Supplement Material

Prevalence and Genomic Characterization of Rotavirus A from Domestic Pigs in Zambia: Evidence for Possible Porcine–Human Interspecies Transmission

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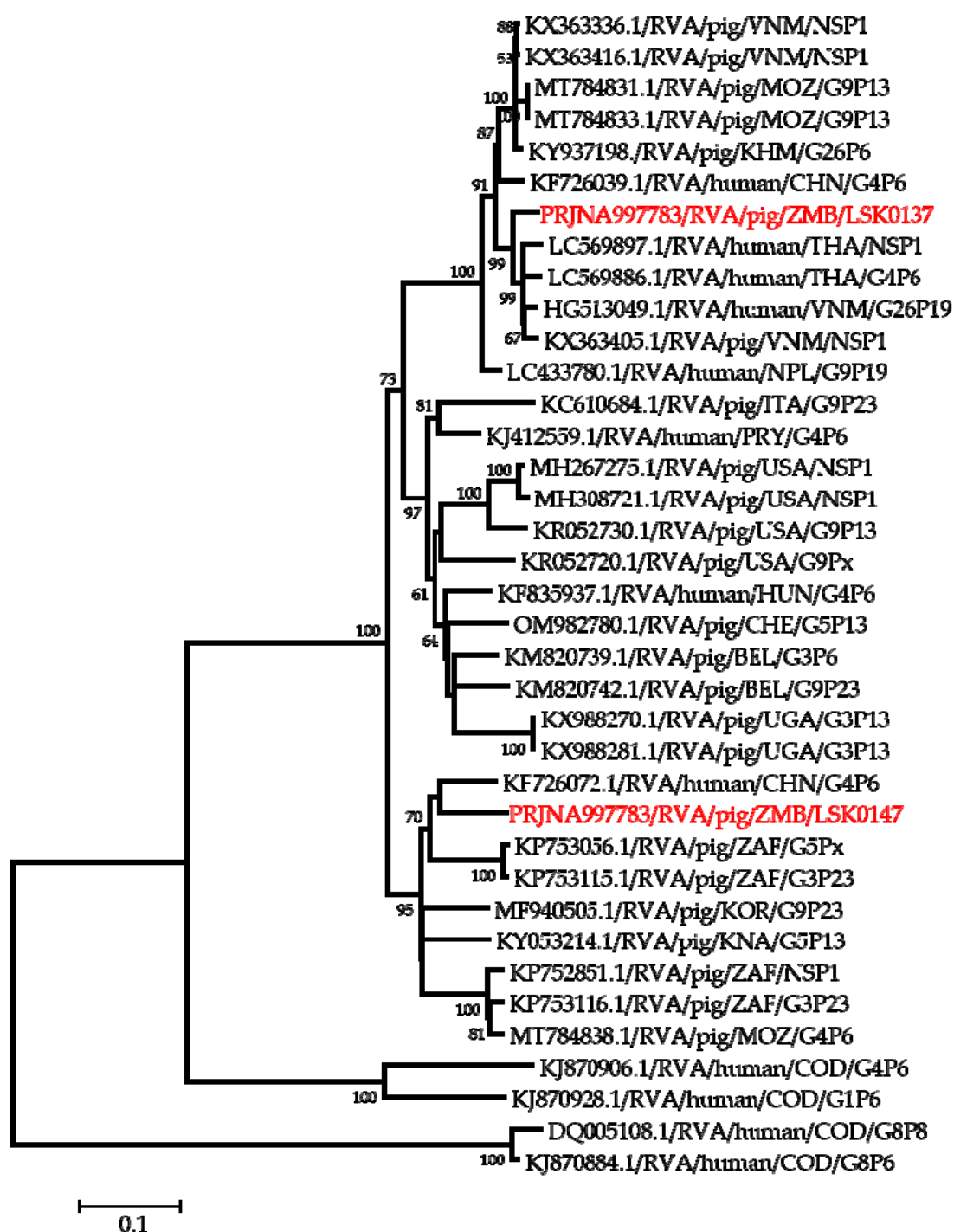
†   These authors contributed equally to this work.
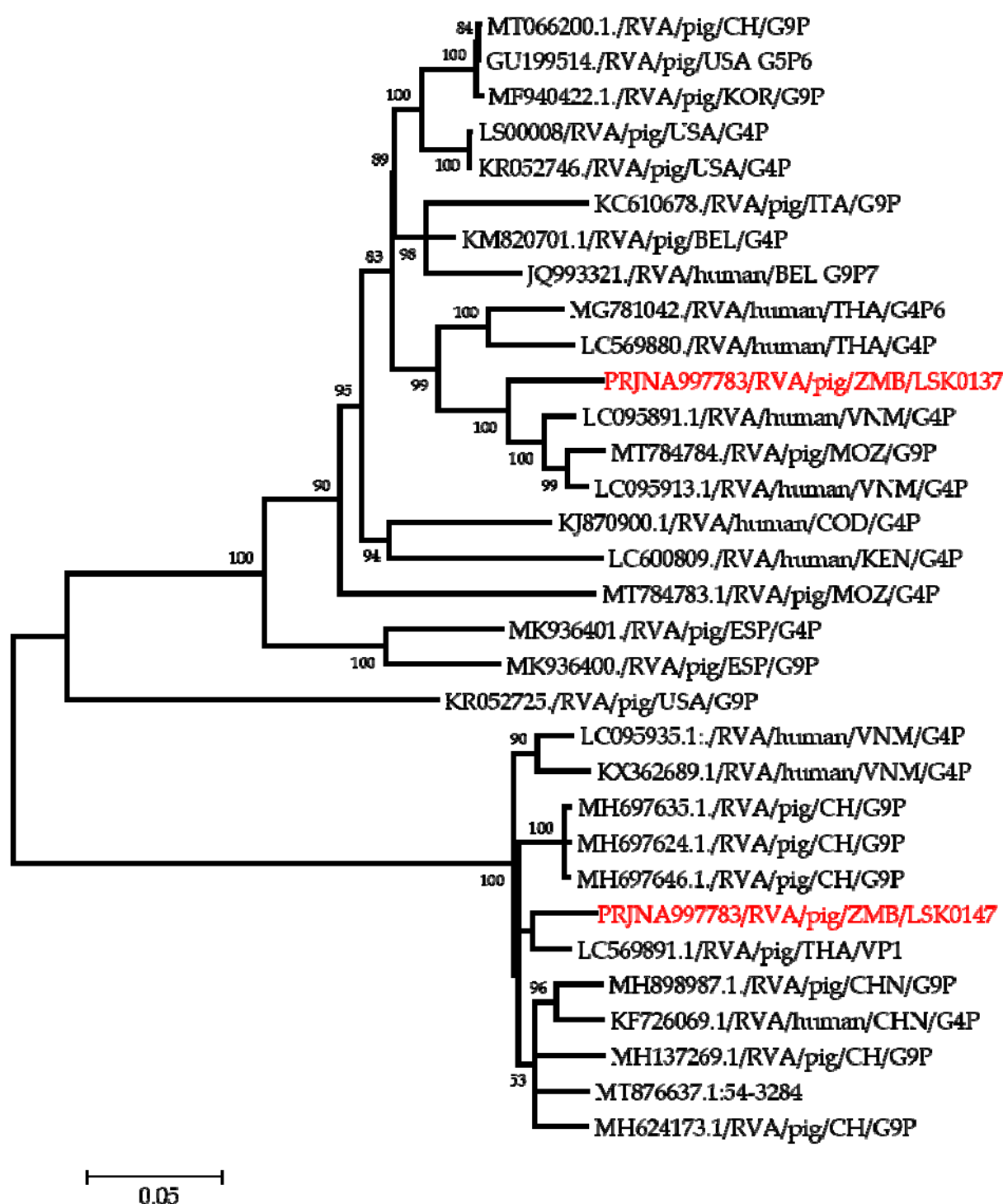
Figure S1. Phylogenetic tree of VP1 genes that belong to genotype R1. The tree was constructed using the general time reversible evolutionary model. The analysis was based on 3218 nucleotides. Bootstrap values on branch nodes ≥ 50% are shown. The GenBank accession number/ Rotavirus group/Species origin/country of origin / G/P-types represent the reference sequences included in the tree. The viruses characterized in this study with their bioproject accession number are shown in red text.
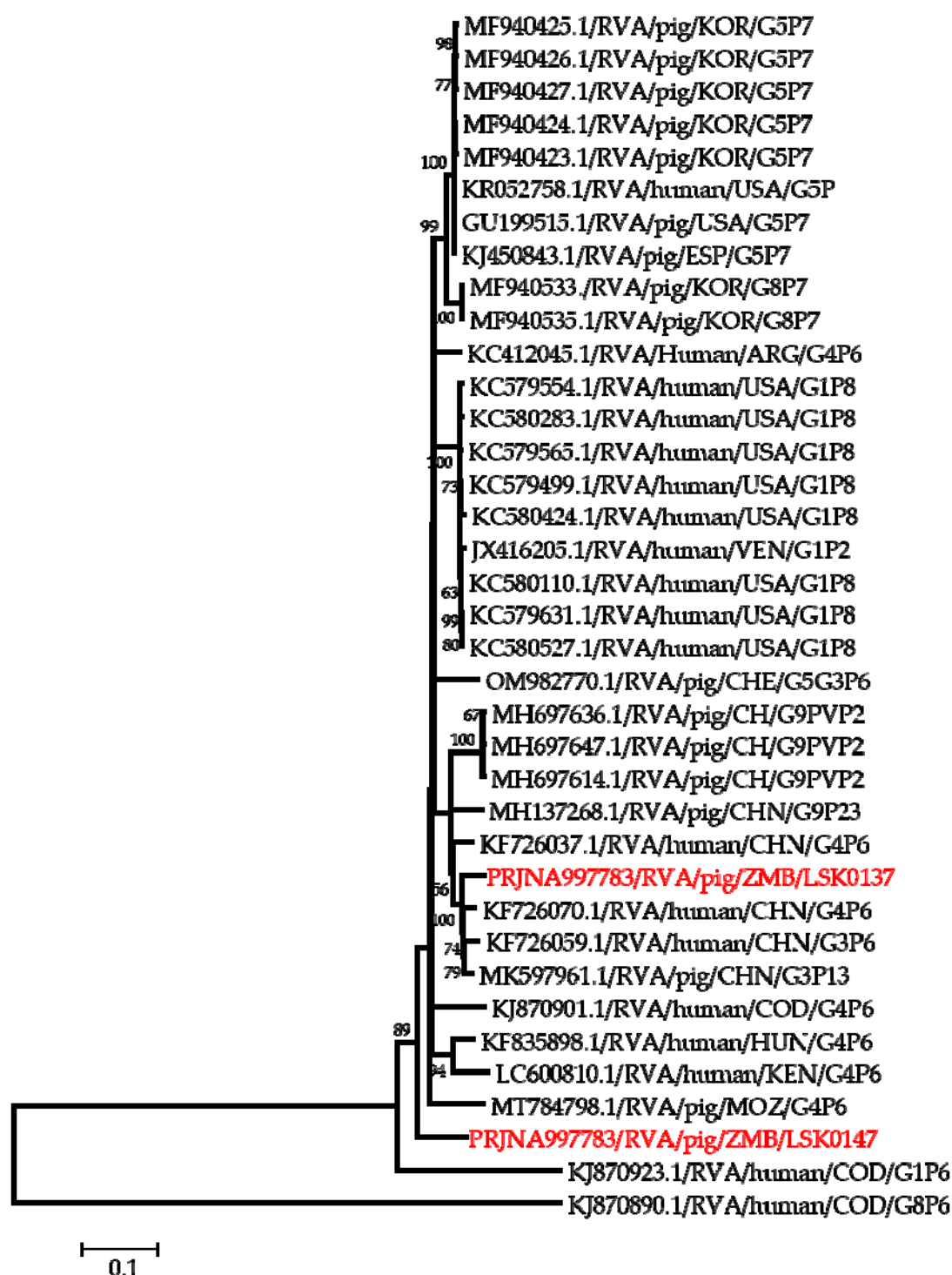
Figure S2. Phylogenetic tree of VP2 genes that belong to genotype C1. The tree was constructed using the general time reversible evolutionary model. The analysis was based on 2605 nucleotides. Bootstrap values on branch nodes ≥ 50% are shown. The GenBank accession number/ Rotavirus group/Species origin/country of origin / G/P-types represent the reference sequences included in the tree. The viruses characterized in this study with their bioproject accession number are shown in red text.
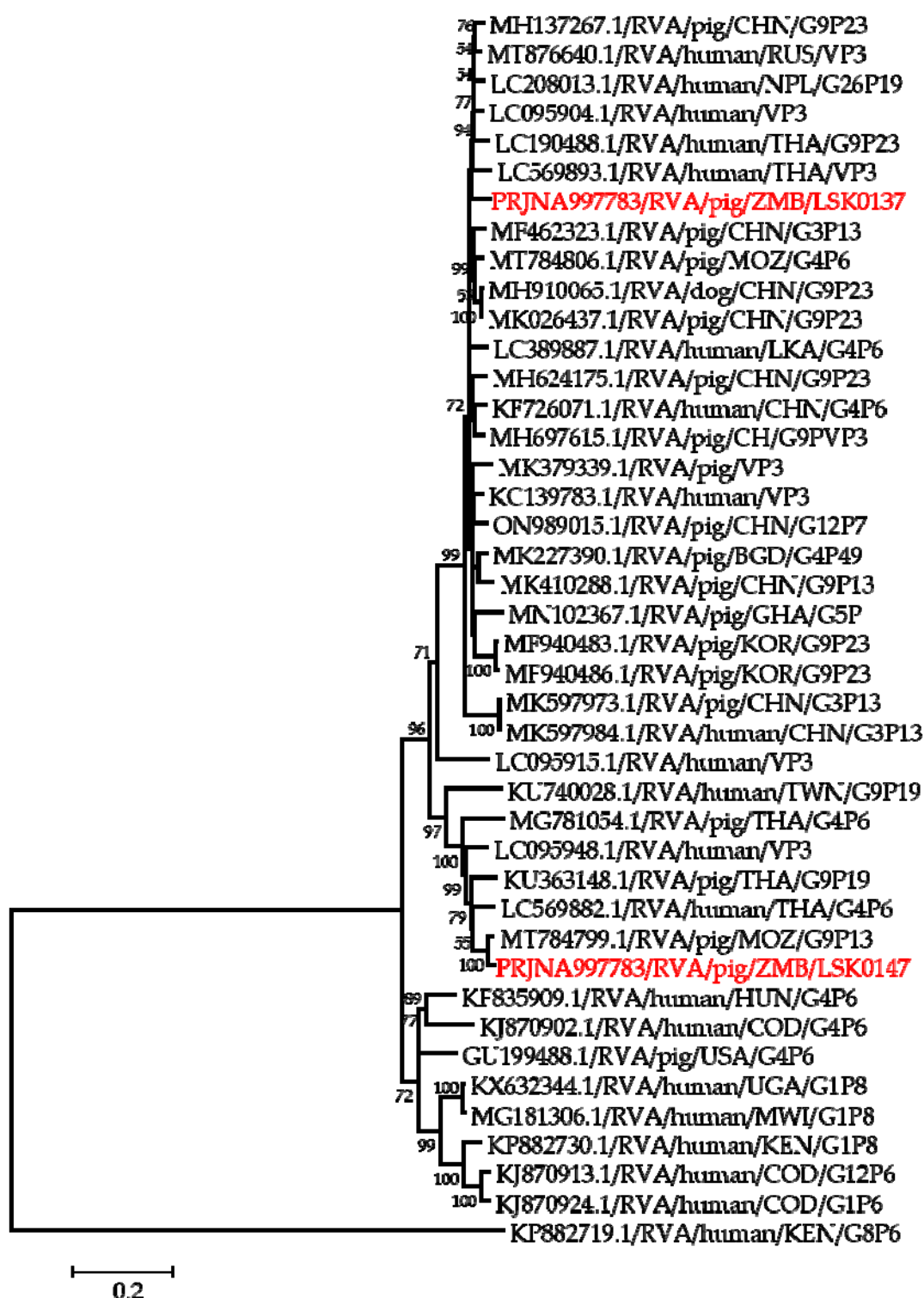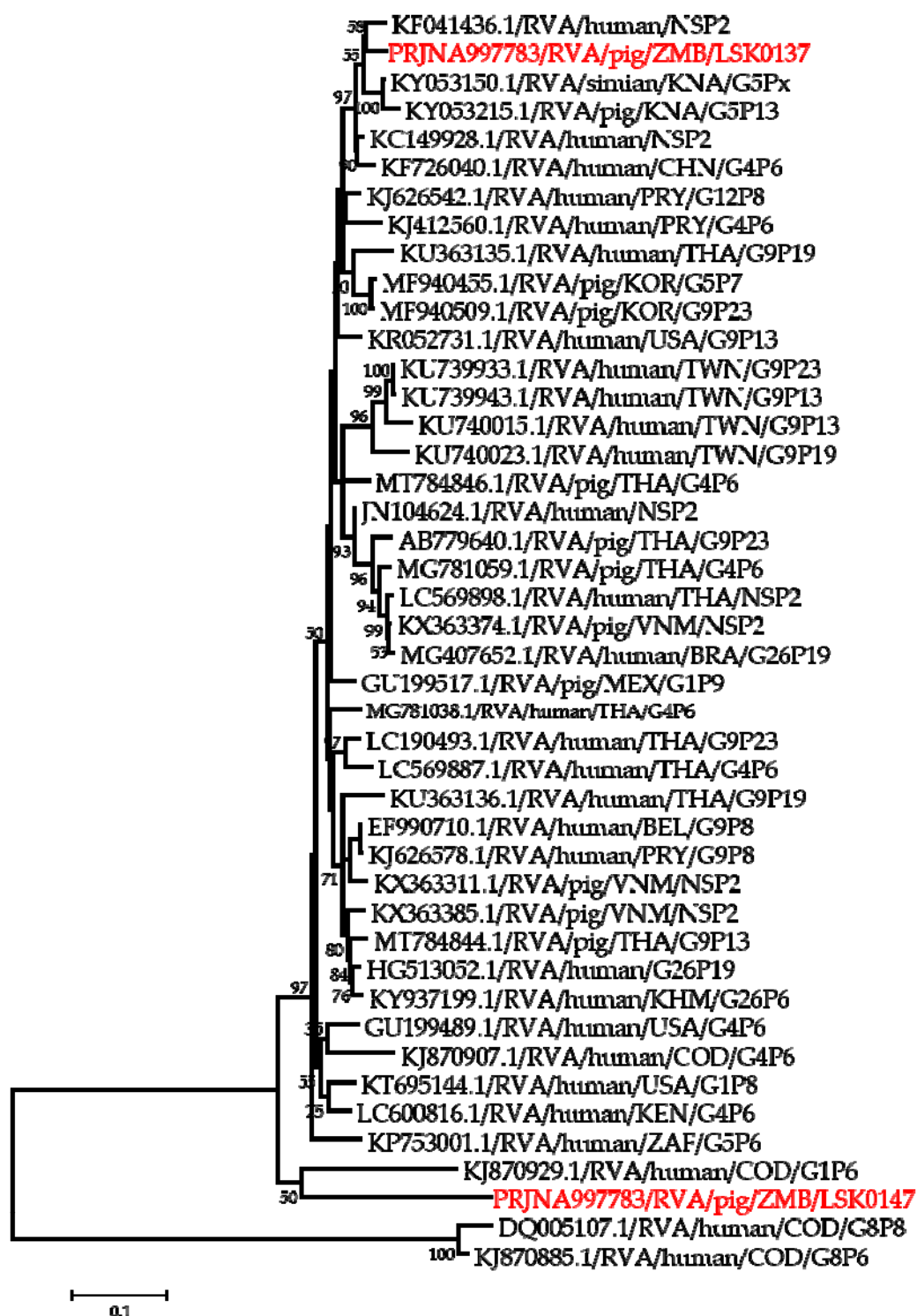
Figure S3. Phylogenetic tree of VP3 genes that belongs to genotype M1. The tree was constructed using the general time reversible evolutionary model. The analysis was based on 2505 nucleotides. Bootstrap values on branch nodes ≥ 50% are shown. The GenBank accession number/ Rotavirus group/Species origin/country of origin / G/P-types represent the reference sequences included in the tree. The viruses characterized in this study with their bioproject accession number are shown in red text.
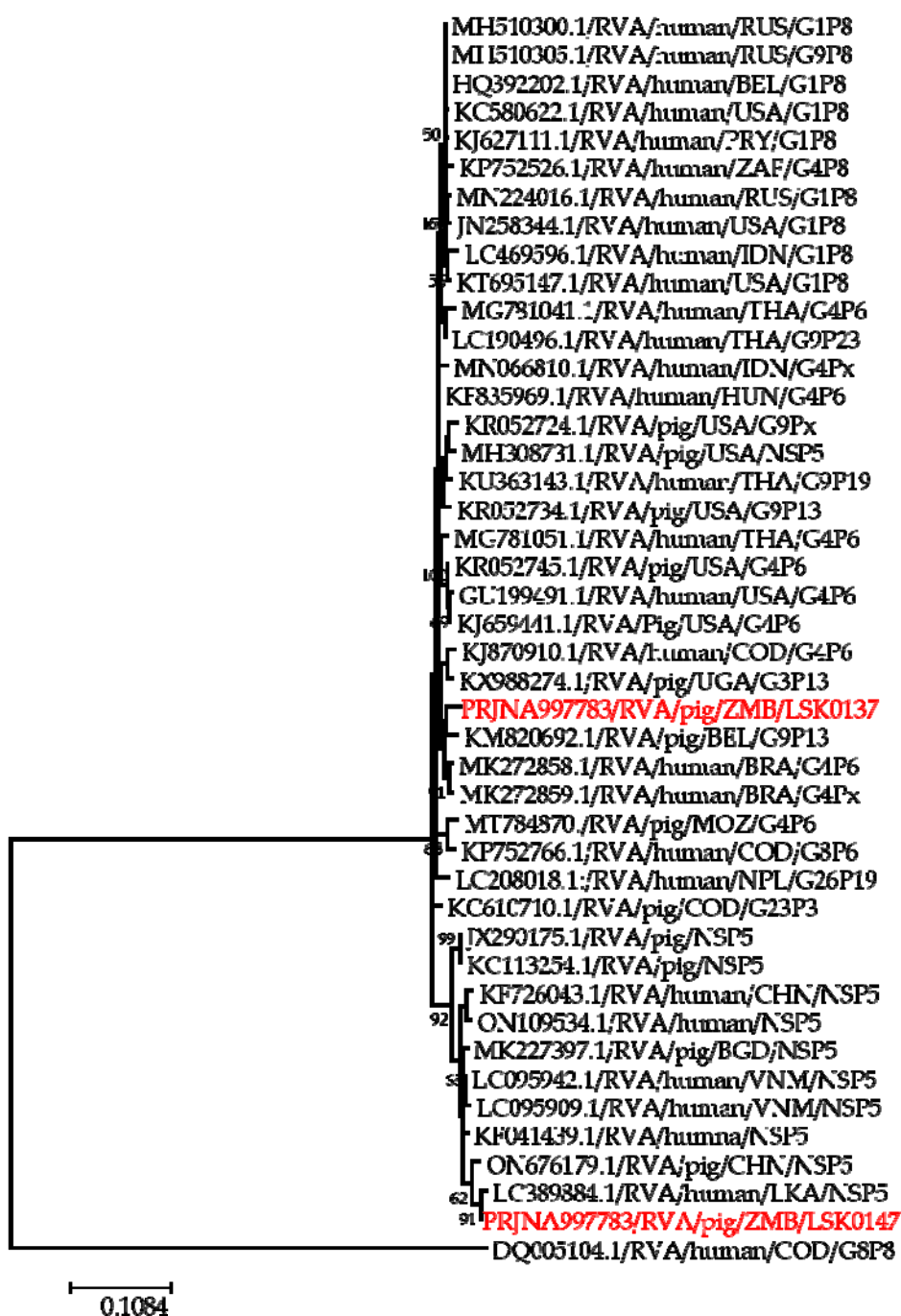
Figure S4. Phylogenetic tree of NSP1 genes. The tree was constructed using the general time reversible evolutionary model. The analysis was based on 1443 nucleotides. Bootstrap values on branch nodes ≥ 50% are shown. The GenBank accession number/ Rotavirus group/Species origin/country of origin / G/P-types represent the reference sequences included in the tree. The virus characterized in this study with its bioproject accession number is shown in red text.

Figure S5. Phylogenetic tree of NSP2 genes that belong to genotype N1. The tree was constructed using the general time reversible evolutionary model. The analysis was based on 804 nucleotides. Bootstrap values on branch nodes ≥ 50% are shown. The GenBank /accession number/ Rotavirus group/Species origin/country of origin / G/P-types represent the reference sequences included in the tree. The viruses characterized in this study with their bioproject accession number are shown in red text.

Figure S6. Phylogenetic tree of NSP5 genes that belong to genotype H1. The tree was constructed using the general time reversible evolutionary model. The analysis was based on 582 nucleotides. Bootstrap values on branch nodes ≥ 50% are shown. The Gen-Bank accession number/ Rotavirus group/Species origin/country of origin / G/P-types represent the reference sequences included in the tree. The virus characterized in this study with its bioproject accession number is shown in red text.