

TABLE S3. Repeats in HCIV-1 genome.

Tandem repeats ^a			
Coordinates ^b	Consensus sequence (size in nt)	Copy number	Match (%)
11044-11088 (ORF 16)	<u>cg</u> tcgccg <u>cc</u> g <u>tc</u> g <u>tc</u> ac (18)	2.5	96
15186-15239 (ORF 24)	<u>cg</u> acgag <u>gc</u> g <u>cc</u> ag <u>cc</u> gc (21)	2.5	81
15449-15503 (ORF 24)	<u>cc</u> gacgag <u>gc</u> g <u>cc</u> acg <u>gc</u> g (22)	2.6	80
15754-15803 (ORF 24)	<u>g</u> acgacg <u>tc</u> gacg <u>g</u> accg <u>tc</u> (21)	2.4	87
30127-30156 (ORF 47)	<u>ag</u> g <u>tc</u> g <u>tc</u> g <u>gc</u> ctcc (15)	2.0	93
30492-30533 (ORF 47)	<u>g</u> tcg <u>tc</u> g <u>tc</u> g <u>cc</u> (12)	3.5	87
31197-31243 (right end of the genome)	<u>gc</u> ggtccgaccg <u>gc</u> ccct (18)	2.6	80
Inverted repeats ^c			
Coordinates ^b	Sequence ^d	Match (%)	
11047-11087/16326-16286 (ORF 16/ORF 25)	<u>cg</u> tcgccg <u>tc</u> g <u>tc</u> accg <u>tc</u> gccg <u>cc</u> g <u>tc</u> g <u>tc</u> accg <u>tc</u> gccg	90	
446-475/20161-20190 (Upstream ORF 1/ between ORF 30 and ORF 31)	<u>ag</u> g <u>gc</u> gacagacg <u>gc</u> ccg <u>tc</u> gagc <u>gc</u> ggtccg	96	
15296-15394/29492- 29590 (ORF 24/ORF 47)	<u>tg</u> g <u>cc</u> gacgag <u>gc</u> g <u>gc</u> gag <u>tc</u> g-caaccag <u>gc</u> g <u>gc</u> g <u>cc</u> gacga g <u>tc</u> g <u>gc</u> g <u>cc</u> ag <u>gc</u> g <u>gc</u> gacgacg <u>cc</u> g <u>cc</u> accg <u>tc</u> g <u>tc</u> gagcagc- ccg <u>gc</u> gacg <u>cc</u> g	75	

^a Tandem repeats found with Tandem Repeats Finder program.

^b Nucleotide coordinates in HCIV-1 sequence.

^c Inverted repeats found with Einverted program.

^d Underlined, sequence mismatch; hyphen, gap in sequence.