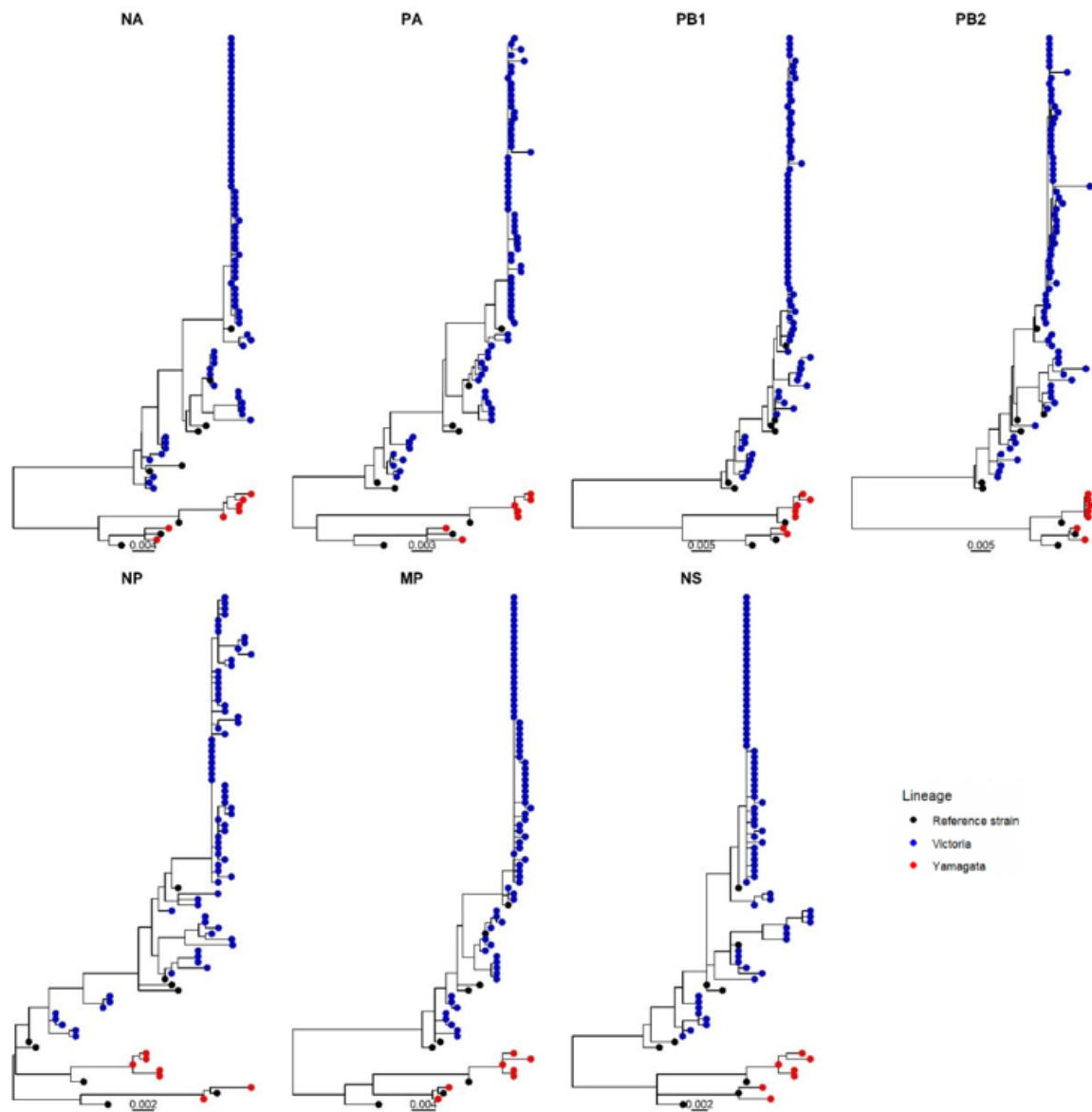
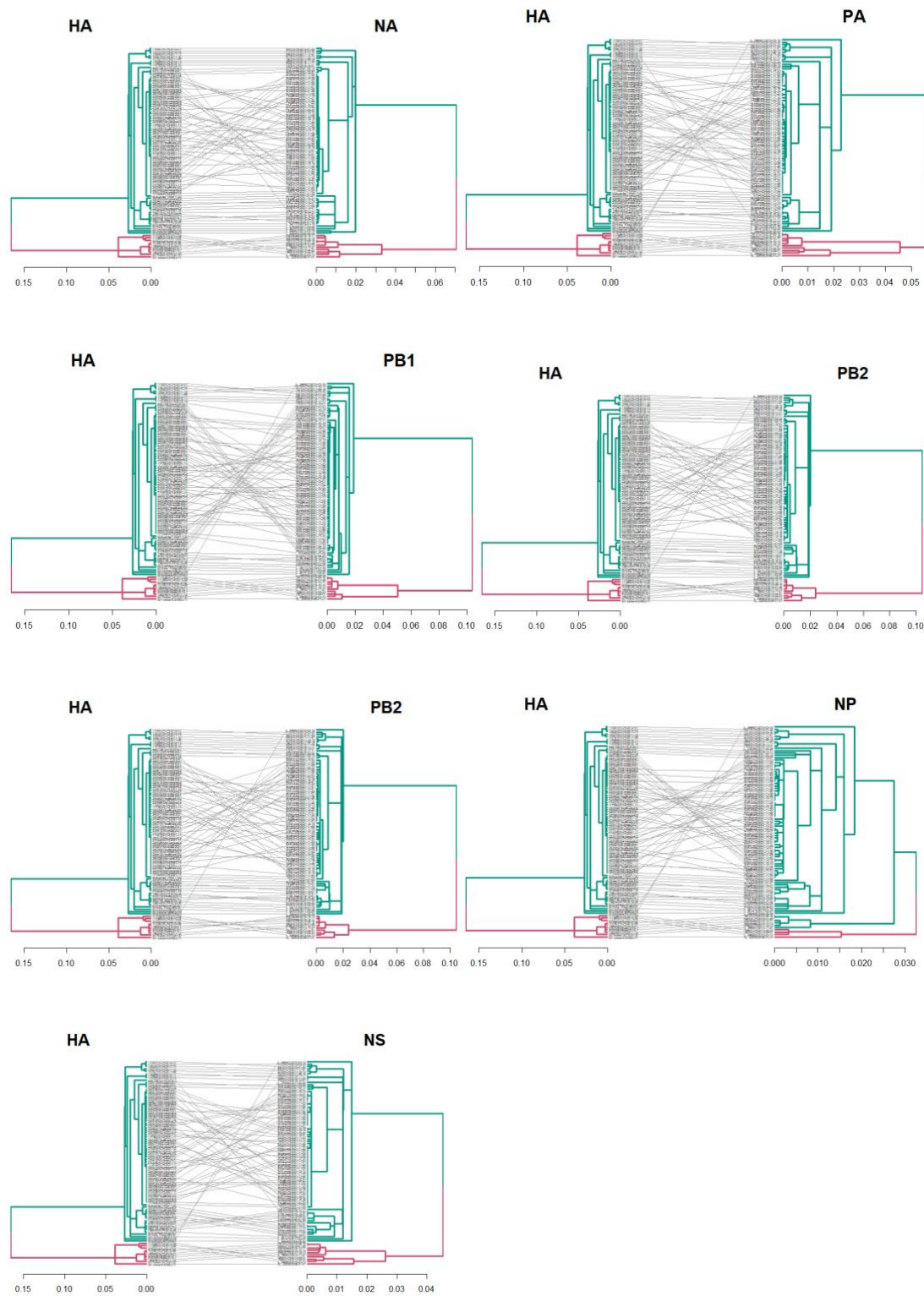


Supplementary figure 2a - Genetic relatedness of Kilifi and Uganda IBV strains.



Per segment maximum likelihood phylogenies were inferred from 91 IBV strains from Kilifi (75), Uganda (6) and 10 reference strains.

Supplementary figure 2b - Tanglegrams showing the phylogenetic congruency between IBV gene segments.



B/Yamagata strains are represented by the red branches while B/Victoria strains are represented by the green branches.