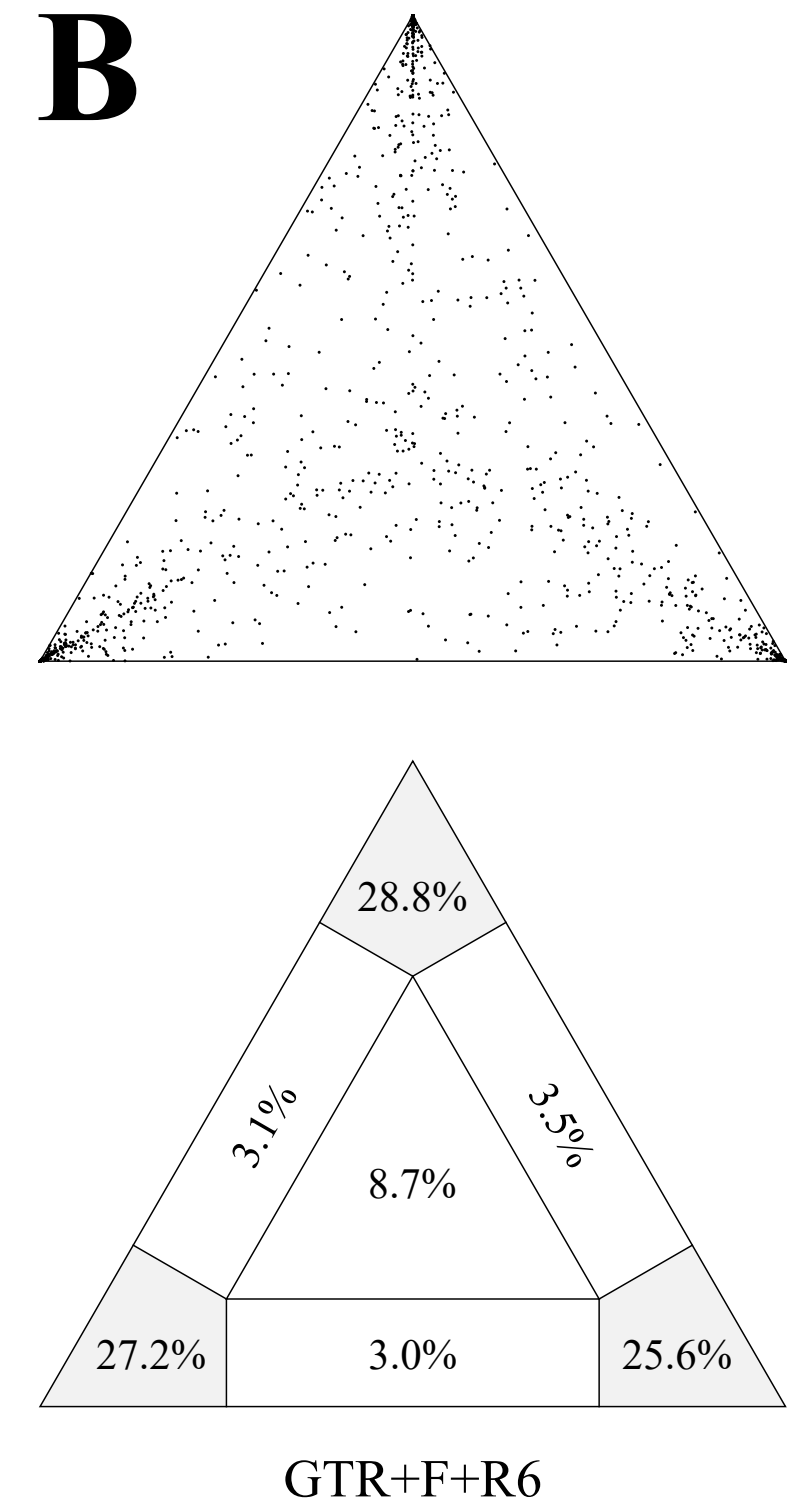
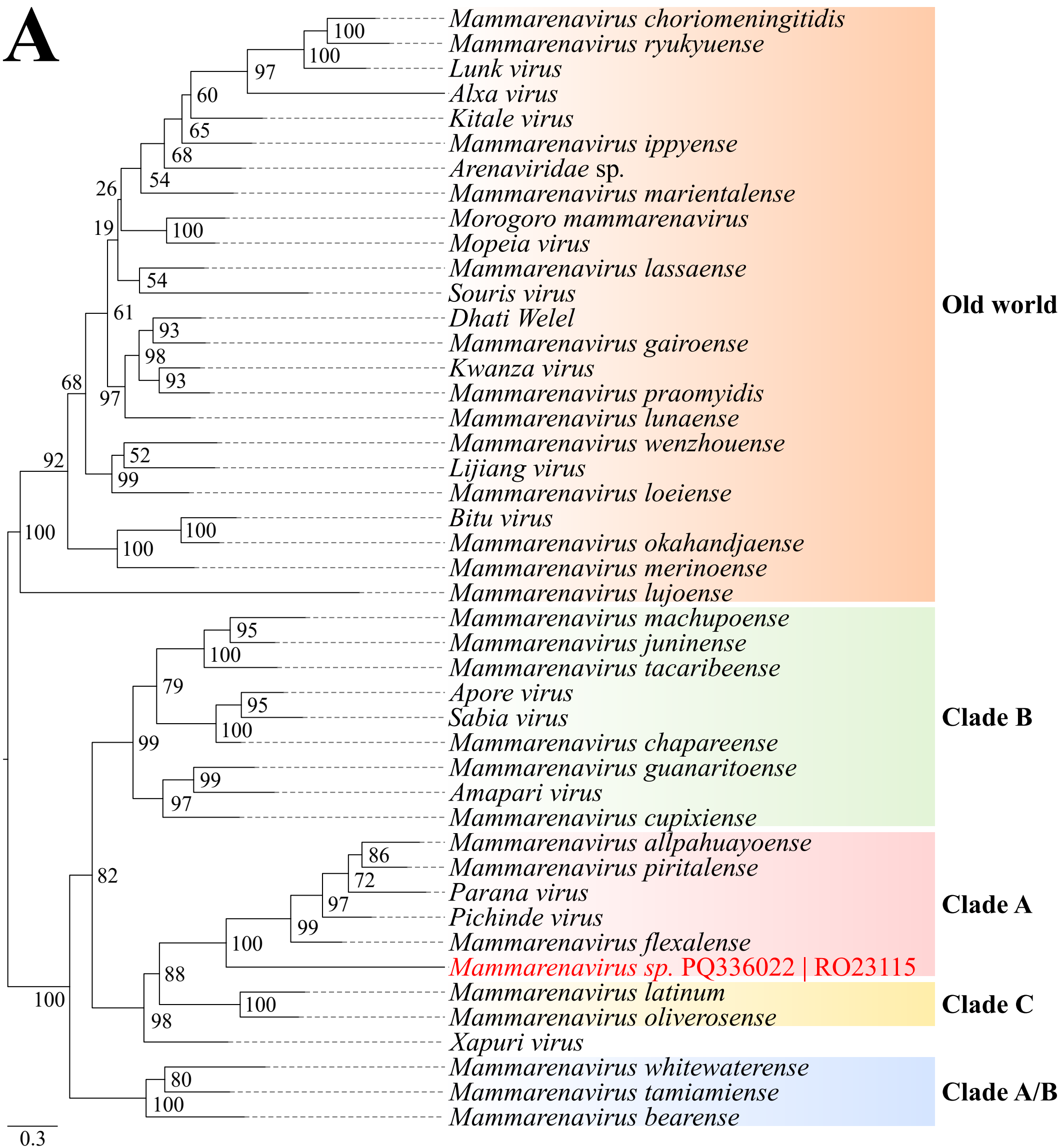




Supplementary Figure 3.(A) Phylogenetic reconstruction using the Maximum Likelihood method based on nucleotide sequences of the glycoprotein region of New and Old World Arenaviruses, including the identified contig highlighted in red. **(B)** Maximum likelihood mapping diagram showing the quality of the phylogenetic signal from the quartet analysis, with 81.6% of quartets resolved.