

Supplementary Fig. S4

Barcode gap analysis of *Limnodrilus* complex COI data generated by ABGD. Histogram **A** showing the distribution of pairwise genetic distances (Jukes-Cantor) between each pair of specimens using the entire COI data set. Ranked distances **B** depicting how number of hypothetical species recovered by the ABGD algorithm varies across increasing prior genetic divergence thresholds. **C** Initial and recursive partitions are obtained by changing prior intra-specific divergence.

