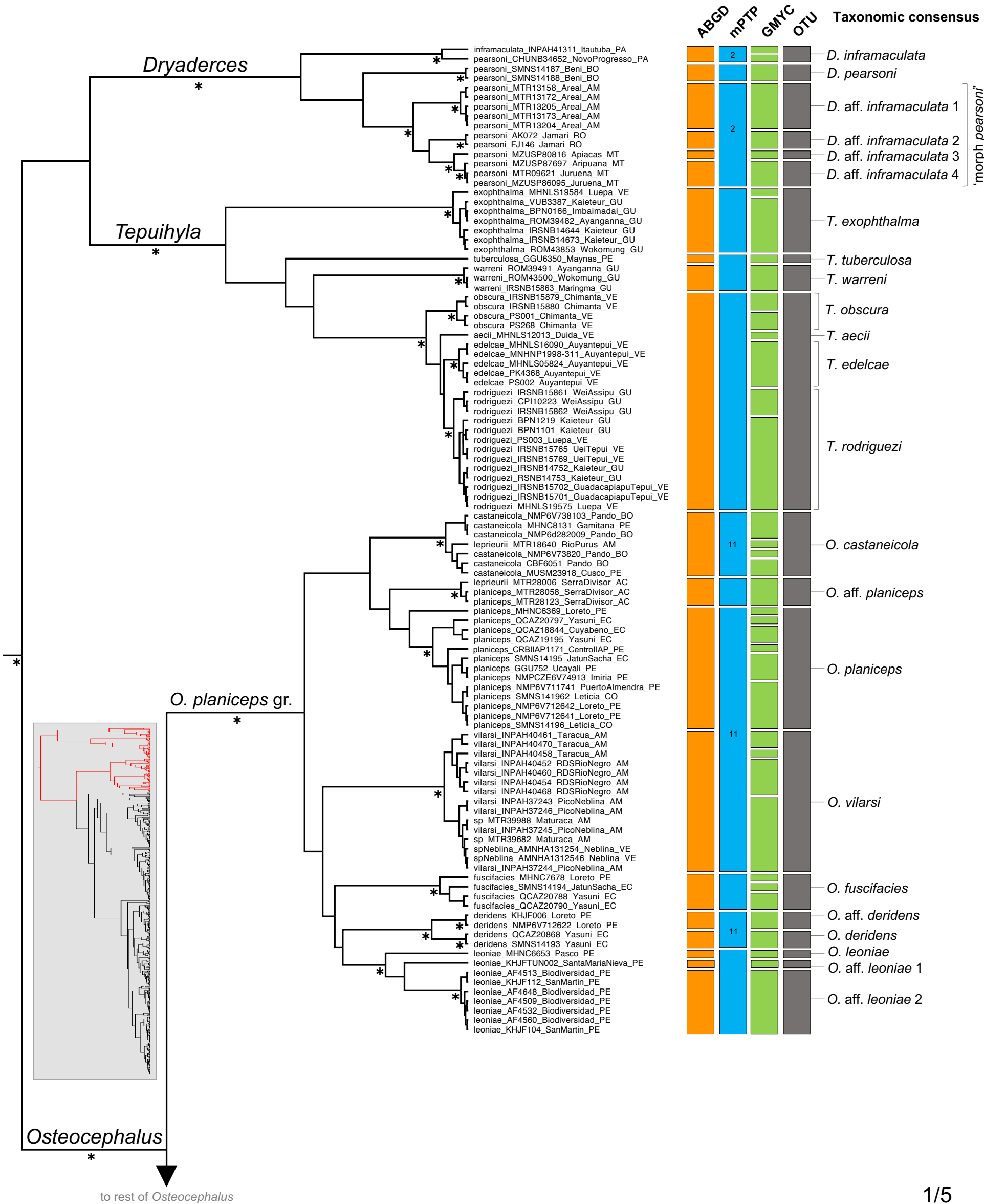
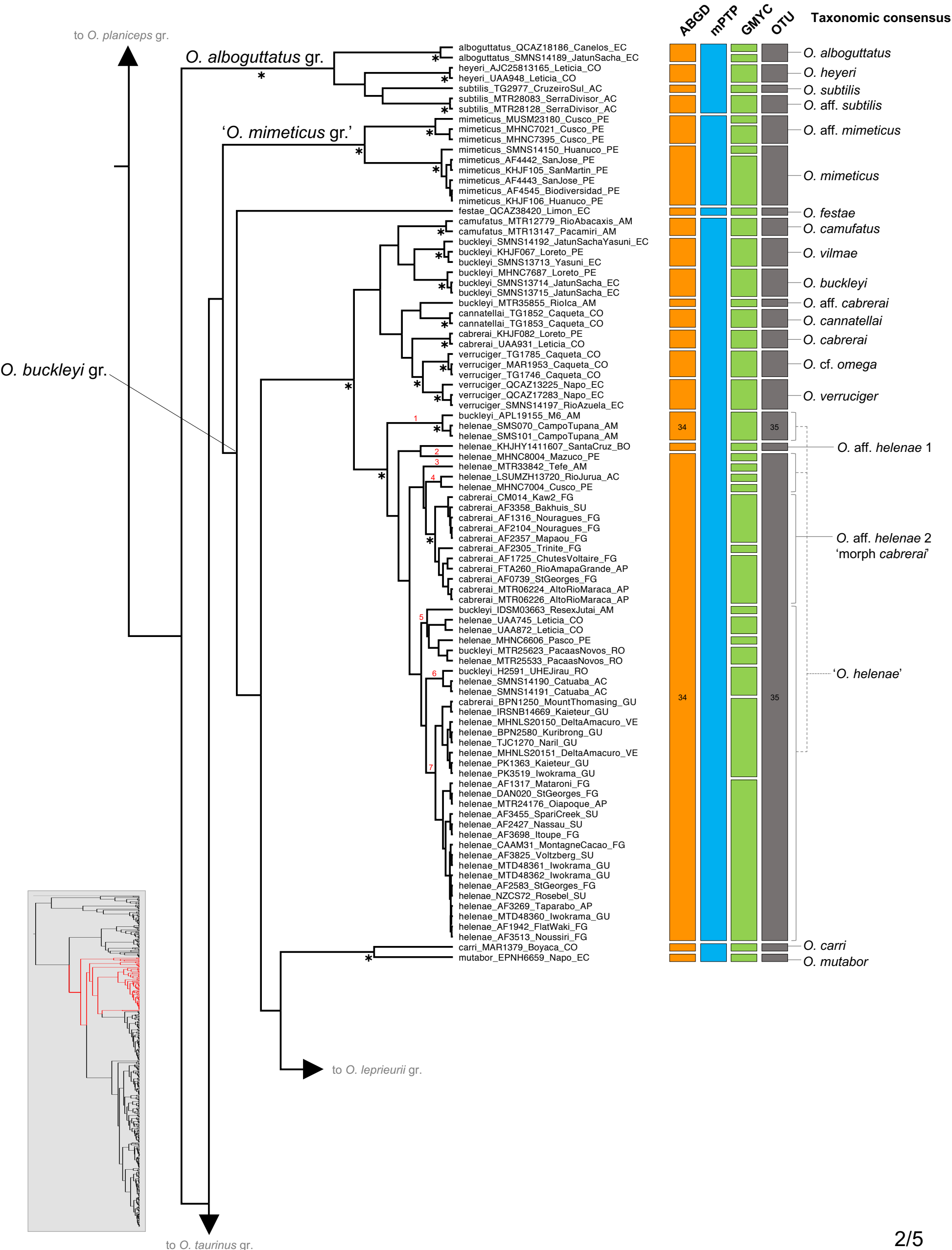
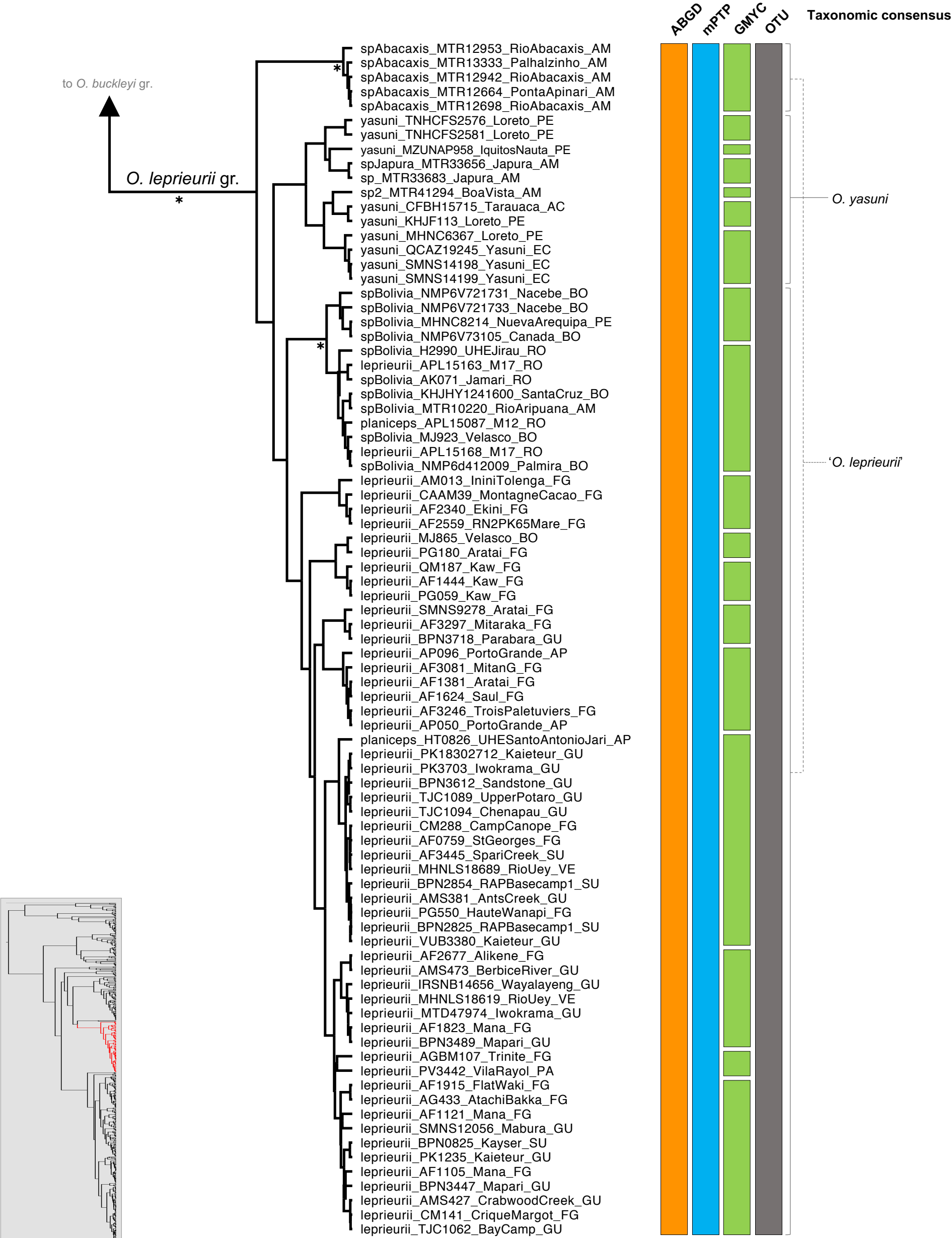
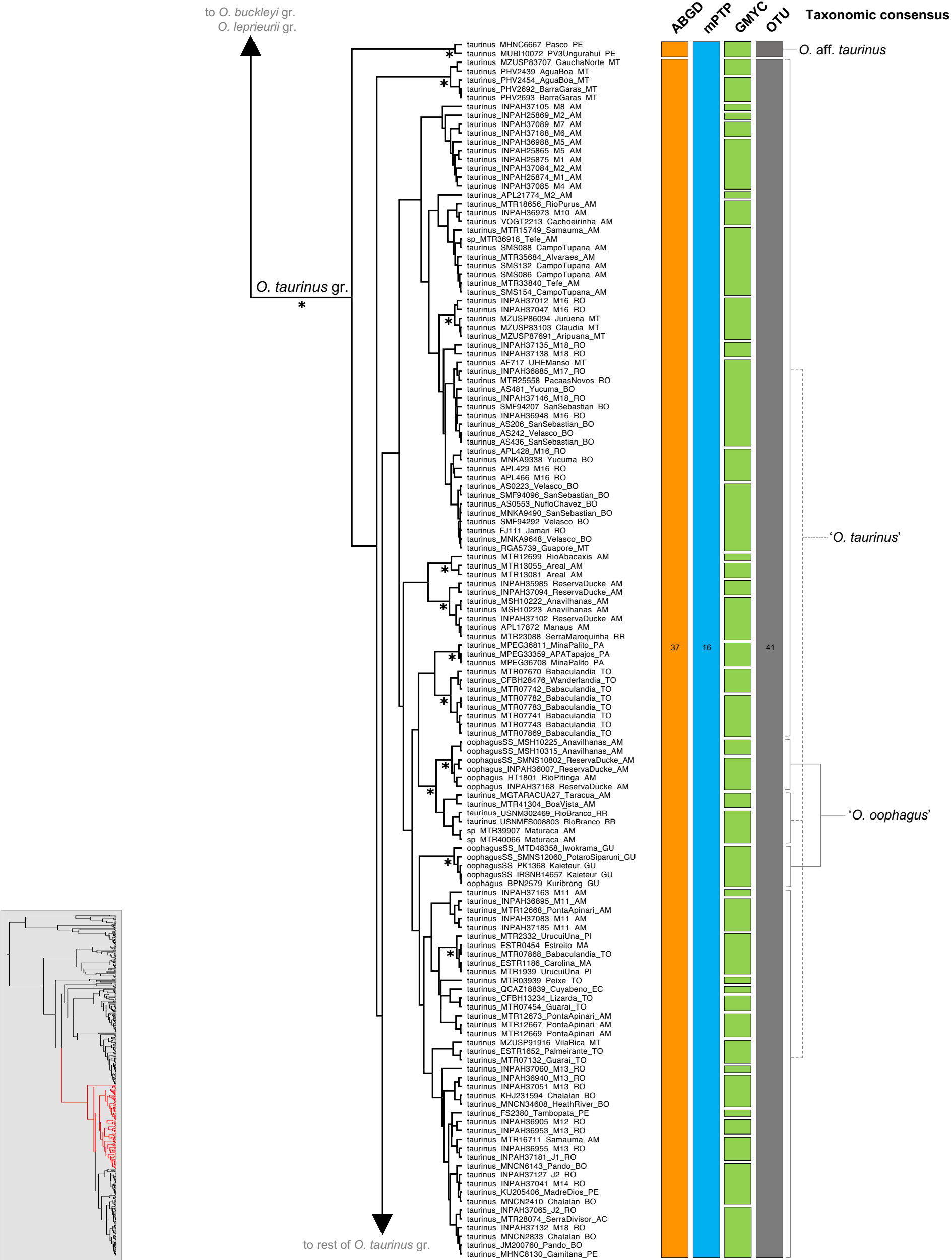


Fig. S2 Results of species delimitation analyses conducted on a 16S rRNA fragment (583 bp) for *Osteocephalus*, *Tepuihyla*, and *Dryaderces* ($n = 557$ sequences) using three methods (ABGD, mPTP, and GMYC) and resulting Operational Taxonomic Units (OTUs) from the majority rule consensus. Each box corresponds to a delimited species. The tree topology corresponds to the Maximum Clade Credibility tree from BEAST analysis (of GMYC), and asterisks represent Posterior Probabilities ≥ 0.95 . Because of this topology, some clades corresponding to the same delimited species in the other methods appear as discontinuous boxes; only in those cases a number corresponding to that particular species is provided (same as in Electronic Supplement 2). See conclusions for ‘Taxonomic consensus’ under ‘Taxonomic account’ in Appendix. Inlet, schematic trees show the section (in red) from the entire tree which is shown in each page



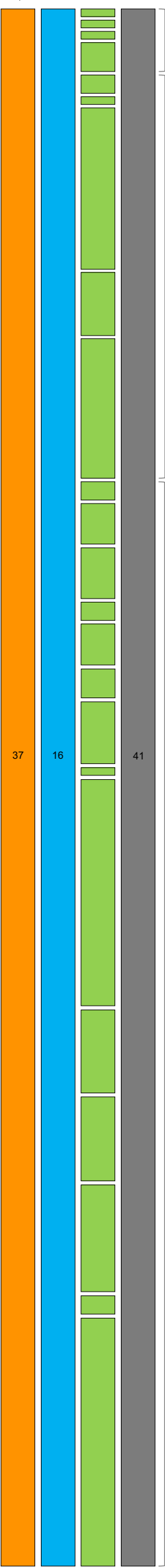
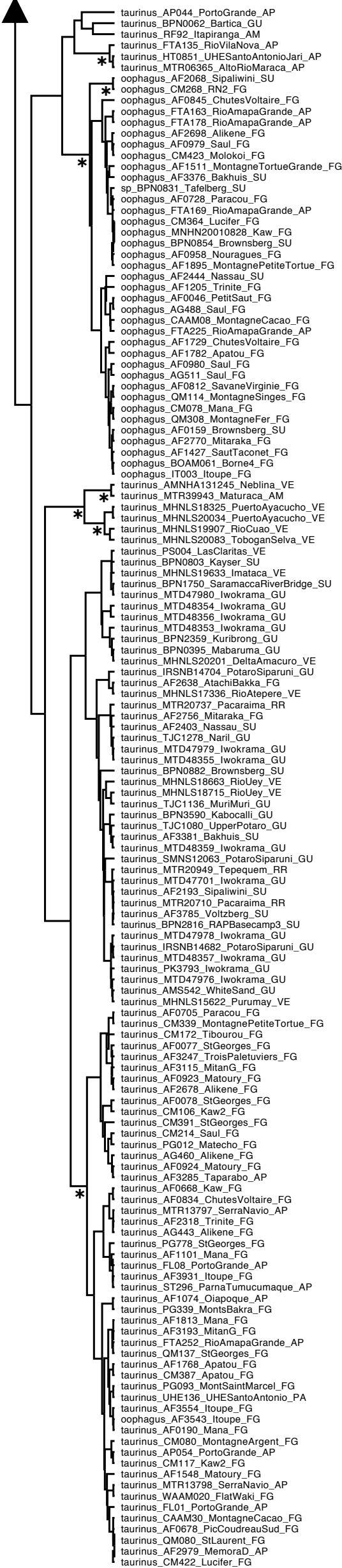






to rest of *O. taurinus* gr.

ABGD mPTP GMYC OTU Taxonomic consensus



O. oophagus

O. taurinus

