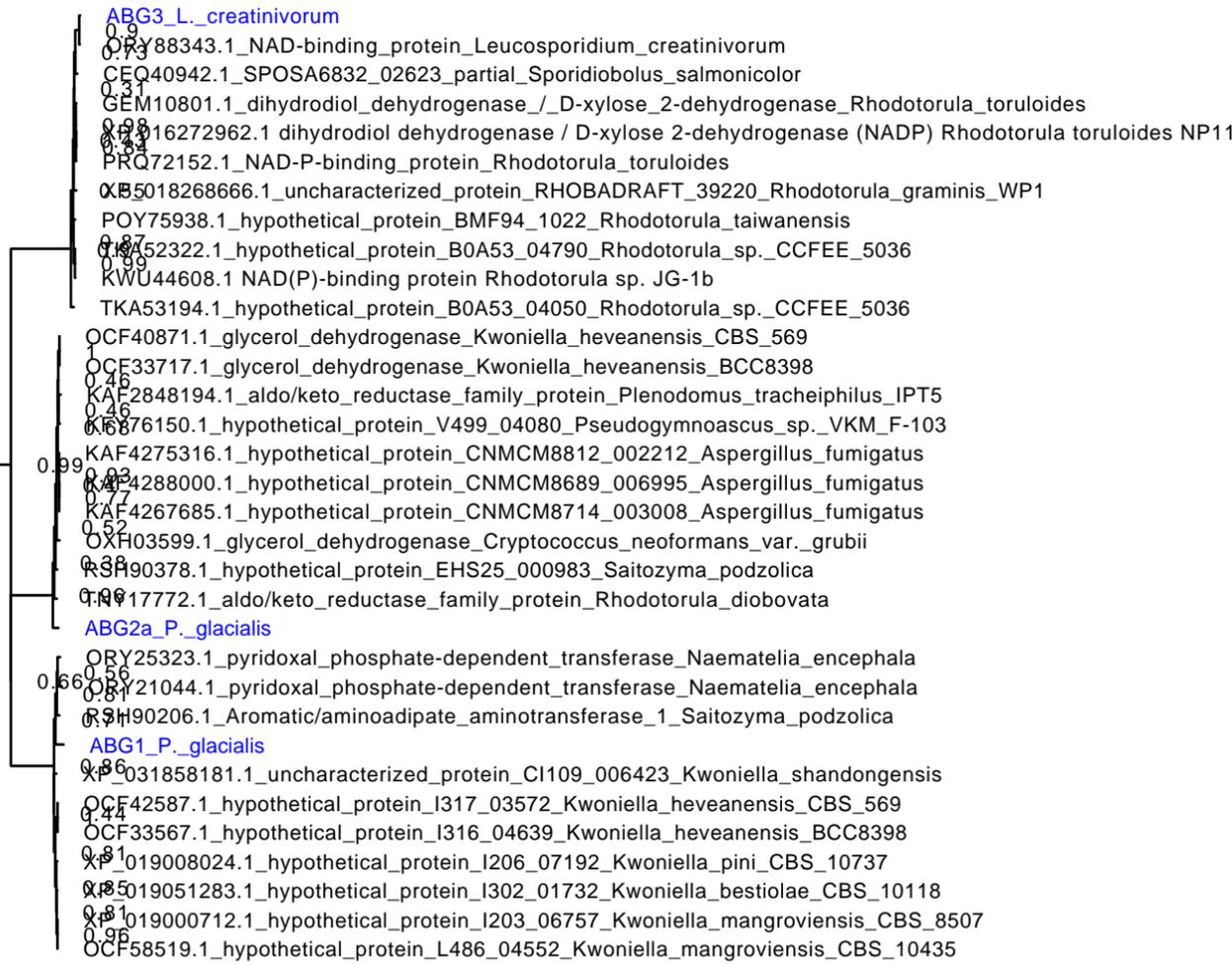
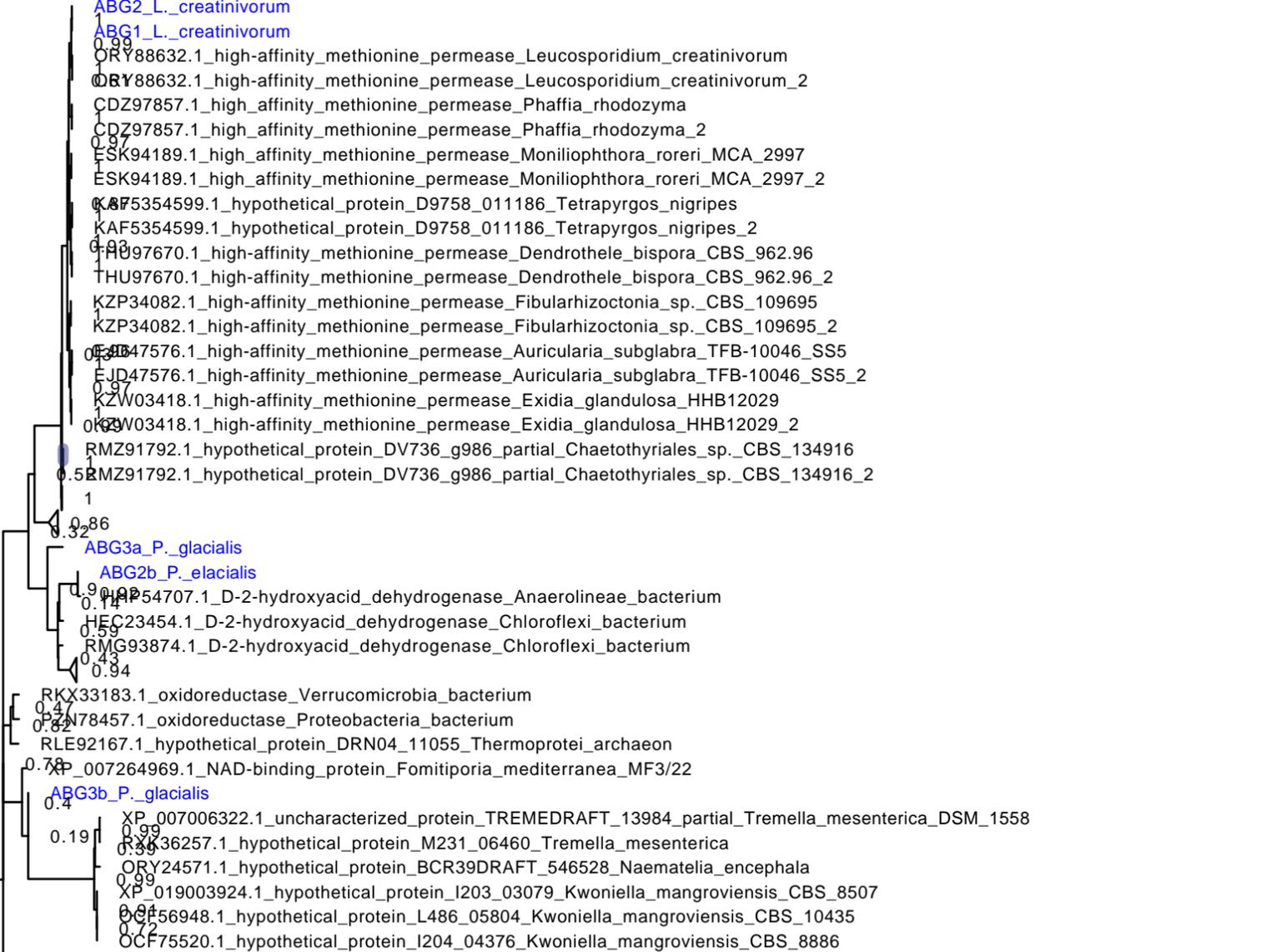


**NRPS  
Core Biosynthetic Genes**

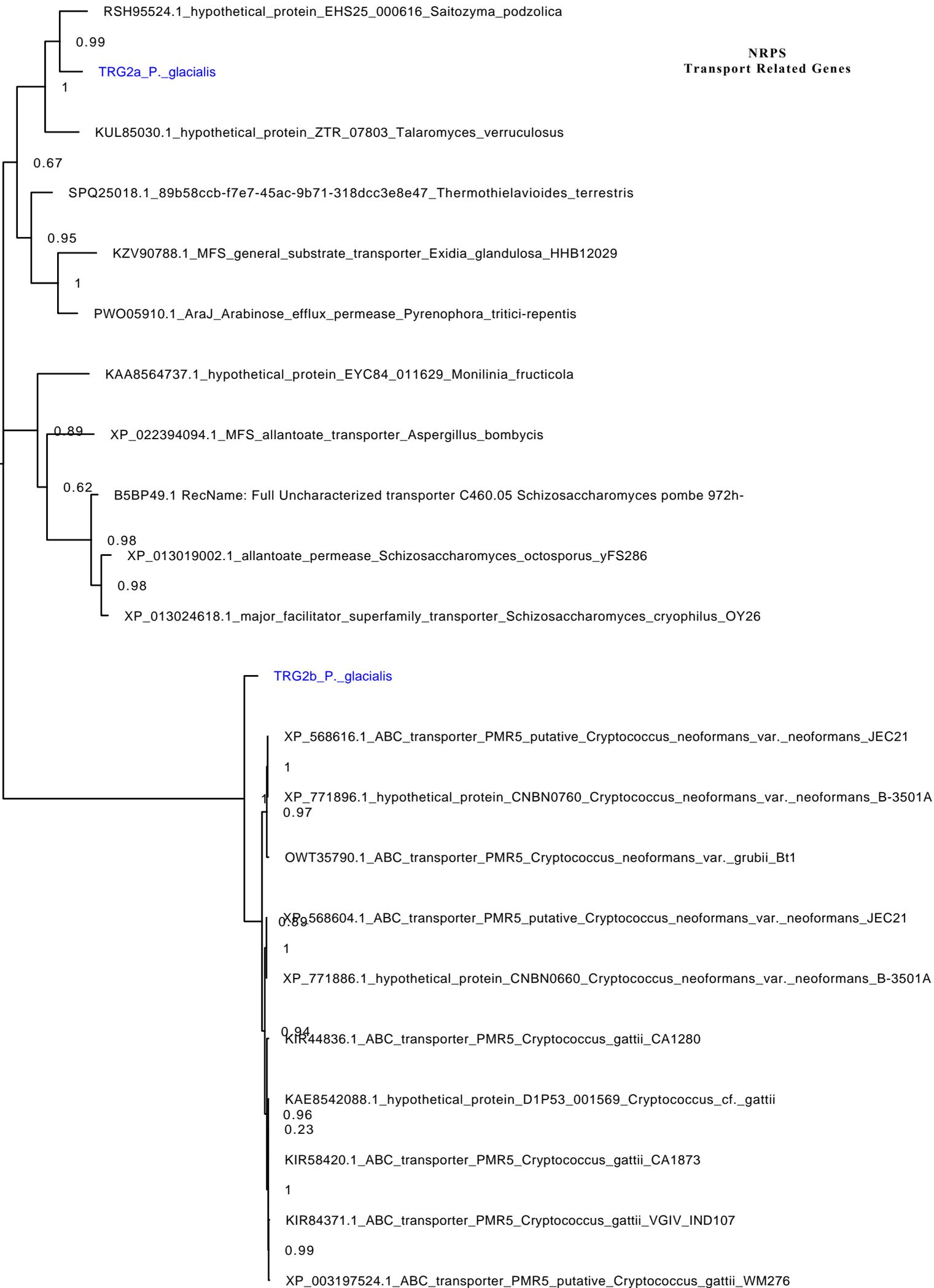


0.6

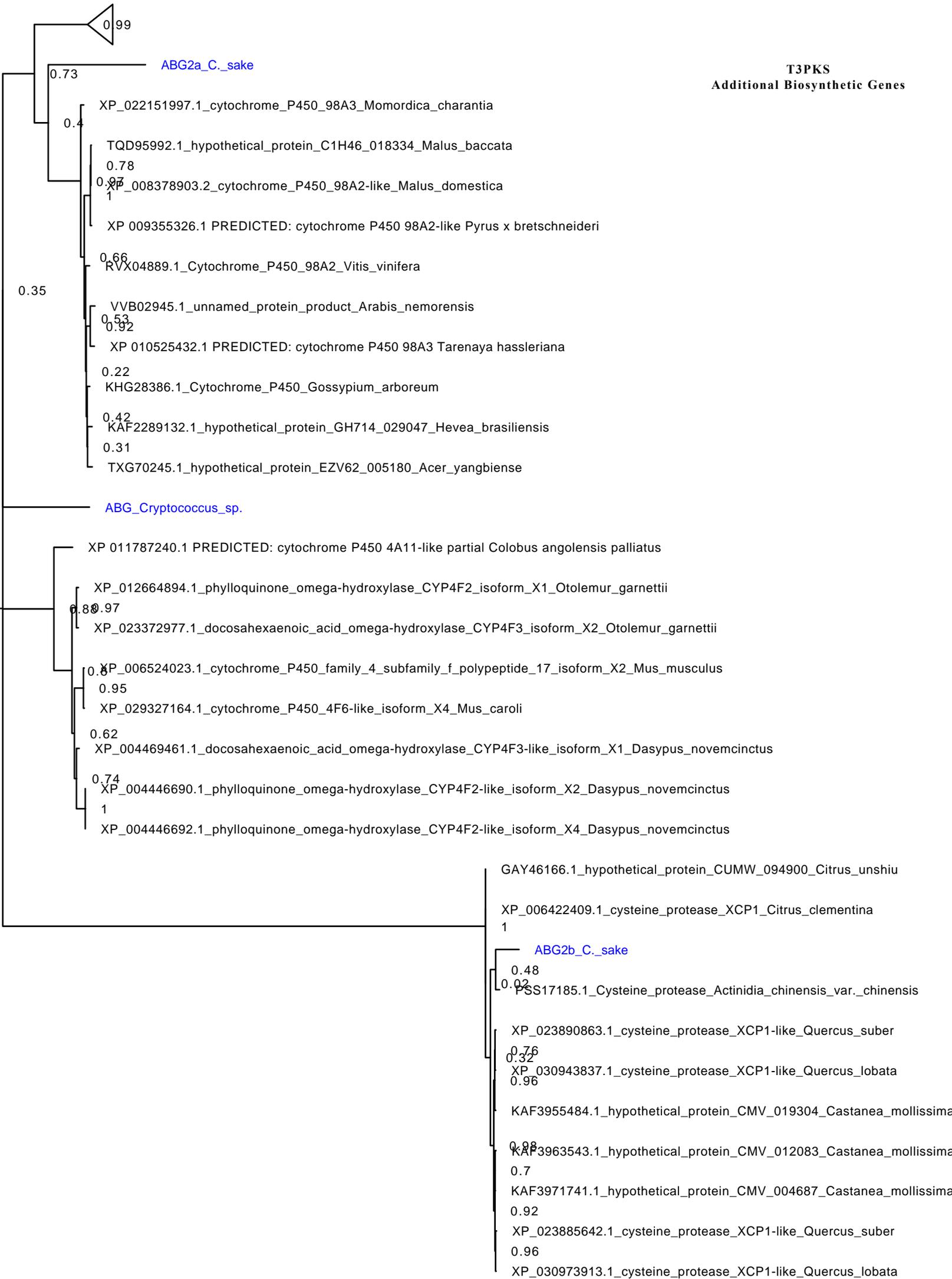
**NRPS**  
**Additional Biosynthetic Genes**



NRPS  
Transport Related Genes



0.4



**T3PKS  
Core Biosynthetic Genes**



0.6

Terpene  
Core Biosynthetic Genes



30.0

The evolutionary history was inferred by using the Maximum Likelihood method and JTT matrix-based model. The tree with the highest log likelihood (-46006.35) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using a JTT model, and then selecting the topology with superior log likelihood value. This analysis involved 79 amino acid sequences. There were a total of 2521 positions in the final dataset. Evolutionary analyses were conducted in MEGA X.