

S1 Table. Classification of the HIV-1 subtype B sequences in the B_{PANDEMIC} or B_{CAR}

Dataset	Country*	Subtype B	B _{PANDEMIC} (%)	B _{CAR} (%)	Putative Recombinants (%)
FL	DO	4	-	4 (100)	-
	HT	6	-	5 (83)	1 (17)
	JM	8	4 (50)	4 (50)	-
	TT	5	-	5 (100)	-
	BR	118	106 (90)	1 (1)	11 (9)
	US	330	306 (93)	9 (3)	15 (5)
	Others	35	34 (97)	-	1 (3)
	Total	506	450 (88)	28 (6)	28 (6)
Years	1978-2015	1978-2015	1983-2011	1986-2012	
<i>gag</i> (HXB2 coordinates 1,264 to 2,148)	DO	4	-	4 (100)	-
	HT	12	3 (25)	9 (75)	-
	JM	18	8 (44)	10 (56)	-
	TT	5	-	5 (100)	-
	BR	107	106 (99)	1 (1)	-
	US	315	306 (97)	9 (3)	-
	Others	34	34 (100)	-	-
	Total	495	457 (92)	38 (8)	-
Years	1978-2015	1978-2015	1983-2011	-	
<i>pol</i> (HXB2 coordinates 2,253 to 3,272)	BS	14	5 (36)	9 (64)	-
	DO	144	39 (27)	105 (73)	-
	HT	5	-	5 (100)	-
	JM	151	78 (52)	73 (48)	-
	TT	5	-	5 (100)	-
	BR	107	106 (99)	1 (1)	-
	US	315	306 (97)	9 (3)	-
	Others	34	34 (100)	-	-
Total	775	568 (74)	207 (26)	-	
Years	1978-2015	1978-2015	1983-2011	-	
<i>env</i> (HXB2 coordinates 6,450 to 8,480)	DO	5	1 (20)	4 (80)	-
	HT	11	-	11 (100)	-
	JM	9	5 (56)	4 (44)	-
	TT	40	-	40 (100)	-
	BR	107	106 (99)	1 (1)	-
	US	315	306 (97)	9 (3)	-
	Others	34	34 (100)	-	-
	Total	529	452 (87)	69 (13)	-
Years	1978-2015	1978-2015	1983-2011	-	
<i>pol</i> -drug naïve (HXB2 coordinates 2,253 to 3,272)	CU	85	84 (99)	1 (1)	-
	DO	143	42 (29)	101 (71)	-
	HT	5	1 (20)	4 (80)	-
	JM	26	11 (42)	15 (58)	-
	GF	255	109 (43)	146 (57)	-
	SR	57	33 (58)	24 (42)	-
	Others	6	1 (100)	5 (100)	-
	Total	577	281 (49)	296 (51)	-
Years	2005-2012	2005-2012	2005-2012	-	

The table summarizes the results of the classification of the full-length (FL) and partial HIV-1 subtype B sequences in the B_{PANDEMIC} or B_{CAR} based on their placement on ML phylogenetic trees displayed in Figures 1 and S1. All sub-datasets are accompanied by their sampling range. *Country codes are in accordance with ISO 3166-1.