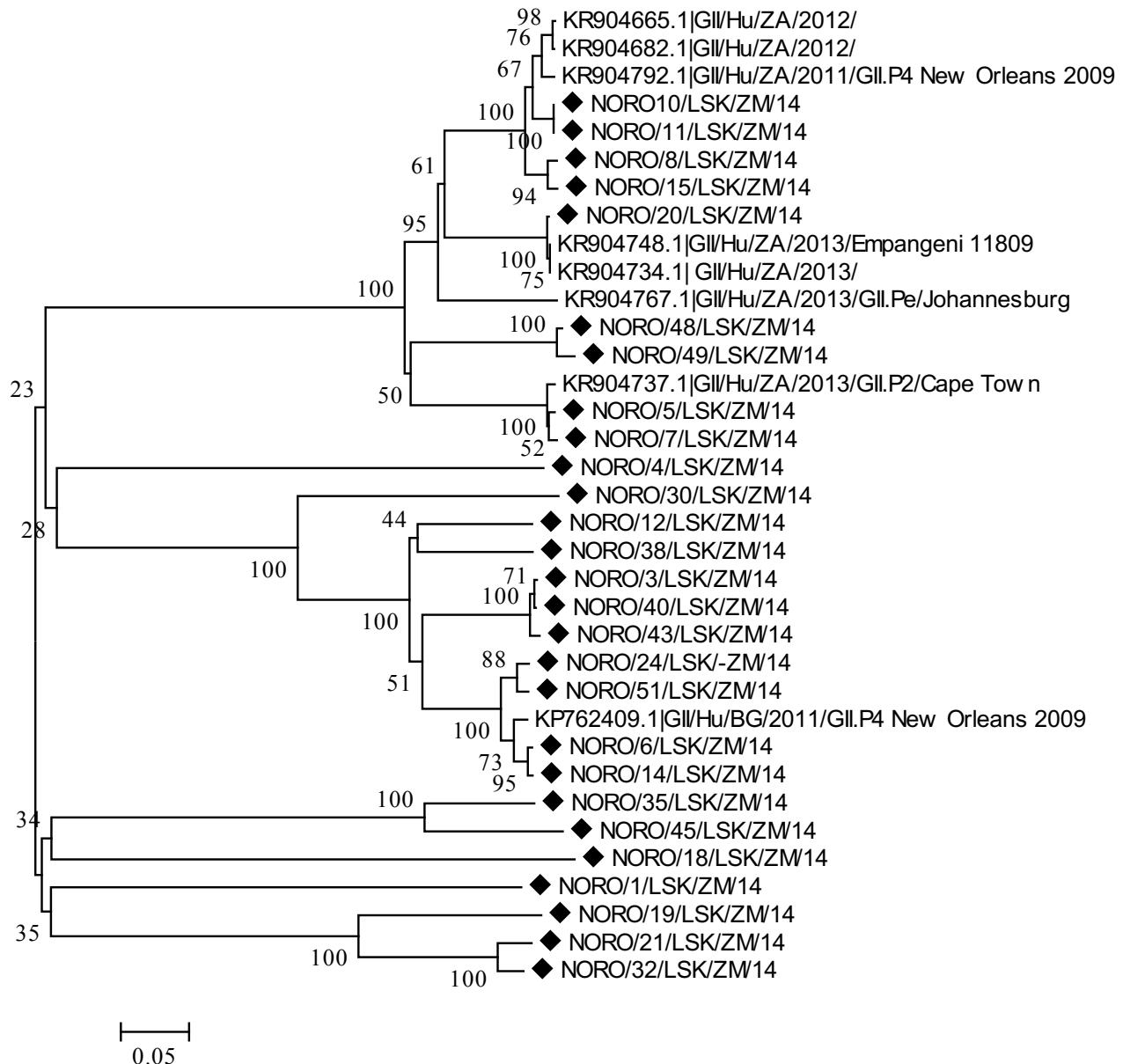


Supplemental Figure 1A. Phylogenetic analysis of a 280-bp region of the partial RNA dependent-RNA polymerase region in NoV Genogroup I detections. Nine genotypes of Genogroup I had sufficient length to be supported in the Mega software. Black circles represent sequences from our study compared to reference sequences from GenBank. NORO=norovirus/ Number of Isolation/Place of isolation/year of isolation; LSK=Lusaka. Branch lengths are indicative of the proportional to the evolutionary distance between sequences, and the distance scale in nucleotide substitutions per position is shown.



Supplemental Figure 1B. Phylogenetic analysis of a 280-bp region of the partial RNA dependent-RNA polymerase region in NoV Genogroup II detections. Twenty-seven genotypes of Genogroup II had sufficient length to be supported in the Mega software. Black circles represent sequences from our study compared to reference sequences from GenBank. NORO=norovirus/ Number of Isolation/Place of isolation/year of isolation; LSK=Lusaka. Branch lengths are indicative of the proportional to the evolutionary distance between sequences, and the distance scale in nucleotide substitutions per position is shown.