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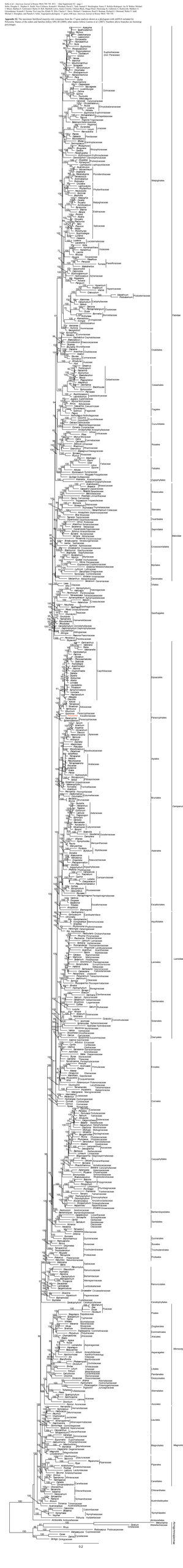
Appendix S2. The maximum likelihood majority-rule consensus from the 7 gene analysis shown as a phylogram with mPTA included for Polyneoa. Names of the orders and families follow APG III (Chase et al. 2009). Other names follow Cantino et al. (2007). Numbers above branches are bootstrap percentages.