

Figure S1. Phylogenetic tree for the partial S segment of "RT-2017" (nt 240-1296 based on GenBank sequence Z84204) constructed by Maximum Parsimony method. Bootstrap values were calculated for 1000 replicates; only values greater than 70% are shown.

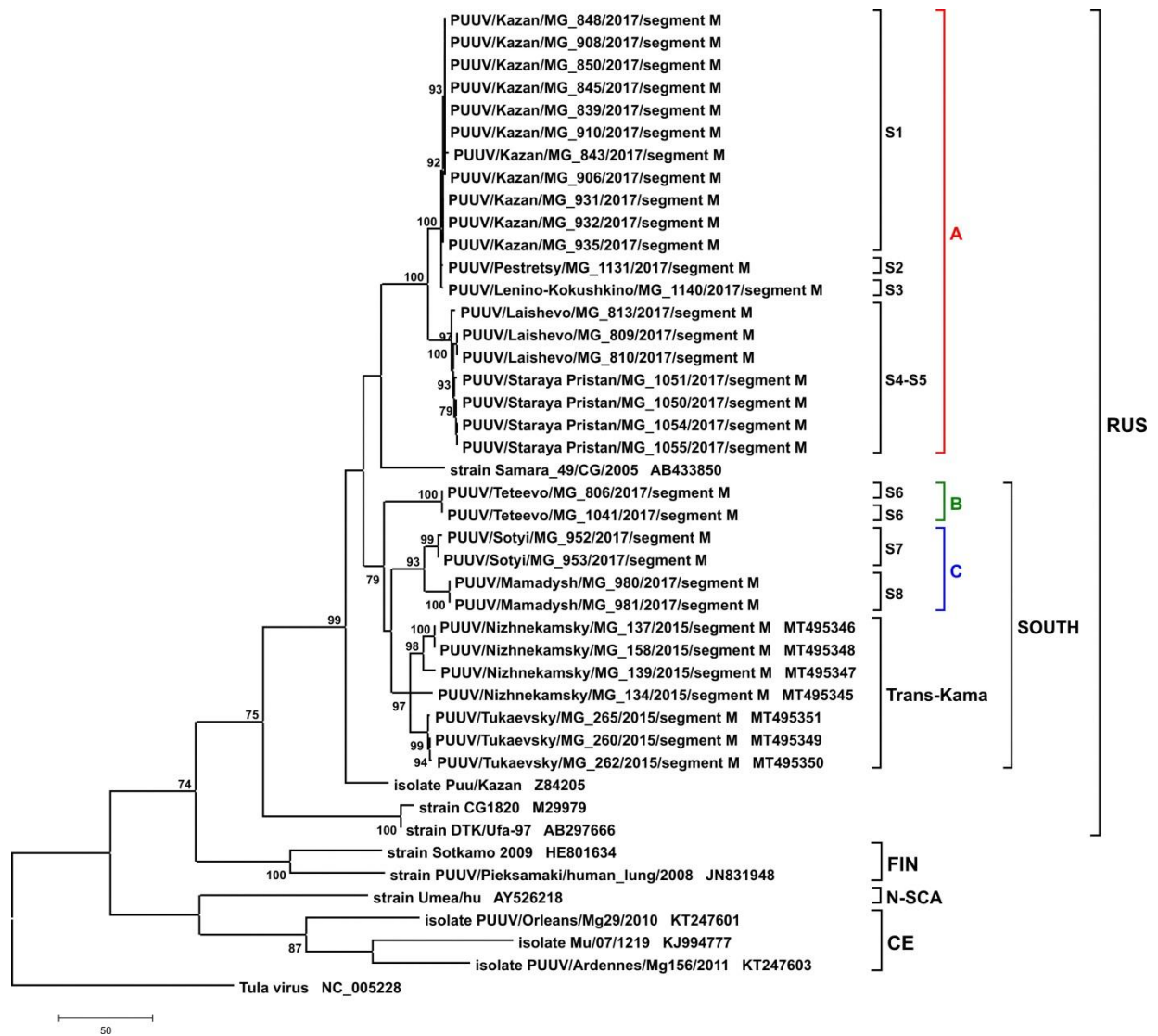


Figure S2. Phylogenetic tree for the partial M segment of "RT-2017" (nt 1499-2512 based on GenBank sequence Z84205) constructed by Maximum Parsimony method. Bootstrap values were calculated for 1000 replicates; only values greater than 70% are shown.

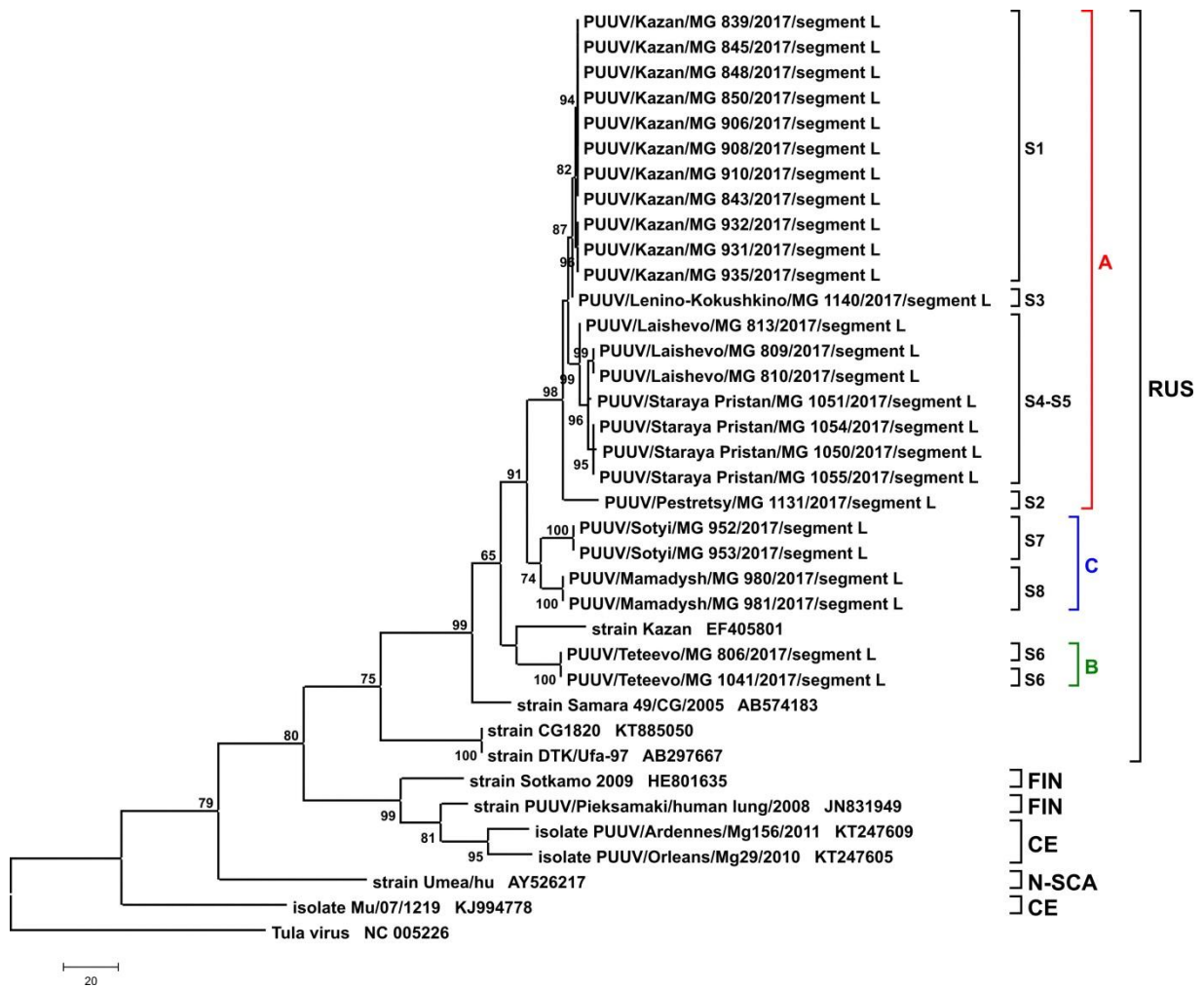


Figure S3. Phylogenetic tree for the partial L segment of "RT-2017" (nt 958-1622 based on GenBank sequence EF405801) constructed by Maximum Parsimony method. Bootstrap values were calculated for 1000 replicates; only values greater than 70% are shown.



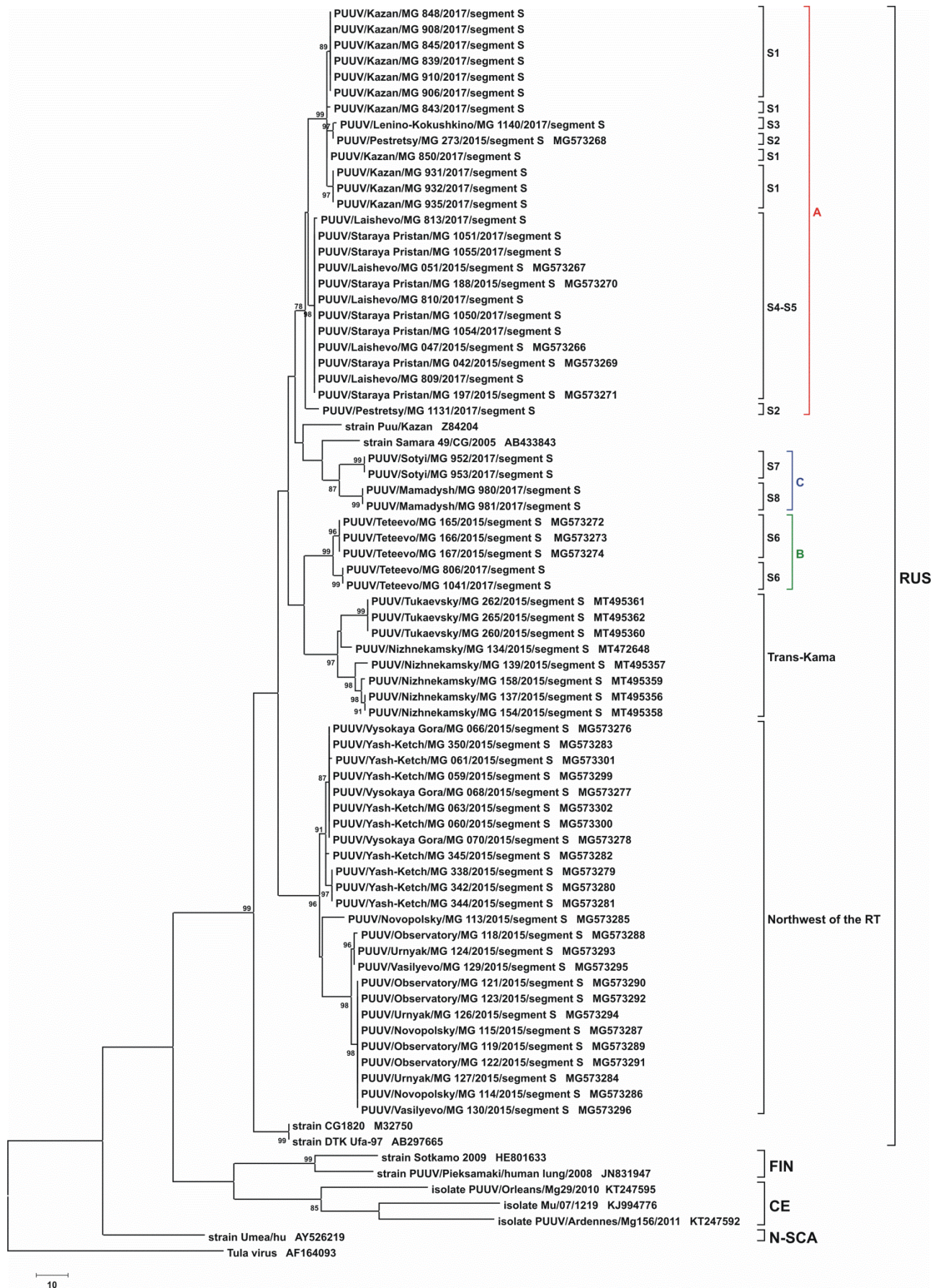


Figure S4. Phylogenetic tree for the partial S segment of PUUV strains from RT (nt 242-805 based on GenBank sequence Z84204) constructed by Maximum Parsimony method. Bootstrap values were calculated for 1000 replicates; only values greater than 70% are shown.