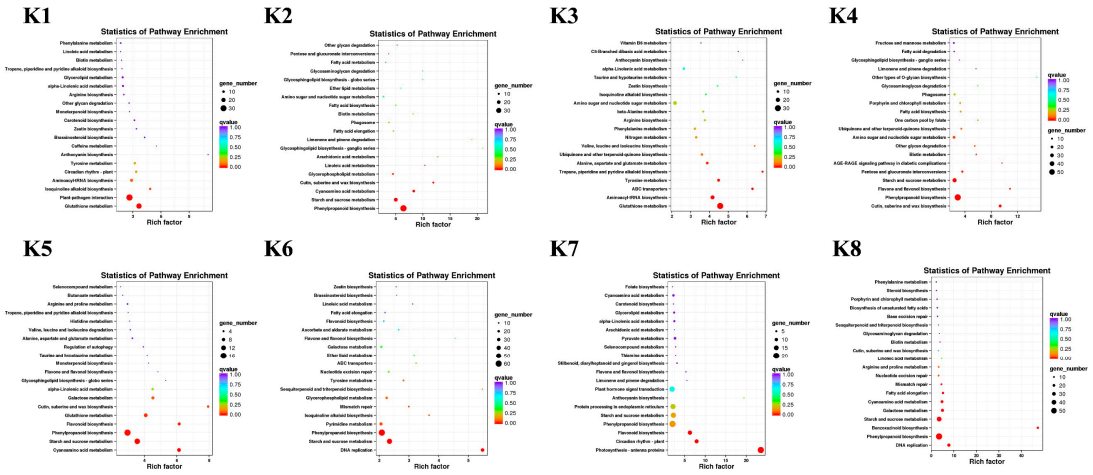

Figure S2. Differentially expressed genes (DEGs) involved top 20 enriched pathways of the eight *K*-means clusters referring to KEGG database