

Electronic Supplementary Material

Premature Stop Codon at Residue 101 within HIV-1 Rev Does Not Influence Viral Replication of Clade BC but Severely Reduces Viral Fitness of Clade B

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A		gp41									
B WT Rev	832 GGG TGG GAA GCC CTC AAA TAT TGG 855 278 G W E A L K Y W 285										
B Rev Q101Stop	832 GGG TGG GAA GCC CTT AAA TAT TGG 855 278 G W E A L K Y W 285										
B		gp41									
BC WT Rev	838 GGG TGG GAA GCC CTT AAA TAT CTG 862 285 G W E A L K Y L 292										
BC Rev Stop101Q	838 GGG TGG GAA GCC CTC AAA TAT CTG 862 285 G W E A L K Y L 292										

Fig. S1 Alignment of DNA and amino-acid sequences at residue 282 within gp41 TM region between wild-type virus and mutated virus. The red character indicates the mutated base. (A) clade B virus; (B) clade BC virus.

Table S1. Primers sequences used in the experiment

Name	Sequence (5' –3')
BC-Stop101Q -F	GGTGGGAAGCCCTCAAATATCTGG
BC-Stop101 Q-R	CCAGATATTTGAGGGCTTCCCACC
BC-E117Stop -F	CTGGAGCTGAAAAGTAGTGCTATTAG
BC-E117Stop-R	CTAATAGCACTACTTTTCAGCTCCAG
B-BH10-Q101Stop-F	GGGTGGGAAGCCCTTAAATATTGGTGGAA
B-BH10-Q101Stop-R	TTCCACCAATATTTAAGGGCTTCCCACCC
BC-ClaI-F	AGCTTAATCGATCTGTAGAAATTG
BC-BamHI-R	TTGCCCCGGATCCTTATTGTAACGCTGC
B-BmtI-F	CAGATAGCTAGCAAATTAAGAG
B-HpaI-R	GAGCAAGTTAACAGCACTATTC