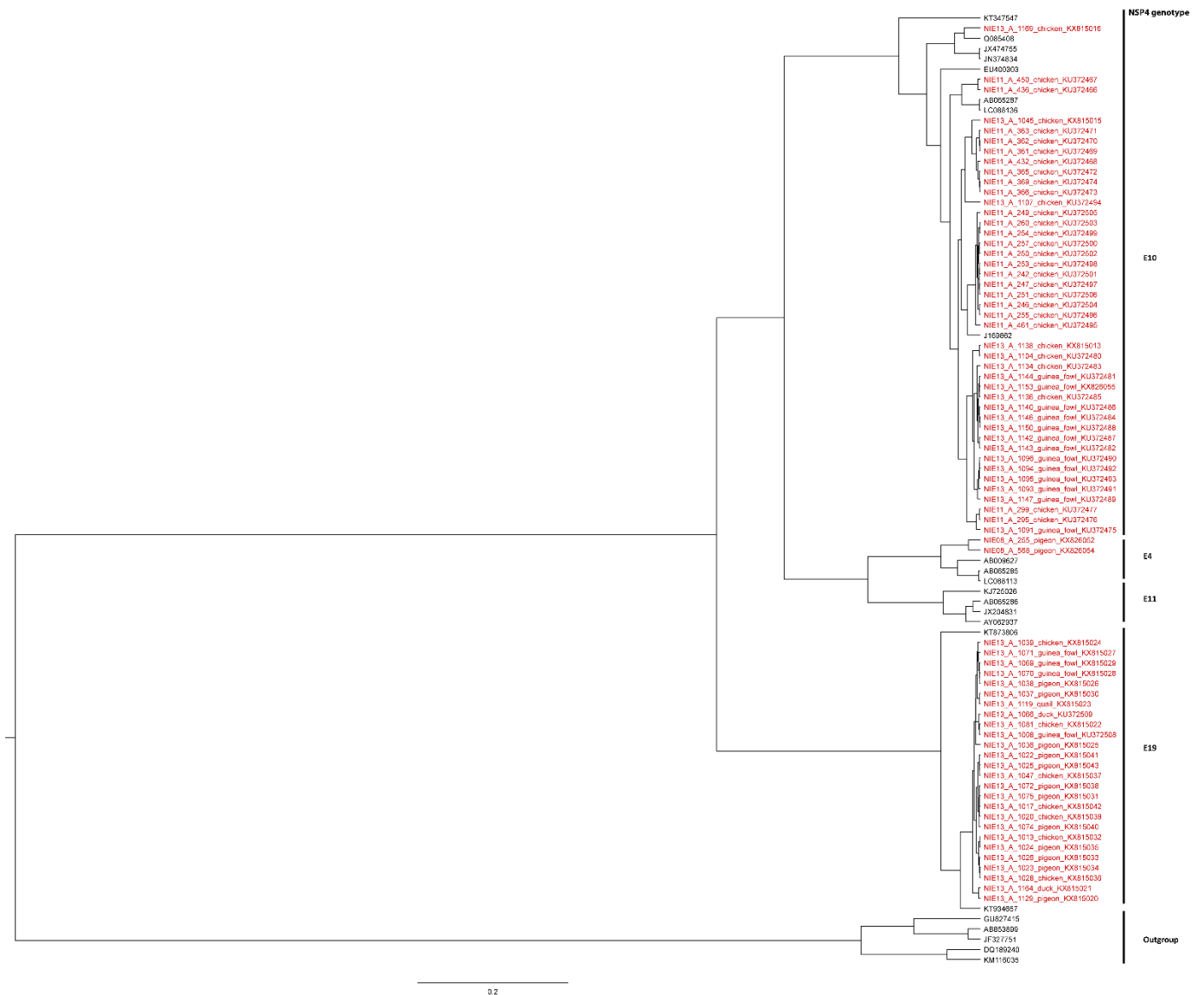


1 Additional File 3

2



3

4 **Maximum clade credibility tree of partial NSP4 gene sequences of Rotavirus group**

5 **A (RVA).** Bayesian analyses of alignments (529 bp) comprising sequences of all available

6 NSP4 sequences that are available in Genbank

7 (<http://www.ncbi.nlm.nih.gov/Genbank/index.html>), as well as all long sequences identified

8 in this study. Tree topology was tested by posterior probability (pp) and only the well

9 supported values are shown (pp>0.7). The RVA strains are represented by their GenBank

10 accession numbers and study sequences are in red. Genotypes were assigned using the
11 nucleotide cut-off values defined before (1).

12 References

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