## Supplementary Data

|                      |                    | <u> </u>               |
|----------------------|--------------------|------------------------|
| <br>Public databases | Number of unigenes | Percentage of unigenes |
| <br>NR               | 34427              | 51.02%                 |
| NT                   | 32373              | 47.97%                 |
| SwissProt            | 14562              | 21.58%                 |
| ALL                  | 67473              | 100.00%                |

Table S1. Statistics of the results from analyzing the unigenes using multiple public databases

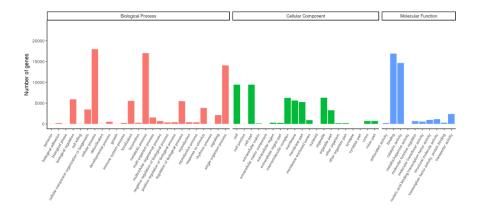


Figure S1. Histogram showing the distribution of the unigenes in Gene Ontology (GO) functional categories.

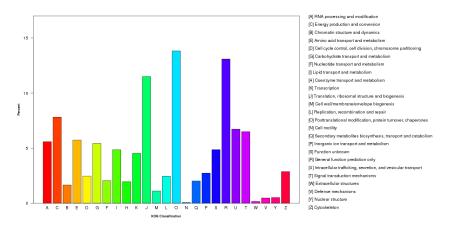


Figure S2. Classification of the unigenes into Orthologous groups.

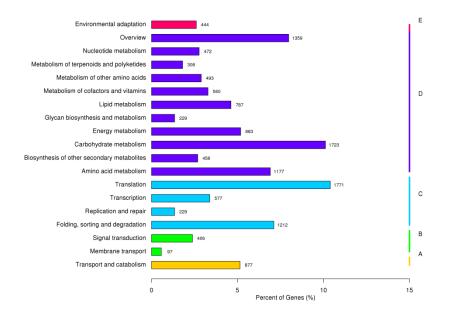


Figure S3. Functional classification and pathway assignment of the unigenes via the use of KEGG.

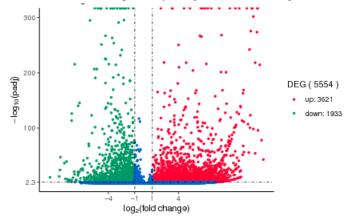


Figure S4. Expression levels of differentially expressed genes in D and H samples. Up-regulated and down-regulated genes are denoted by red and green dots, respectively. Blue dots correspond to those that are not differentially expressed.