

- SEM.1 Index for the supplement (File name Supplementary\_material\_index)
- SEM.2 Full character list and specimens studied (File name diversity-1700431-Characters)
- SEM.3 Phylogenetic matrix in nexus format used in the analyses in the article (File name  
"Phylogeny\_Batomorphii\_morphological\_characters\_revisited\_DATA\_MATRIX.nex").
- SEM.4 Phylogenetic matrix in TNT format used in the parsimony analyses in the article (File name "TNT\_Data\_matrix.tnt").
- SEM.5 Commands used in the Parsimony analysis, in an executable script for TNT (File name "TNT\_ANALYSIS\_SCRIPT.tnt").
- SEM.6 Commands used to estimate the Bremer support of the groups recovered by the parsimony analysis, in an executable script for TNT (File name  
"TNT\_BREMER\_SCRIPT.tnt").
- SEM.7 Command for calculating the tree metrics on TNT (File name "STATS.RUN")
- SEM.8 Commands used in the Maximum Likelihood analysis, in an executable script for PAUP (File name "PAUP\_ANALYSIS\_SCRIPT.paup").
- SEM.9 Commands used to map the characters in the ML tree, in an executable script for TNT (File name "TNT\_map\_Script.tnt").
- SEM.10 Commands used in the Bayesian inference analysis, in an executable script for MrBayes (File name "Mr\_Bayes\_Script.bay").
- SEM.11 Log file of the parsimony analysis (File name "TNT\_ANALYSIS.log").
- SEM.12 Log file of the ML analysis (File name "PAUP\_ANALYSIS.log").
- SEM.13 Log file of the BI analysis (File name "Mr\_Bayes\_ANALYSIS.log").
- SEM.14 Log file of the mapping of characters for the parsimony tree (File name  
"TNT\_map.log").
- SEM.15 Log file of the mapping of characters for the ML tree (File name  
"PAUP\_map.log").