

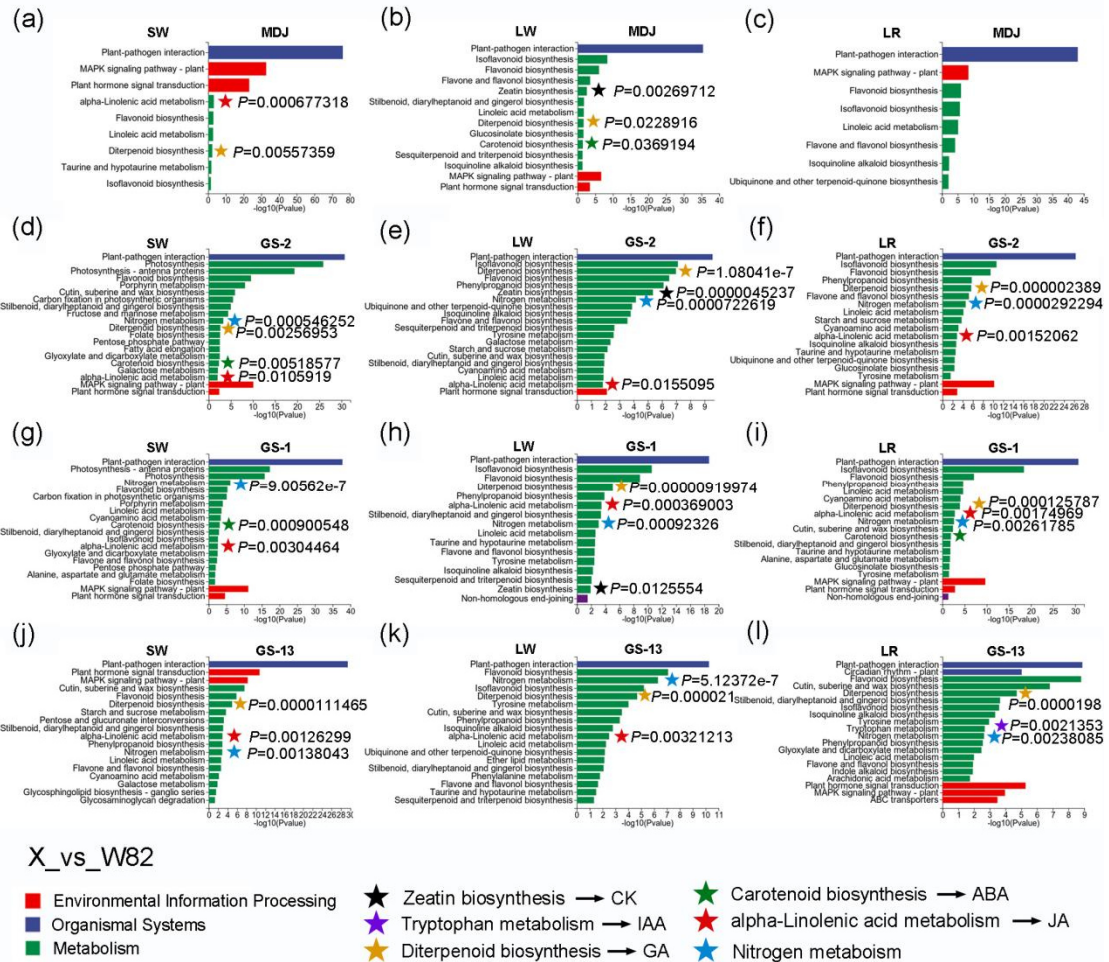


Fig. S6 KEGG pathway enrichment analysis of differentially expressed genes in shoot apex under different light conditions using W82 as the reference genome. (a–c) MDJ in SW, LW, and LR; (d–f) GS-2 in SW, LW, and LR; (g–i) GS-1 in SW, LW, and LR; (j–l) GS-13 in SW, LW, and LR. Shoot apices were collected from different soybean accessions grown for 10 days under long-day white:red = 6:1 (LR), long-day white (LW), and short-day white (SW) conditions for transcriptome sequencing. Bar plots show the top 20 enriched KEGG pathways. Red, blue, and green bars represent Environmental Information Processing, Organismal Systems, and Metabolism, respectively. 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.