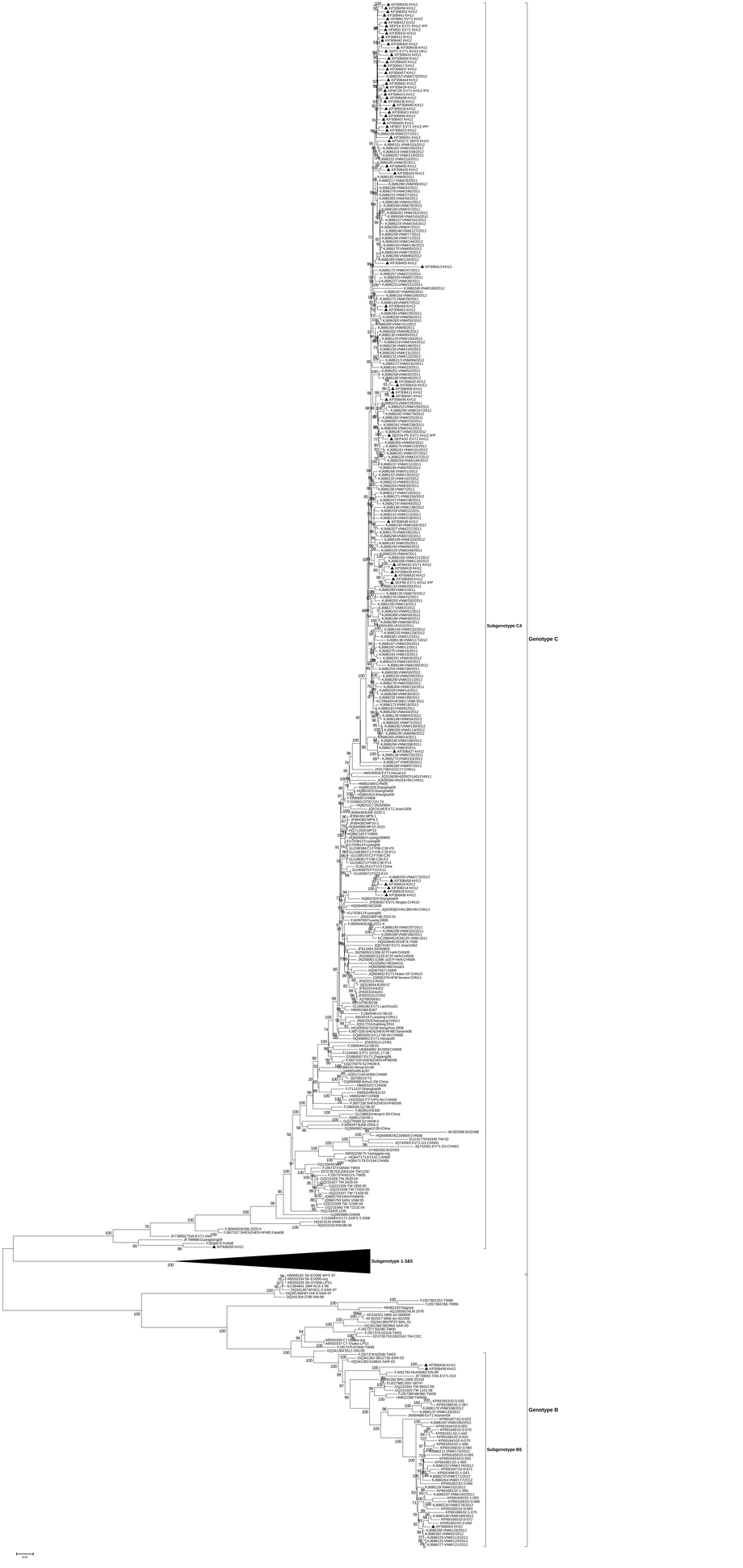

Supplementary Figure S2: Maximum likelihood (ML) phylogenetic tree of 467 EV-A71 full-genome sequences. The tree was built using the ML method based on the GTR+G4 model. The robustness of nodes was assessed with 100 bootstrap replicates. Bootstrap values lower than 70 are not shown. Cambodian sequences are marked with black triangles.