



**Supplementary Figure 2.** Maximum likelihood estimate of phylogenetic relationships amongst the HIV-1 M group subtypes and the CRF<sub>x</sub>\_BFs with a focus on subtypes B and F. Lineages shown with dashed lines have <70% bootstrap support, whereas lineages shown in solid lines have ≥70% bootstrap support. Note phylogenetic relationships among subtypes are impacted by recombination, yet our target group of CRF47\_BF sequences form a well supported monophyletic group.