



Supplementary Figure S2: Maximum likelihood phylogenetic tree with extended taxon sampling from the genera *Totivirus* and *Victorivirus*. Multiple sequence alignment was done by PAGAN v.1.53 and the Phylogenetic inference was carried out by using IQ-TREE v.1.6.1 with the LG+G4 evolutionary model. Statistical support of branches was calculated with 5000 UFBoot replicates. Only values higher than 95% are shown.