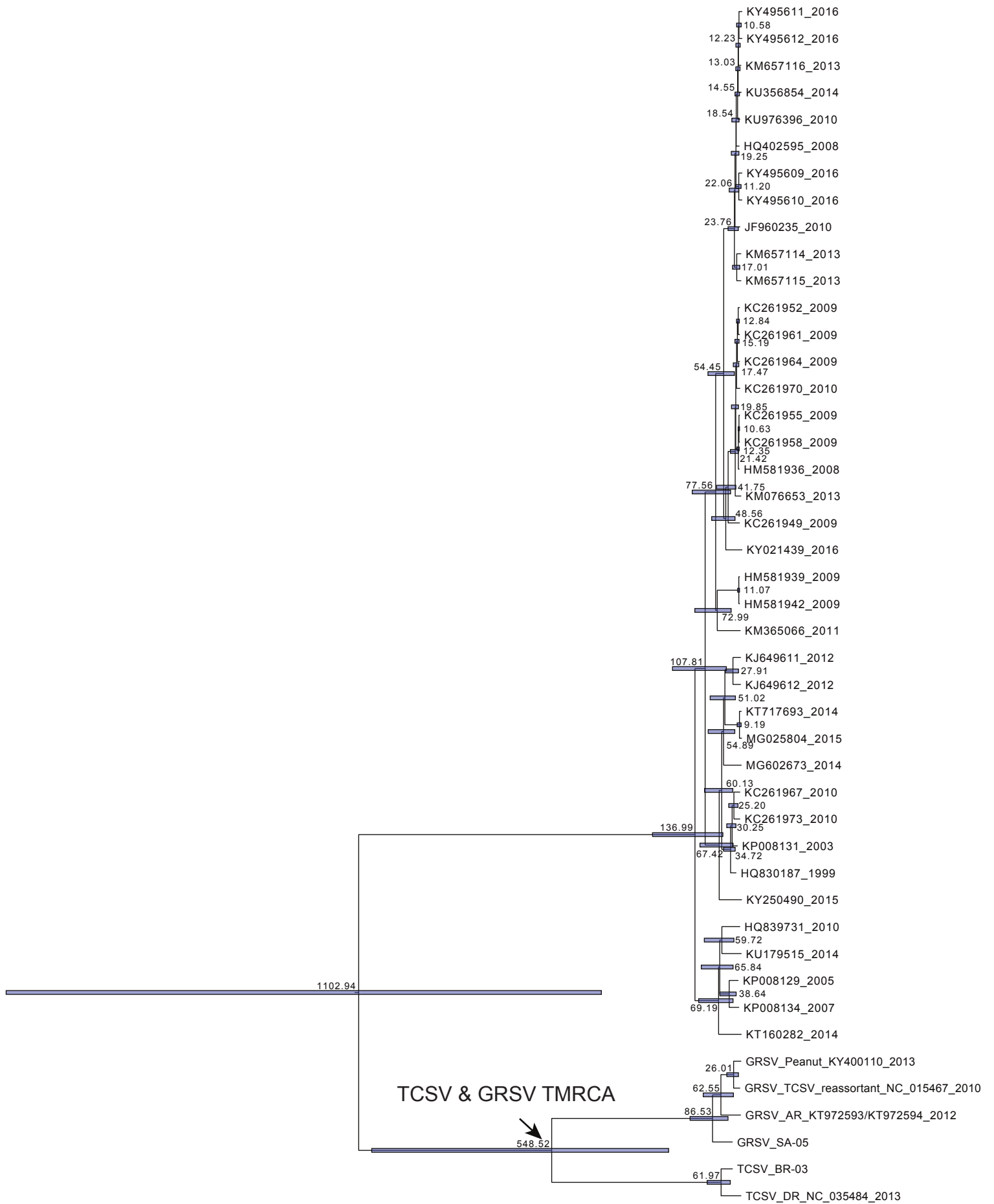
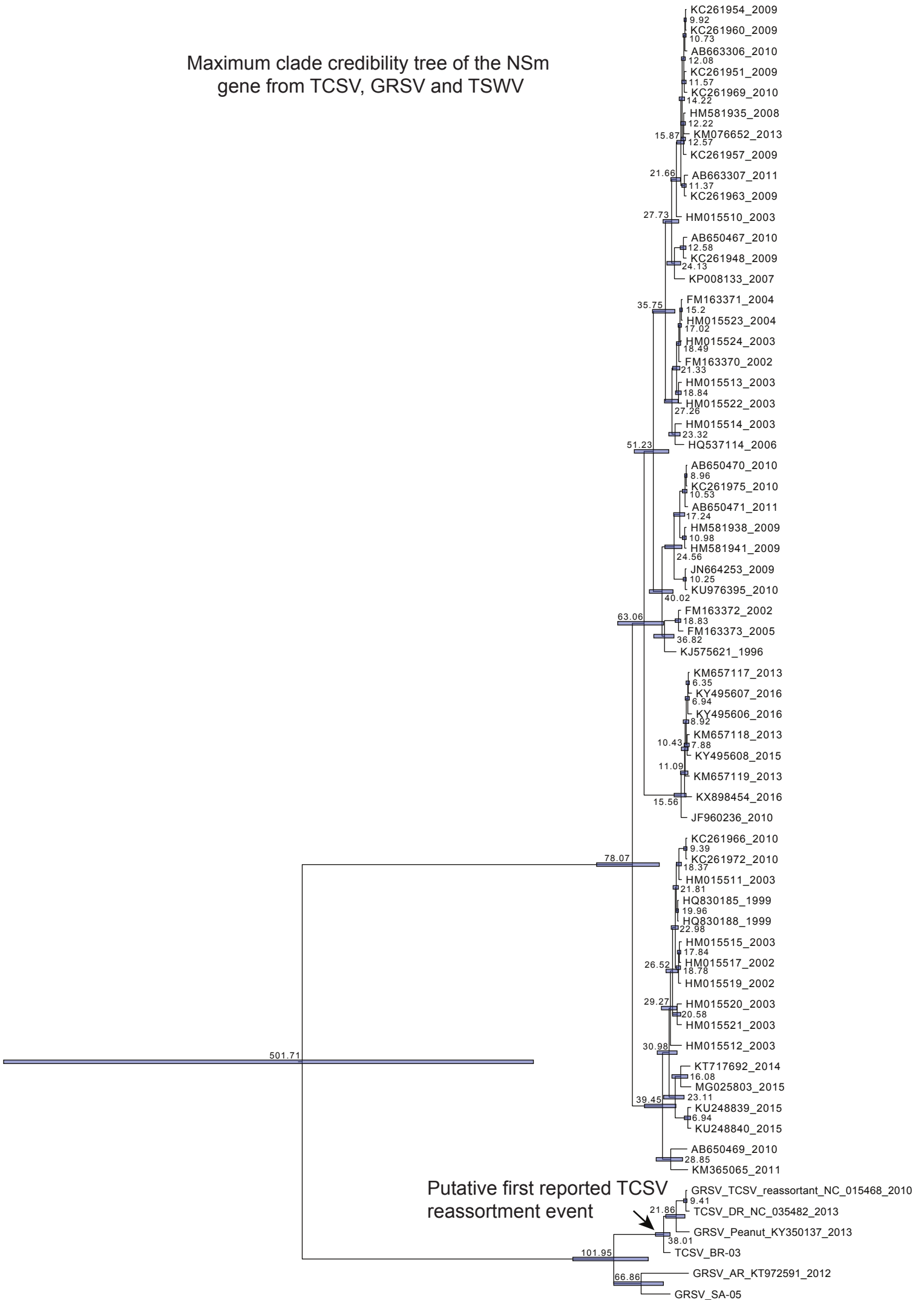


Maximum clade credibility tree of the S segment from TCSV, GRSV and TSWV



Maximum clade credibility tree of the NSm gene from TCSV, GRSV and TSWV



Maximum clade credibility tree of the L segment from TCSV, GRSV and TSWV

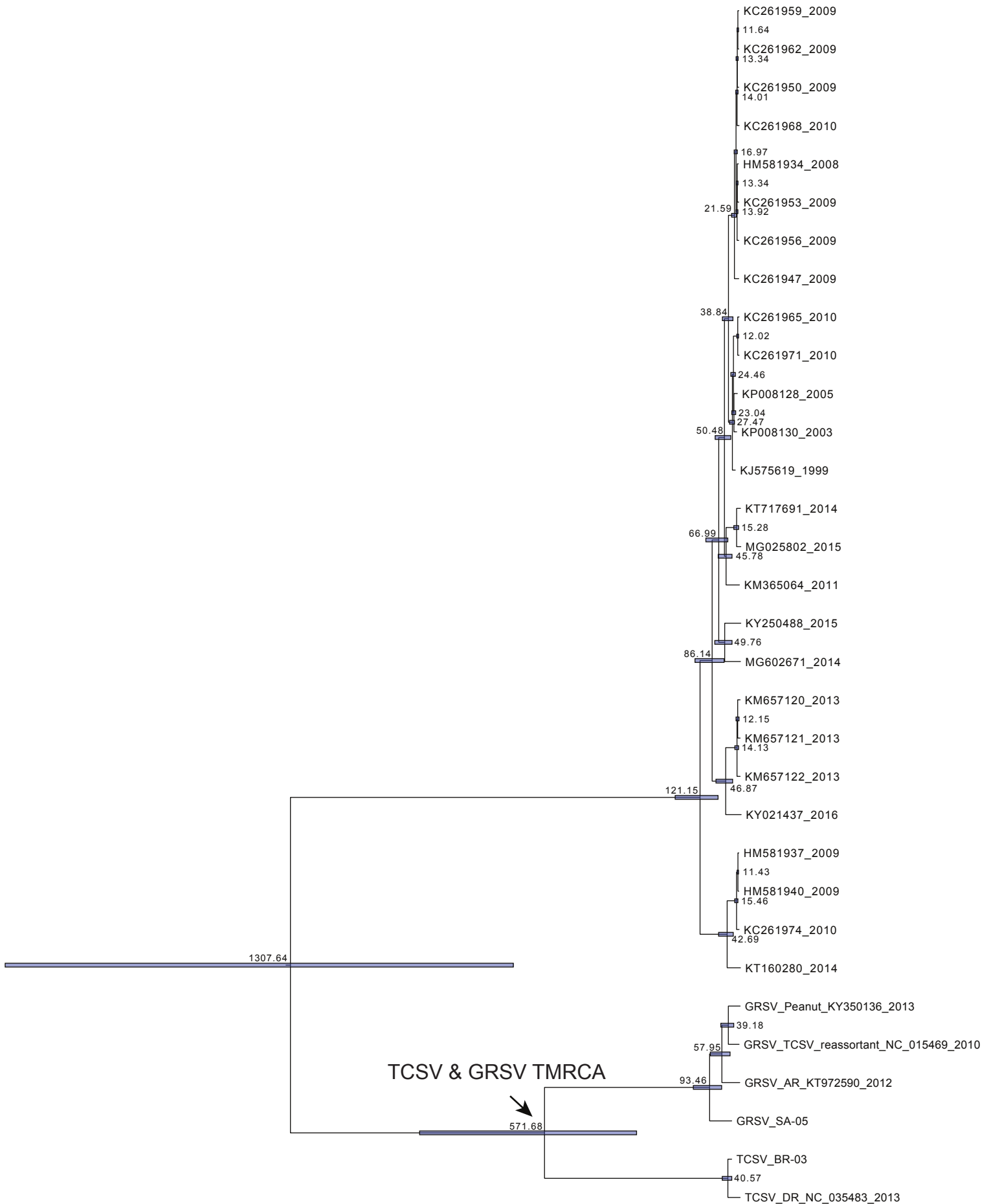


Figure S1. Bayesian phylogenetic analysis of the S, M (NSm) and L segments of TCSV, GRSV and TSWV. Maximum clade credibility trees of the S, M (NSm) and L RNAs of TCSV, GRSV and TSWV. Node heights represent the mean heights of each MCMC run. Blue bars represent the 95% HPD interval of the tree heights. The TMRCA between TCSV and GRSV is shown on the S and L segment trees, and the putative first reassortment event between TCSV and GRSV is shown on the NSm tree.