**Supplemental Digital Content 1. Methods used for next generation sequencing (NGS).**

Next generation sequencing (NGS) was performed using the MiSeq System (Illumina, Inc., San Diego, CA, USA) using methods adapted from a previous study (Dudley DM, Bailey AL, Mehta SH, et al. Cross-clade simultaneous HIV drug resistance genotyping for reverse transcriptase, protease, and integrase inhibitor mutations by Illumina MiSeq. *Retrovirology.* 2014;11:122). Five percent (5%) denatured PhiX beads were used as a sequencing control; samples were loaded into 600-cycle MiSeq cartridges and sequenced. Data was analyzed by CLC Genomics Workbench v9.0 software (Qiagen, Asrhus, Denmark). Paired end reads were trimmed for quality (limit=0.05) and ambiguity (2-nt maximum). PCR primer sequences were removed. Reads <50 bases in length were discarded. Trimmed reads were aligned to a reference sequence (HXB2 #NC\_001802). The following alignment settings were applied: mismatch 2, insertion 3, deletion 3, length fraction 0.7, and similarity fraction 0.8. The frequency of drug resistance mutations was determined using the Low Frequency Variant Detection Tool from the CLC Bio software (cut-off for significance: 2%; minimum frequency for variants: 1000 reads). Default settings were used for error rate calculations.