**Supplement Material**

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

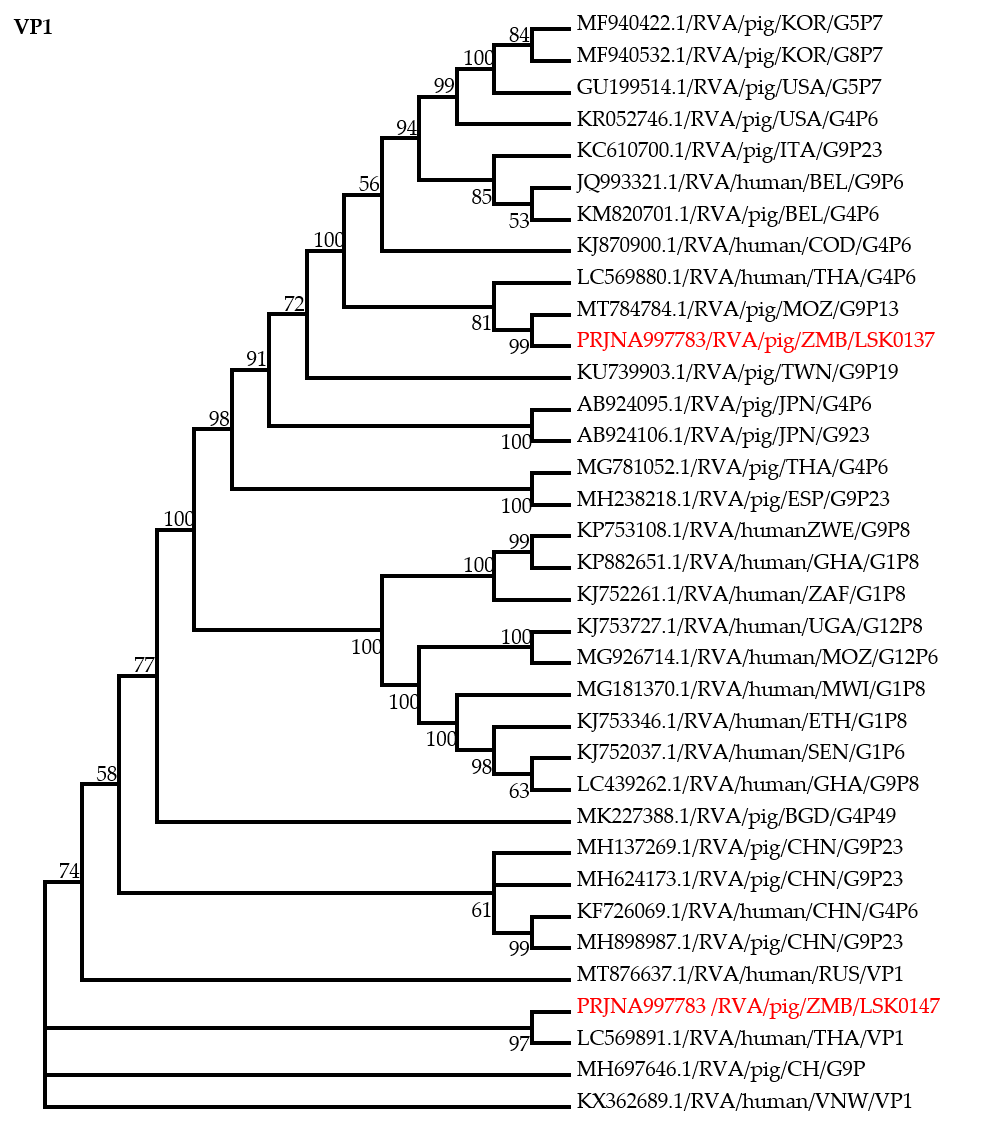
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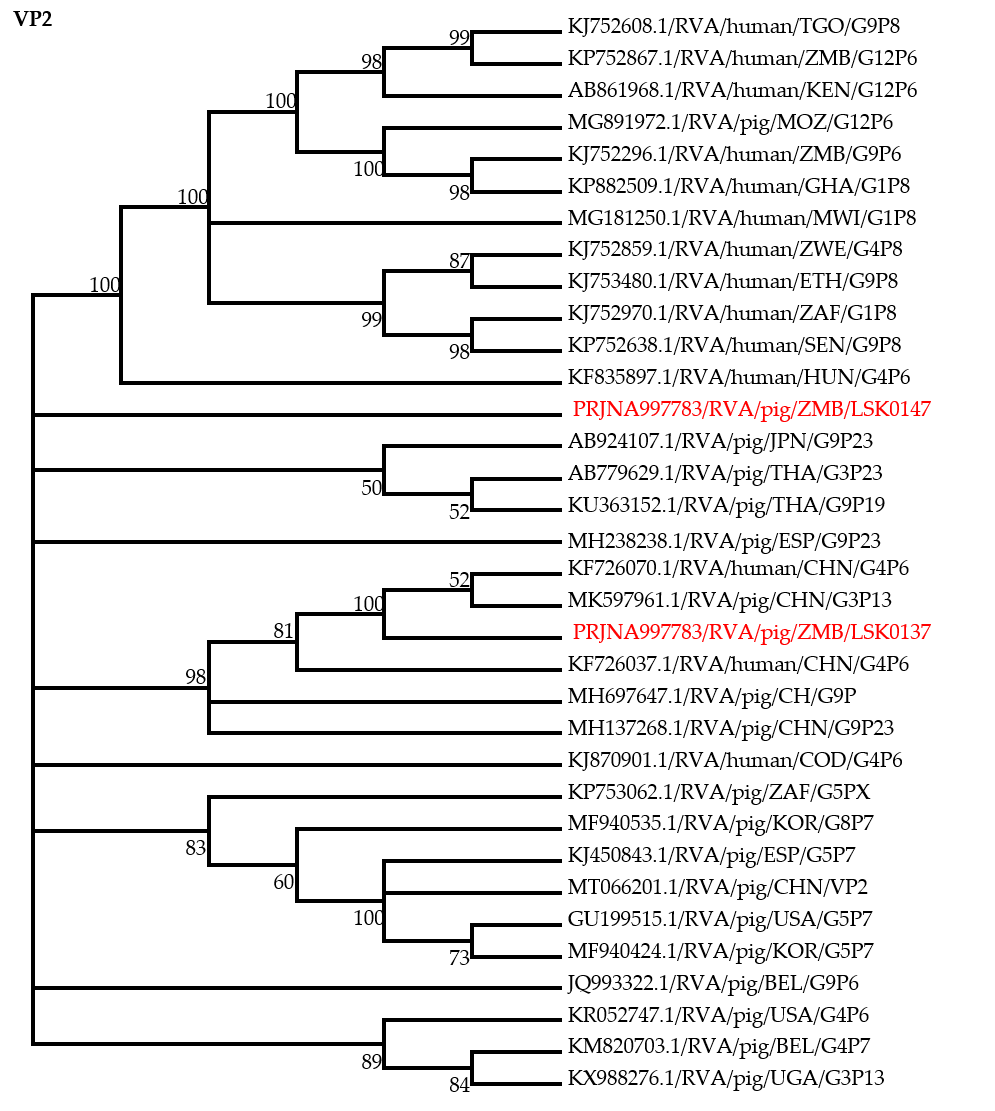
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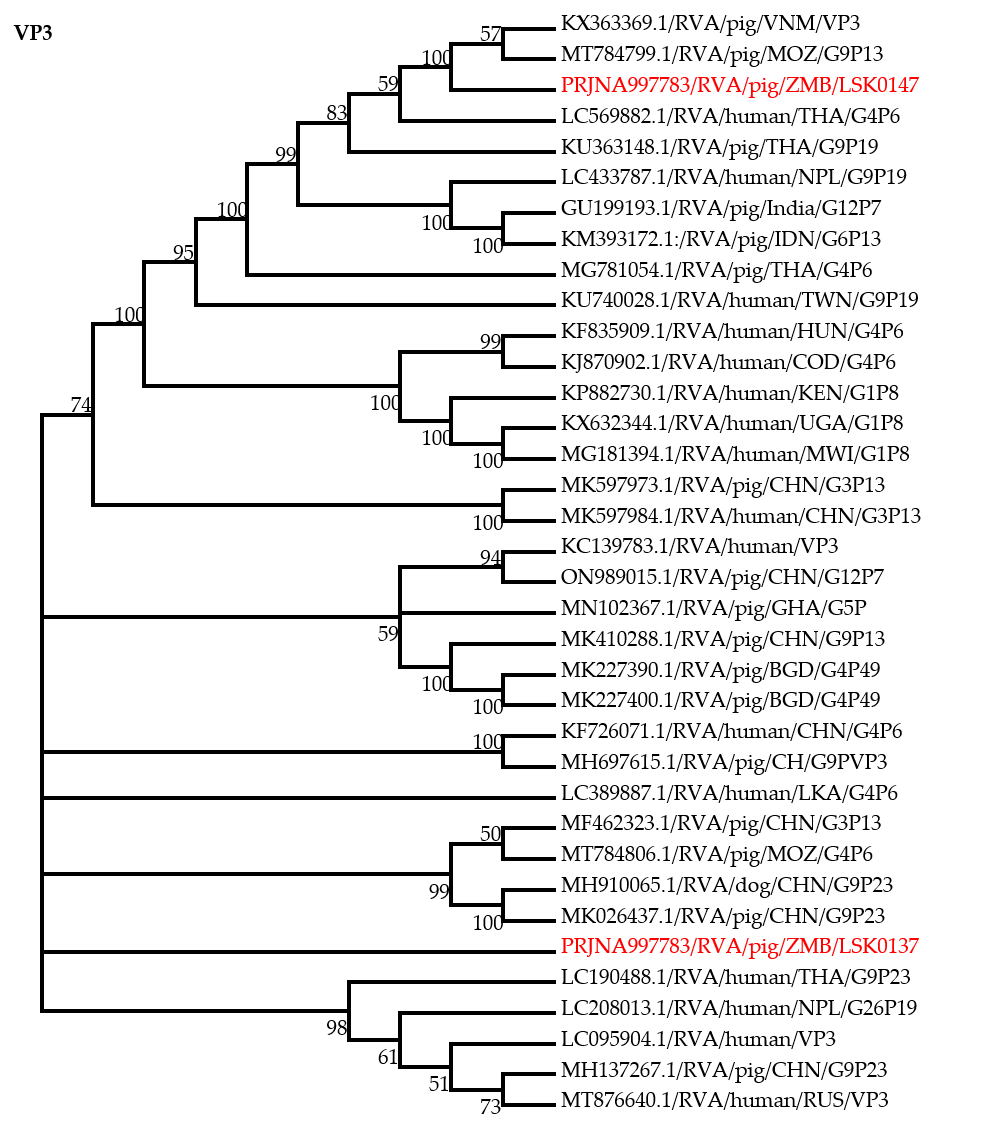
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**Figure S1**.Phylogenetic tree of VP1 genes that belong to genotype R1. The analysis was based on 3218 nucleotides. Bootstrap values on branch nodes ≥ 50% are shown. The GenBank accession number/ Rotavirus group/Species origin/country of origin / 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.

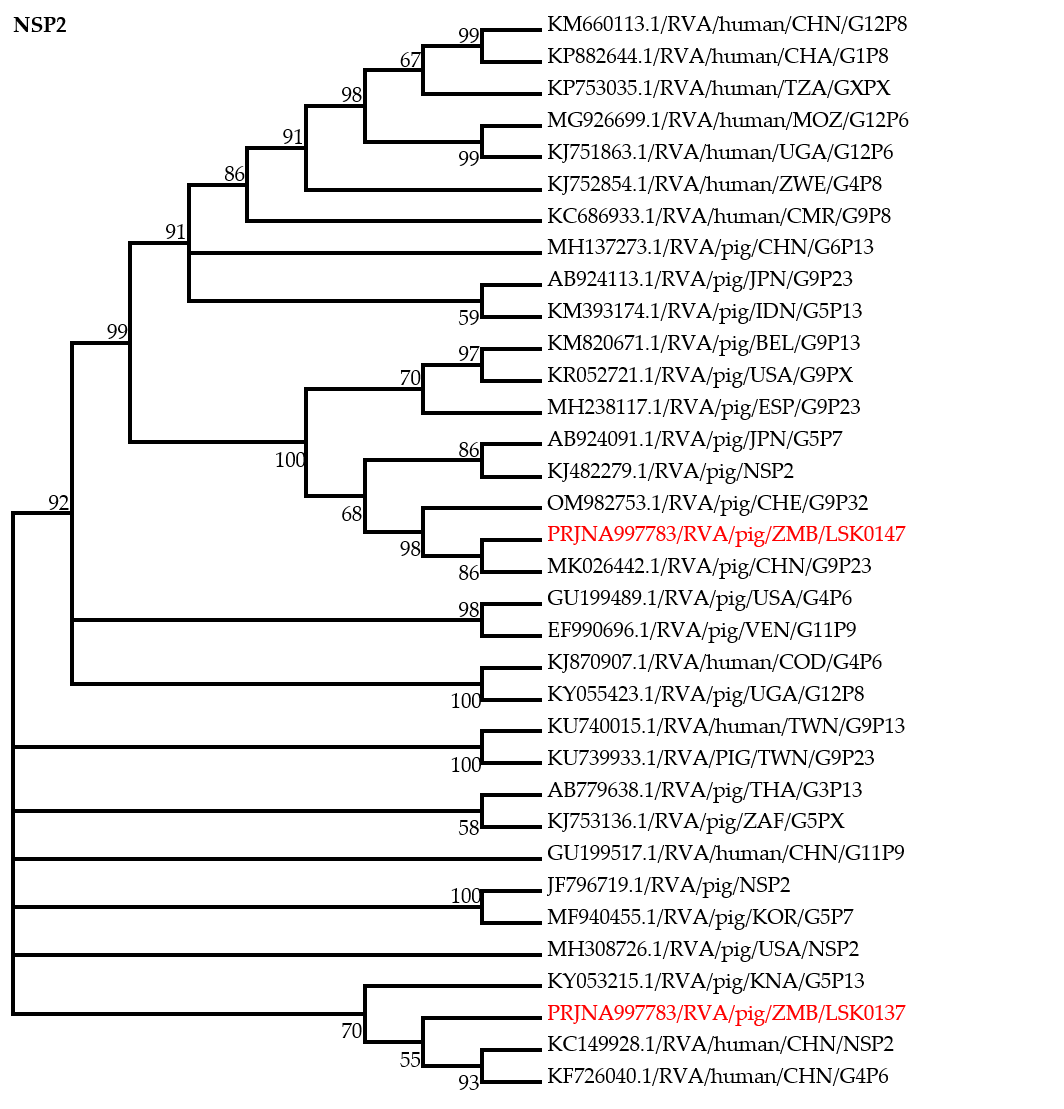
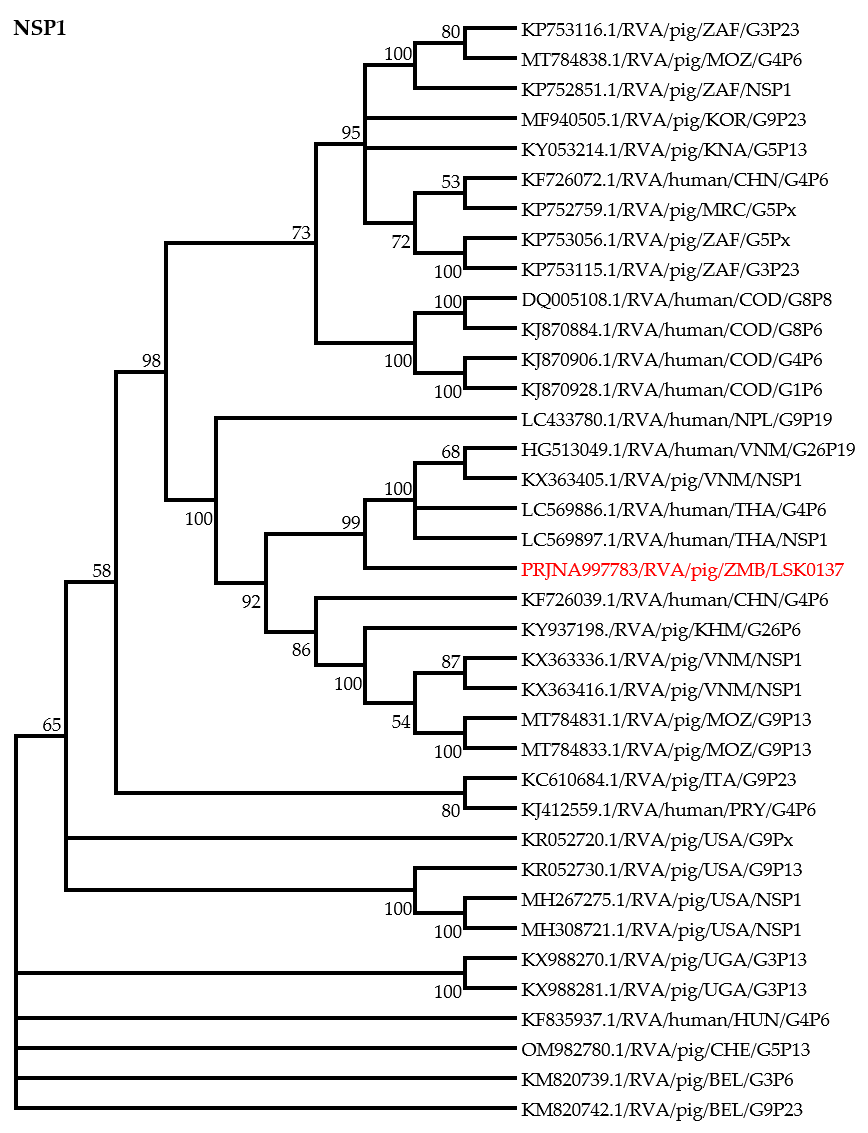


**Figure S2.** Phylogenetic tree of VP2 genes that belong to genotype C1. The analysis was based on 2605 nucleotides. Bootstrap values on branch nodes ≥ 50% are shown. The GenBank accession number/ Rotavirus group/Species origin/country of origin / G/P-types represent the reference sequences included in the tree. The viruses characterized in this study with their Bioproject accession number are shown in red text.

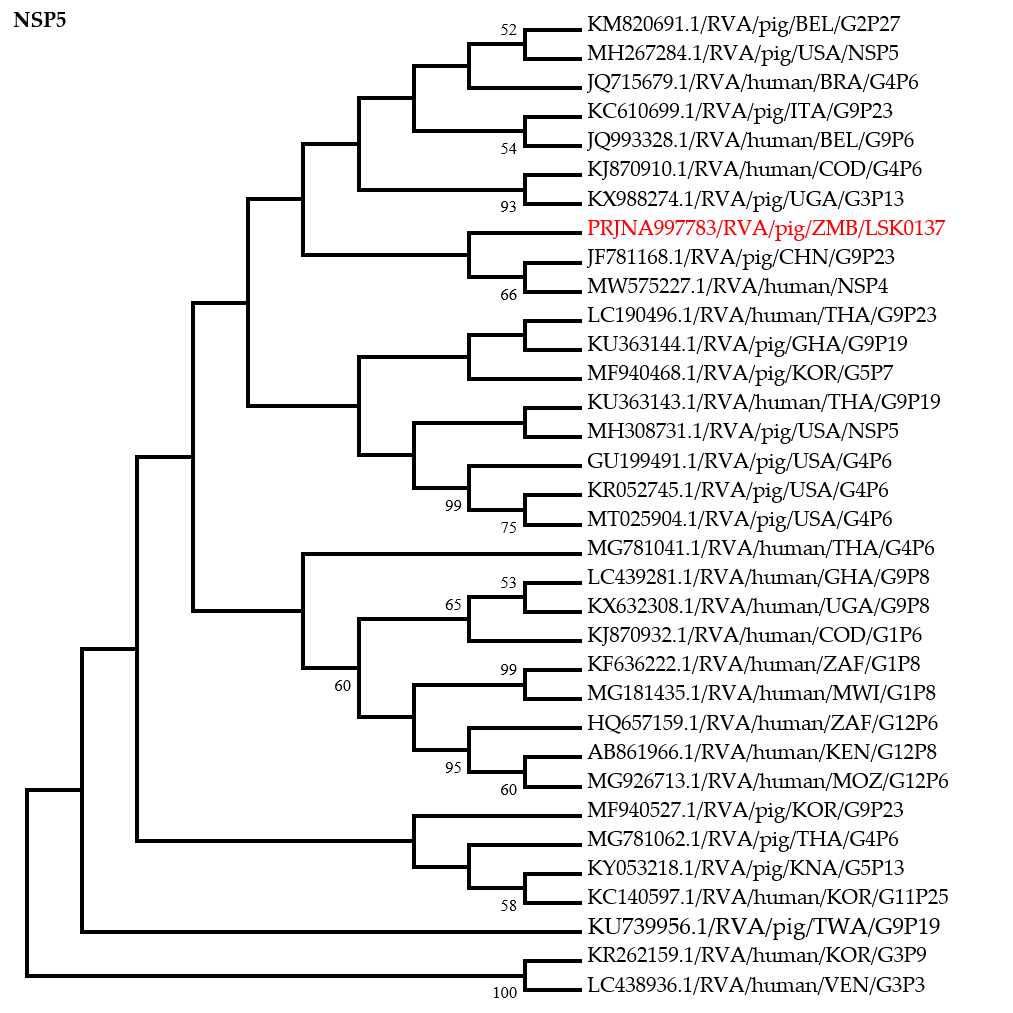


**Figure S3.** Phylogenetic tree of VP3 genes that belongs to genotype M1. The analysis was based on 2505 nucleotides. Bootstrap values on branch nodes ≥ 50% are shown. The GenBank accession number/ Rotavirus group/Species origin/country of origin / G/P-types represent the reference sequences included 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 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 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 analysis was based on 582 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.