Supplementary Meterial S4. The phylogenetic trees of VP6, VP1, VP2, VP3, NSP1, NSP2, NSP3, NSP4.

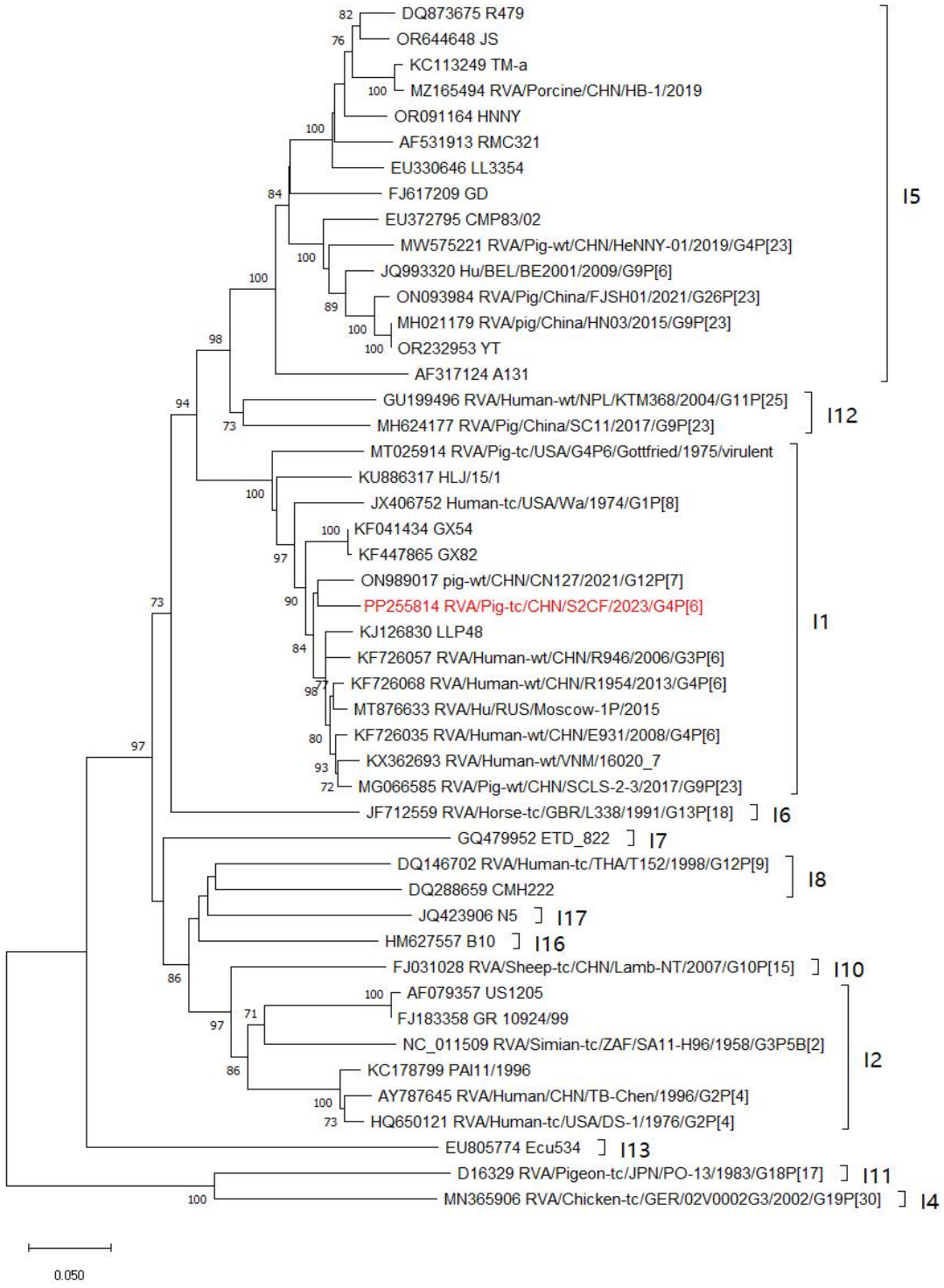


Figure S1. Phylogenetic tree based on VP6 was constructed using neighbor-joining method with 1,000 bootstrap replicates under the K2 + G model. The bootstrap values over 70% are indicated at each branch node represents substitutions per nucleotide site. The S2CF strain isolated in this study was marked in red. Abbreviation: K2= Kimura 2-parameter, G= Gamme sites.

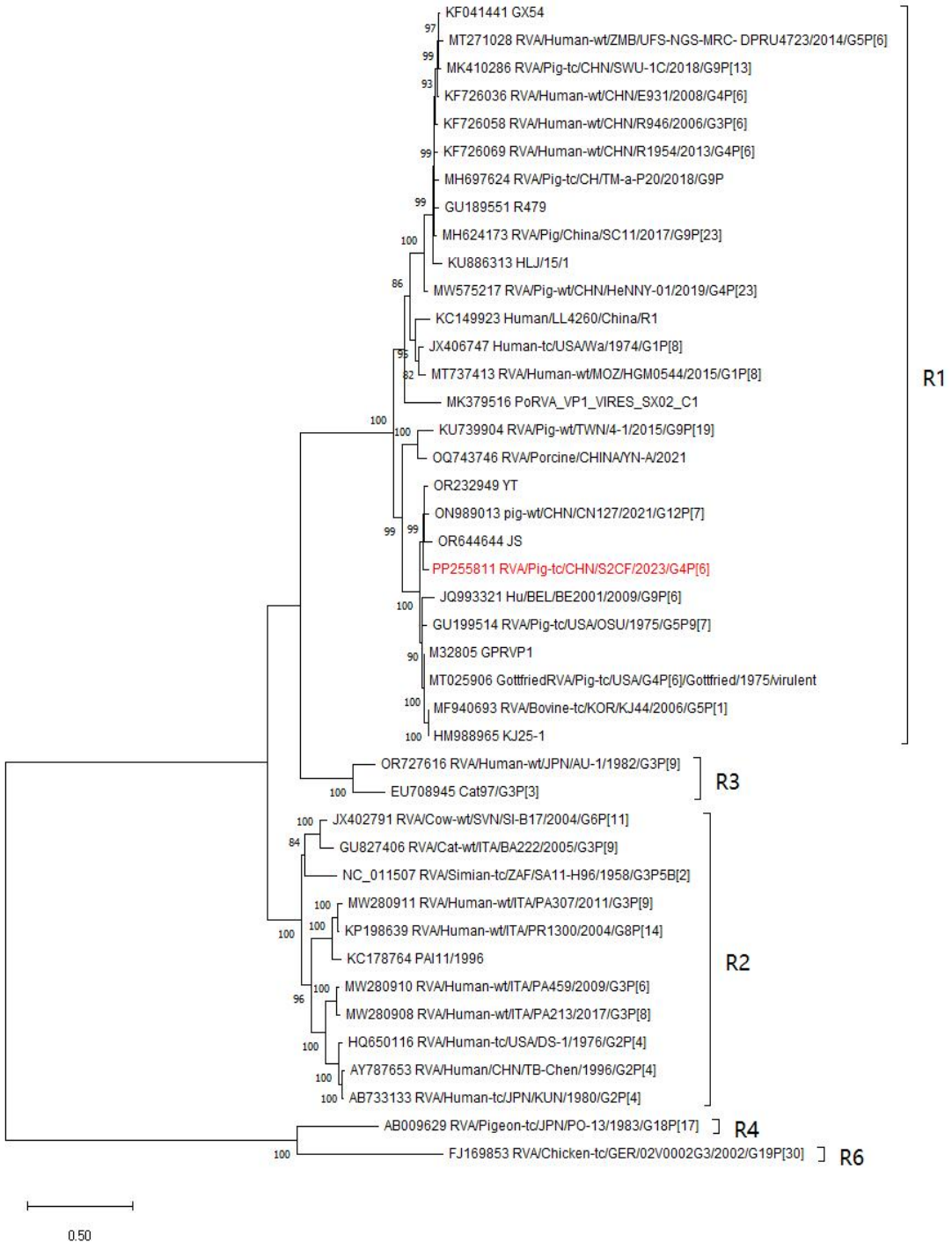


Figure S2. Maximum-likelihood phylogenetic tree based on the VP1 was finished using genetic distances calculated with 1,000 bootstrap replicates under the GTR + G + I model. Bootstrap values ⩾ 70%. The S2CF strain isolated in this study is marked with red. Abbreviation: GTR= General Time Reversible, G= Gamme sites, I= Invariant sites.

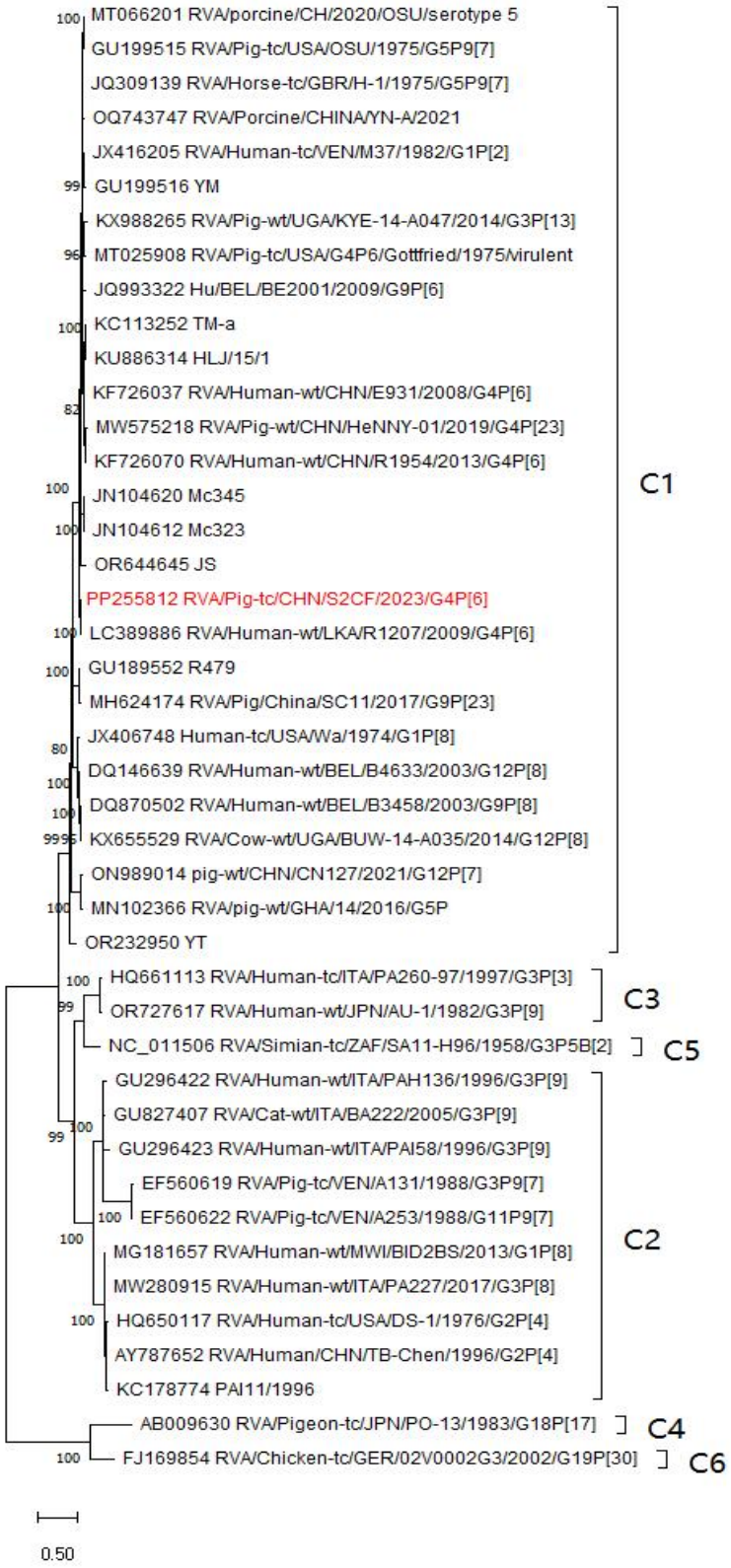


Figure S3. Phylogenetic tree of VP2 was finished using genetic distances calculated by maximum likelihood with 1,000 bootstrap replicates under the GTR + G + I model. Node labels represents bootstrap values $\geqslant$ 70% are shown. The S2CF strain isolated in this study is marked with red.

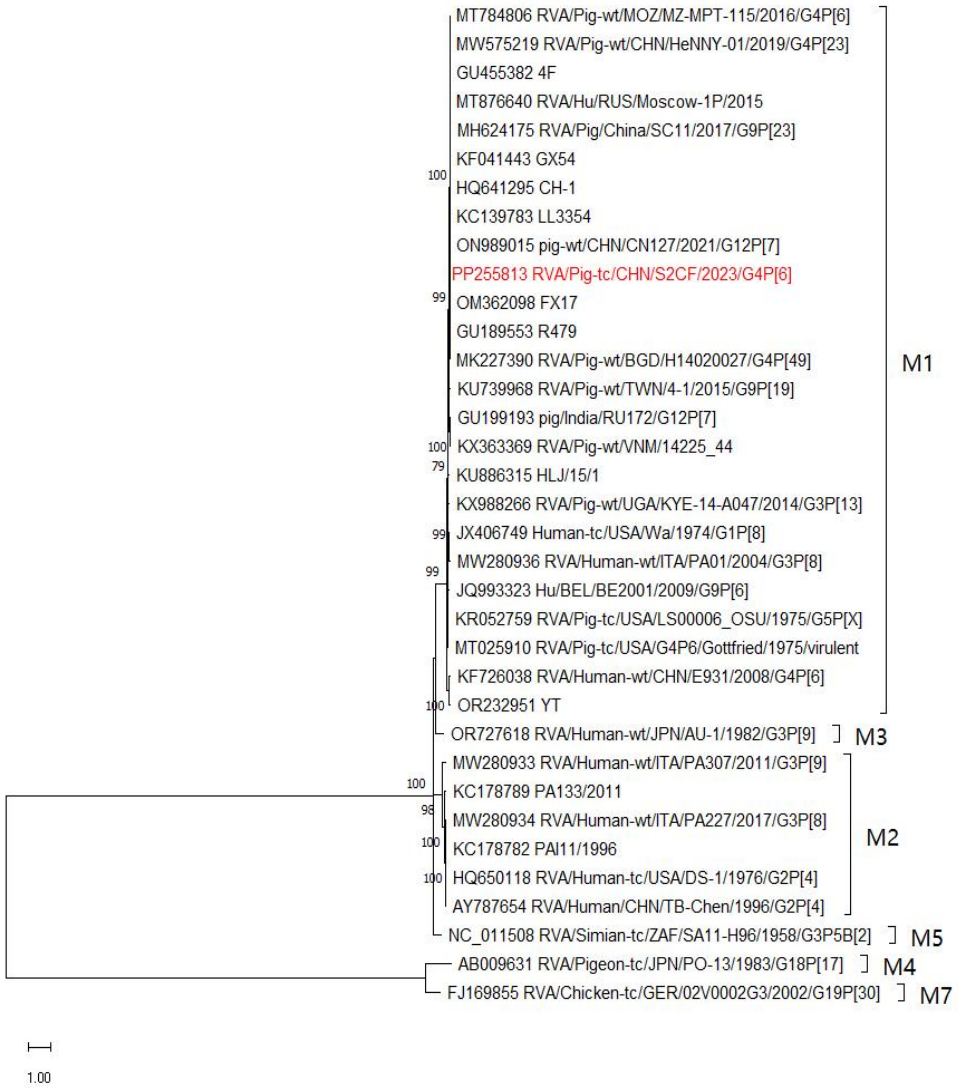


Figure S4. Phylogenetic tree of VP3 was finished using genetic distances calculated by maximum likelihood with 1,000 bootstrap replicates under the GTR + G + I model. Node labels represents bootstrap values ⩾ 70% are shown. The S2CF strain isolated in this study is marked with red.

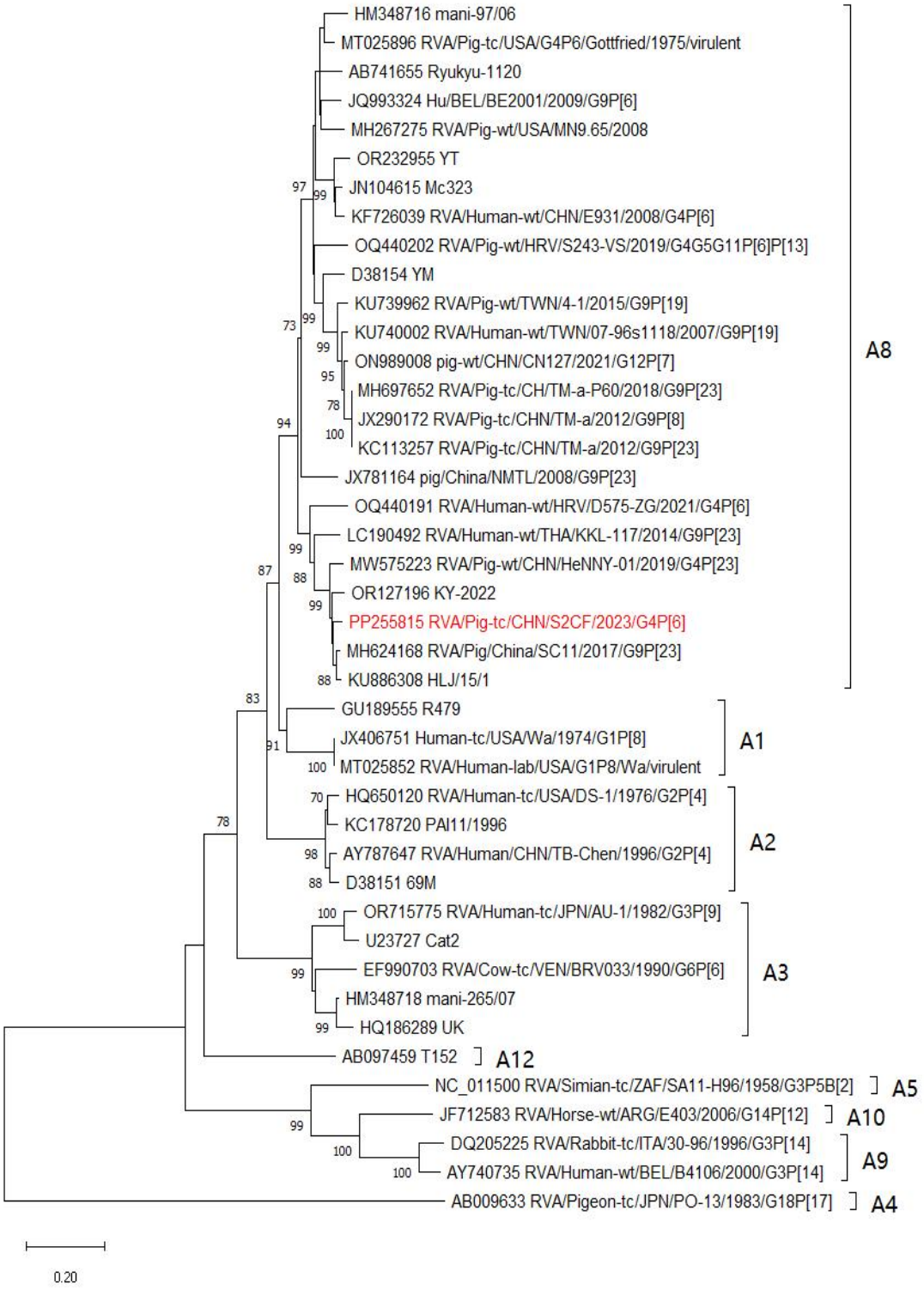


Figure S5. Phylogenetic tree based on NSP1 was constructed using neighbor-joining method with 1,000 bootstrap replicates. The model was K2+G. The bootstrap values ⩾ 70% are indicated at each branch node represents substitutions per nucleotide site. The S2CF strain isolated in this study was marked in red.

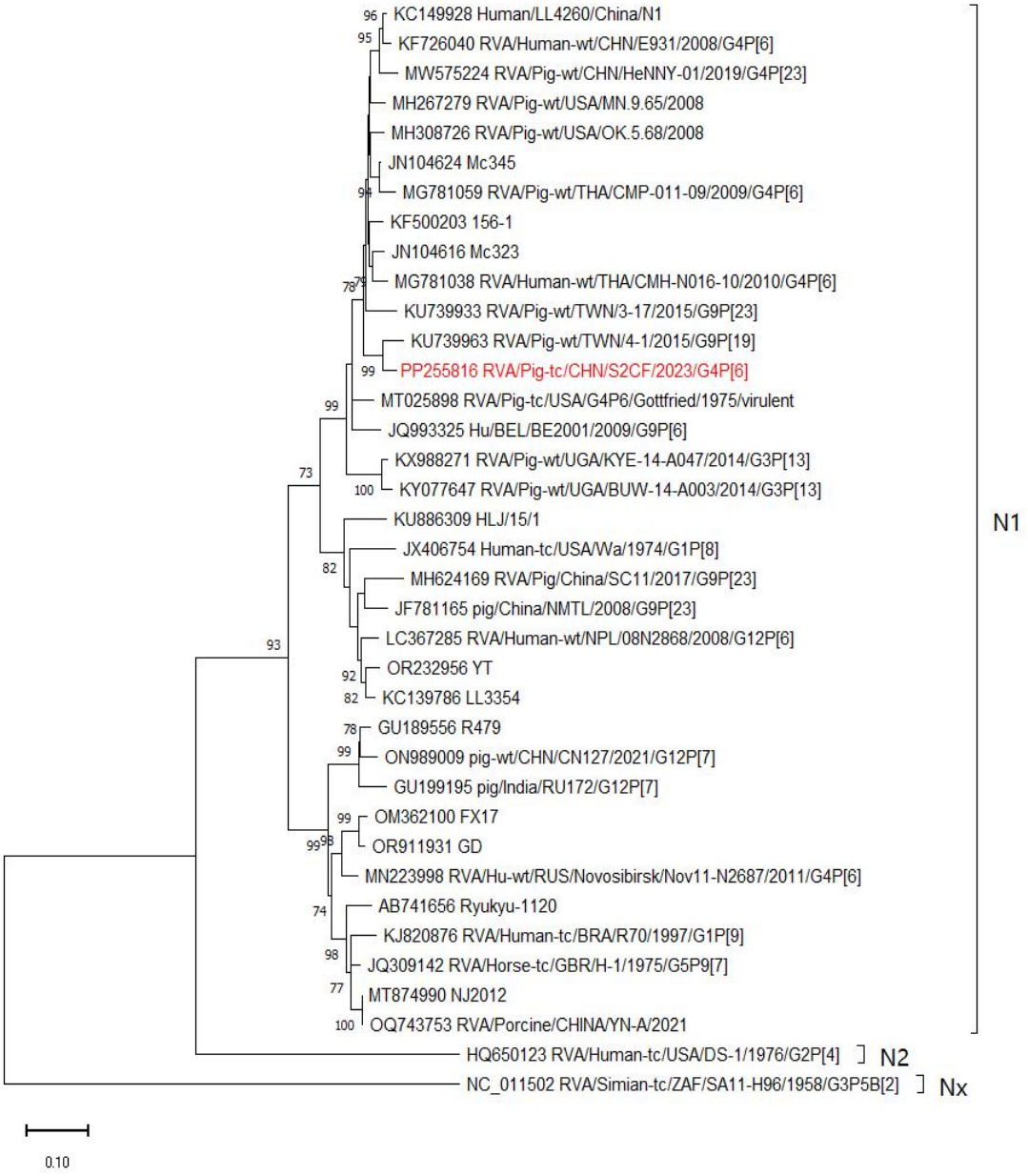


Figure S6. The phylogenetic tree constructed from the nucleotide of NSP2 based on the maximum likelihood method under the T92 + G model and boot-strapped with 1000 repetitions. The bootstrap values ⩾ 70%r are indicated at each branch node represents substitutions per nucleotide site. The S2CF strain isolated in this study was marked in red.

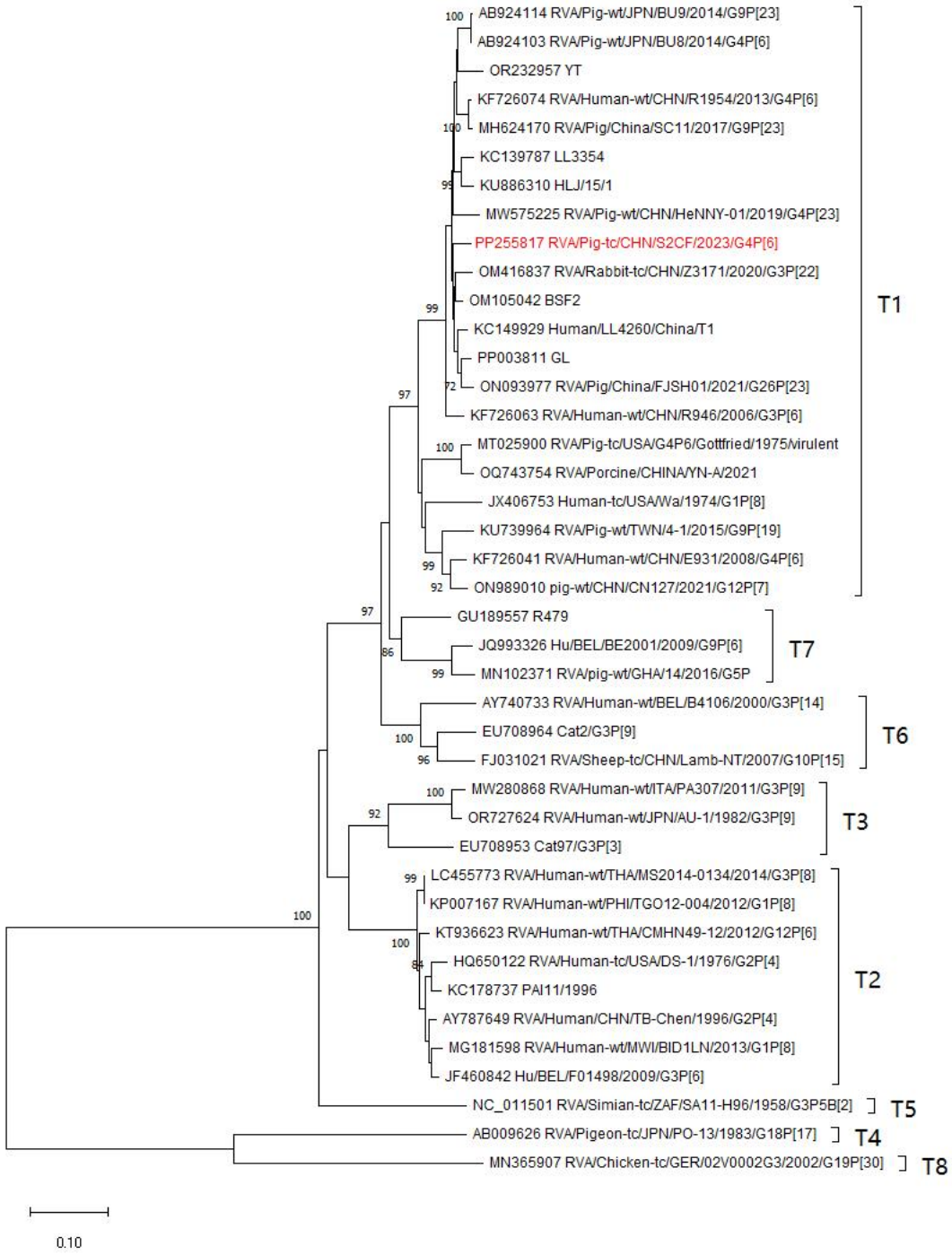


Figure S7. Phylogenetic tree of NSP3 was constructed using neighbor-joining method with 1,000 bootstrap replicates. The bootstrap values ⩾ 70% are indicated at each branch node represents substitutions per nucleotide site. The S2CF strain isolated in this study was marked in red.

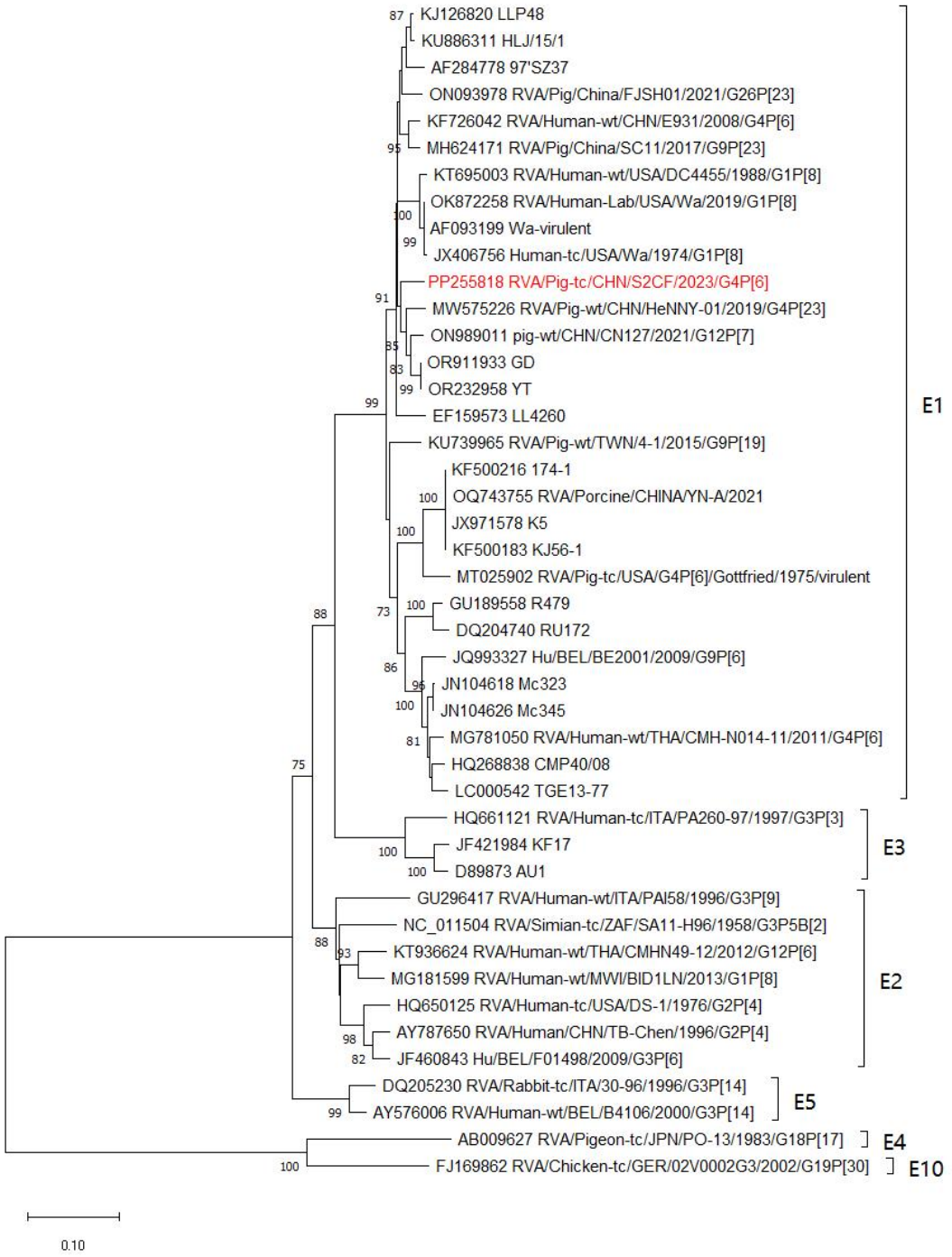


Figure S8. Phylogenetic tree of NSP4 was constructed using neighbor-joining method with 1,000 bootstrap replicates. The bootstrap values ⩾ 70% are indicated at each branch node represents substitutions per nucleotide site. The S2CF strain isolated in this study was marked in red.