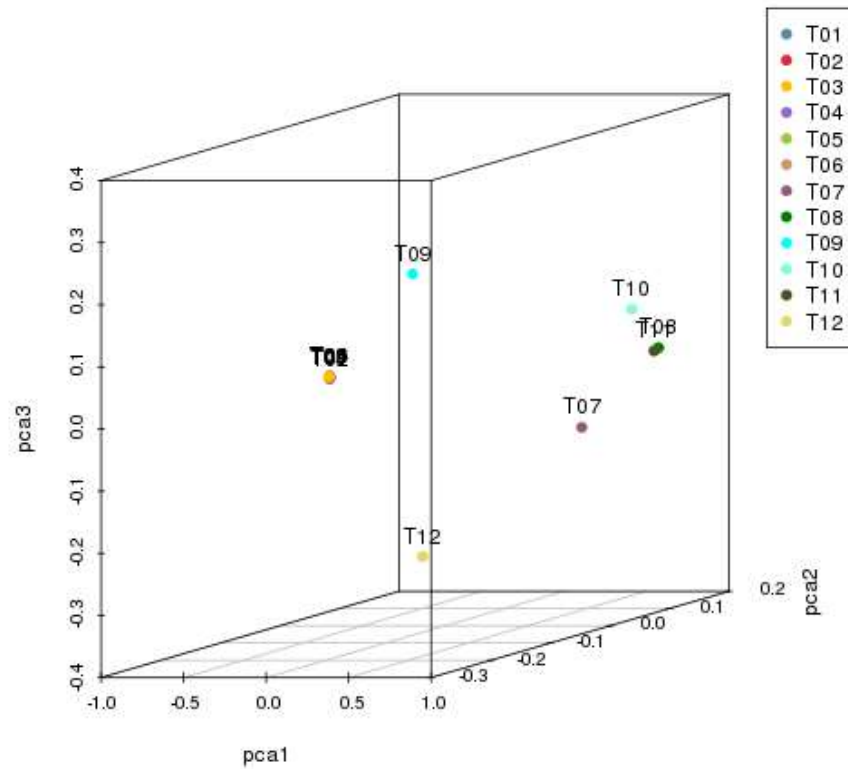


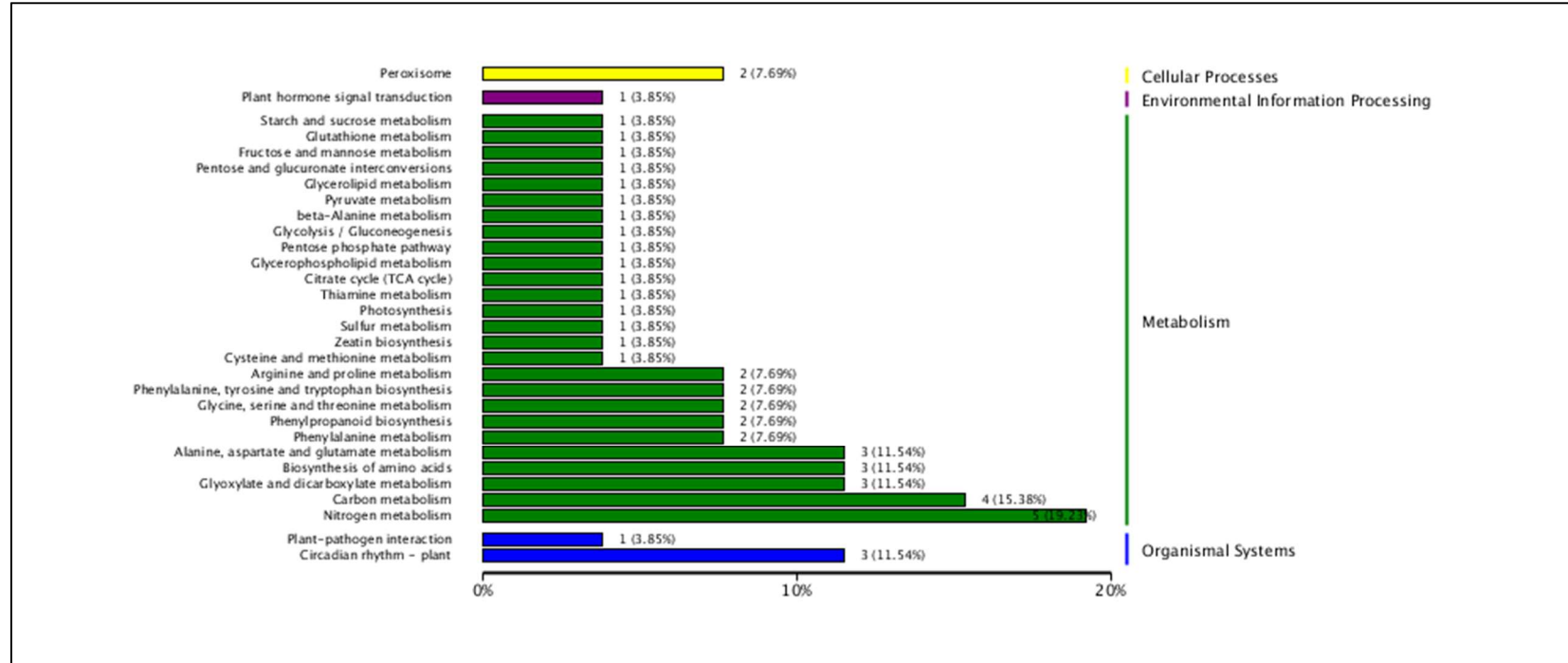
**Figure S1.** Pearson correlation coefficient analysis of biological replicates of different samples within two maize inbred lines with contrasting drought tolerance under different treatment conditions. The correlation coefficient ( $R^2$ ) between two corresponding ( $x$ - and  $y$ -axis) samples was calculated based on the FPKM (fragments per kilobase of exon model per million mapped reads) values of those samples. The  $x$ - and  $y$ -axis shows the corresponding biological samples for different treatment conditions. T01-T03, tolerant line YE8112 under water-sufficient (control) condition; T04-T06, tolerant line YE8112 under water-deficit (drought) condition; T07-T09, sensitive line MO17 under control condition; T10-T12, sensitive line MO17 under drought condition.



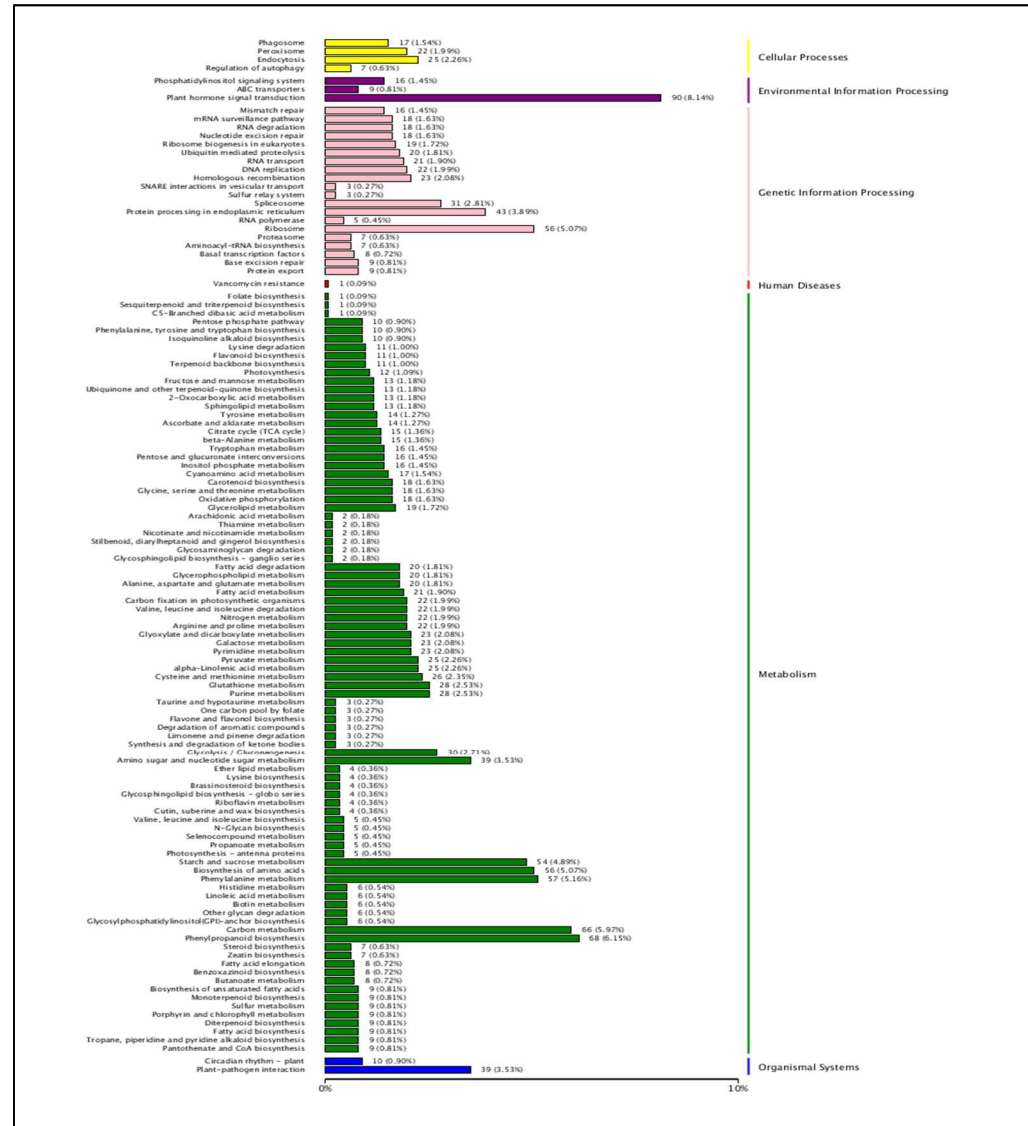
**Figure S2.** Principal Component Analysis (PCA) of the similarities and differences between the twelve samples used for RNA-Sequencing. The PCA analysis showed that there was low consistence amongst the three replicates of the two (one drought-stress and one control) samples probably due to a technical failure. Thus, sequencing results were analyzed by retrieving samples T07 (MO17 water control) and T12 (MO17 water deficit).

Supplementary Figure 3 (Top 20 KEGG Pathways in Different Experimental Comparisons)

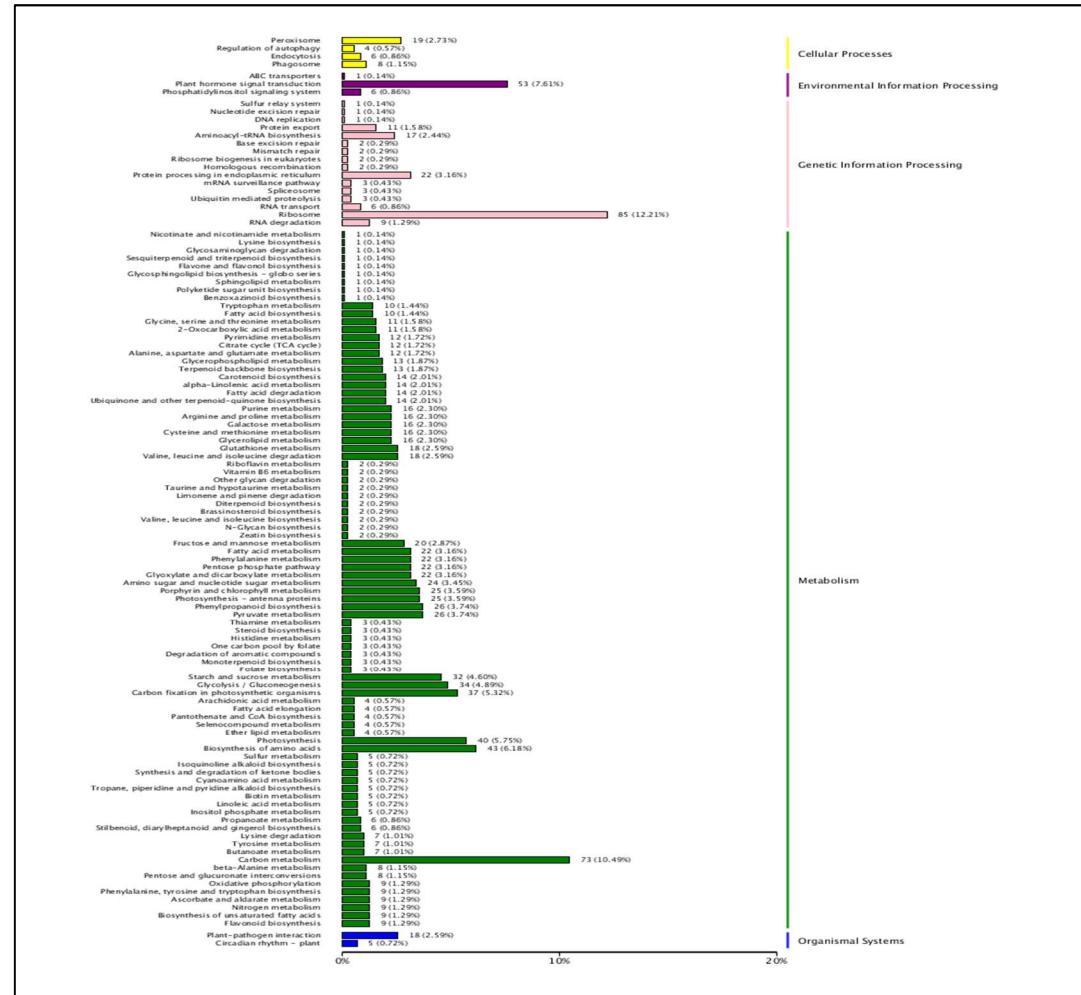
a) Pathways enriched in TC TD comparison



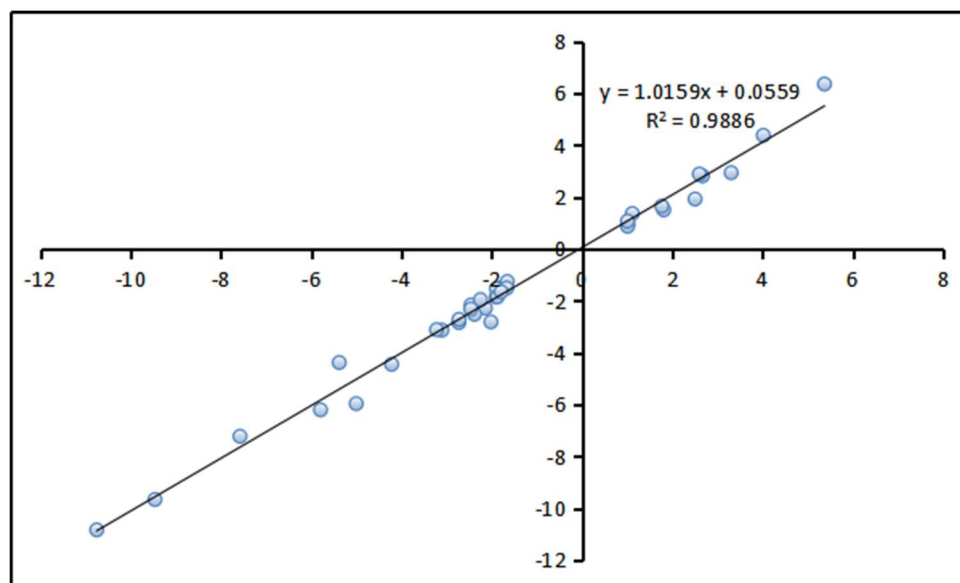
## b) Pathways enriched in SD TD comparison



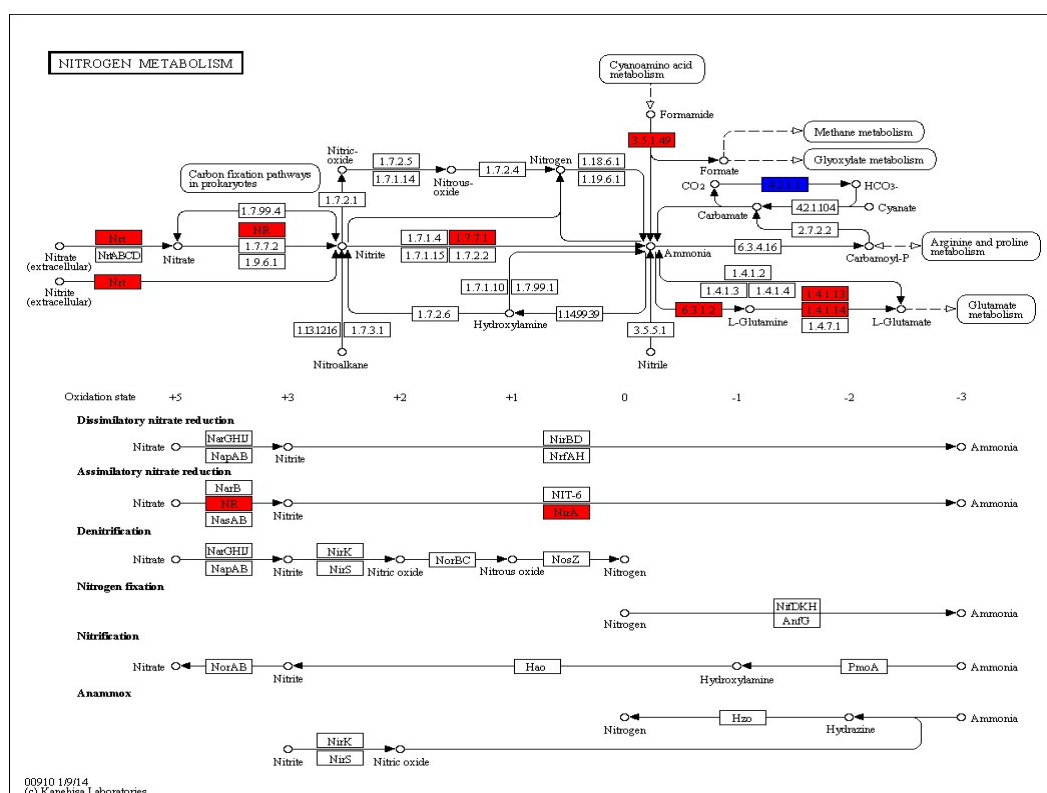
c) Pathways enriched in SC SD comparison



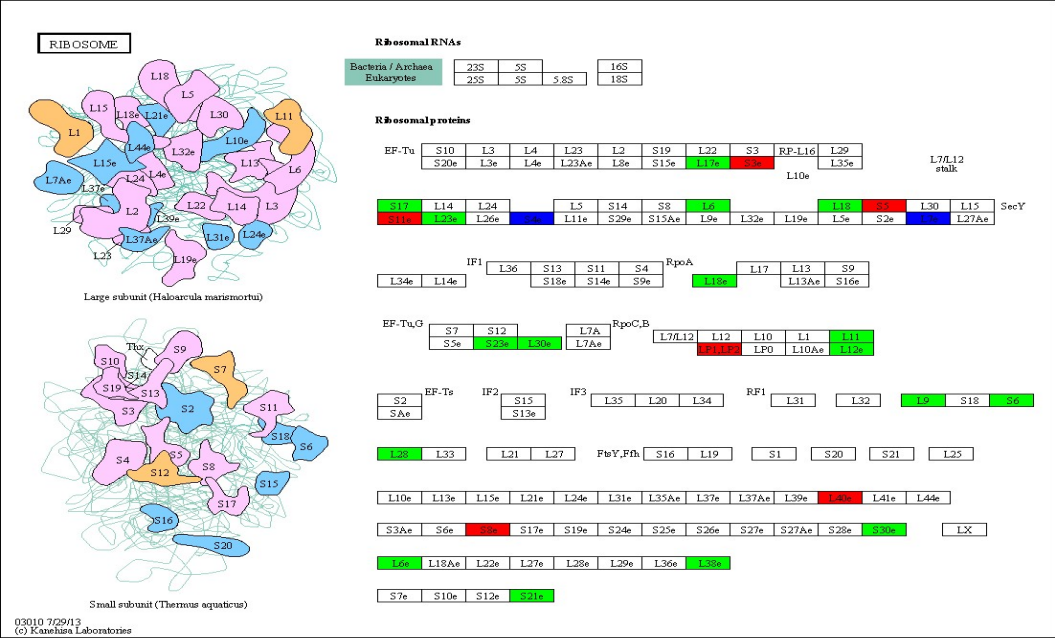
**Figure S3.** Top 20 KEGG pathway enrichment analysis of the differentially expressed genes (DEGs) in different experimental comparisons. (A) TC\_TD comparison; (B) SD\_TD comparison; and, (C) SC\_SD comparison. The whole number above the bar (blue) graph represents number of DEGs enriched in the corresponding pathway.



**Figure S4.** Validation of RNA-seq expression data by qRT-PCR analysis. Validation was performed using 20 randomly selected differentially expressed genes (DEGs). The plots demonstrate the expression ratio in log scale with base of two. The X-axis indicates qRT-PCR log scale; the Y-axis indicates RNA-seq log scale.



(A)



(B)

**Figure S5.** Most significantly enriched metabolic pathways in the two contrasting maize inbred lines under drought stress. (A) Nitrogen metabolism pathway significantly enriched in tolerant line YE8112; (B) Ribosome pathway significantly enriched in sensitive line MO17. Up-regulated genes are shown in red, down-regulated genes in green, and genes expressed in both cases are shown in blue.