

**Supplementary Fig. 1.** Rectangular cladogram showing phylogenetic relationships among organisms that were selected for the identification of γ-form tyrosinase genes. The public databases, where complete genomic sequence information is available, are also shown in the tree.

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**Supplementary Fig. 2.** Phylogenetic analysis of tyrosinases (TYR) and tyrosinase-related proteins (TYRP) identified in *Clonorchis sinensis* (bold letters) and other animal taxa. The maximum likelihood tree was constructed using PhyML based on their amino acid sequence alignment rooted with the *Suberites domuncula* protein (CAE01389). The identity of each protein was distinguished by its GenBank accession number and the scientific name of its donor organism in parenthesis. Italicized accession numbers with asterisks denote proteins, for which sequence information was predicted using mRNA sequences. Branch support values of > 0.50, which were obtained by the Shimodaira-Hasegawa-like approximate likelihood ratio test, are indicated at the nodes. Proteins conserving a signal peptide and transmembrane domain are marked with ‘S’ and ‘T’, respectively. P\_clade 1 and 2 categorize members of two major lineages detected in the subtree of platyhelminth proteins. Solid diamonds indicate nodes that represent the gene duplication events, which may have occurred in the common ancestors of turbellarians and neodermatans.