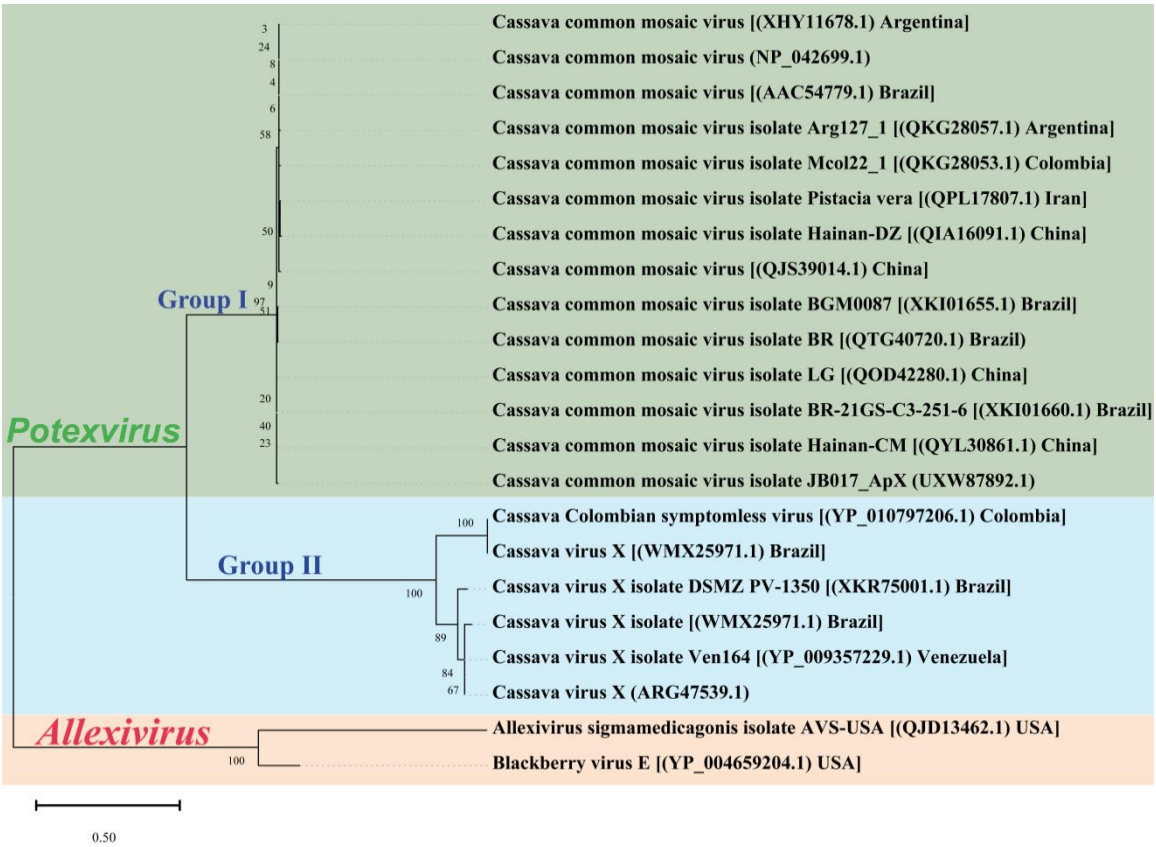

Supplementary Figure 2: Phylogenetic analysis of Cassava Common Mosaic Virus (CsCMV) Coat protein (CP). MEGA12 was utilized to infer the phylogenetic tree by constructing maximum likelihood phylogenetic trees, using best-fit substitution models LG + G + I, with 1,000 bootstrap replicates. Virus sequences were downloaded from the National Center for Biotechnology Information (NCBI) database. Allexiviruses were used as an outgroup.