



**Supplementary Figure 2.** Subtyping of the near full-length HIV-1 consensus sequences, obtained by deep sequencing, was performed using the Recombination Identification Program (RIP 3.0) from the Los Alamos HIV Sequence Database as described (1). The similarity plots show distance measurements between the query sequence (patient-derived HIV-1) and the reference HIV-1 sequences from different subtypes.

1. Siepel A.C., Halpern A.L., Macken C, and Korber B.T. (1995). A computer program designed to screen rapidly for HIV type 1 intersubtype recombinant sequences. *AIDS Res Hum Retroviruses* 11:1413-6