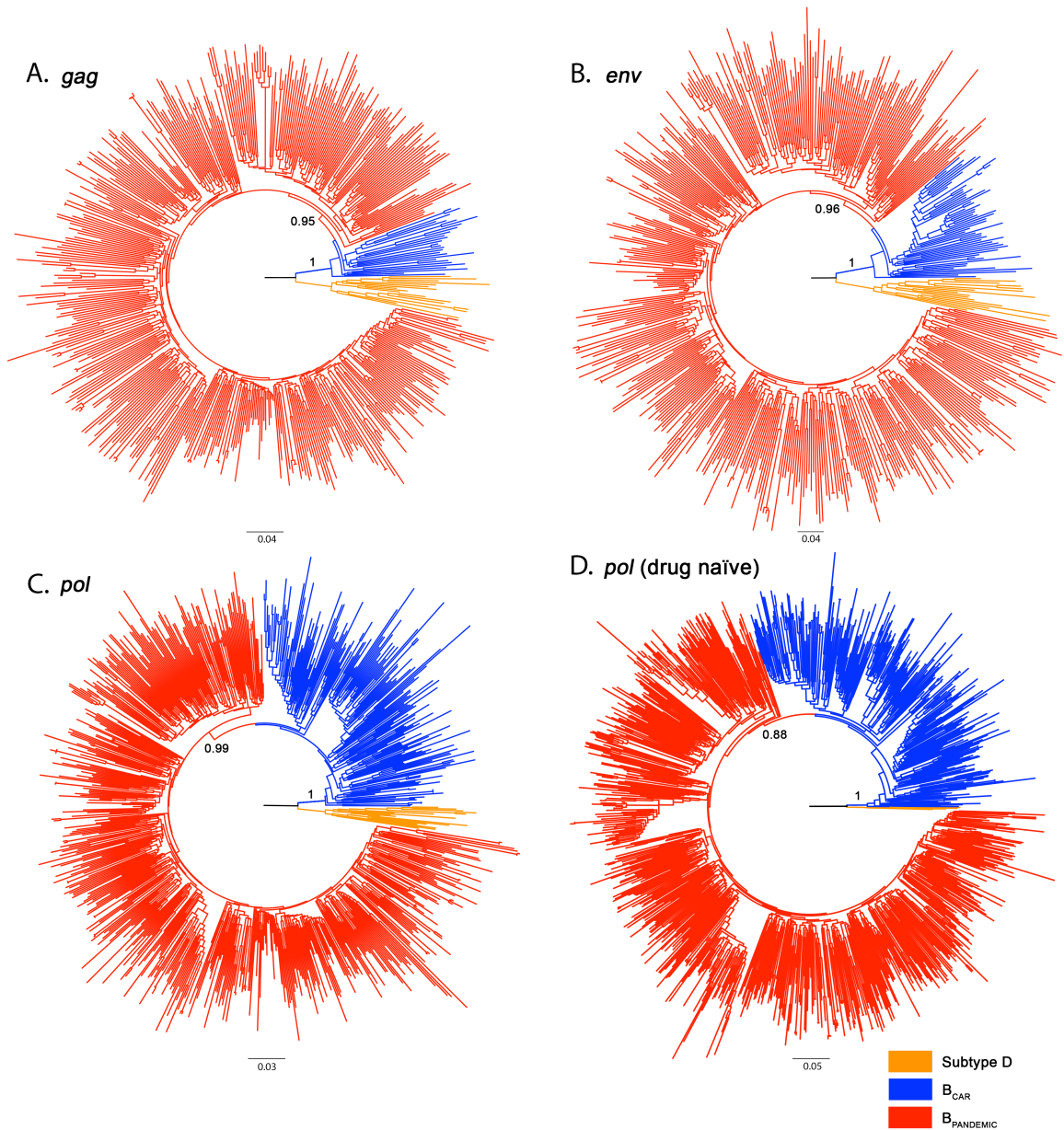


Supplementary Figures:



**Figure S1:** ML phylogenetic trees of HIV-1 subtype B American sequences on specific regions of *gag*, *pol*, and *env*. Partial HIV-1 sequences covering (A) *gag* (1,264 to 2,148), (B) *env* (6,450 to 8,480), (C) *pol* (2,253 to 3,272), and (D) *pol* from drug naïve individuals (2,253 to 3,272) were classified into  $B_{PANDEMIC}$  (red branches) and  $B_{CAR}$  (blue branches) lineages according to the topology obtained in each tree. Node support (SH-aLRT) for subtype B and  $B_{PANDEMIC}$  monophyletic groups are indicated. The trees were rooted using HIV-1 subtype D sequences. Branch lengths are drawn to scale with the bar at the bottom indicating nucleotide substitutions per site.