

## **The marine fishes from southern Mindanao, Philippines, including a DNA barcode reference library of commercially important species**

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Appendix Figure 1. Maximum likelihood phylogenetic tree inferred from the cytochrome oxidase I (COI) barcoding region (no. of sequences = 497; sequence length = 534 bp) using the General Time Reversible model with gamma rate variation and proportion of invariant sites (GTR+G+I). Tip labels indicate the BOLD process ID, species name, specimen ID, BOLD Barcode Index Number (BIN), and GenBank Accession No. Nodes with bootstrap support values  $\geq 50\%$  are shown. *Neotrygon orientalis* was used as the outgroup to root the tree.