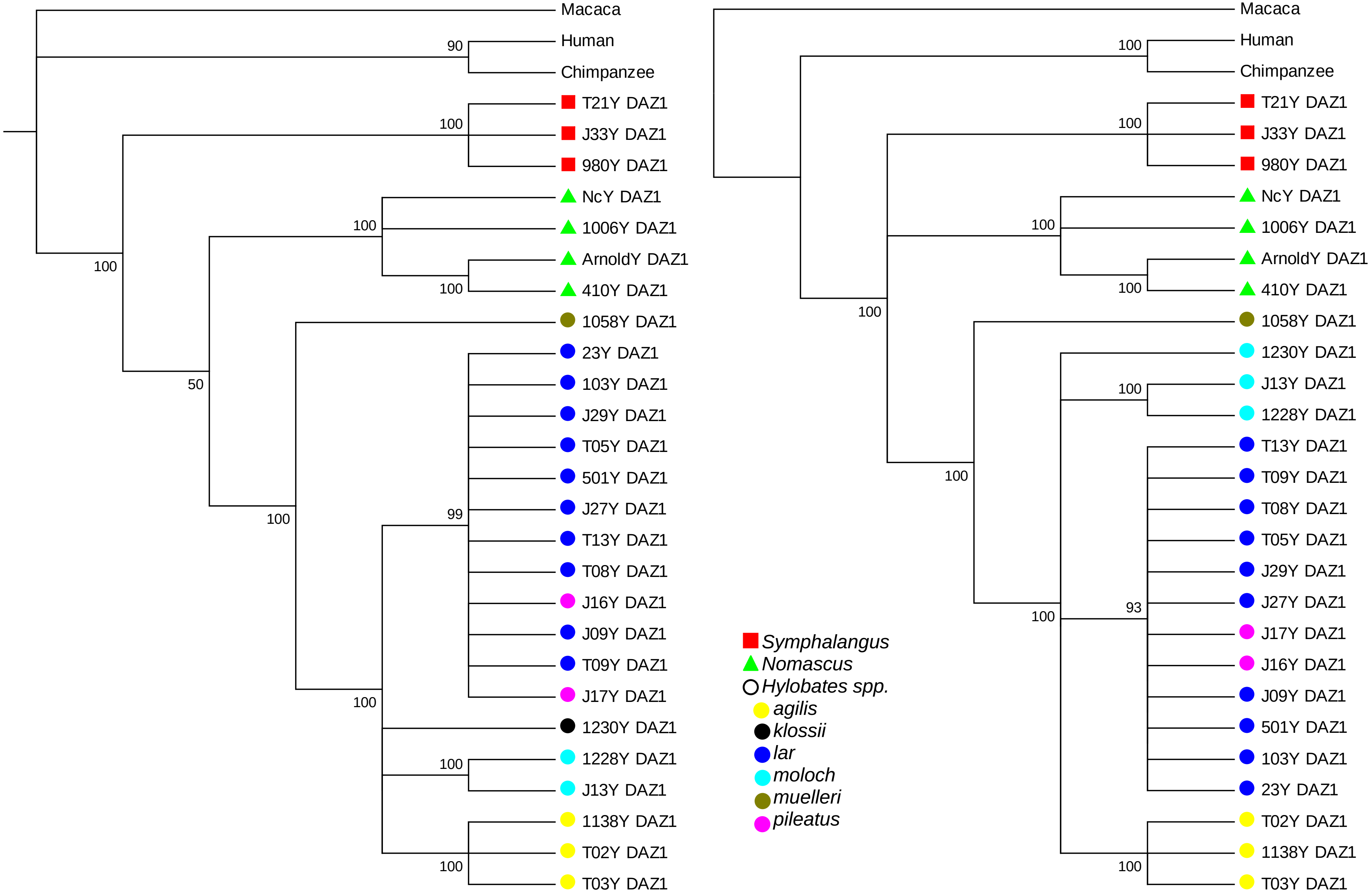
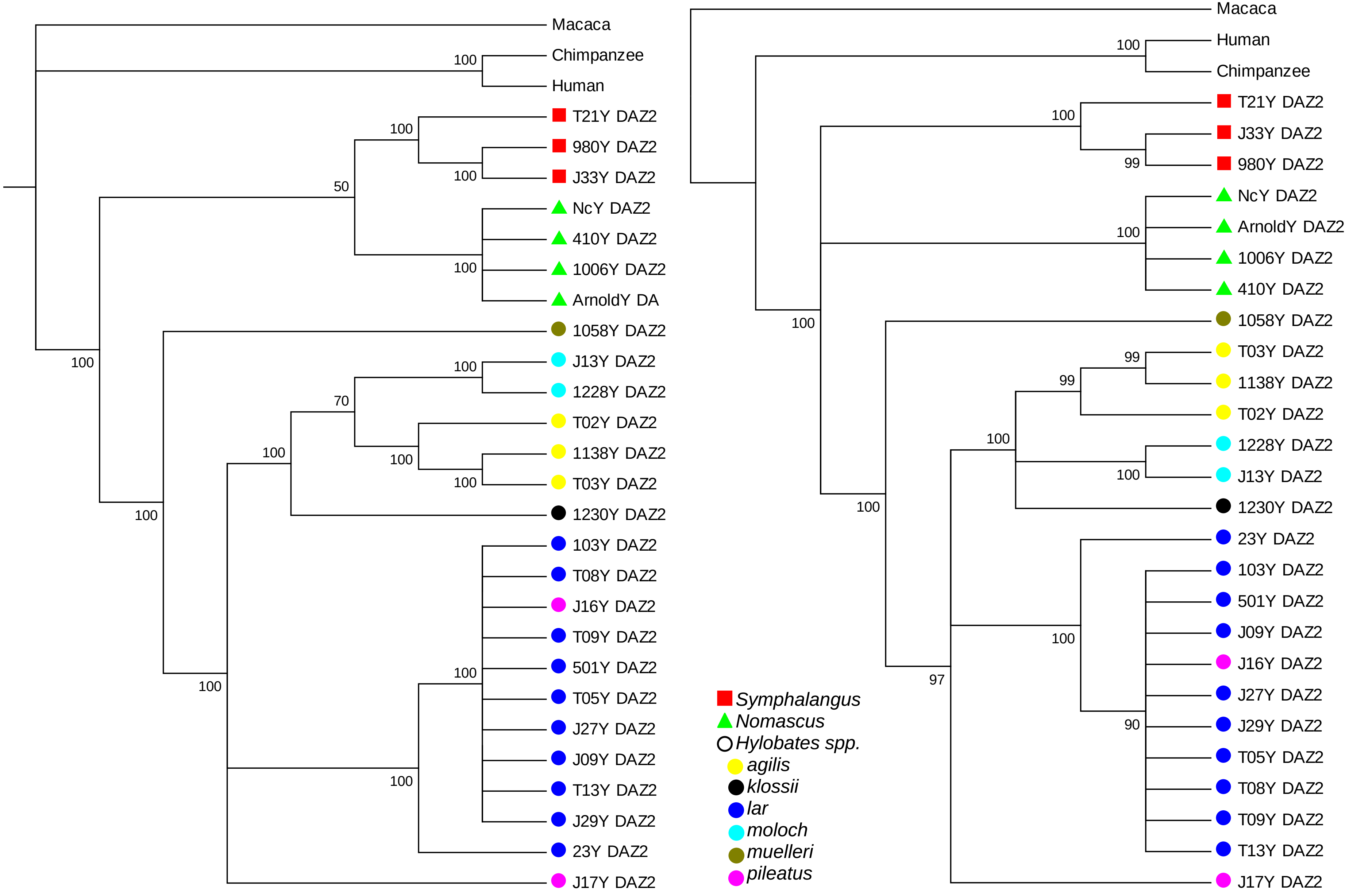
Figure S1 Phylogeny trees of individual Y chromosomal amplicons:
Maximum likelihood (ML) and Bayesian (BI) majority-rule trees of gibbon phylogenies based on the sequences from different Y chromosomal amplicons: DAZ-1, DAZ-2, DBY, RPS4Y, SMCY, TSPY and UTY. The ML trees are on the left and Bayesian trees on the right.

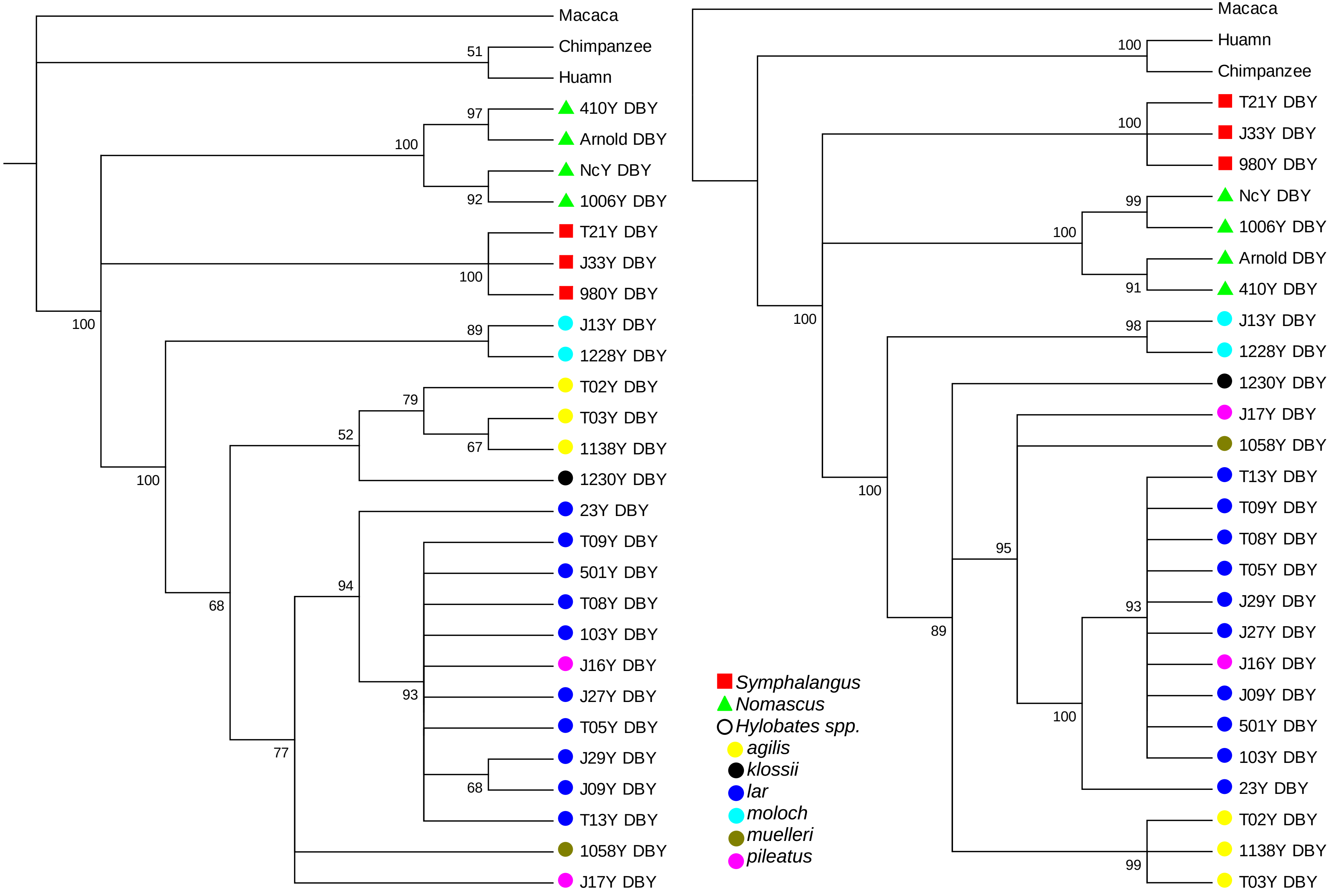
ML and BI trees of DAZ-1



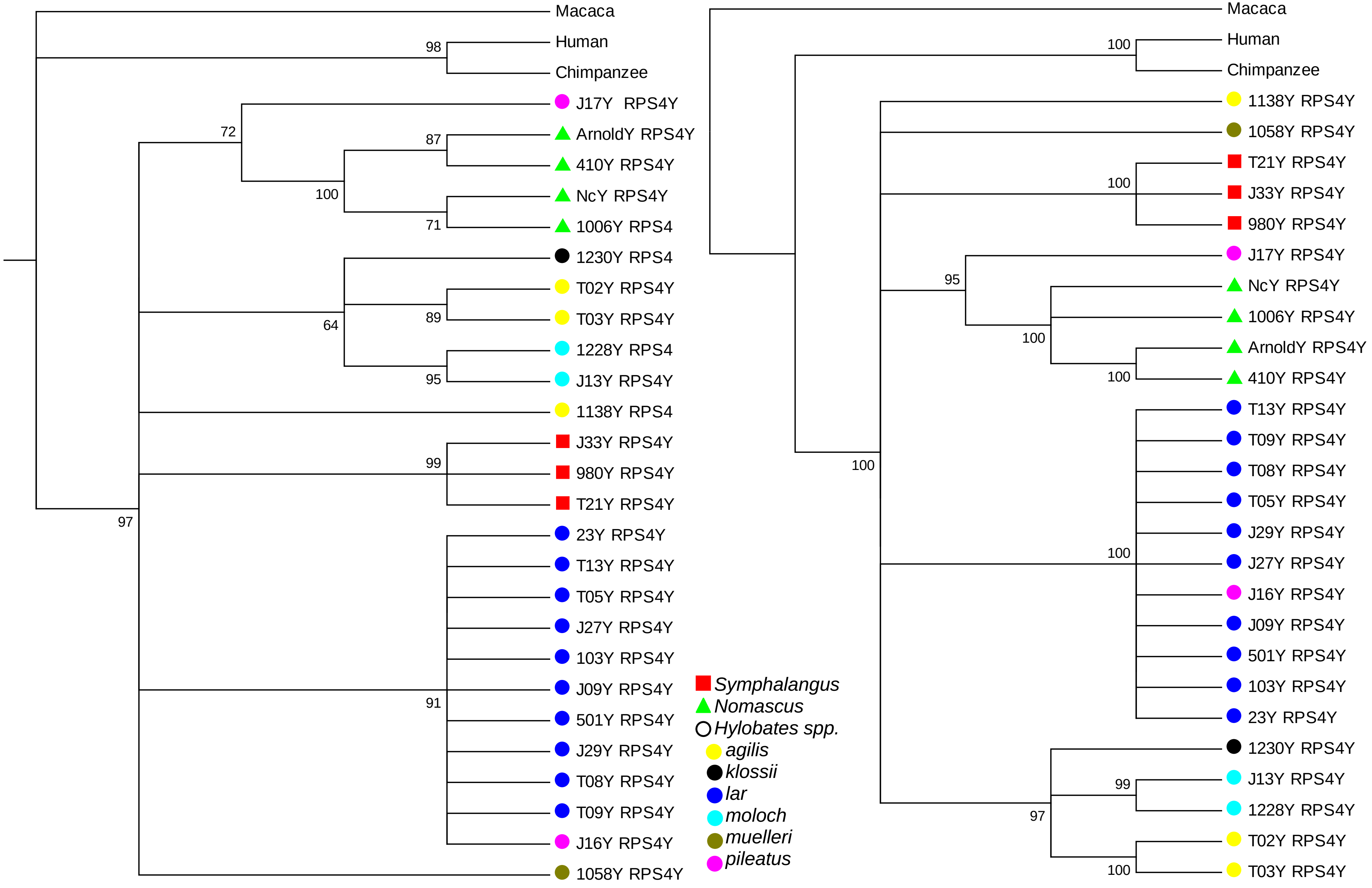
ML and BI trees of DAZ-2



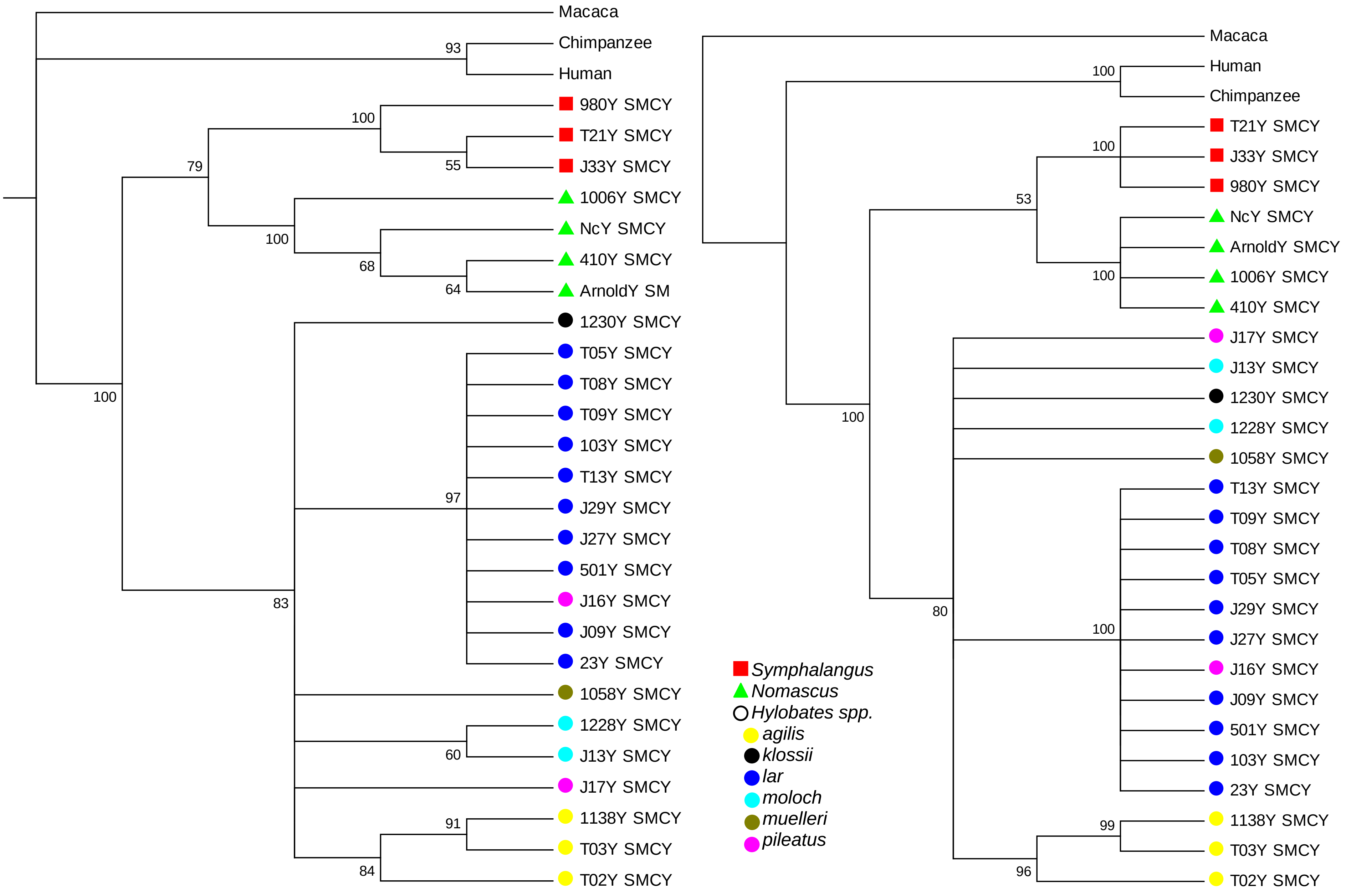
ML and BI trees of DBY



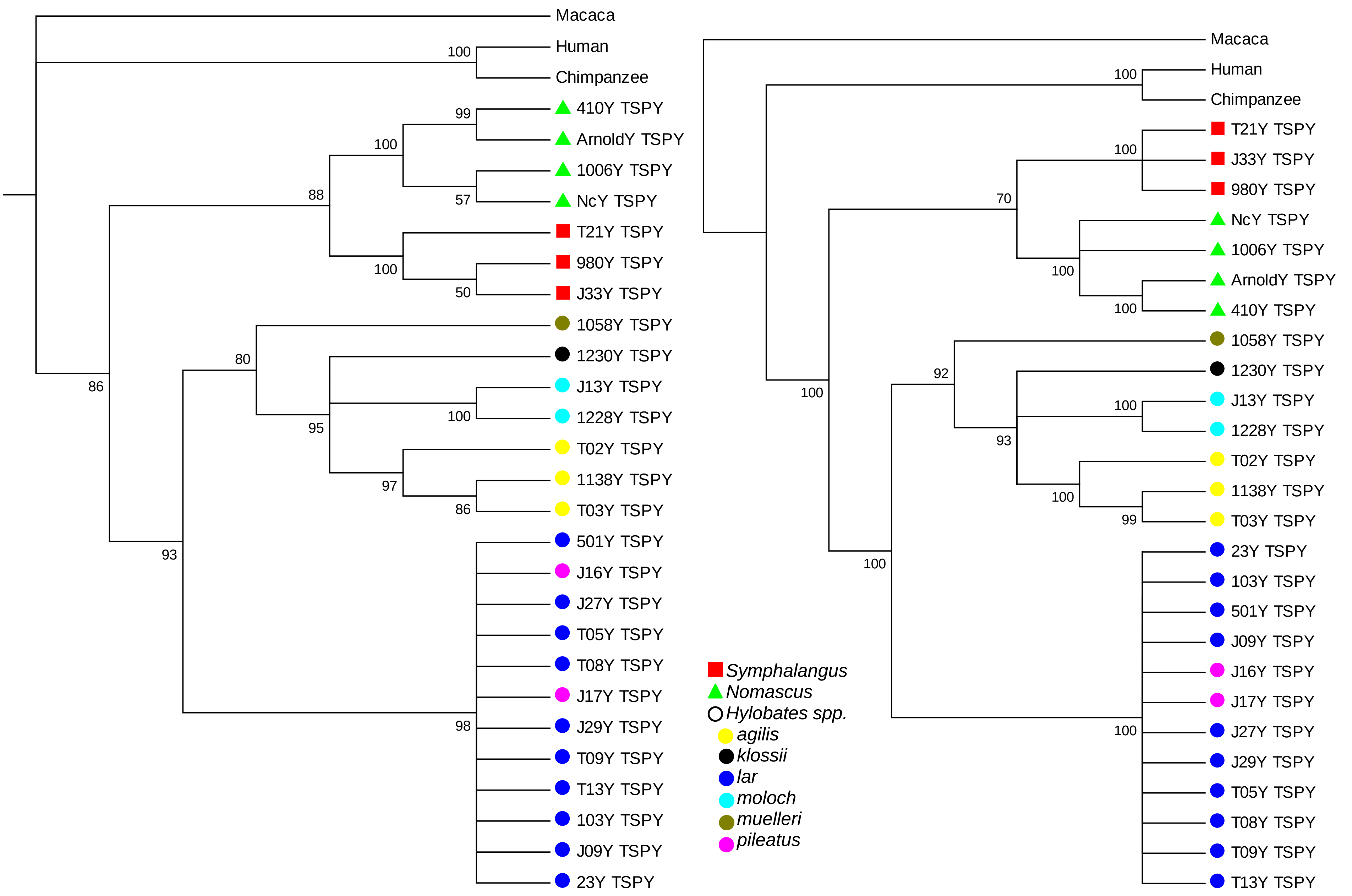
ML and BI trees of RPS4Y



ML and BI trees of SMCY



ML and BI trees of TSPY



ML and BI trees of UTY