



0.1
 Supplemental Figure 1. Phylogenetic tree of full protease/reverse transcriptase amplicons. Tree contains 523 sequences representing 43 subjects at a total of 187 visits. Tree was generated using the maximum likelihood method employed in DIVEIn web analysis software (<http://indra.mullins.microbiol.washington.edu/DIVEIN/>). Branches of reference strains are black. The scale bar represents the number of nucleotide substitutions per site.