

Supplementary table 1. Amplification and genotyping outcomes by viral load groups

	Amplification success		Sequencing Success**	
	HIV PRRT	HIV IN	HIV PRRT	HIV IN
Total (n=100)	68 (68.0%)	71 (71.0%)	49/68 (72.1%)	51/71 (71.8%)
LLV (200-999 copies/mL) (n=30)	16 (53.3%)	21 (70.0%)	9/16 (56.3%)	11/21 (52.4%)
VL \geq 1000 copies/mL (n=70)	51 (72.9%)	52 (74.3%)	40/51 (78.4%)	40/52 (76.9%)

*HIV IN-HIV integrase region; HIV PRRT- HIV protease and reverse transcriptase region; n-total number of samples; ** Sequencing success was calculated using the number of successfully amplified samples as the denominator.*