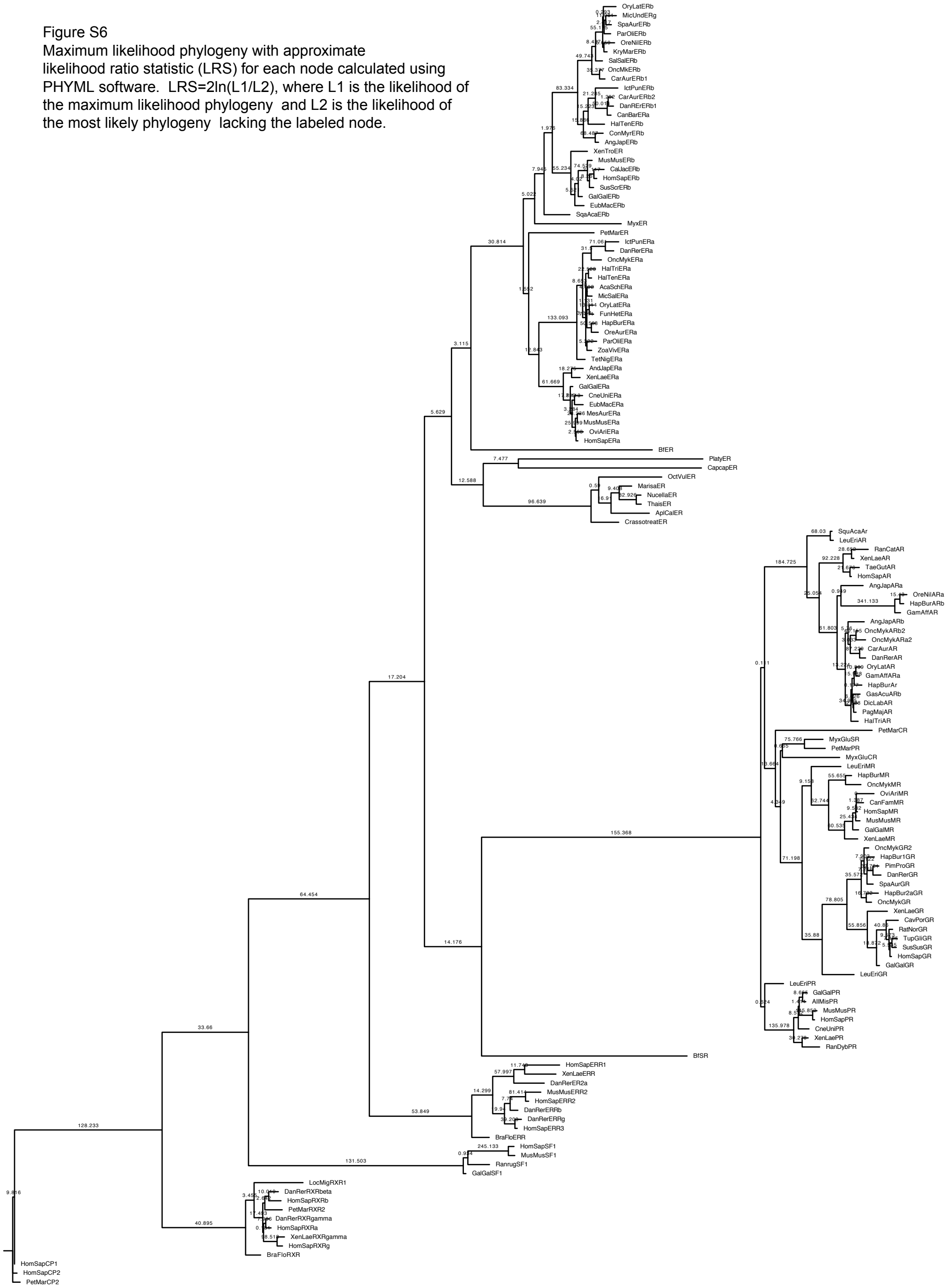Figure S6
Maximum likelihood phylogeny with approximate likelihood ratio statistic (LRS) for each node calculated using PHYML software. LRS=2ln(L1/L2), where L1 is the likelihood of the maximum likelihood phylogeny and L2 is the likelihood of the most likely phylogeny lacking the labeled node.