

Table 2: Evolution of antiretroviral resistance mutations in HIV-1 individuals with dual infections

Case	Time points	Primary subtype		Secondary subtype	
		Prot	RT	Prot	RT
C1	S1	NONE	M41L/ M184V/ Y188L/ L210W/ T215Y ²¹ <i>V106I, H221Y and D67N^(A)</i>	NONE	NONE
	S2	L10I/ I15V/ M46I/ L63P/ I84V/ I85V/ L90M ¹² <i>M36I and F53L/ A71T^(A)</i>	M41L/ D67N/ L210W/ T215Y ¹²	NON DETECTED	
C2	CRF12_BF		B subtype		
	NONE	NONE	I84V/ L90M	M41L/ K70E/ L210W/ T215Y	
C3	B subtype		CRF12_BF		
	NONE	K103N ¹	NONE	NONE	
C4	CRF12_BF		B subtype		
	S1	I47V ¹	NONE	NONE	NONE
S2	NONE	K70R ¹	NON DETECTED		
C5	CRF12_BF		BF recombinant (not CRF12)		
	S1	NONE	Y181C/ H221Y ²	NON DETECTED	
S2	NONE	Y181C ¹	NONE	NONE	

A mean of sixteen sequences and/ or clones per sample were analyzed with Stanford software. Resistance mutations separated by bars indicate combination of mutations in the sequences. The number indicated by superscript shows the number of sequences or clones with the corresponding mutation or combination of mutations.

(A) Each mutation in different sequences and carrying the combination of mutations indicated.