

# Analysis of phytochemicals in colored-grain wheat (*Triticum aestivum*. L) and effects on gene expression and biochemical responses under water deficit condition

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## Abstract

Nutritious and functional foods from crop have received great attention in recent years. Colored-grain wheat contains high phenolic compound and a large number of flavonoid. One of plant pigments, wheat anthocyanin is increasingly emerging as natural compounds for consumer's health and condition. Total phenolic compound, flavonoid, and anthocyanin of four wheat groups classified by color degree were measured to examine the biological and physiological effects by phytochemical in colored-grain. Activities of anti-oxidant enzyme and MDA contents in four wheat groups were also determined. In addition, we analyzed genome wide transcripts in seedling of colored-grain wheat response to ABA and PEG treatment. Drought response pathway, such as ABA signaling, water and ion channels, detoxification signaling, enzymes of osmolyte biosynthesis, phospholipid metabolism, signal transduction, and transcription factors related DEGs were selected to explain response mechanism under water deficit condition. Anthocyanin, phenol compound, and DPPH radical scavenging activity were measured and antioxidant activity enzyme assays were conducted to show biochemical adaptation under water deficit condition. The accumulation of total anthocyanin and phenol contents were observed in colored wheat seedlings, and antioxidant capacity was promoted by upregulation of genes involved in maintaining redox state and activation of antioxidant scavengers, such as CAT, APX, POD, and SOD in colored wheat seedlings under water deficit condition. This work may provide valuable and basic information for further investigation of the molecular responses of colored-grain wheat to water deficit stress and for further gene-based studies

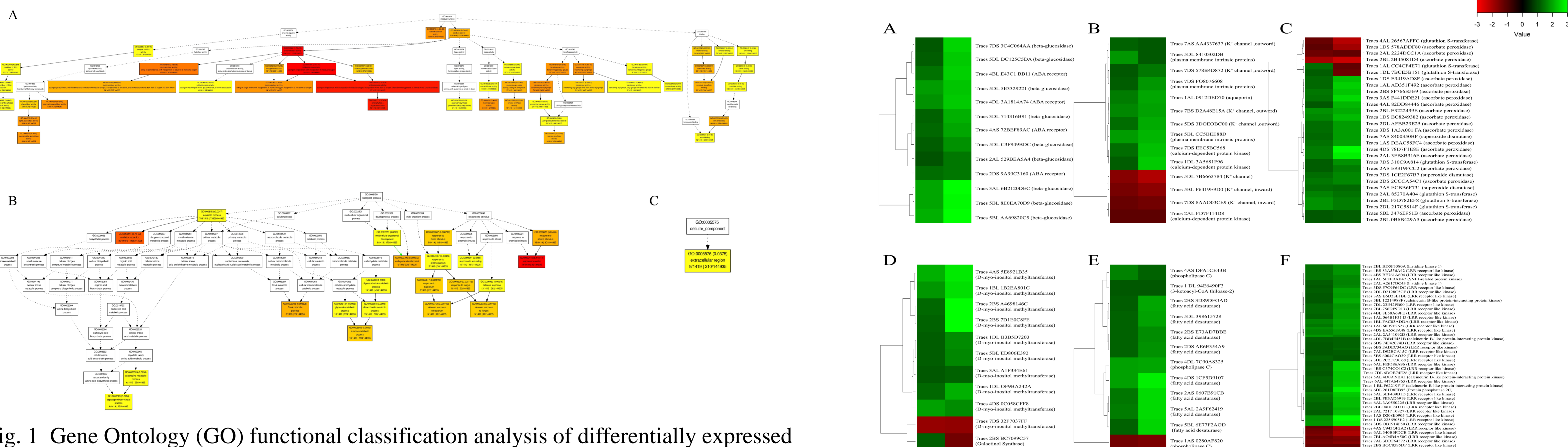


Fig. 1 Gene Ontology (GO) functional classification analysis of differentially expressed genes (DEGs), based on RNA-Seq data. Significant GO terms in in three GO categories, biological process, cellular component, and molecular function were shown.

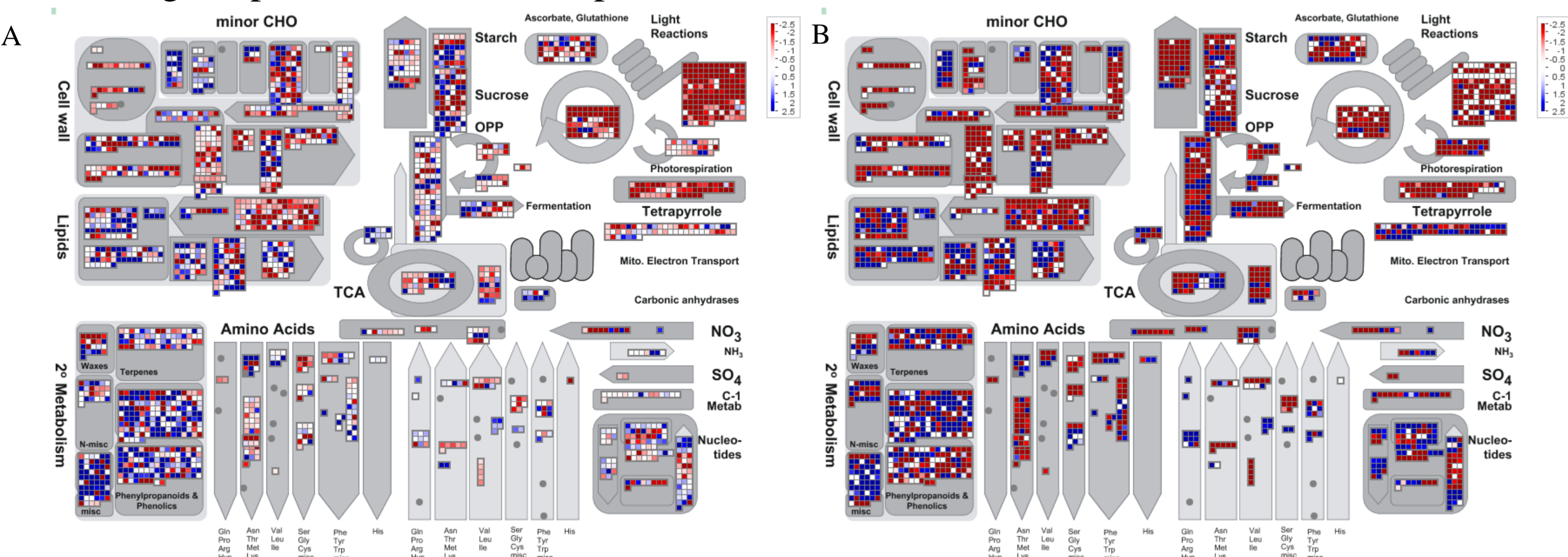


Fig. 2 Overview of the MapMan visualization of differences in transcript levels during seed development stage. (A) ABA and (B) PEG treatments

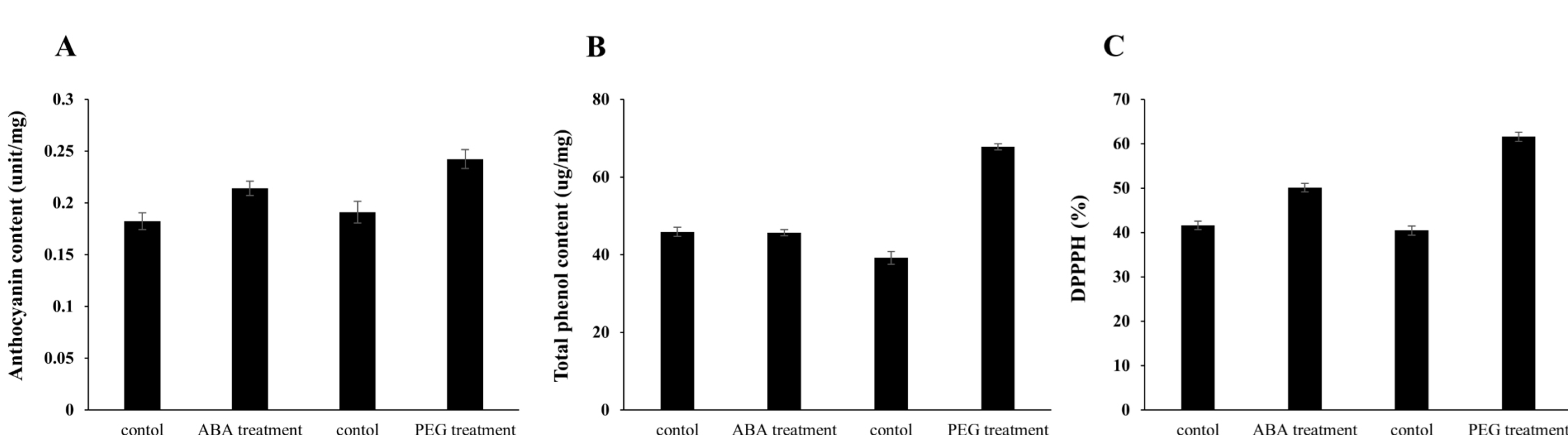


Fig. 4. Comparison of (A) anthocyanin and (B) phenol contents of abscisic acid (ABA)- and polyethylene glycol (PEG)-treated colored-grain wheat seedlings. (C) Effects of ABA and PEG treatment on DPPH radical-scavenging activity in colored-grain wheat seedlings. Values and error bars represent means  $\pm$  SD for an average of three independent experiments each.

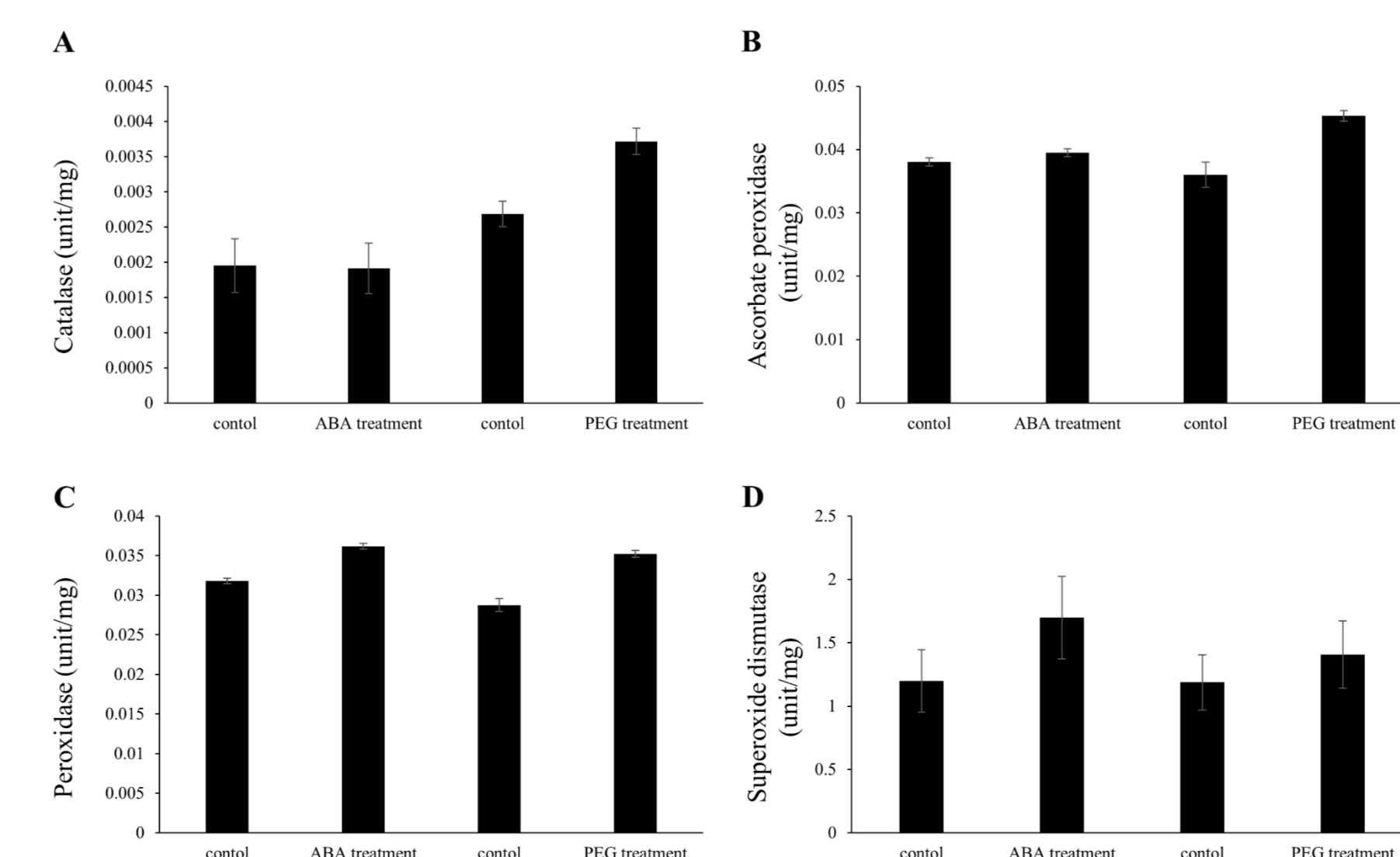


Fig. 5. Effect of abscisic acid (ABA) and polyethylene glycol (PEG) treatments on the activities of various antioxidant enzymes in colored-grain wheat seedlings.

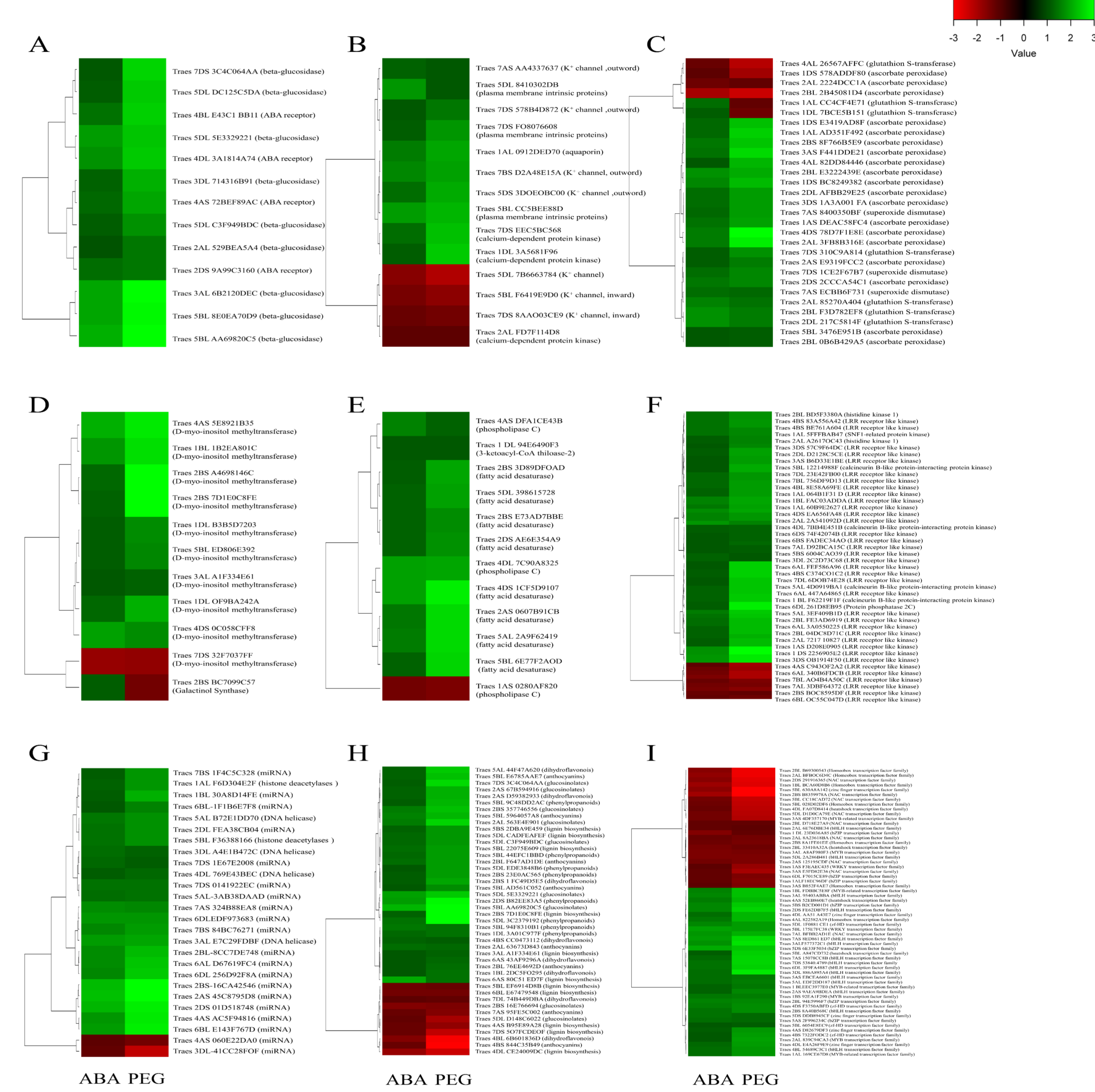


Fig. 3. Expression profiles of transcripts that were differentially expressed under abscisic acid (ABA)- and polyethylene glycol (PEG)-mediated stress showed by heatmap. (A) ABA signaling, (B) water and ion channeling, (C) detoxification signaling, (D) osmolyte biosynthesis, (E) phospholipid metabolism, (F) signal transduction, (G) gene expression, (H) flavonoid biosynthesis, and (I) transcription factors.

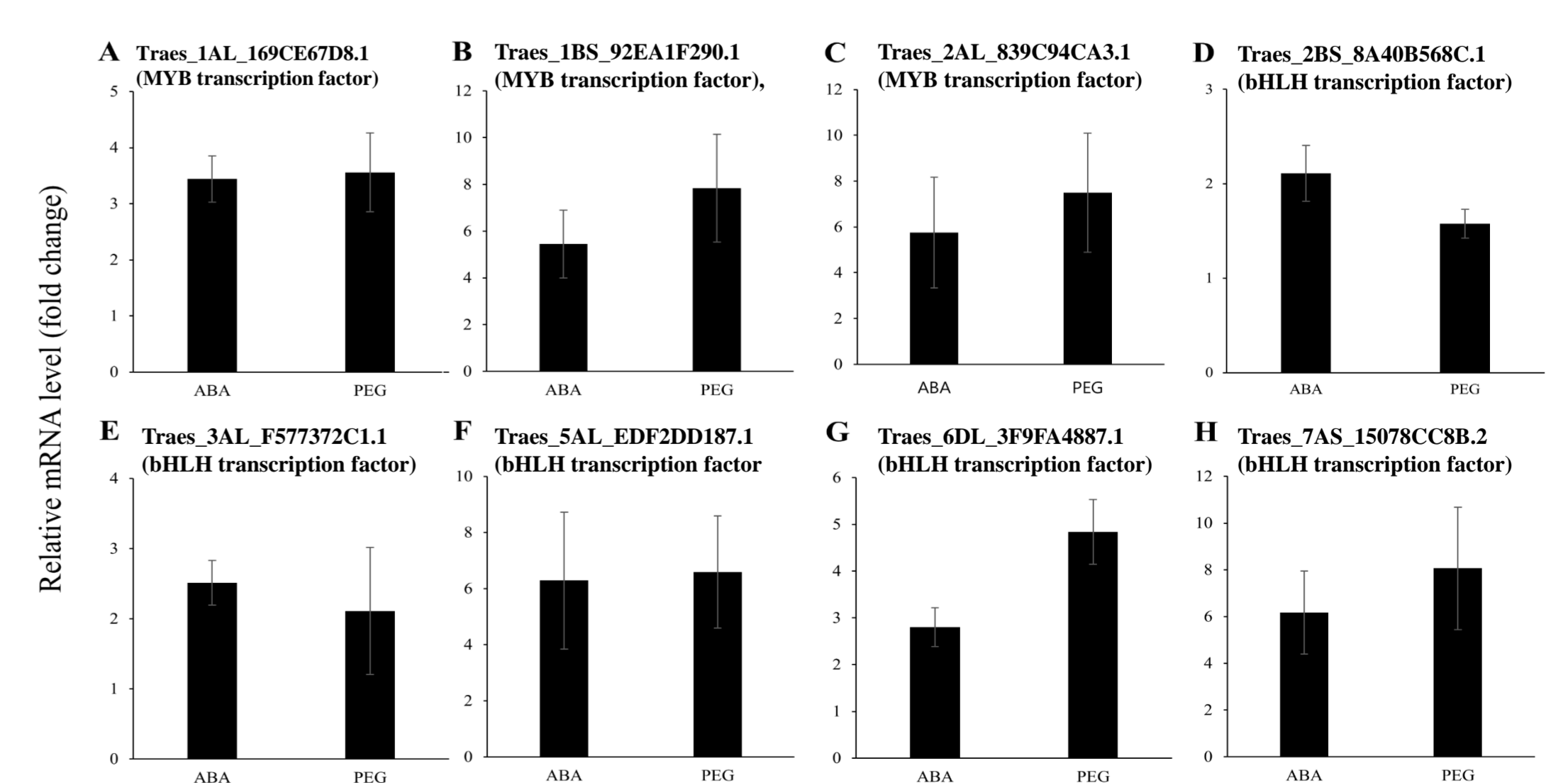


Fig. 6. Expression of selected transcription factor genes, as revealed by qRT-PCR. Values and error bars represent means  $\pm$  SD (n = 3).

