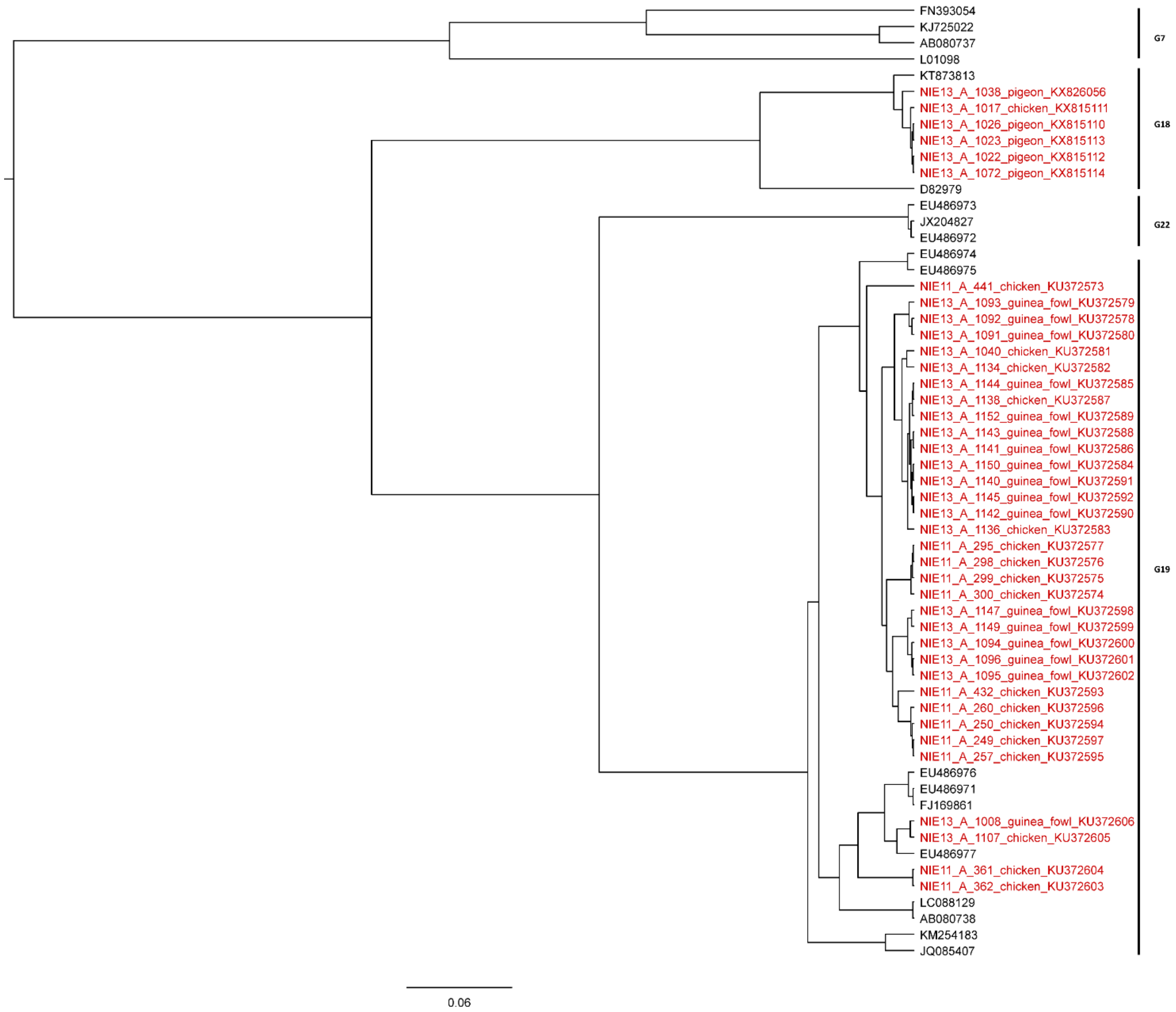
Additional File 6



Maximum clade credibility tree of partial VP7 gene sequences of Rotavirus group A (RVA). Bayesian analyses of alignments (699 bp) comprising sequences of all available VP7 sequences that are available in Genbank (http://www.ncbi.nlm.nih.gov/Genbank/index.html), as well as all long sequences identified in this study. Tree topology was tested by posterior probability (pp) and only the well supported values are shown (pp>0.7). The RVA strains are represented by their GenBank accession numbers and study sequences are in red. Genotypes were assigned using the nucleotide cut-off values defined before (1).

References

1. **Matthijnssens J, Ciarlet M, McDonald SM, Attoui H, Banyai K, Brister JR, Buesa J, Esona MD, Estes MK, Gentsch JR, Iturriza-Gomara M, Johne R, Kirkwood CD, Martella V, Mertens PP, Nakagomi O, Parreno V, Rahman M, Ruggeri FM, Saif LJ, Santos N, Steyer A, Taniguchi K, Patton JT, Desselberger U, Van Ranst M.** 2011. Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG). Arch Virol **156:**1397-1413.