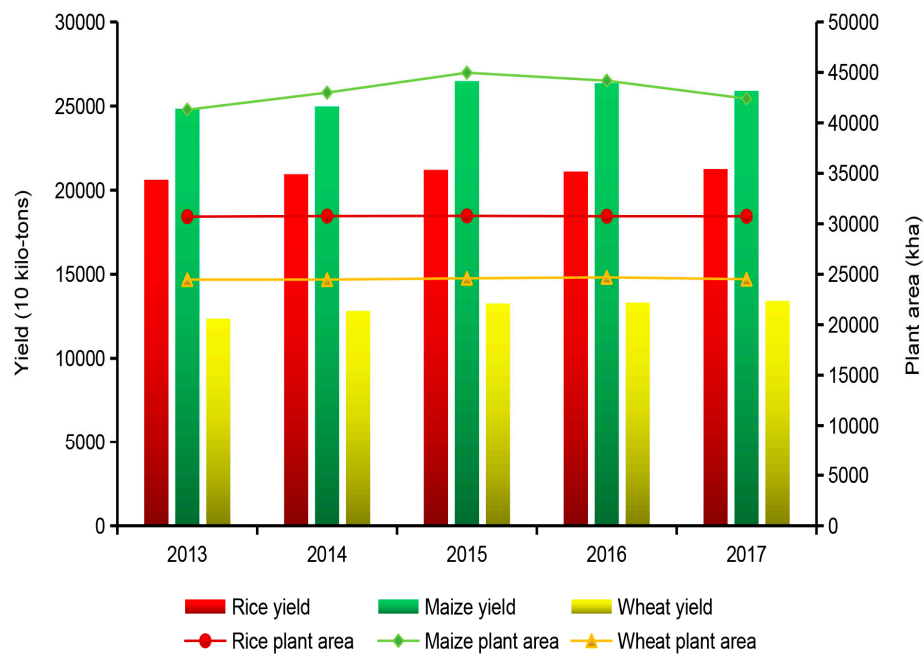
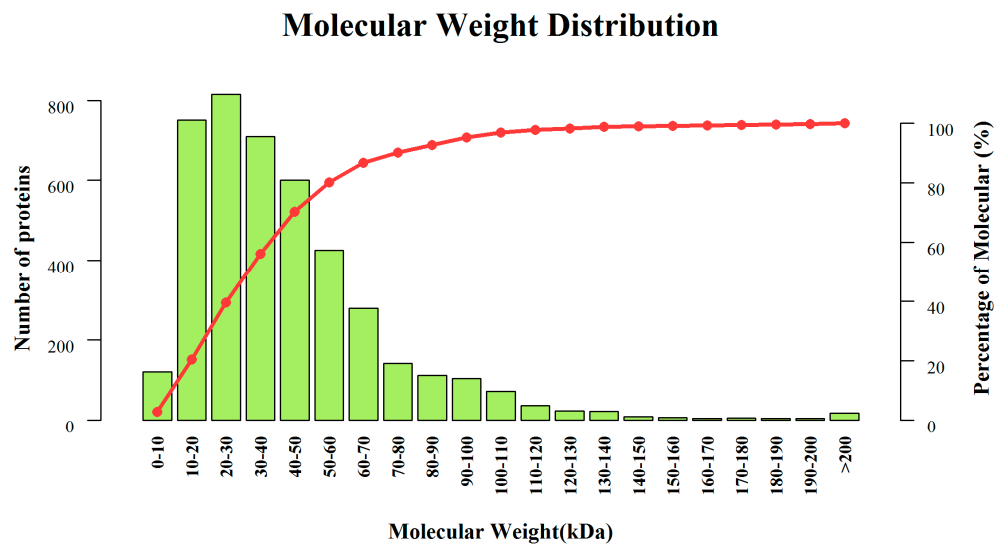


Supplementary Figures (Total 7)

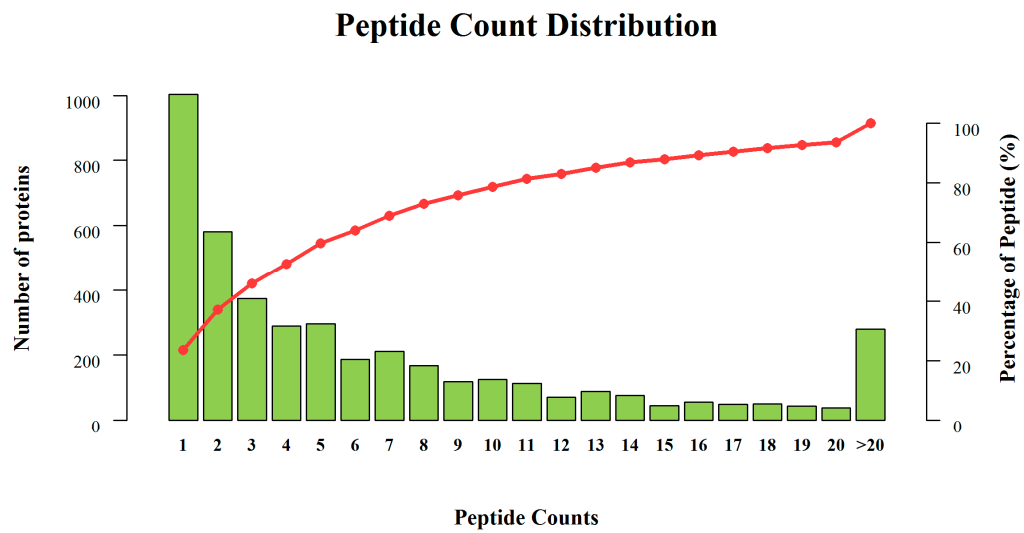


Supplementary Figure 1. The main food crops planting area and yield in recent years (2013-2017) in China (<http://data.stats.gov.cn/index.htm>)

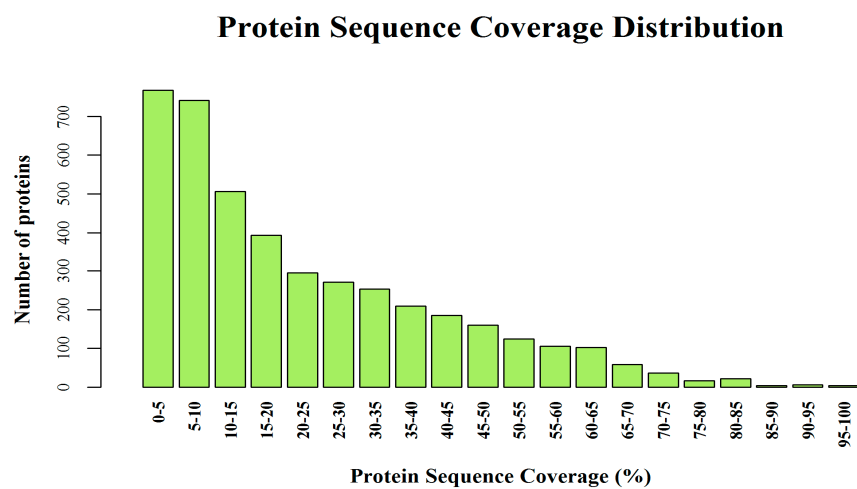
2A



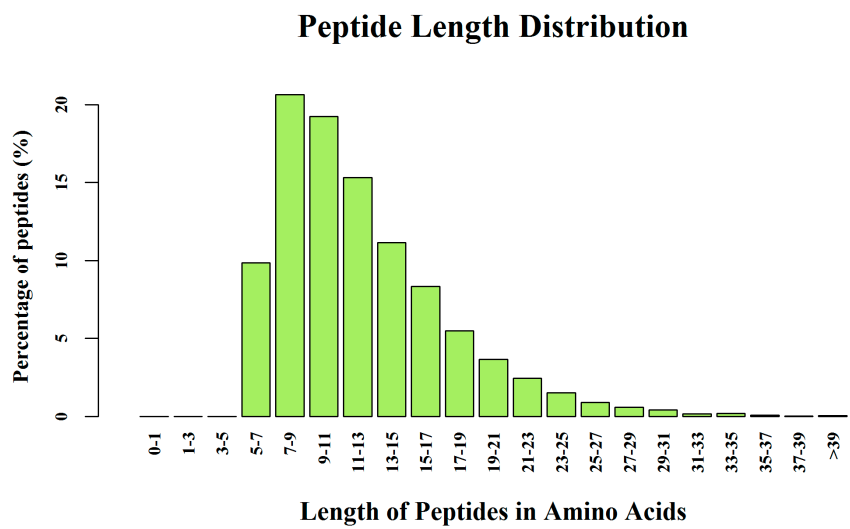
2B



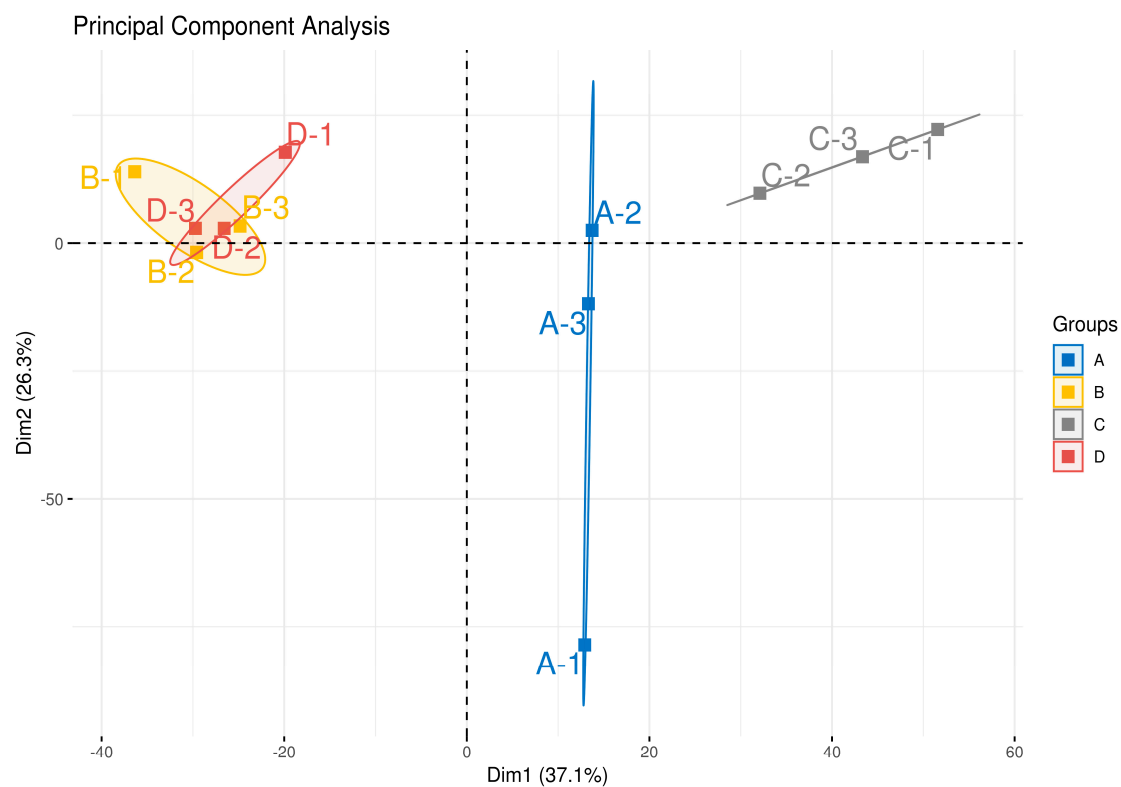
2C



2D

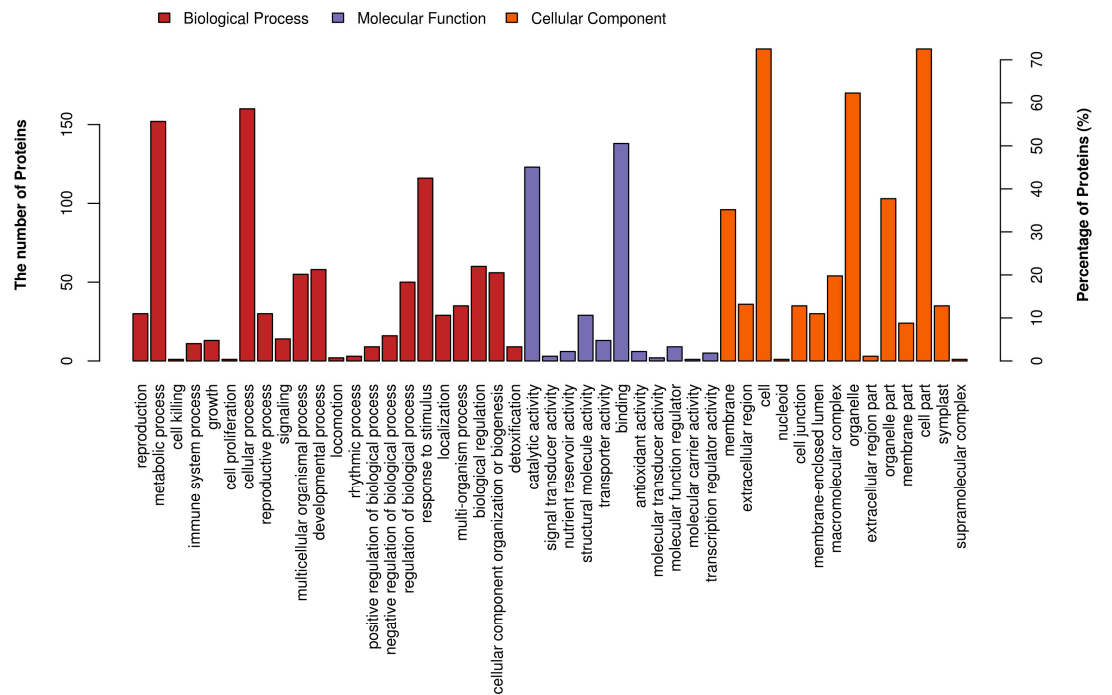


Supplementary Figure 2. Basic isobaric tags for relative and absolute quantification (iTRAQ) proteomics analysis output details. **(A)** Mass distribution of the identified proteins; **(B)** numbers of peptides that were matched to proteins; **(C)** sequence coverage range of the identified proteins; **(D)** length distribution of peptides defining each protein.

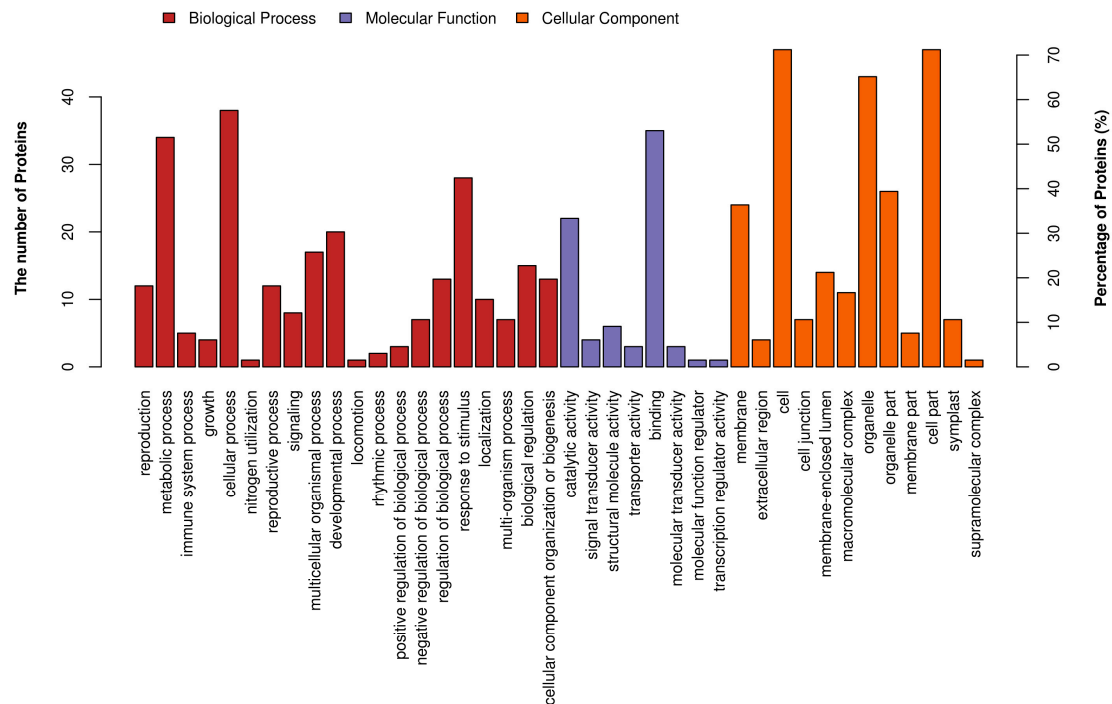


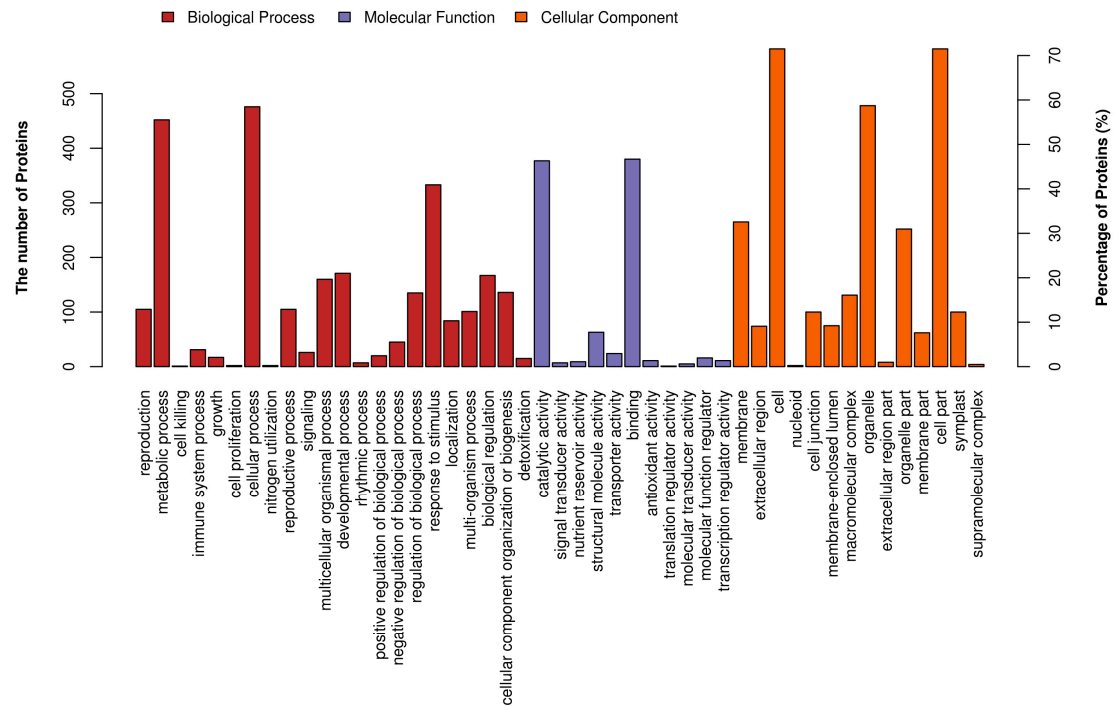
Supplementary Figure 3. Principal component (PCA) analysis of the twelve maize germinating-seed-tissue samples. PCA analysis was conducted using the dimension reduction and clustering visualization procedure. An orthogonal transformation was used to identify the principal components, which equal a linear combination of the protein levels. The distance of between two sample points represents the similarity level of those samples; the closer the distance, the higher the similarity between the samples. X axis represents the degree of contribution of a principal component N (PCN) in the two-dimensional graph to distinguish samples; Y axis represents the contribution of a principal component M (PCM) in the two-dimensional graph to distinguish samples.

4A

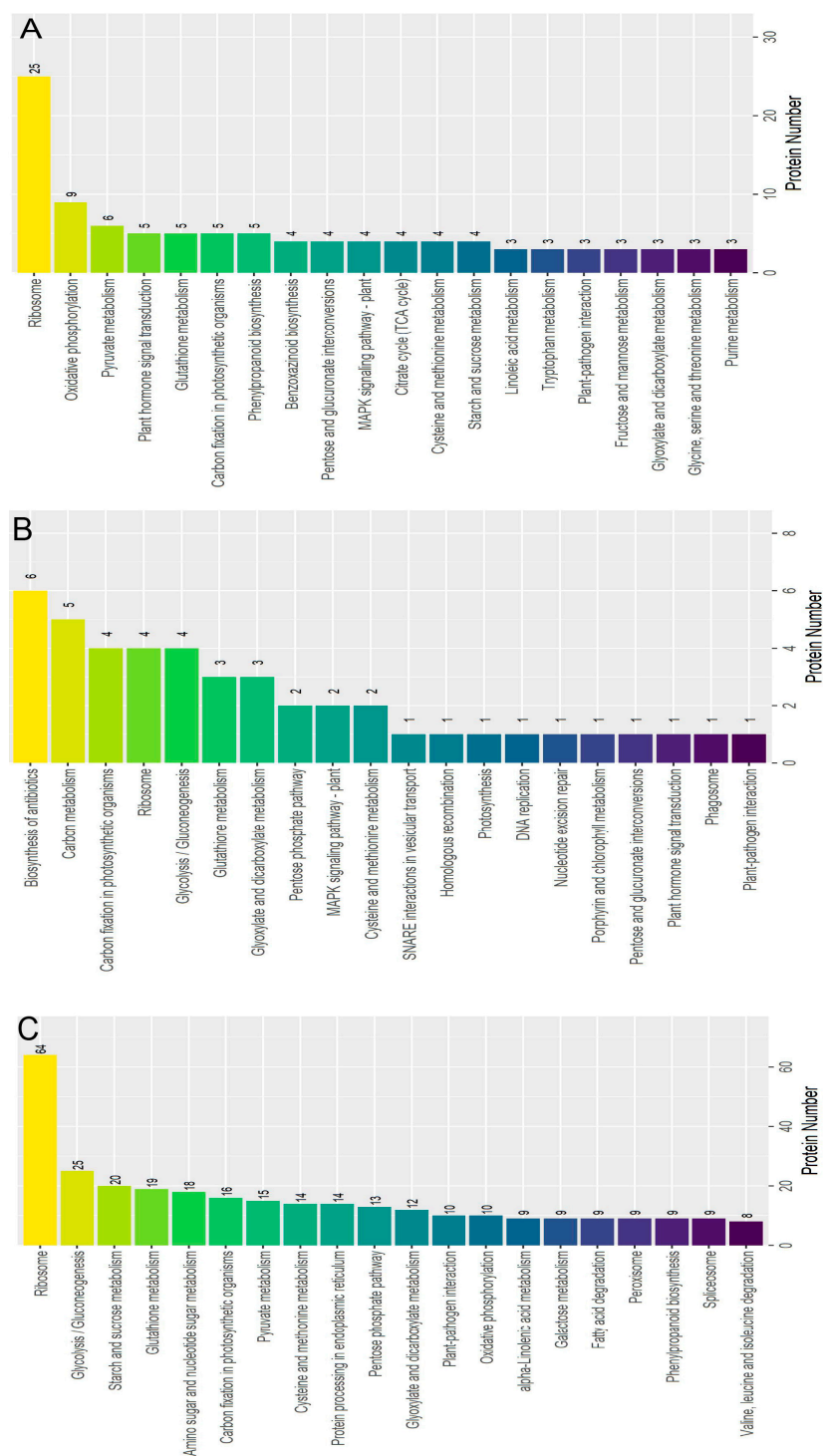


4B



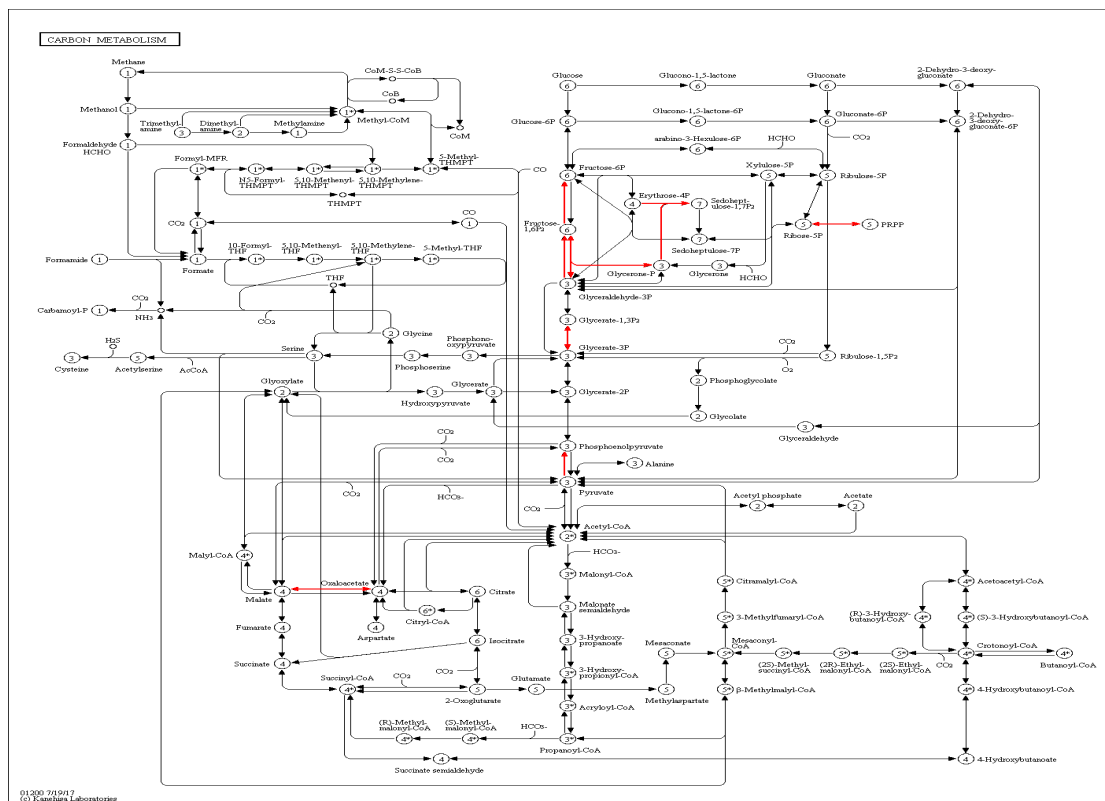


Supplementary Figure 4. Gene ontology (GO) functional classification of drought responsive differentially abundant proteins (DAPs) in different experimental comparisons. **(A)** WC_WD specific DAPs; **(B)** MC_MD specific DAPs; and **(C)** WD_MD specific DAPs. Y-axis represents the number of proteins in each function (and %); The X-axis shows the function of the protein, which is divided into three broad biological functional groups-biological process (BP), molecular function (MF) and cellular component (CC).

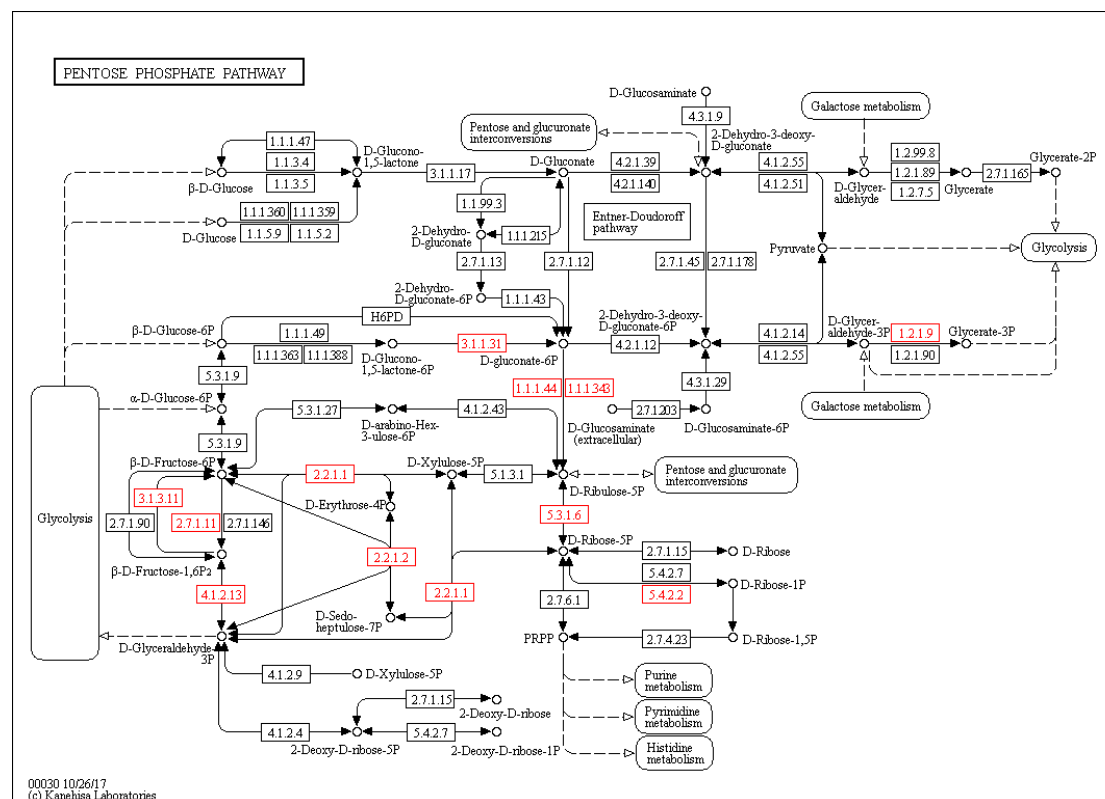


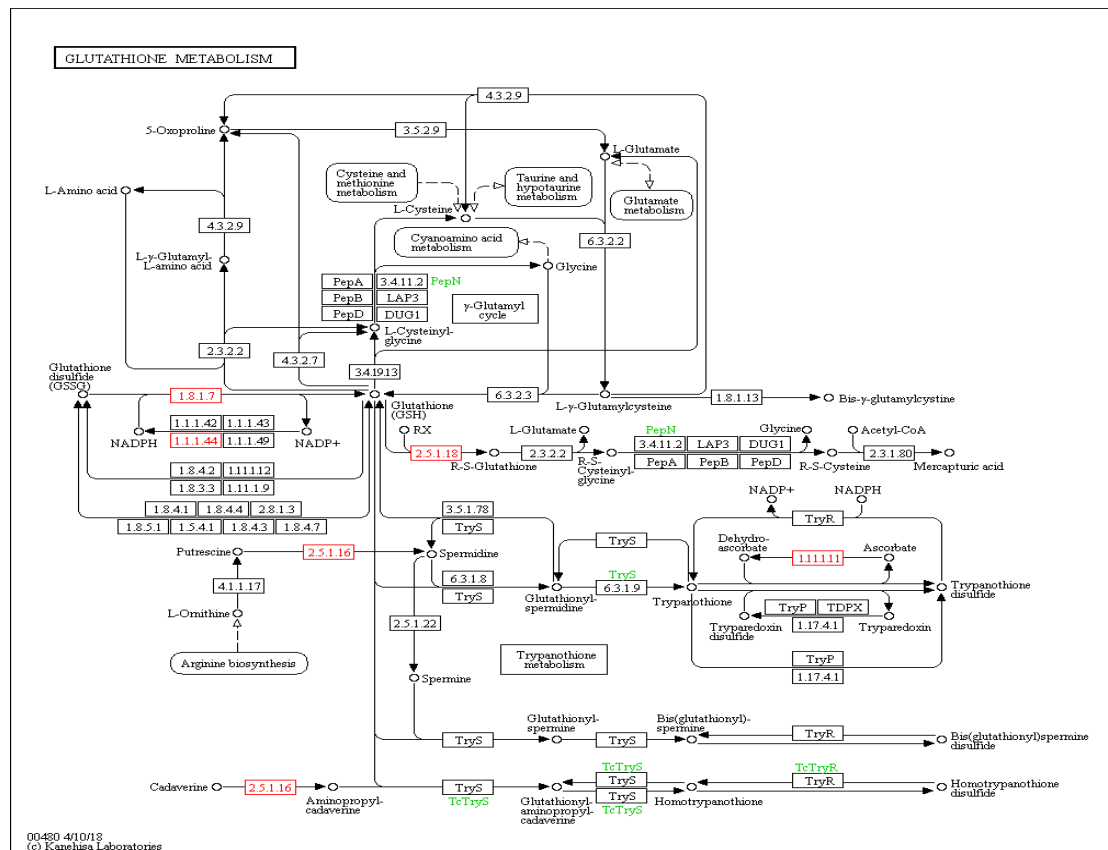
Supplementary Figure 5. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of the DAPs based on the KEGG database. **(A)** WC_WD; **(B)** MC_MD; and **(C)** WD_MD experimental comparisons. The y-axis represents number of DAPs enriched in the corresponding pathway, and the x-axis indicates the specific sub-categories of DAPs in that main pathway.

6A

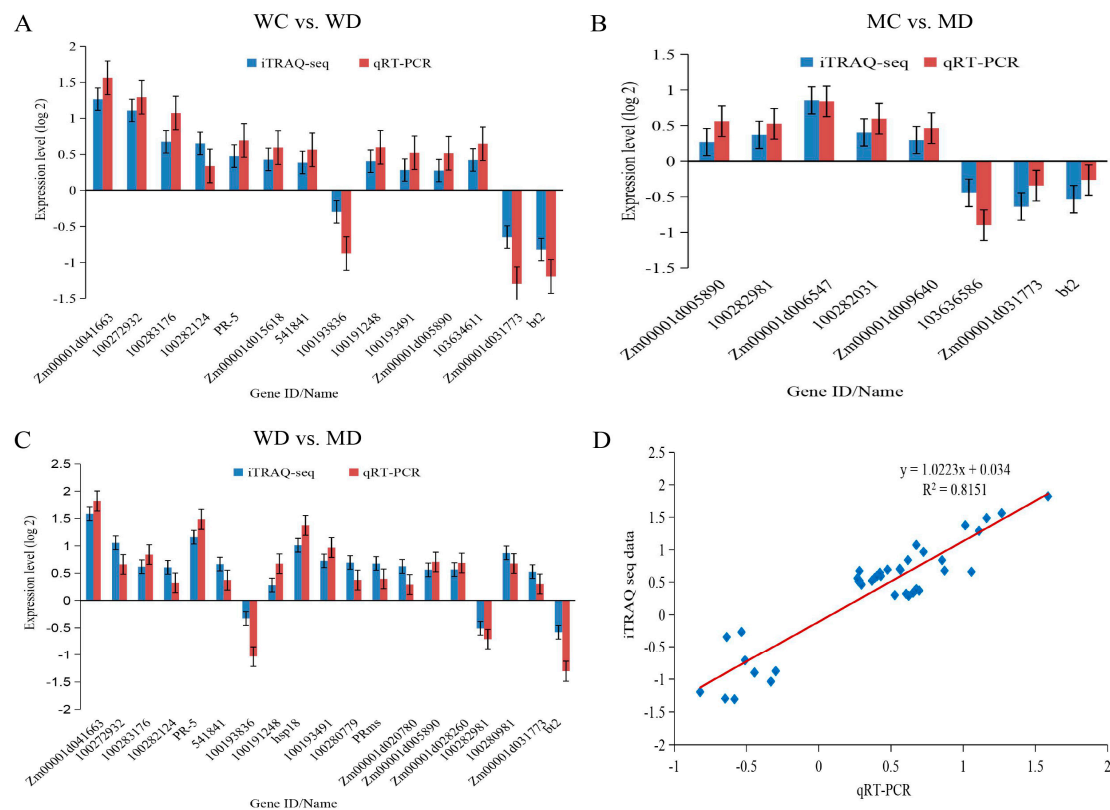


6B





Supplementary Figure 6. Top most significantly enriched KEGG pathways in two maize lines under PEG-induced drought stress conditions. The red boxes are proteins that were differentially expressed under PEG treatment conditions. **(A)** ‘Carbon metabolism’ pathway was significantly enriched in tolerant line mutant vp16; **(B)** ‘Pentose phosphate’ pathway was significantly enriched in WD_MD and MC_MD experimental comparisons; and **(C)** ‘Glutathione metabolism’ pathway was significantly enriched in WD_MD comparison.



Supplementary Figure 7. Confirmation of iTRAQ-seq results by qRT-PCR analysis. Quantitative RT-PCR analysis of the expression patterns of the maize germinating seeds genes encoded by differentially abundant proteins (DAPs) from different experimental comparisons. (A) DAPs in the WC_WD; (B) DAPs in MC_MD; and (C) DAPs in WD_MD comparisons. (D) DAPs expression tendencies in both iTRAQ sequencing data and qRT-PCR experimental results. The x-axis shows the results of qRT-PCR, and the y-axis represents the DAPs relative expression level.