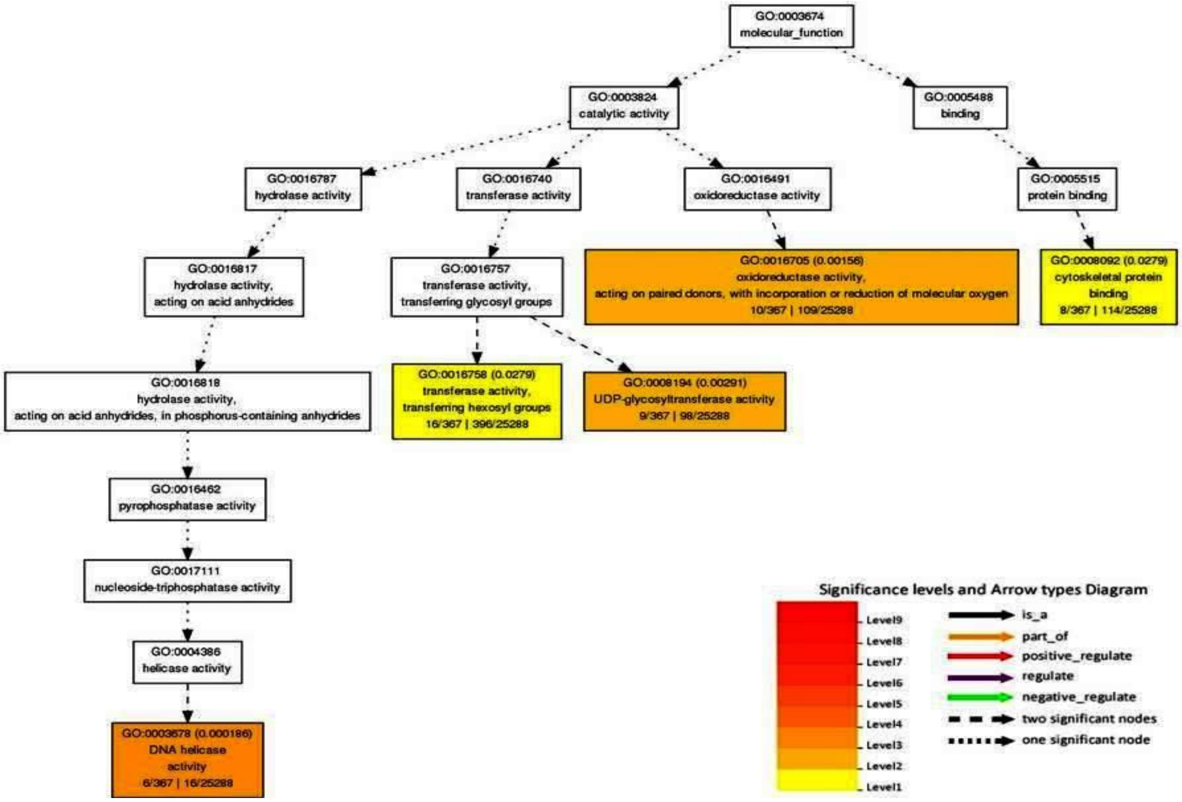
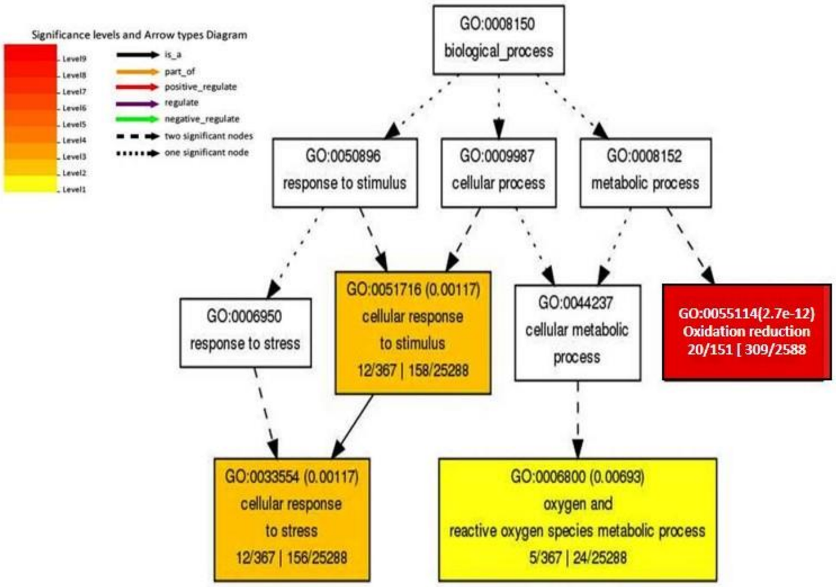
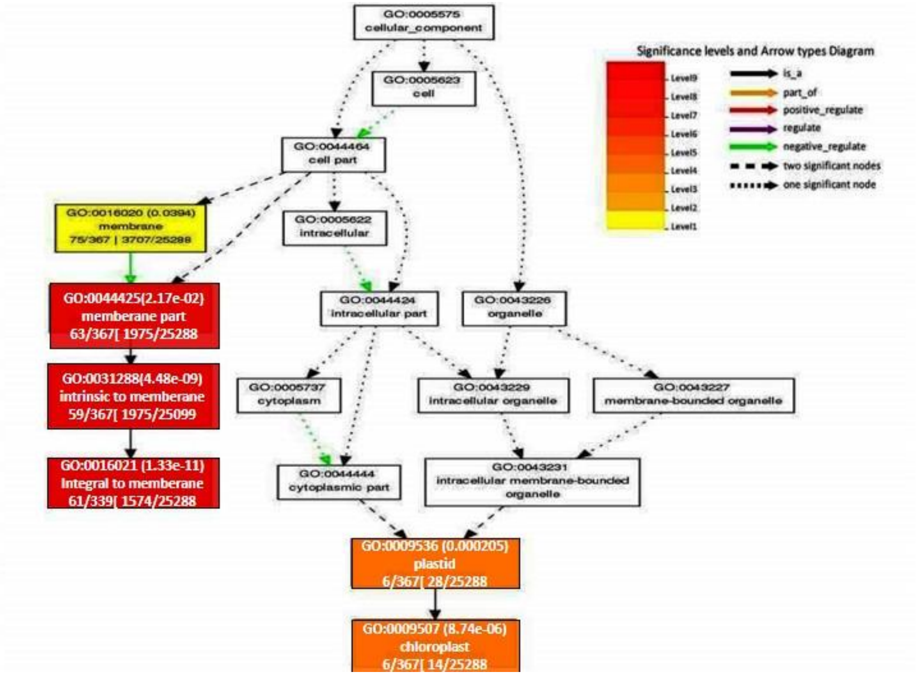


Supplementary Figure 1. The gene ontology category enrichment analysis for the differentially expressed genes (DEGs), using AgriGO (v 2.0) based on molecular function for the DEGs transcripts at grain filling stage of C7 and MO17 corn genotypes.

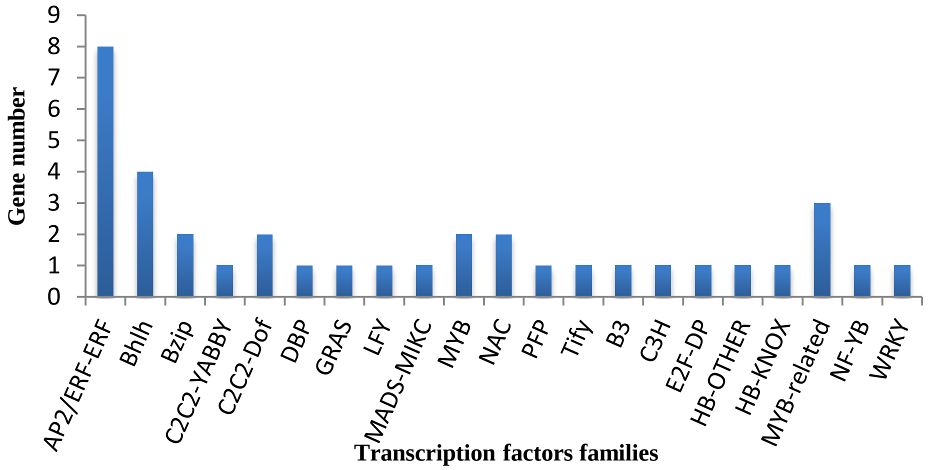


Supplementary Figure 2. The gene ontology category enrichment analysis for the differentially expressed genes (DEGs), using AgriGO (v 2.0) based on the biological process for the DEGs transcripts at grain filling stage of C7 and MO17 corn genotypes.

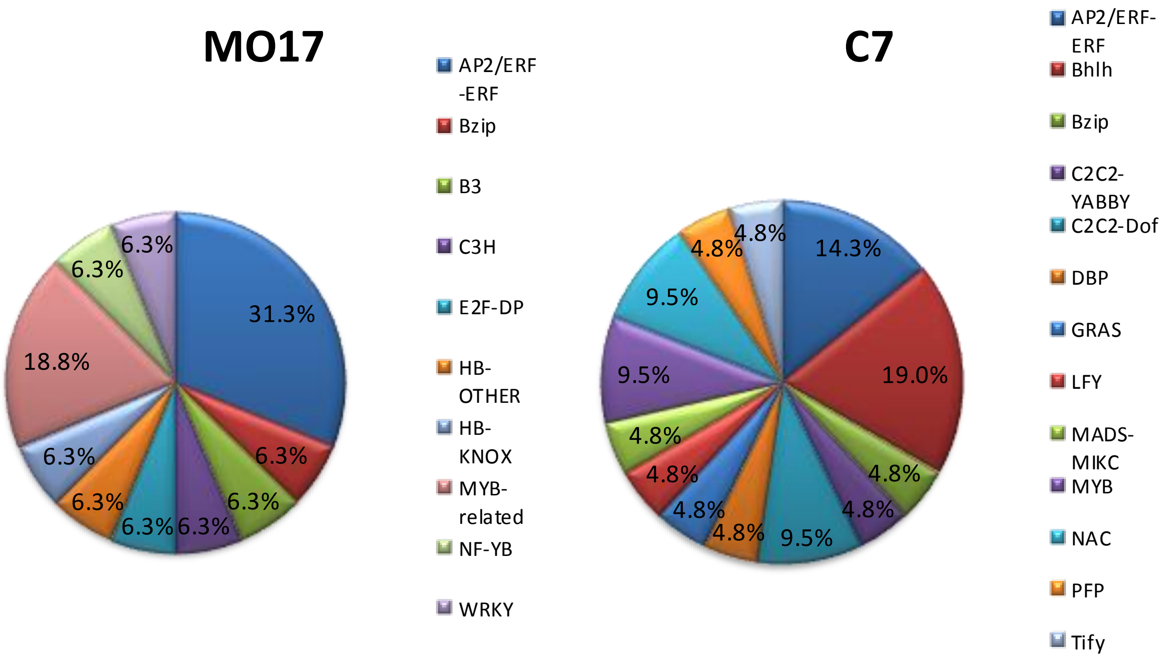
.



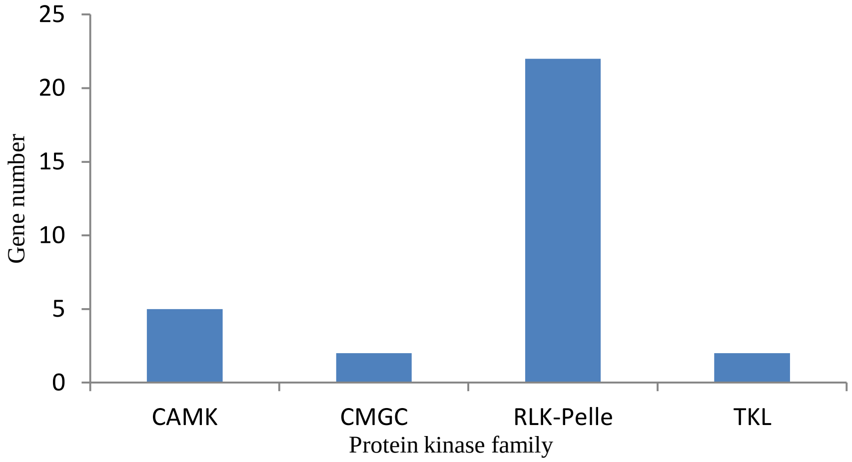
Supplementary Figure 3. The gene ontology category enrichment analysis for differentially expressed genes (DEGs), using AgriGO (v 2.0) based on cellular components' function for the DEGs transcripts at grain filling stage of C7 and MO17 corn genotypes.



Supplementary Figure 4. Families of transcription factors identified among genes with the differential expression at the grain filling stage of C7 and MO17 corn genotypes.



Supplementary Figure 5. Frequency distribution of transcription factor families (FTs) at the grain filling stage of C7 and MO17 corn genotypes.



Supplementary Figure 6. Protein kinase family identified among genes with differential expression in the C7 and MO17 corn genotypes.