



SUPPLEMENTARY FIG. S1. Phylogenetic maximum likelihood tree of HIV RT sequences from the Dominican Republic (DR) sampled from 2001 to 2010. A reference set of 66 sequences was downloaded from the Los Alamos HIV database (<http://www.hiv.lanl.gov>). The reference set includes sequences from Haiti (HT, $n=30$), the United States (USA, $n=10$), Martinique (MQ, $n=5$), Trinidad-Tobago (TT, $n=5$), Puerto Rico (PR, $n=10$), and Jamaica (JAM, $n=5$). Bootstrap values higher than 80% are marked at the branches (●). The tree was rooted using reference sequence HXB2. Branch lengths were estimated with the best fitting nucleotide substitution model and were drawn to scale with the bar at the bottom indicating 0.03 nucleotide substitutions per site. Sequences from the DR are identified by the year of sampling followed by the sample number.