

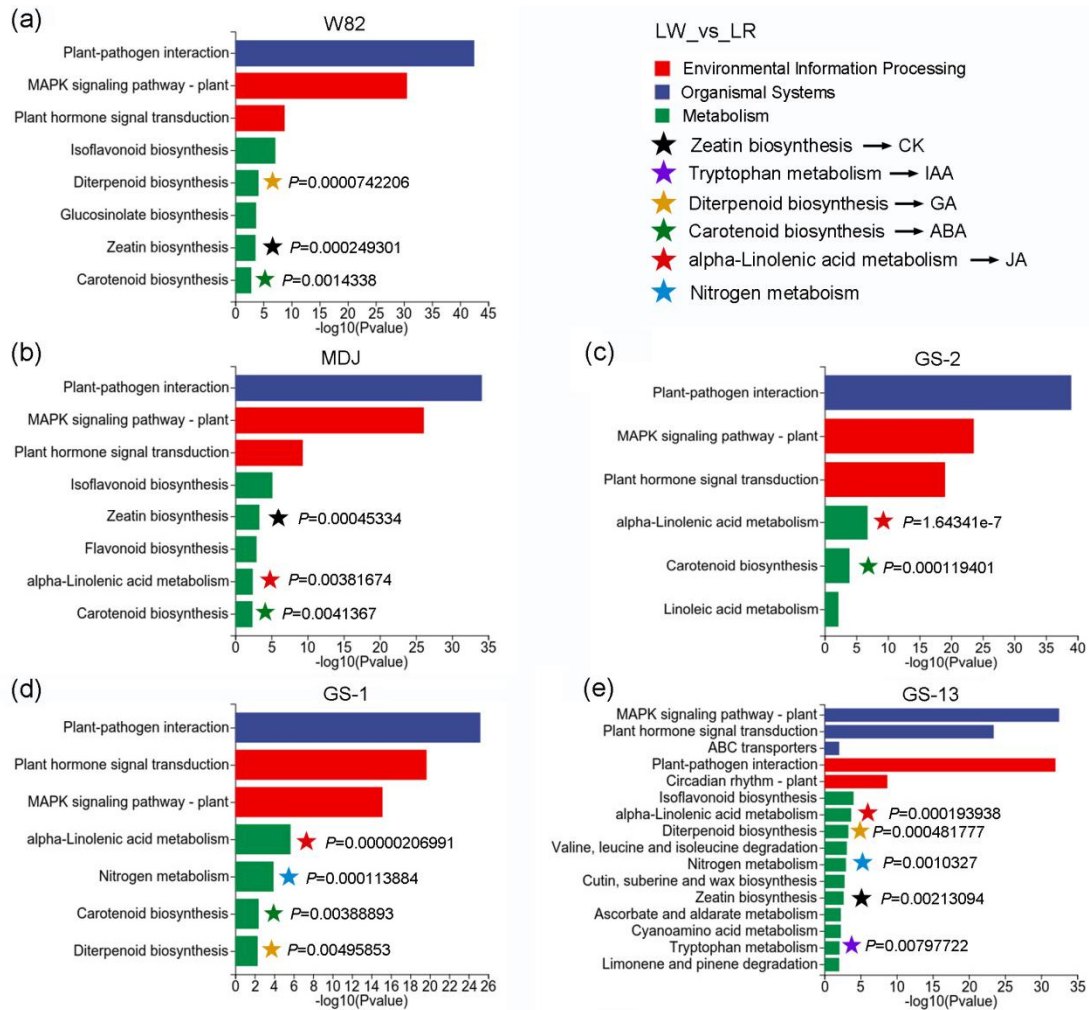


Fig. S7 KEGG pathway enrichment analysis of differentially expressed genes in five soybean accessions under long-day white light (LW) versus long-day white:red = 6:1 (LR) comparison. (a) W82, (b) MDJ, (c) GS-2, (d) GS-1, and (e) GS-13. Shoot apices were collected from different soybean accessions grown for 10 days under LR and LW conditions for transcriptome sequencing. Bar graphs display the most significantly enriched KEGG pathways. Key pathways are labeled with colored stars: black star for zeatin biosynthesis (CK), yellow star for diterpenoid biosynthesis (GA), purple star for tryptophan metabolism (IAA), green star for carotenoid biosynthesis (ABA), red star for α -linolenic acid metabolism (JA), and blue star for nitrogen metabolism.