



Supplementary Material

Candidate Chemosensory Genes Identified in the *Procambarus clarkii* (Decapoda: Cambaridae) by Antennules Transcriptome Analysis

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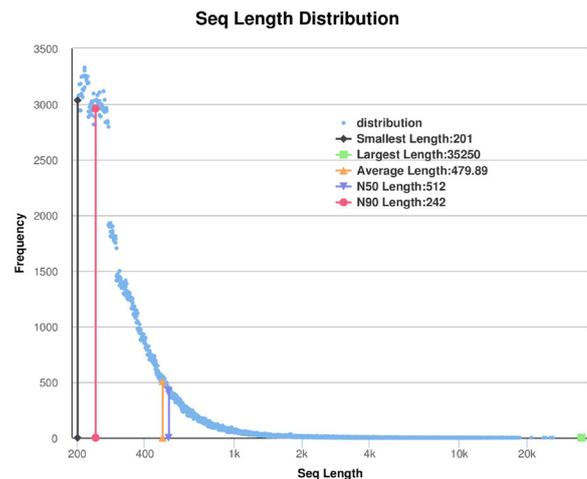
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Supplementary Table S I. Statistics for de novo transcriptome assembly.

	Total	Min length	Mean length	Max length	N50	N90	GC (%)
Unigenes	582,398	201	479.89	35,250	512	242	45.02
transcripts	755,807	179	642.89	35,250	957	261	44.59



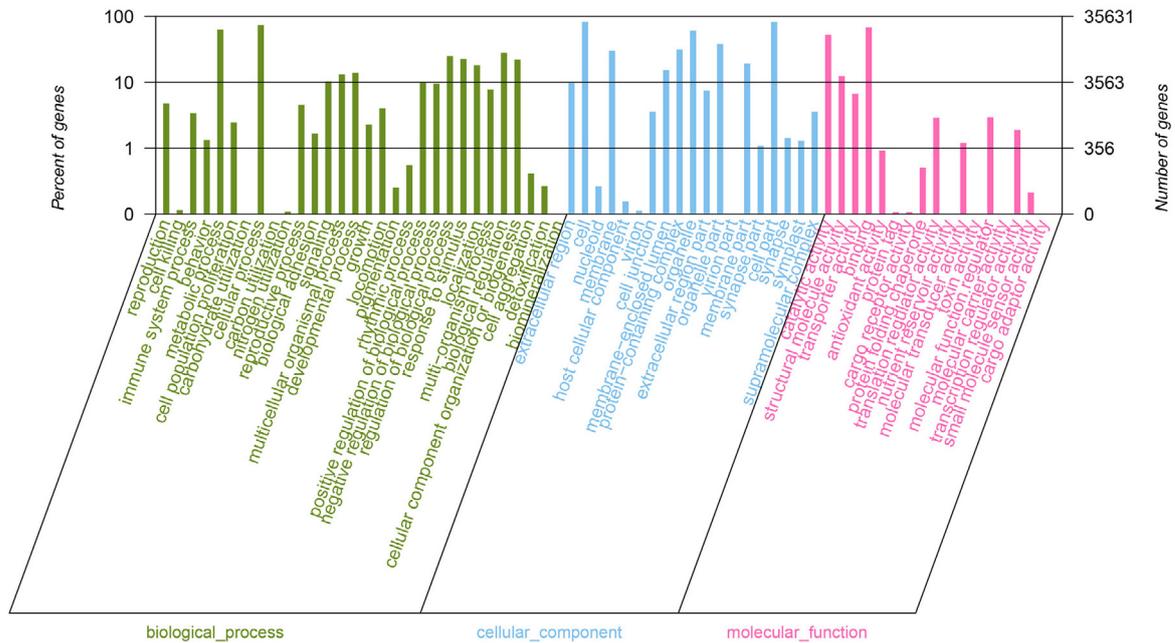
Supplementary Fig. S1. Distribution of *Procambarus clarkii* unigenes length.

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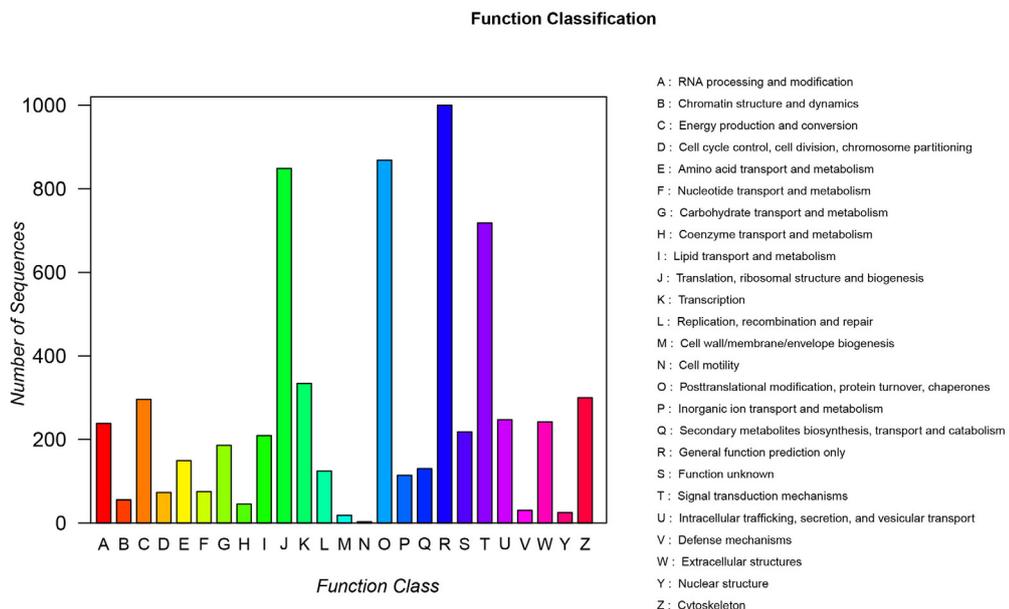


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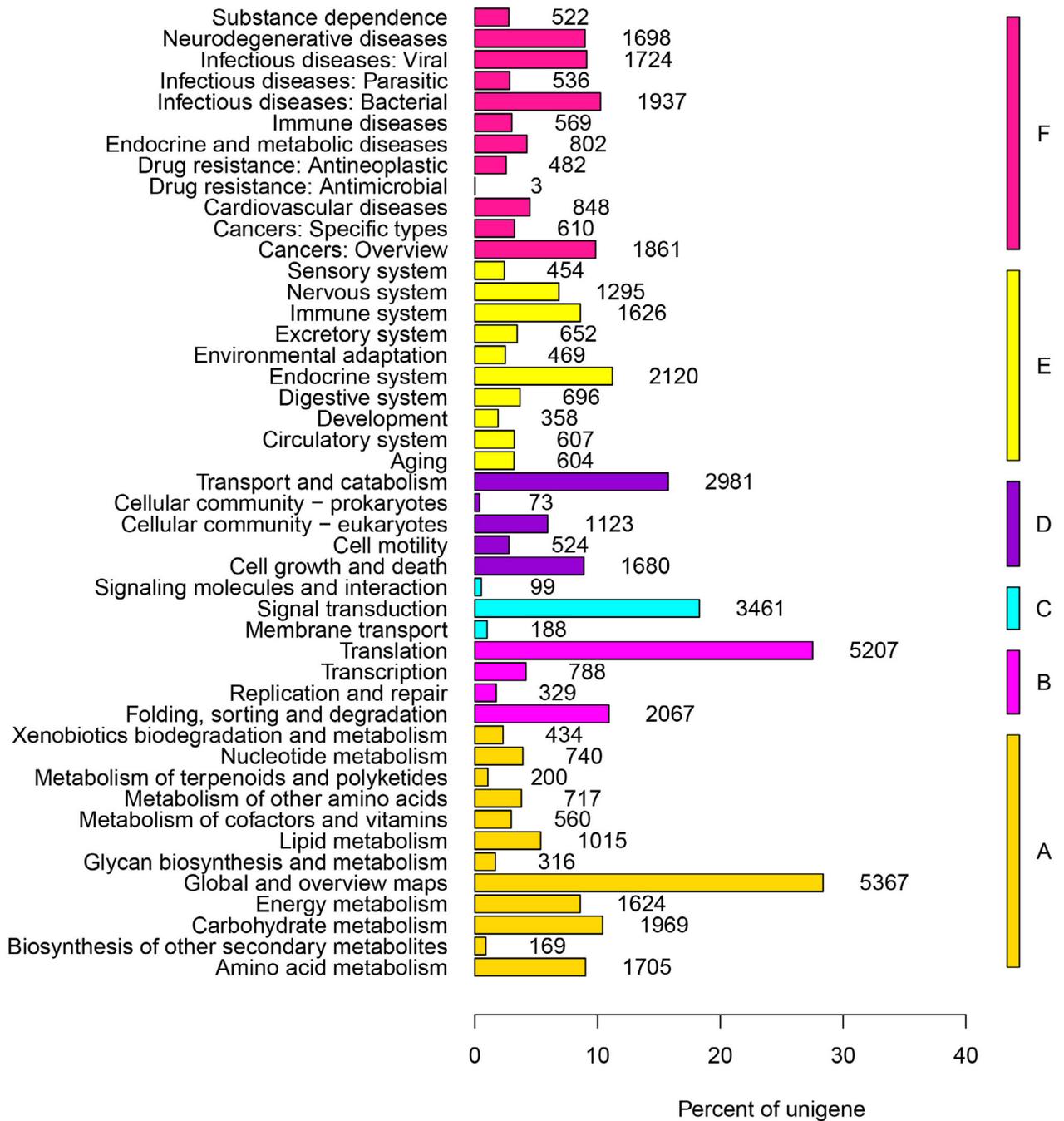
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Supplementary Fig. S2. Distribution of Gene Ontology (GO) categories (level 2) of transcripts for *Procambarus clarkii*. In the figure, the abscissa represents the secondary classification term of GO, the left ordinate represents the percentage of isogenic contained in the secondary classification, the right ordinate represents the number of isogenic compared with the secondary classification, and the three colors represent the three categories, in which green represents the biological process, blue represents a cellular component, and red represents the molecular function.



Supplementary Fig. S3. Histogram presentation of the results from the classification using EuKaryotic Orthologous Groups (KOG). In the figure, each color column represents A functional classification of KOG (represented by capital letters A~Z, the specific meaning is marked on the right), and the height of the column, namely the vertical coordinate, represents the transcript number with this kind of function.



Supplementary Fig. S4. Distribution of *Procambarus clarkii* differentially expressed genes among Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. The ordinate is the name of the KEGG metabolic pathway, and the abscissa is the number of genes annotated into the pathway and the proportion of the number of genes in the total number of genes annotated. According to the KEGG metabolic pathways involved, genes are divided into five branches: Metabolism (A), Genetic Information Processing (B), Environmental Information Processing (C), Cellular Processes (D), and organic Systems (E).