

low-K stress conditions. ~~GO enrichment analysis of functional significance was used~~. Gene
 Ontology (GO) is an internationally standardized gene functional classification system ~~and a~~
~~strictly defined concept to for~~ comprehensively describing the properties of genes and their
 products in any organism. GO has three ontologies: molecular functions, cellular components,
 and biological processes. The basic unit of GO is the GO-term. Every GO-term belongs to a
 type of ontology. In gene expression profiling analysis, GO enrichment analysis of functional
 significance ~~applies-uses~~ hypergeometric testing to map all differentially expressed genes to
 terms in the GO database (<http://www.geneontology.org/>); looking for ~~significantly enriched~~
 GO terms ~~that are significantly enriched in a given DEG relative to their DEGs comparing to~~
~~the~~ genome background.

In our study, ~~apart from the unknown transcripts~~, predicted ~~or and~~ known transcripts ~~sa~~ were
~~categorized according to their divided into groups~~: molecular function transcripts, cellular
 component transcripts, and biological process transcripts. Of these, 4813 differentially
 expressed transcripts ~~can be were categorized-divided~~ into 50 functional groups (Figure 2). ~~In~~
~~aspect of the-For~~ molecular function, the most significant enrichment was observed among the
the various binding genes (GO: 0005488), including 40 DEGs encoding ~~eneoded~~ calcium ion
 binding proteins (GO: 0005509), 66 DEGs encod~~inged~~ iron ion binding proteins (GO:
 0005506), 55 DEGs ~~eneoded-encoding~~ zinc ion binding proteins (GO: 0008270), and 4 DEGs
~~eneoded-encoding~~ potassium ion binding proteins (GO: 0030955). ~~280-Two hundred and~~
~~eighty~~ DEGs were found to ~~encoded~~ transferase activity (GO: 0016740). ~~which-These~~
 included ~~the~~ kinase activity genes (GO: 0016301). ~~94-Ninety-four~~ DEGs were found to
~~encoded~~ transporter activity (GO: 0005215). ~~which-These~~ included transmembrane