

Figure S1. Homology analysis of *P. striolata* unigenes. (A) NR-value distribution. (B) NR-identity distribution. (C) NR-species distribution.

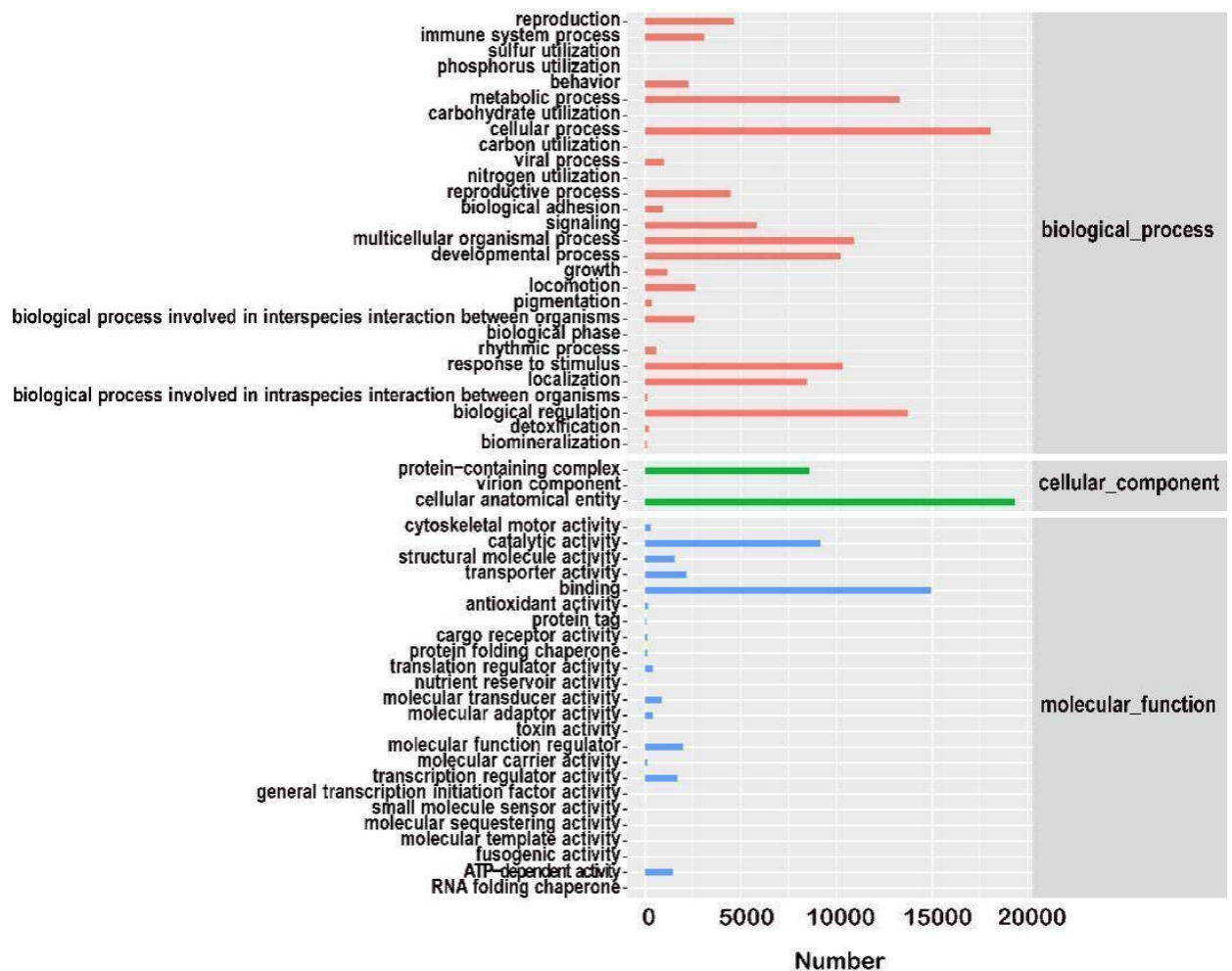


Figure S2. Gene-ontology (GO) assignment of *P. striolata* unigenes. EggNog-mapper software was used to complete GO annotation and the default parameters of EggNog-mapper were used for annotation. The GO-annotation results corresponded to GOTerm and the number of annotated genes in the second-level classification was counted. There were three categories in the GO analysis: biological process (BP), cellular component (CC) and molecular function (MF).

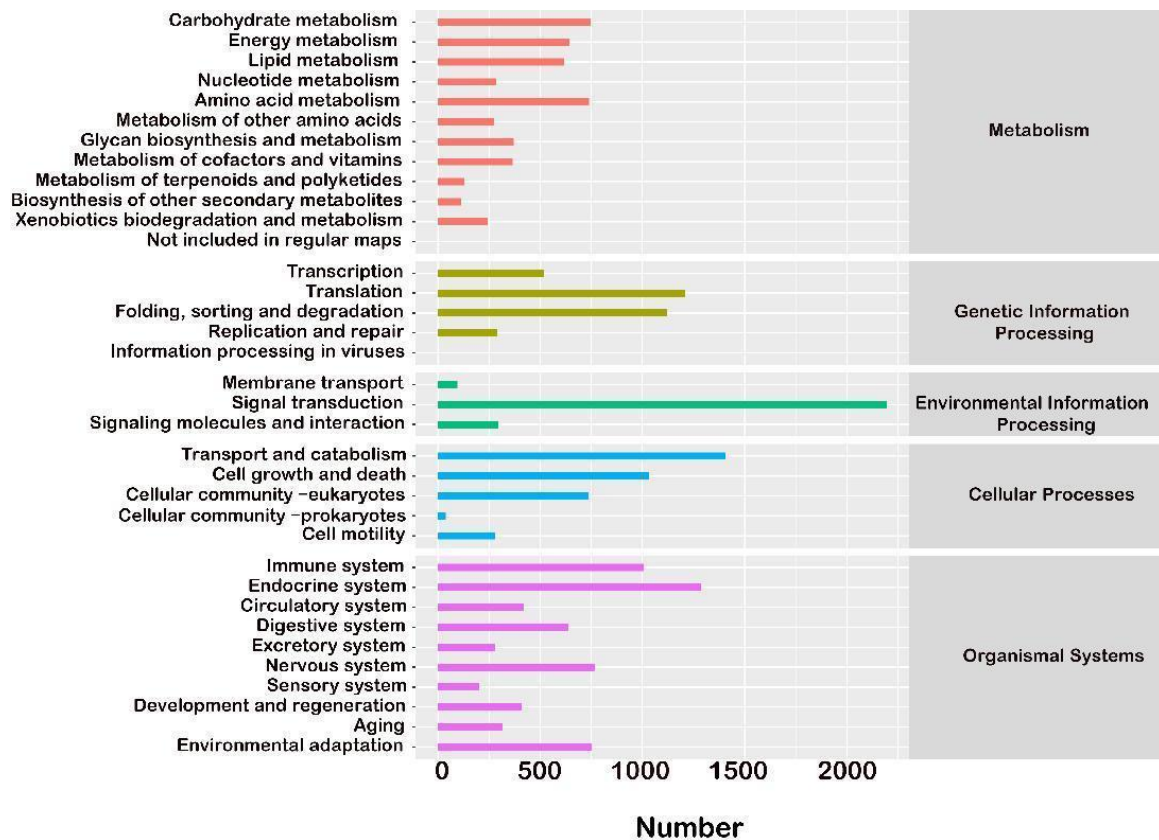


Figure S3. Kyoto Encyclopedia of Genes and Genomes (KEGG) classification of *P. striolata* unigene. KO and pathway annotations were mainly completed by KOBAS annotation system (<http://kobas.cbi.pku.edu.cn/>). Gene sets selected large groups of species (animals, plants, etc.). KO was mapped to the corresponding KEGG pathway after KO annotation was completed. KEGG classification included five main categories: cellular processes, environmental-information processing, genetic-information processing, metabolism and organism systems.