

Schmidt et al. Figures

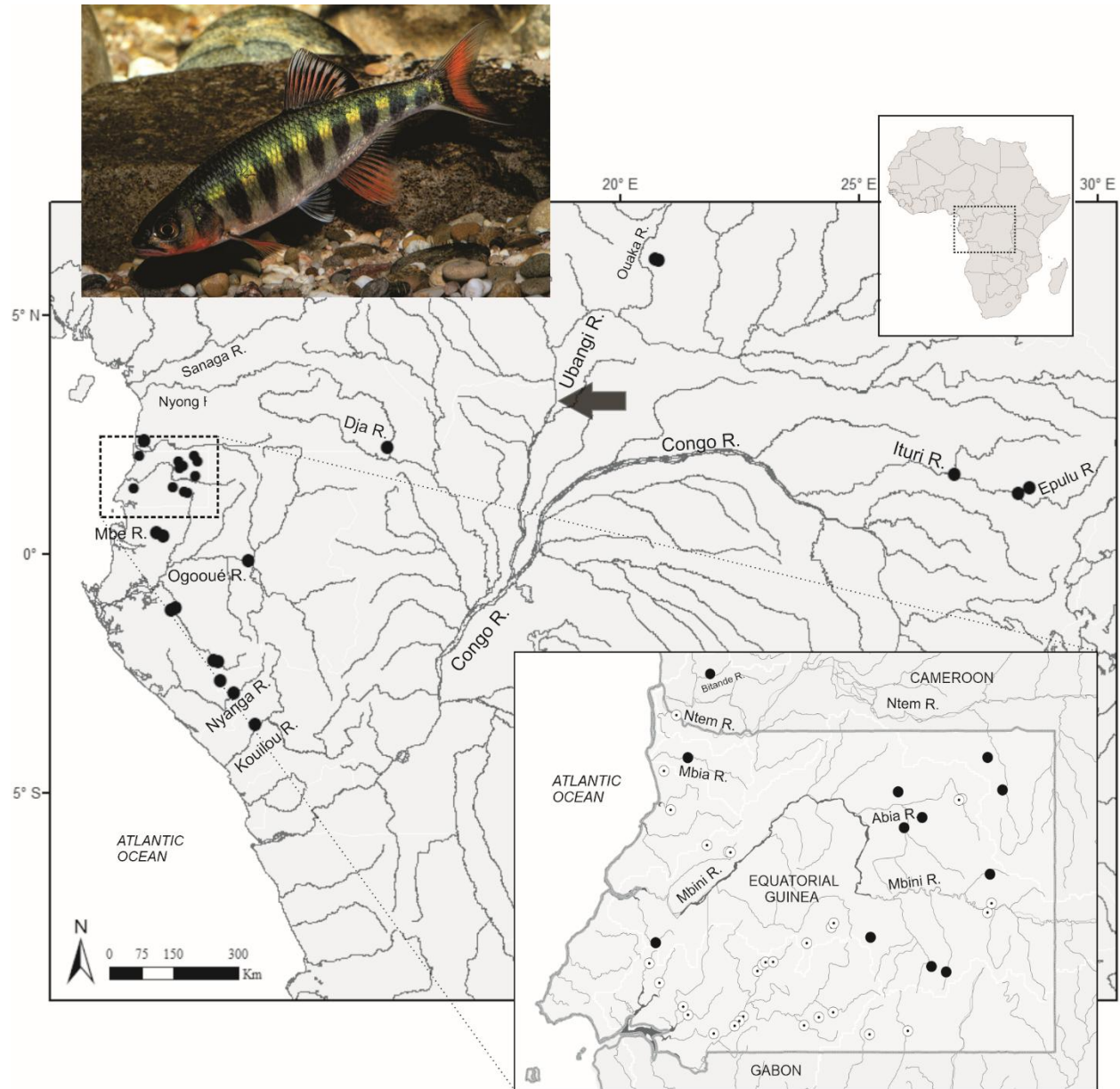


Figure 1. Localities of *Opsaridium ubangiense* included in the analyses. Note that the Ubangi River basin is the type locality for *O. ubangiense* (indicated by arrow). Open circles within Equatorial Guinea are collection events that didn't yield *Opsaridium ubangiense*. Inset picture of *Opsaridium ubangiense* from the Sognok River, a tributary to the Sanaga River, in Cameroon. Photograph by M.C.W. Keijman.

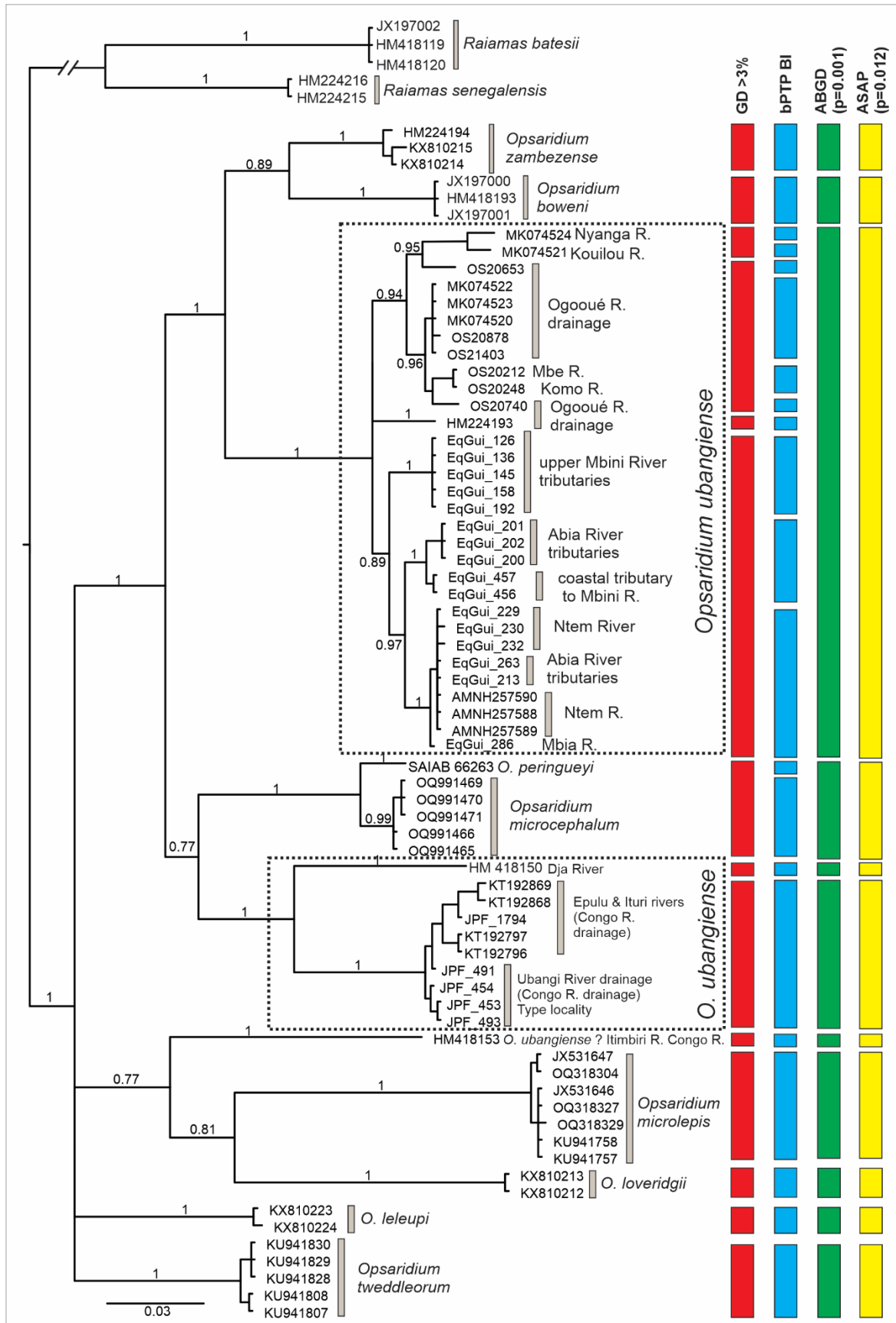


Figure 2. Phylogeny inferred from partial CO1 (651 bp) from 75 specimens. Branch support values are posterior probabilities from the Bayesian Inference analysis. Groups identified by different delimitation methods are shown on the left of the tree. All specimens currently considered *O. ubangiense* are enclosed in dashed box. Metadata for specimens included in this analysis can be found in supplemental table 1.

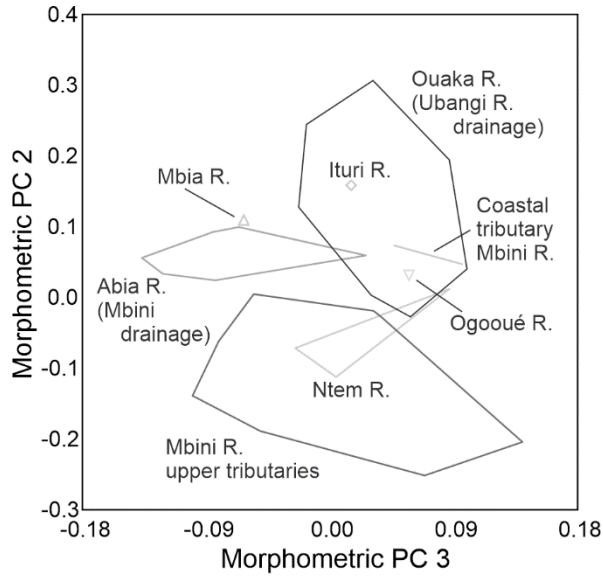
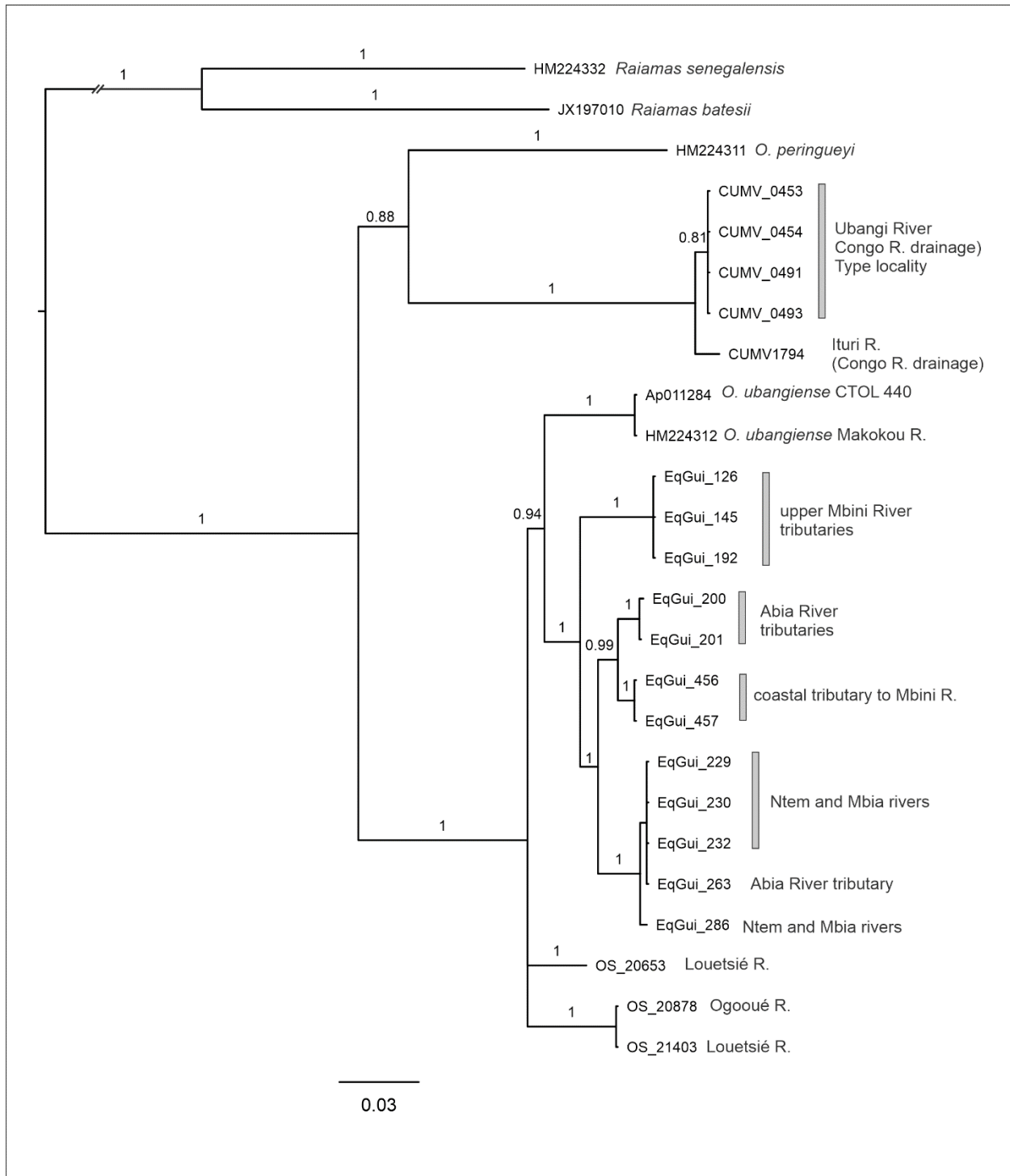
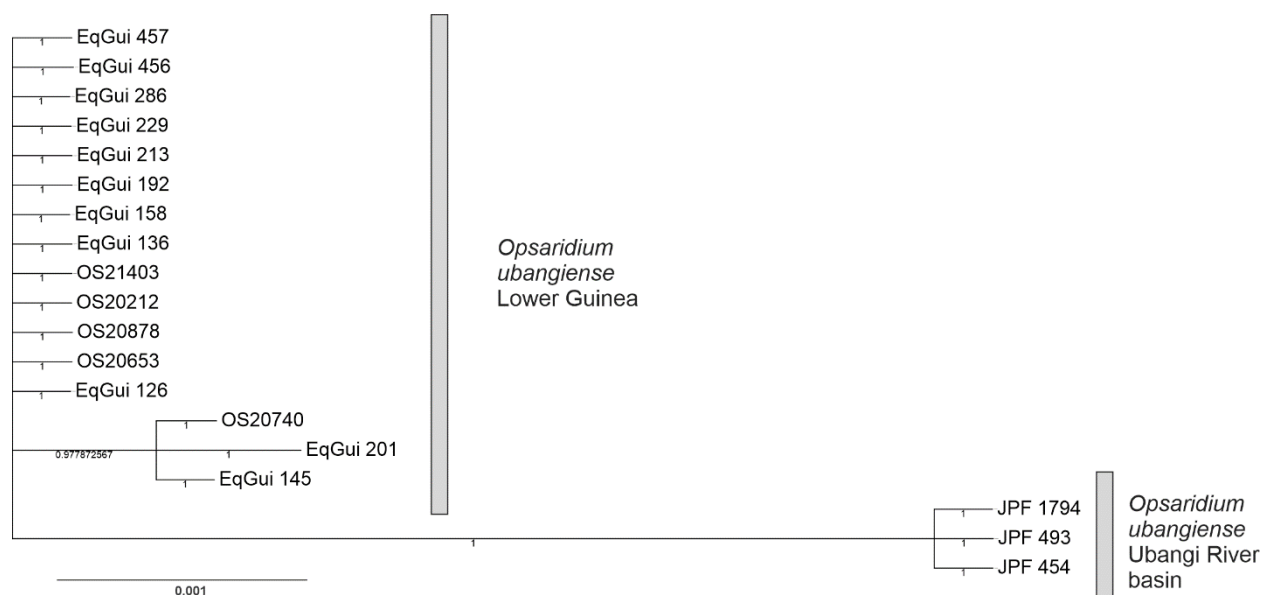


Figure 3. Scatter plot of PC2 vs. PC3 from principal components analysis of 18 log-transformed linear measurements from 50 specimens.

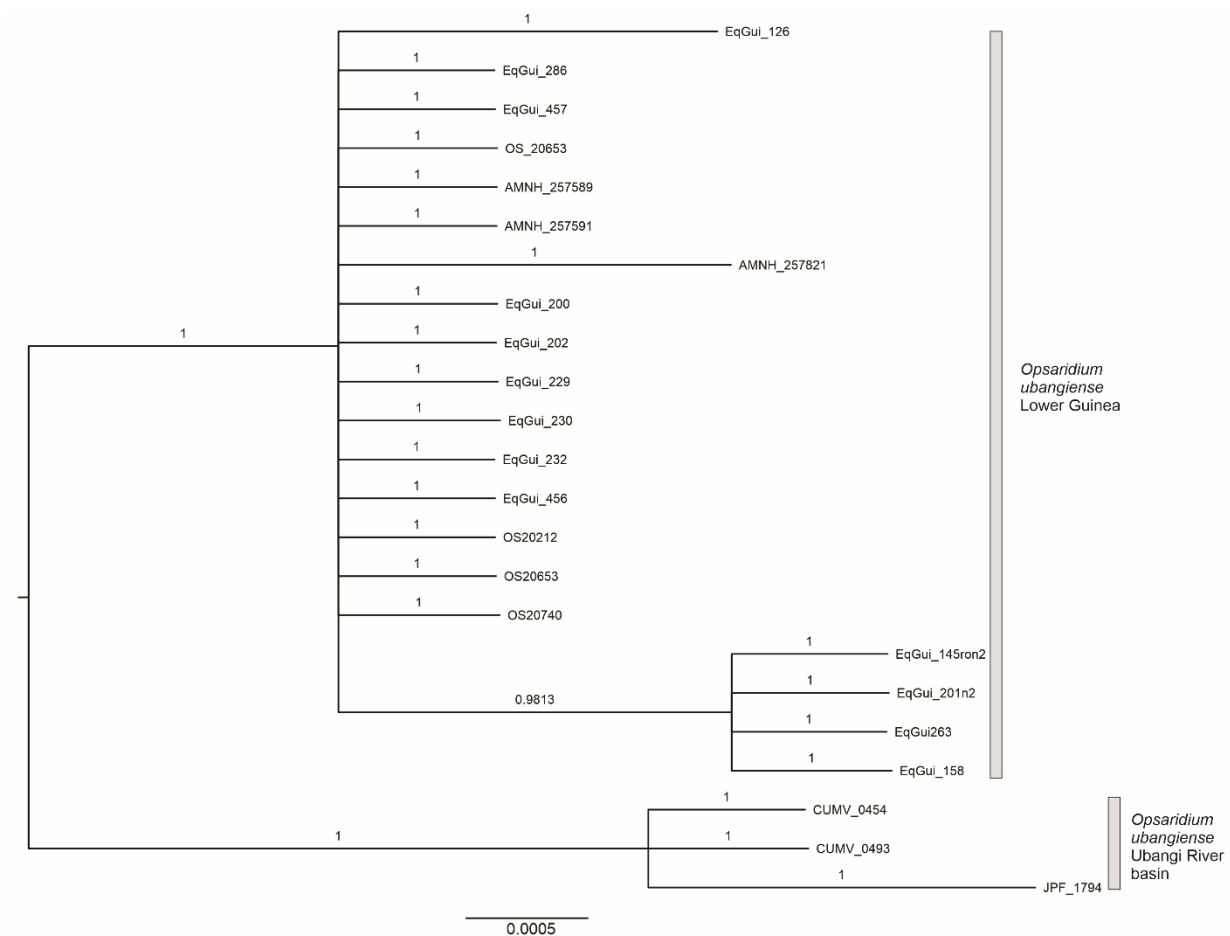
Supplementary Figures



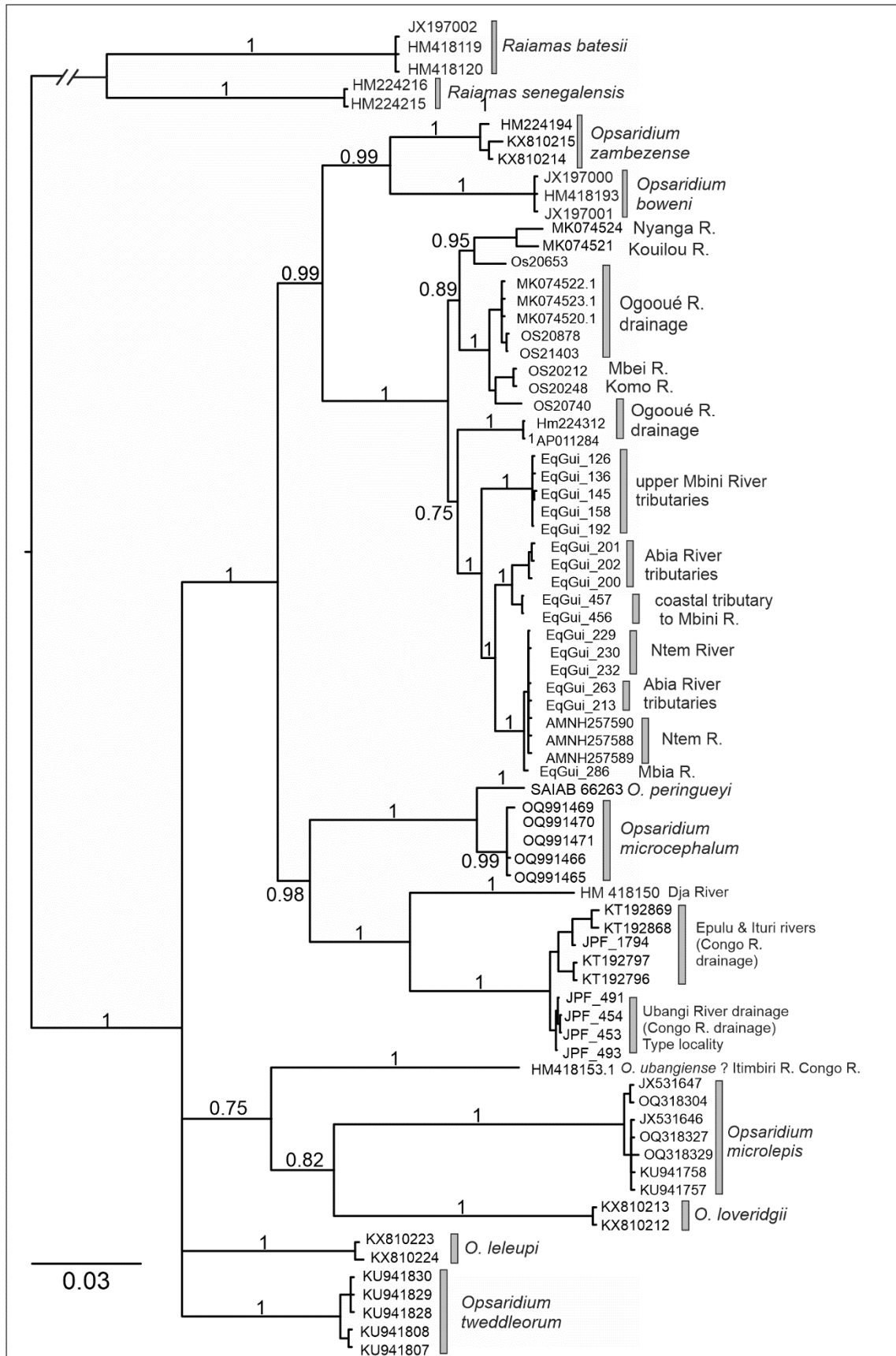
Supplementary Figure 1. Gene tree inferred from partial CYTB (1044 bp) from 25 taxa. Branch support values are posterior probabilities from the Bayesian Inference analysis. Metadata for specimens included in this analysis can be found in Supplemental Table 1.



Supplementary Figure 2. Unrooted phylogeny inferred from partial MYH6 (786 bp) from 19 specimens. Branch support values are posterior probabilities from the Bayesian Inference analysis. Metadata for specimens included in this analysis can be found in Supplemental Table 1.



Supplemental Figure 3. Unrooted phylogeny inferred from GH intron 2 (146 bp) from 23 specimens. Branch support values are posterior probabilities from the Bayesian Inference analysis. Metadata for specimens included in this analysis can be found in Supplemental Table 1.



Supplemental Figure 4. Phylogeny inferred from concatenated CO1, CYTB, MYH6, and GH (2621 bp) from 76 taxa. Branch support values are posterior probabilities from the Bayesian Inference analysis. Metadata for specimens included in this analysis can be found in Supplemental Table 1.