

Fig. S1. Comparison of mitochondrial genomes from three spionids. Codon usage patterns indicated by codons per thousand codons (CDsp T) (**A**) and relative synonymous codon usage (RSCU) value (**B**) of 13 PCGs among two *Lindapsio polybranchiata*, *Lindaspio sp. (NES)* and *Rhynchospio aff. asiatica*. The specimens collected in the South China Sea were denoted *Lindaspio sp. (CSC)* and specimens in New England Seep 2 were denoted *Lindaspio sp. (NES)*.

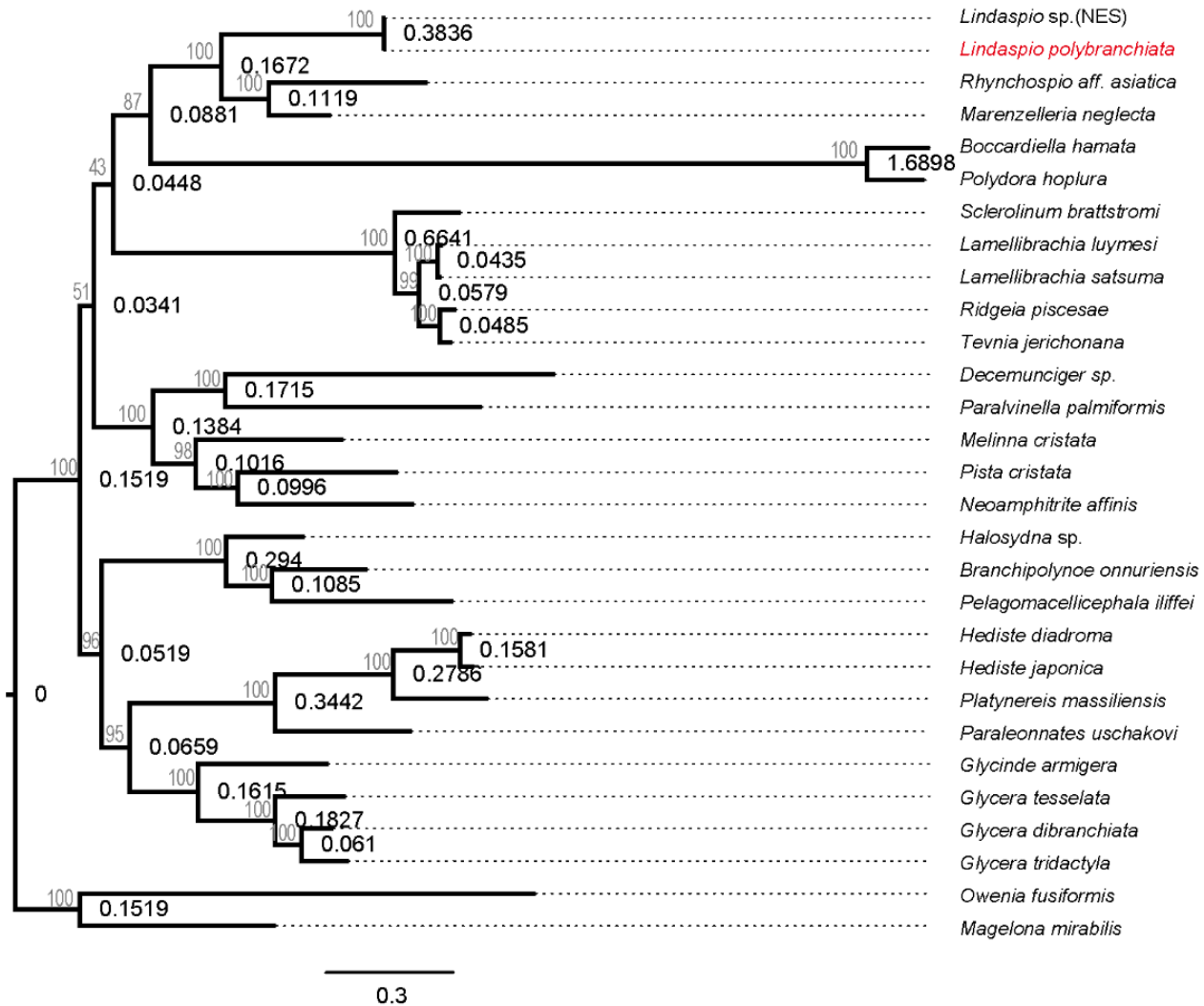


Fig. S2. Maximum likelihood phylogenetic tree inferred from nucleotide sequence of 12 concatenated mitochondrial PCGs with the GTR substitution model. The grey number value on each node is the branch length and the grey number is percentage bootstrap values with 1000 replications.



Fig. S3. Comparison of mitochondrial gene rearrangements among spionids. Genes for tRNAs was displayed with a single letter in red. Green and orange indicated protein-coding genes and RNA, respectively. Blue rectangles indicated regions where the gene order was rearranged.

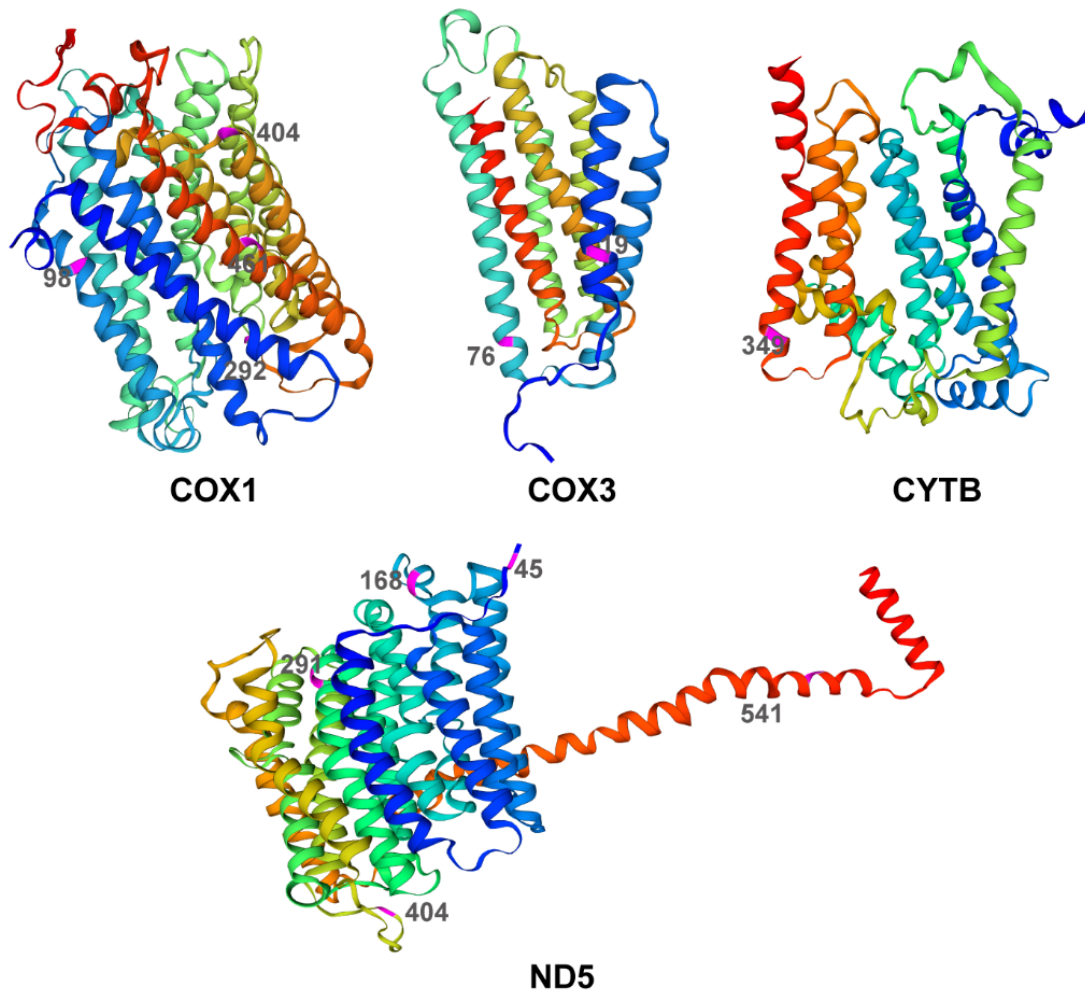


Fig. S4. Distribution of positively selected sites inferred by CODEML are marked in the three-dimension (3D) structure of COX1, COX3, CYTB, and ND5.