Additional files

Figure S1 - Characteristic analysis of the homology search for transcriptome unigenes against the NR database

(A)E-value distribution of BLAST hits for each unique sequence with a cut-off E-value of 1.0E-5; (B) Similarity in distribution of the top BLAST hits for each sequence; (C) Species distribution is shown as a percentage of the total homologous sequences with an E-value of at least 1.0E-5. We used the first hit of each sequence for analysis.

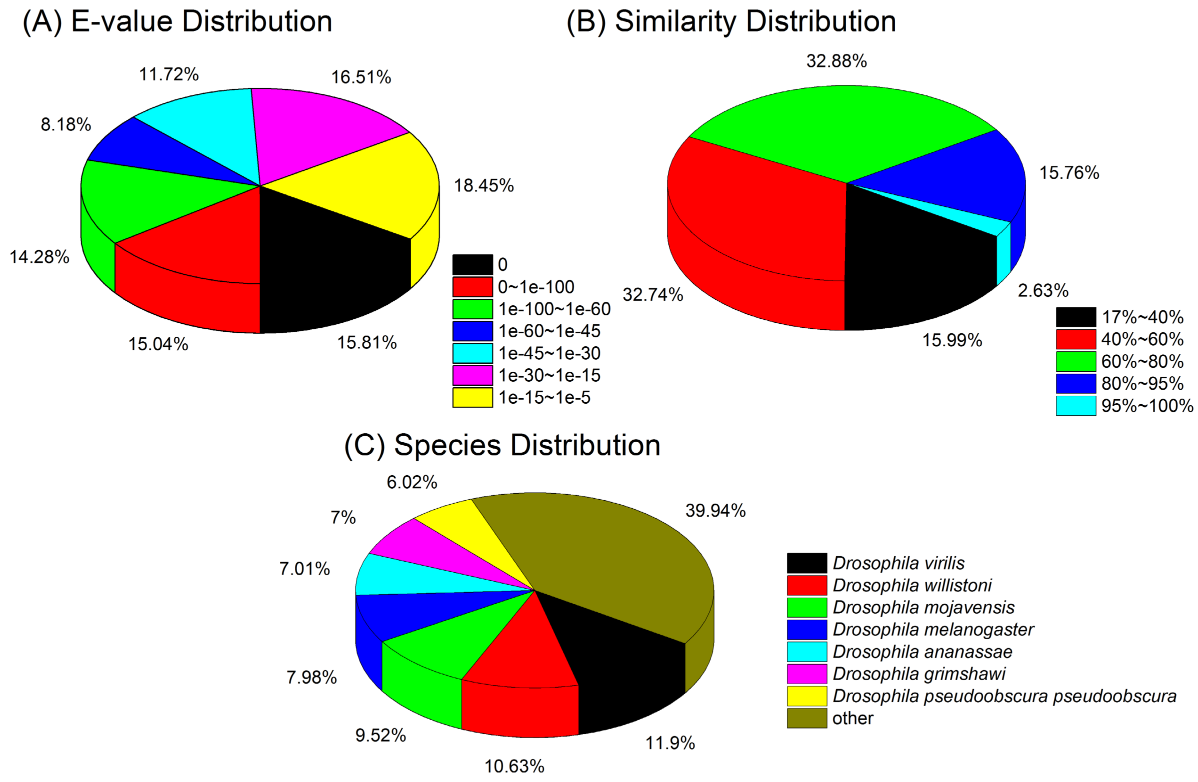


Figure S2 - Histogram presentation of the (A) gene ontology (GO) and (B) clusters of orthologous group (COG) classification

(A) The results are listed in three categories: biological process, cellular component and molecular function. (B) Out of 28,779 BLAST hits, 10,784 sequences are classified into 25 COG categories.

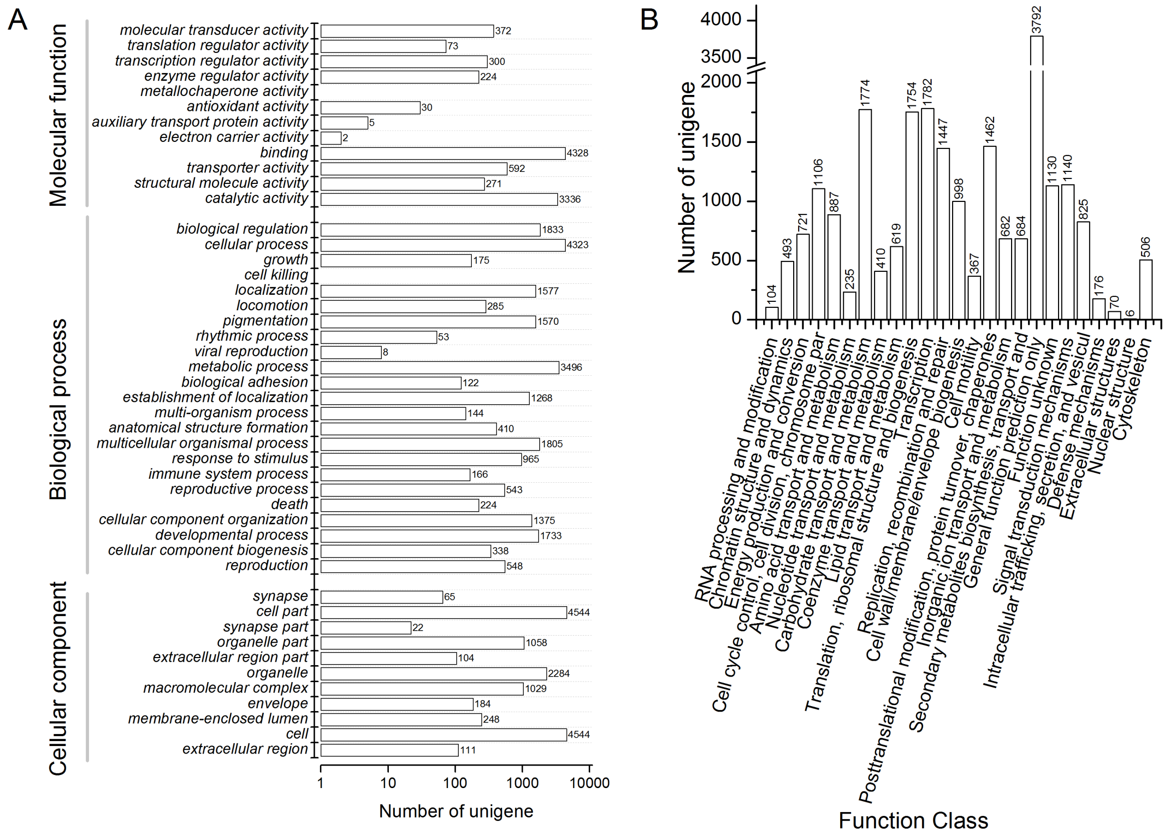


Figure S3 – Different components of the raw tags and distribution of distinct tags in each sample.

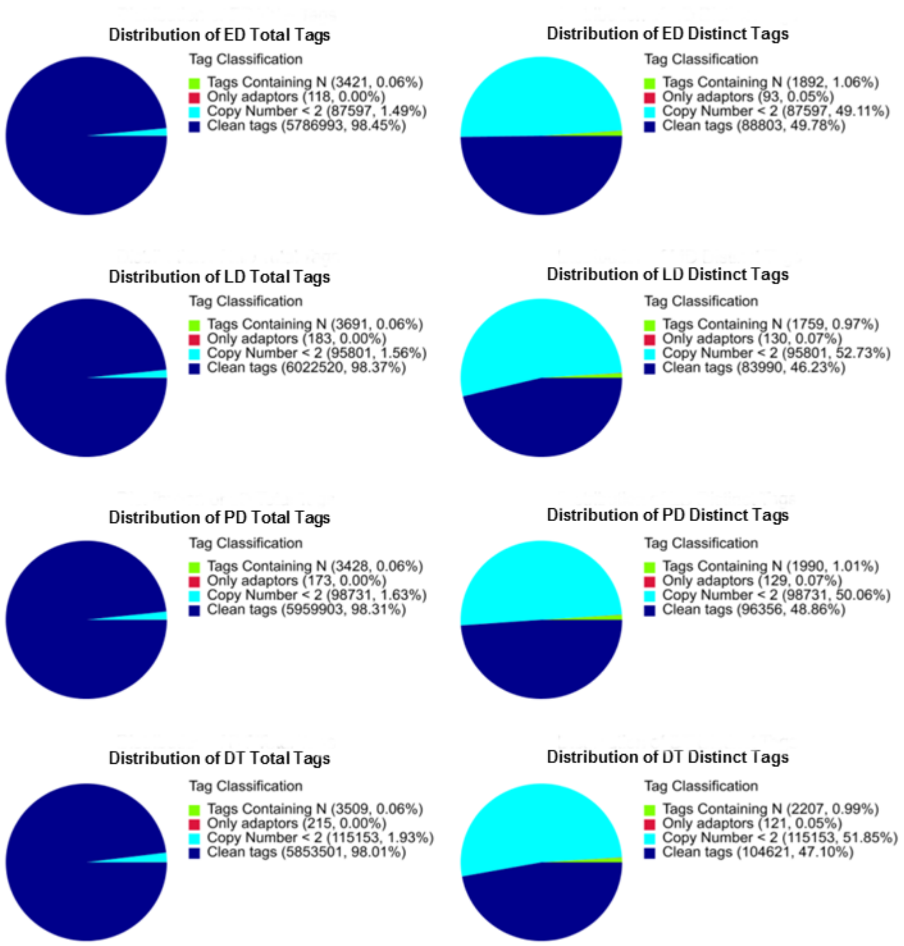
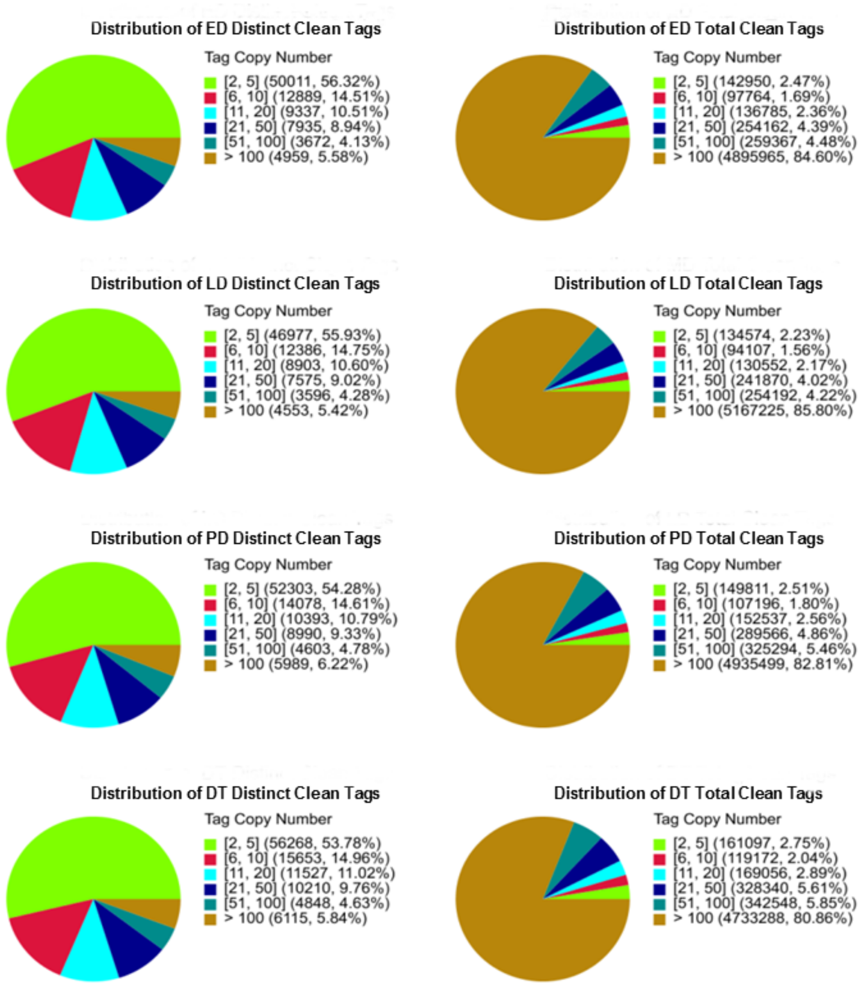


Figure S4 –Distribution of total tags and distinct tags in each sample.



Distribution of ED Distinct Clean Tags

Distribution of ED Total Clean Tags

Distribution of LD Distinct Clean Tags

Distribution of LD Total Clean Tags

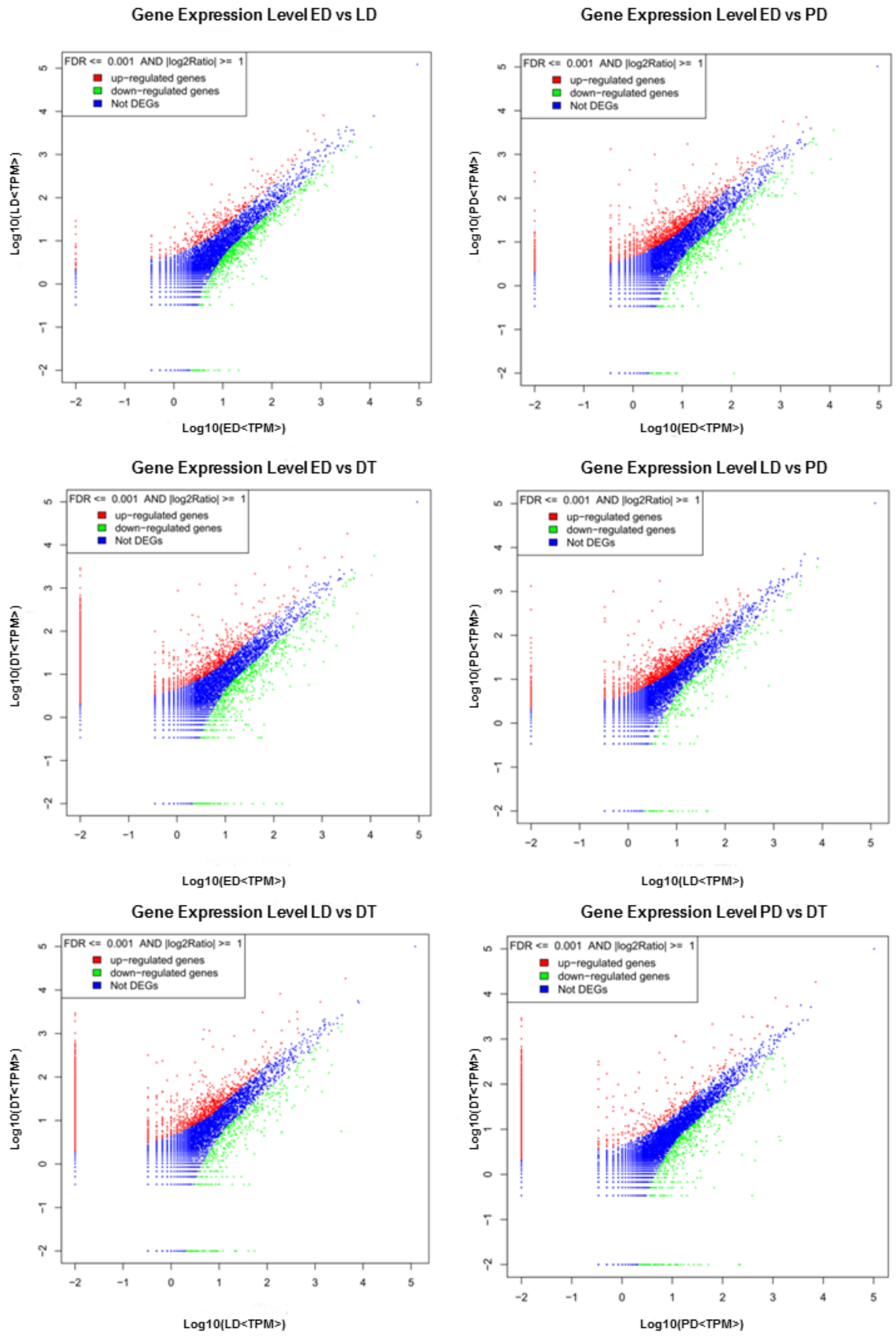
Distribution of PD Distinct Clean Tags

Distribution of PD Total Clean Tags

Distribution of DT Distinct Clean Tags

Distribution of DT Total Clean Tags

Figure S5 – The gene expression level in all comparisons.



Gene Expression Level ED vs LD

Gene Expression Level ED vs PD

Gene Expression Level ED vs DT

Gene Expression Level LD vs PD

Gene Expression Level LD vs DT

Gene Expression Level PD vs DT

Table S1 – Sample collection and RNA extraction strategy.

(XLSX)

Table S2 – The specific primers used in qRT-PCR to validate differentially expressed genes.

(XLSX)

Table S3 – Use of Sanger sequencing to verify the quality of RNA-seq results.

(XLSX)

Table S4 – Top hits obtained by BLASTX against NR database for the total unigenes.

(XLSX)

Table S5 – The GO annotation of unigenes.

(XLSX)

Table S6 – KO annotation of unigenes.

(XLSX)

Table S7 – Tag analysis statistics.

(XLSX)

Table S8 –Differentially expressed tags were filtered with the absolute value of log2Ratio $\geqslant 1$ based on the FDR < 0.001 from the tandem comparison of samples i.e., LD *vs* DT, PD *vs* DT, ED *vs* LD, ED *vs* PD, ED *vs* DT, LD *vs* PD.

(XLSX)

Table S9 – GO enrichment analysis in different comparisons.

(DOC)

Table S10 – KO enrichment analysis in different comparisons.

(XLSX)

Table S11– Differentially expressed genes filtered accordingtothe absolute value of log2Ratio ⩾ 1 based on the FDR < 0.001 among ED, LD and PD were annotated indifferent databases.

(XLSX)

Table S12– Putatively identified Heat shock protein were filtered with the absolute value of log2Ratio ⩾ 1 based on the FDR < 0.001 among ED, LD and PD.

(XLSX)