5	7	22977
ES24	Tcells:CD4+	chr1+111605702	LINC01160 *	U3:U5	5	7456
ES24	Tcells:CD4+	chrX+129586366	OCRL *	U3:U5	3	4653
ES24	Tcells:CD4+	chr11+66088645	PACS1 *	U3:U5	2	9317
ES24	Tcells:CD4+	chr21+46568571	DIP2A *	U5	2	9240
ES24	Tcells:CD4+	chr1-67334888	IL12RB2 *	U3:U5	2	895
ES24	Tcells:CD4+	chr7-100546895	AGFG2 *	U3	2	14
ES24	Tcells:CD4+	chr1+243035757	LINC01347	U3:U5	2	9
ES24	Tcells:CD4+	chr10-38469695	LINC00999	U5	2	2
ES24	Tcells:CD4+	chr20-519598	CSNK2A1 *~	U3:U5	2	2
ES24	Tcells:CD4+	chrY-24301096	GOLGA2P3Y	U5	2	2
ES24	Tcells:CD4+	chr8-68301074	C8orf34-AS1	U3	1	13826
ES24	Tcells:CD4+	chr19+9618298	ZNF561 *	U3	1	12728
ES24	Tcells:CD4+	chr22-17218184	ADA2 *	U3	1	10702
ES24	Tcells:CD4+	chr19+43759400	SMG9	U5	1	8164
ES24	Tcells:CD4+	chrX+45182310	CXorf36 *	U3	1	7112
ES24	Tcells:CD4+	chr6-90015830	BACH2 *~	U3	1	2312
ES24	Tcells:CD4+	chrX-71540482	OGT *	U3	1	2181
ES24	Tcells:CD4+	chr17+44469357	GPATCH8 *	U5	1	657
ES24	Tcells:CD4+	chr1+150420900	RPRD2 *	U3	1	433
ES24	Tcells:CD4+	chr19-1974779	CSNK1G2 *	U5	1	417
ES24	Tcells:CD4+	chr11+63893432	MARK2 *	U5	1	388
ES24	Tcells:CD4+	chr22+40106897	TNRC6B *	U5	1	170
ES24	Tcells:CD4+	chr17-81878965	ARHGDI A	U3	1	44
ES24	Tcells:CD4+	chr18+2949476	LPIN2 *	U5	1	33
ES24	Tcells:CD4+	chr7-44411464	NUDCD3 *	U3	1	17
ES24	Tcells:CD4+	chr10+126033432	ADAM12 *~	U3	1	10
ES24	Tcells:CD4+	chr19-47153461	SAE1 *	U5	1	7
ES24	Tcells:CD4+	chr20+47258233	ZMYND8 *~	U5	1	5
ES24	Tcells:CD4+	chr6+128375	LINC00266-3	U3	1	4
ES24	Tcells:CD4+	chr10-38406250	SEPT7P9	U5	1	2
ES24	Tcells:CD4+	chr11+170382	SCGB1C1	U5	1	2
ES24	Tcells:CD4+	chr2+86163183	IMMT *	U3	1	2
ES24	Tcells:CD4+	chr19+12654658	MAN2B1 *	U5	1	1
ES24	Tcells:CD4+	chr20-64306882	LINC00266-1	U3	1	1
ES24	Tcells:CD4+	chr7+6334995	FAM220A *	U5	1	1
ES24	Tcells:CD4+	chr8+188554	RPL23AP53	U5	1	1
ES24	Tcells:CD4+	chrY+25369046	GOLGA2P3Y	U5	1	1

**Supplementary Table 5. Epitopes targeted in Gag and Nef by Pt169 CD8+ T cells**

SFC per million	Gag AA#	Consensus sequence	AA Δ compared to	
			2010 Pt169 sequences	2017 clonal Pt169 sequence
270	9-23	SGGELDRWEKIRLRP		
50	37-51	ASRELERFAVNPGLL		
25	77-91	SLYNTVATLYCVHQR	V82I, R91N (3/3)	V82I, R91N
40	241-255	STLQEQIGWMTNPP	N252S (3/3)	N252S
35	265-279	WIILGLNKIVRMYP		
510	353-364	VGGPGHKARVLAEAM	G357A (3/3)	G357A
<b>Nef AA#</b>				
440	6-19	WSKRSVVGWPTVRER	R8S, V10I, T15A, V16I, R17G (2/3) R8S, V10I, T15A, V16I (1/3)	R8S, V10I, T15A, V16I
40	12-26	WPTVRERMRRAEPA	T15A, V16I, R17G (2/3) T15A, V16I (1/3)	T15A, V16I
30	182-195	MDDPEREVLEWKFDS	R186K (3/3)	R186K

**Supplementary Table 6. Epitopes targeted in Gag and Nef by ES24 CD8+ T cells**

SFC per million	Gag AA #	Consensus sequence	AA Δ compared to	
			2014 ES24 sequences	2017 clonal ES24 sequence
382.5	24-39	GKKKYKLVHIVWASR		
447.5	93-107	EVKDTKEALEKIEEE	E93D (13/13)	E93D
622.5	141-155	QMVHQAISPRTLNAW		
140	161-175	EKAFSPEVPMFSAL		
310	237-251	AGTTSTLQEQIGWMT		
60	269-283	GLNKIVRMYSPTSIL		
27.5	297-311	VDRFYKTLRAEQASQ		
82.5	333-347	ILKALGPAATLEEMM		
32.5	365-379	EAMSQVTNSATIMMQ	M378I (13/13)	M378I
45	433-447	FLGKIWPSHKGRPGN		
40	453-467	PEPTAPPEESFRFGE		
25	483-497	KELYPLASLRSLFGN		
<b>Nef AA#</b>				
35	65-79	EVGFPVRPQVPLRPM	R71T (1/12) V74I (11/12)	V74I
107.5	81-95	YKAAVDLSHFLKEKG		
80	89-103	HFLKEKGGLEGLIYS		
47.5	113-127	WVYHTQGYFPDWQNY		
85	133-47	IRYPLTFGWCFKLVP	I133T (12/12) F139Y (11/12)	I133T, F139Y

Note: Red indicates known B57 epitope