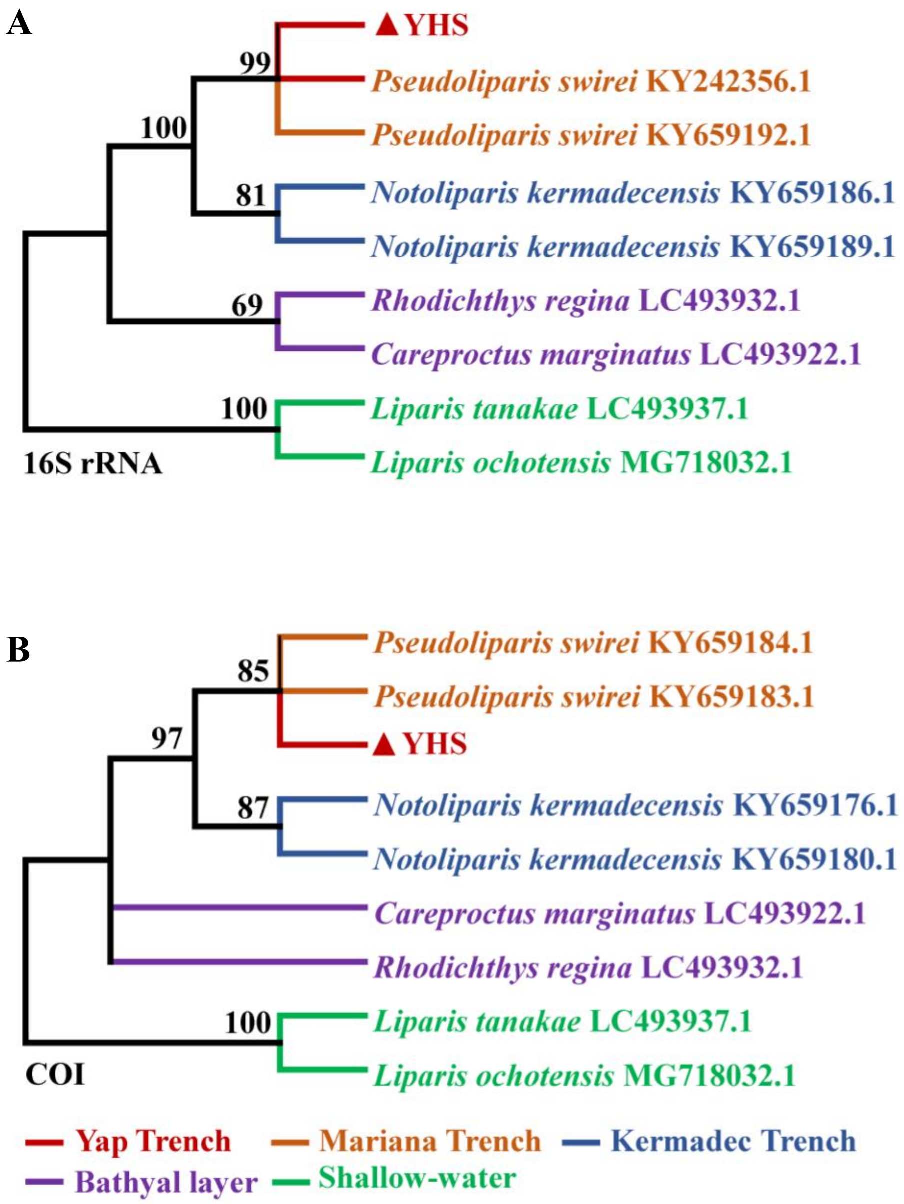

S1 Fig. Phylogenetic relationships among the hadal snailfish (YHS) from the Yap trench and other snailfish species. Maximum likelihood (ML) trees were constructed based on 16S rRNA (A) and cytochrome c oxidase subunit I (COI; B) genes. The 16S rRNA and COI gene sequences of the two Yap hadal snailfish specimens were consistent. ML bootstrap support values (> 50%) are shown. Branches with < 50% support have been collapsed.