**Identification of CRF89\_BF, a new member of an HIV-1 circulating BF intersubtype recombinant form family widely spread in South America.**

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**Supplementary Fig. S1. Analysis of root-to-tip divergence vs. year of sample collection of 65 CRF12\_BF Pr-RT sequences with TempEst.** The analysis was done after removing 8 outlying sequences identified in initial analyses.

**Supplementary Fig. S2.** **Bootscan analyses of 6 Pr-RT sequences of the BF cluster (a-f) and 3 of CRF12\_BF (g-i).** The horizontal axis represents the position from the 3’ end of protease of the mid-point of a 250 nt window moving in 20 nt increments and the vertical axis represents bootstrap values supporting clustering with subtype reference sequences.

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**Supplementary Fig. S3. Bootscan plots of two sequences of ~7 kb of the BF cluster from UK.** The horizontal axis represents the position in the HXB2 genome of the mid-point of a 250 nt window moving in 20 nt increments and the vertical axis represents bootstrap values supporting clustering with subtype reference sequences. The bootscan plot of the NFLG sequence of BOL0137 is shown on top for comparison.

**Supplementary Fig. S4. Maximum clade credibility tree of CRF89\_BF Pr-RT sequences with location traits of some sequences from Bolivian and Peruvian individuals residing in Spain changed to Spain.** Theanalysis was done with the same parameters as an earlier analysis (whose posterior tree distribution is summarized in the MCC tree shown in Fig. 7), only changing the location traits of some samples from Peruvian (M1079, MS0360) or Bolivian (P2345, P3177) individuals residing in Spain belonging to clusters of relatively recent origin from Peru or Bolivia to Spain. The rest of the figure description is as in the legend of Fig. 7.

**Supplementary Fig. S5.** **Maximum clade credibility tree of CRF12\_BF Pr-RT sequences.** MeantMRCA and 95% HPD interval at the root are shown.