



Figure 4 Phylogenetic relationships between kobuviruses and other picornaviruses based on nucleotide sequences of complete polyprotein gene. The tree is generated by the maximum-likelihood method based on the General Time Reversible (GTR) model (Gamma distributed with Invariant sites [G+I] and partial deletion) with 1000 bootstrap replicates. Representative members of family *Picornaviridae* are marked with letters and some with blue circles). Black diamond symbol indicates the sequences of MuKVs identified in the present study.