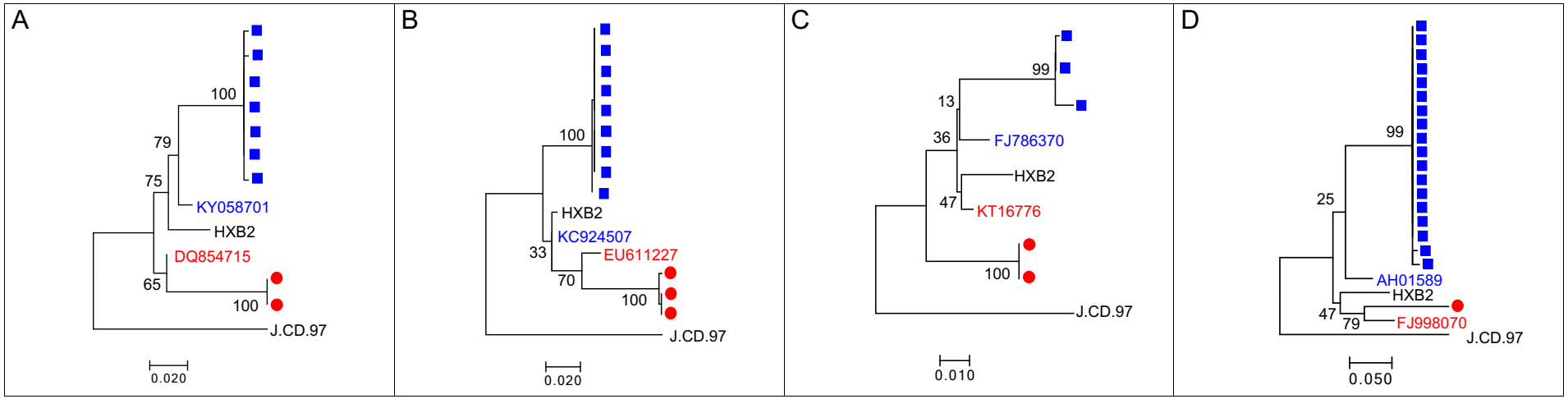
Supplementary Figure 1.



Phylogenetic analyses of patient derived sequences using the maximum likelihood method[24] were performed on coding sequences derived from June 9th blood samples the patient (red circle) and suppressed partner (blue square) in A) protease B) reverse transcriptase without drug resistance mutation sites C) integrase and D) the V3 region of HIV envelope. Bootstrapping was performed 1000 times and values are indicated. In panels A and B the scale bar represents 0.020 nucleotide substitutions (ns) per site; in Panel C 0.010 ns per site and Panel D 0.050 ns per site. The closest sequences searched by BLAST are indicated in red for the patient's strain and in blue for the partner's strain.

NRTI[1] resistance mutations:		**K65R[3], M184V**	
NNRTI[2] resistance mutations:		**K103S, E138Q, Y188L**	
Other mutations:		K46M, S68G, G93E, A98S, I142T, S163Y, Q174K, V179I, T200A, Q207E, R211K, F214L, V245M	
NRTI		NNRTI	
lamivudine (3TC)	high-level resistance	efavirenz (EFV)	high-level resistance
abacavir (ABC)	high-level resistance	etravirine (ETR)	low-level resistance
zidovudine (AZT)	susceptible	nevirapine (NVP)	high-level resistance
stavudine (D4T)	intermediate resistance	rilpivirine (RPV)	high-level resistance
didianosine (DDI)	high-level resistance		
emtricitabine (FTC)	high-level resistance		
tenofovir (TFV)	high-level resistance		

1. Nucleoside reverse transcriptase inhibitors
2. Non-nucleoside reverse transcriptase inhibitors
3. Amino acid substitutions in bold are known resistance conferring mutations.

Supplementary Table 1. Reverse transcriptase drug resistance profile