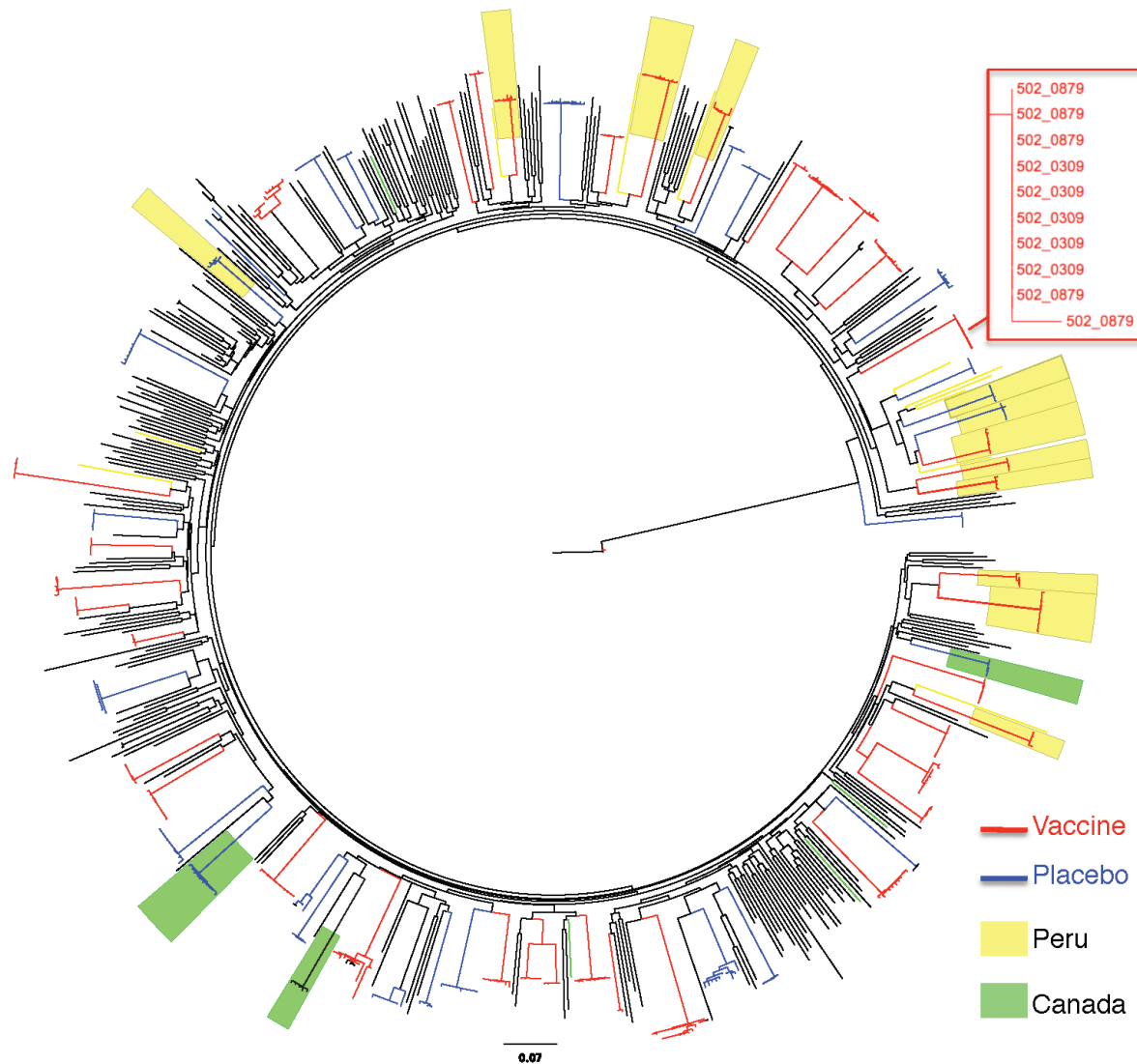


Supplementary Fig. 1



Supplementary Fig. 1. Maximum-Likelihood phylogenetic tree using *env* nucleotide sequences. Four hundred and fifty nine HIV-1 *env* sequences from infected trial participants are shown, with placebo recipient taxa shown in blue and vaccine recipient taxa in red. Also included are contemporary sequences from the US (in black), from Canada (in green) and from Peru (in yellow). Likewise, sequences isolated from trial participants in Canada are highlighted in green, and sequences isolated from individuals in Peru are highlighted in yellow. The inset represents sequences from two individuals with closely related viruses.