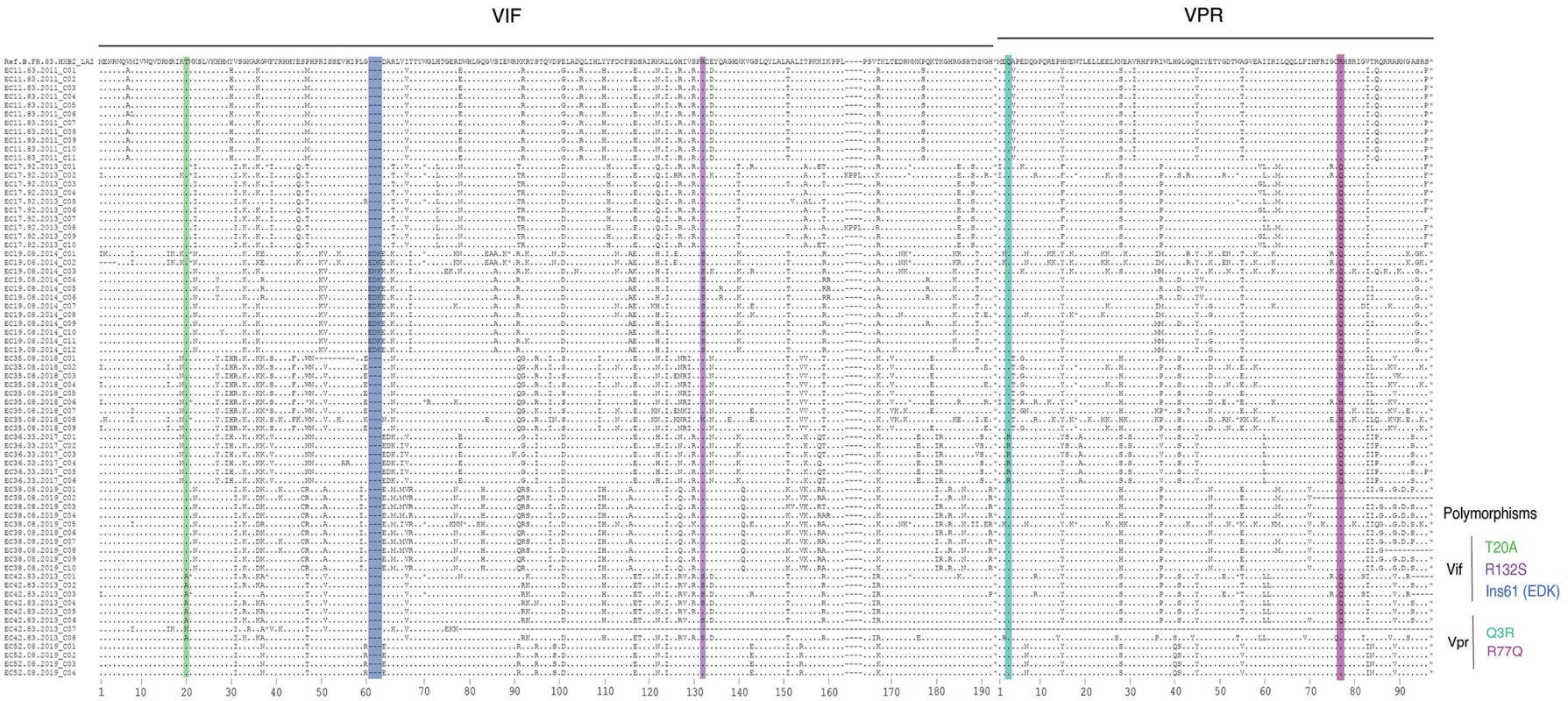

Alignment of all amino acid clones sequences generated for the Vif and Vpr proteins of ECs. Dots indicate amino acids identical to those in the HXB2 reference sequence, which is shown on the top line. Asterisks indicate regions with premature and final stop codons for each protein. Gaps were identified with a dash (-). The highlighted colors in the amino acid sequences indicate polymorphisms described as enriched in LTNPs [Vif: R132S and Ins61 (EDK); Vpr: Q3R and R77Q] or not (Vif: T20A), as shown in the legend.

TABLE I

Amplification strategy of *vif* and *vpr* HIV-1 accessory genes

1° PCR amplification	Fragment Size*	2° PCR amplification	Fragment Size*
SCCOS(Fw): 5'TACAGTGCAGGGGAAAGAATARTAGACATAATA 3	1,170pb	SCCNS (Fw): 5'CAAAATTTCCGGGTTTATTACAGGGACA 3'	1,087pb
ED3AS (Rv): 5'CCTGCCATAGGARATGCCTAA 3'		ED3AS (Rv): 5'CCTGCCATAGGARATGCCTAA 3'	

PCR: polymerase chain reaction; Fw: forward; Rv: reverse; *Fragment size in relation the HXB2.

TABLE II

Summary of HIV-1 genetic mutations in *vif* and *vpr* accessory genes

Protein	Polymorphism	Enriched in ECs/LTNPs	Functional impact	Reference
Vif	T20A	Not determined	Reduced Vif stability and HIV-1 replication in PBMCs	(46)
	E88A+W89A		Reduced Vif expression and HIV-1 replication in H9 cells	(55)
	C114A/S		ΔVif phenotype	(47,56)
	F115A			
	R132A			
	C133A/S			
	I107T	Yes	Reduced HIV-1 replication in PBMCs	(12)
	R132S			(33)
	Ins61(DS)			(30)
	V13I		Not determined	(11)
	V55T			
	L81M			
	K22E		Reduced HIV-1 infectivity	(57)
	S32P			
	Y40H			
	E45G			
	F115S			
	G138R			
	L150P			
Vpr	Q3R	Yes	Reduce the cytopathicity	(35)
	Q65R		Failed to induce G2-arrest and cell death	(58)
	F72L		Reduce incorporation of Vpr into the forming virions	(38)
	R77Q		Reduce the cytopathicity	(8,9,13,37)
	R90N		Not determined	(13)
	L23F	Not determined	1) Nucleoporin binding mutant, diffuse nucleocytoplasmic distribution, 2) unable to cause G2/M arrest	(59)
	E24R, R36P		Selectively disrupts Vpr binding to helicase-like transcription factor (HLTF) without disturbing the UNG2 degradation	(60,61)
	K27M		1) Nucleoporin binding mutant, diffuse nucleocytoplasmic distribution, 2) no G2 arrest, 3) no apoptosis induction, 4) no accumulation at the nuclear envelope	(62)
	A30F		Unable to bind gag and package into particles	(63)
	F34I		1) Decreased Vpr incorporation into virions compared to WT Vpr, 2) Unable to bind the nuclear envelope but causes G2/M arrest	(23,64)
	P35N		Unable to interact with cyclophilin A	(65)
	Y50A		G2/M arrest defective mutant	(13)
	W54R		Defective for UNG2 loading onto CRL4 but retains binding to DCAF	(62)
	G56A		Defective for HLTF degradation, ability to arrest cell cycle maintained	(66)
	L68A		Nuclear export mutant	(67)
	F69A		DCAF binding mutant, but associates with Exo1 like wild type Vpr	(68)
	H71R		1) DCAF binding mutant, unable to induce G2/M cell cycle arrest, 2) Decreased Vpr incorporation into virions	(25,64,69)
	R73A/S		Reduce the cytopathicity	(37,70)
	R90K		Relieves IL-12 suppression	(71)
	R85QRR		Impaired nuclear targeting by the virus	(72)

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