

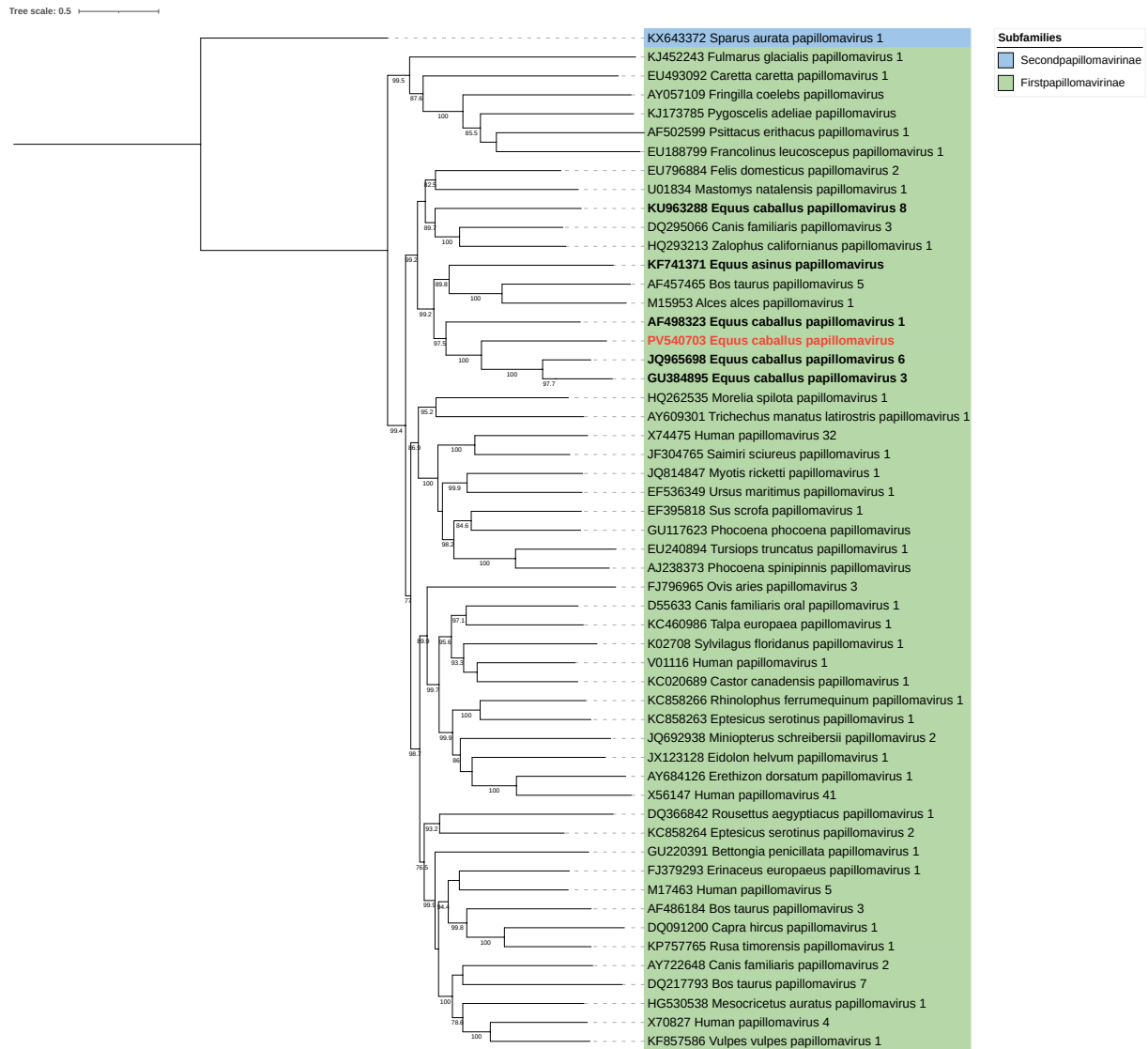


Figure S1 Whole genome phylogenetic analysis of *Papillomaviridae*. Maximum likelihood tree of representative member species from each genus within the *Papillomaviridae* family. The tree was constructed using with the Best-fit model (GTR+F+I+G4) selected based on the Bayesian Information Criterion (BIC). Bootstrap analysis was performed with 1,000 ultrafast bootstrap replicates, and bootstrap values ≥ 70 are displayed. Colored labels indicate different subfamilies. The sequence obtained in this study (PV540703) is highlighted in bold red, while other papillomaviruses from *Equus* are shown in bold.

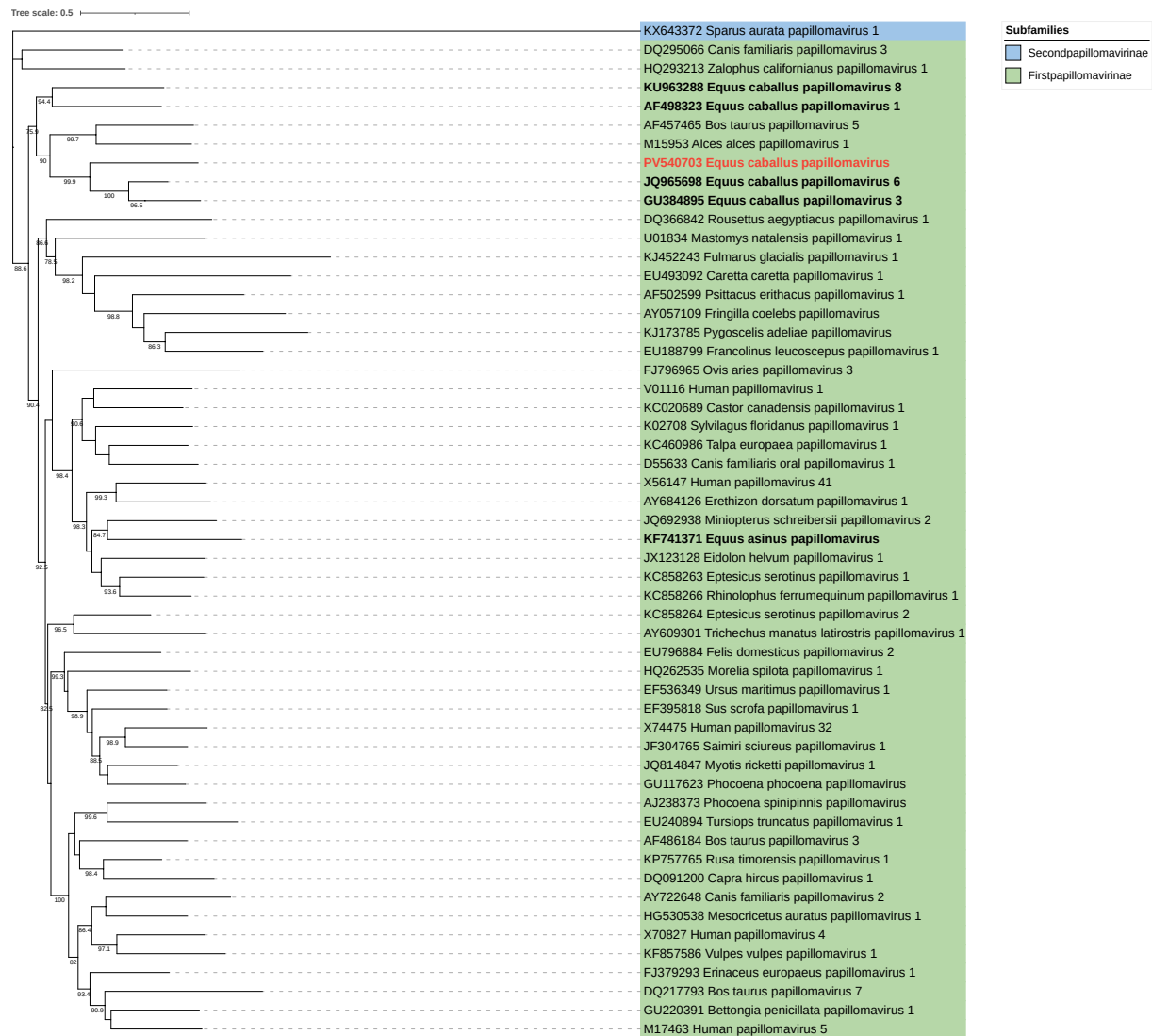


Figure S2 L1 phylogenetic analysis of *Papillomaviridae*. Maximum likelihood tree of representative member species from each genus within the *Papillomaviridae* family. The tree was constructed using the L1 gene with the Best-fit model (GTR+F+I+G4) selected based on the Bayesian Information Criterion (BIC). Bootstrap analysis was performed with 1,000 ultrafast bootstrap replicates, and bootstrap values ≥ 70 are displayed. Colored labels indicate different subfamilies. The sequence obtained in this study (PV540703) is highlighted in bold red, while other papillomaviruses from *Equus* are shown in bold.