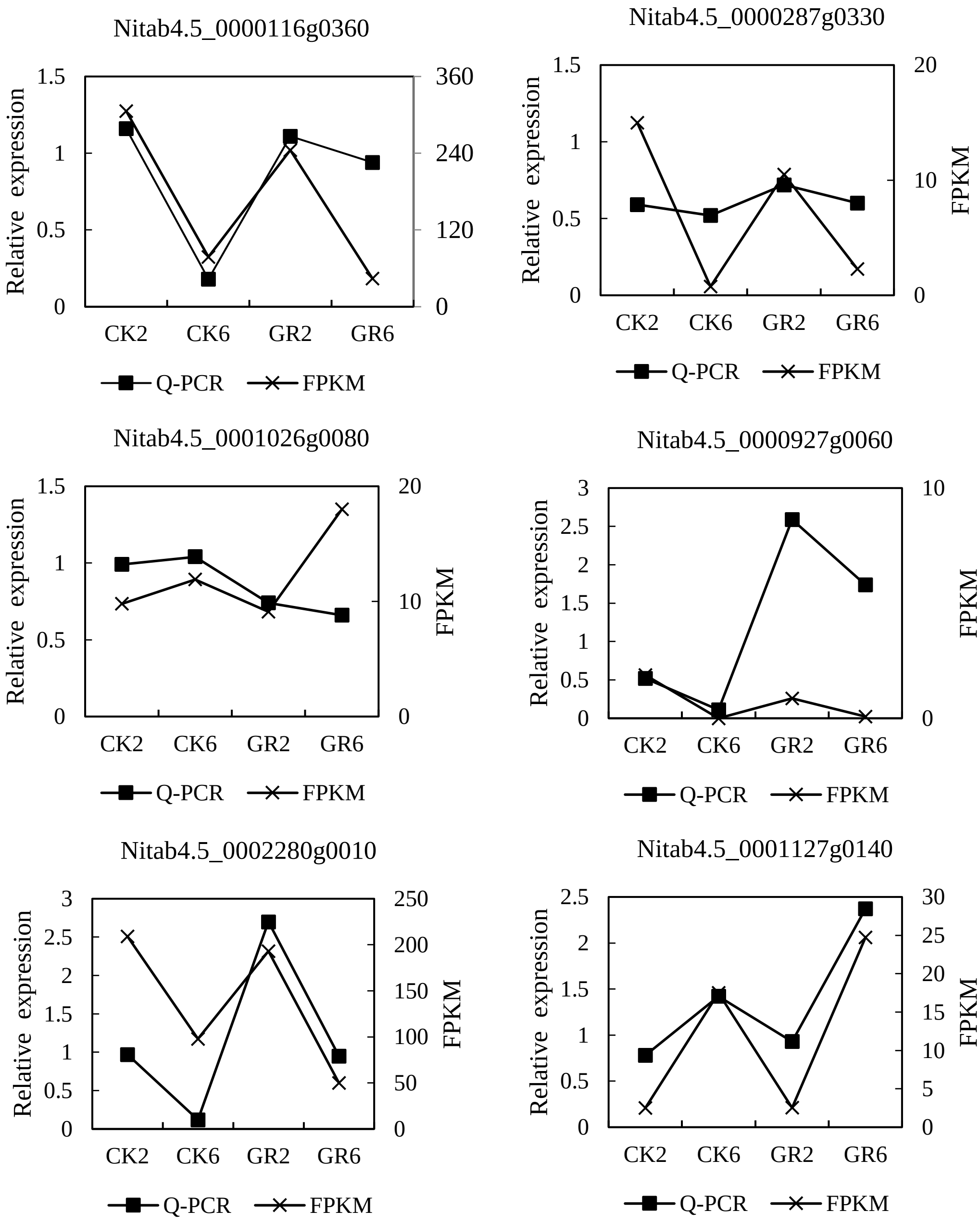

Fig. 1 Suppl. Expression analysis of 6 DEGs in different samples. Transcription levels and qRT-PCR results of 6 genes selected from RNA sequencing. The left y-axis shows the relative gene expression levels analyzed by qRT-PCR, and the right y-axis shows the corresponding RNA-Seq expression data (FPKM).

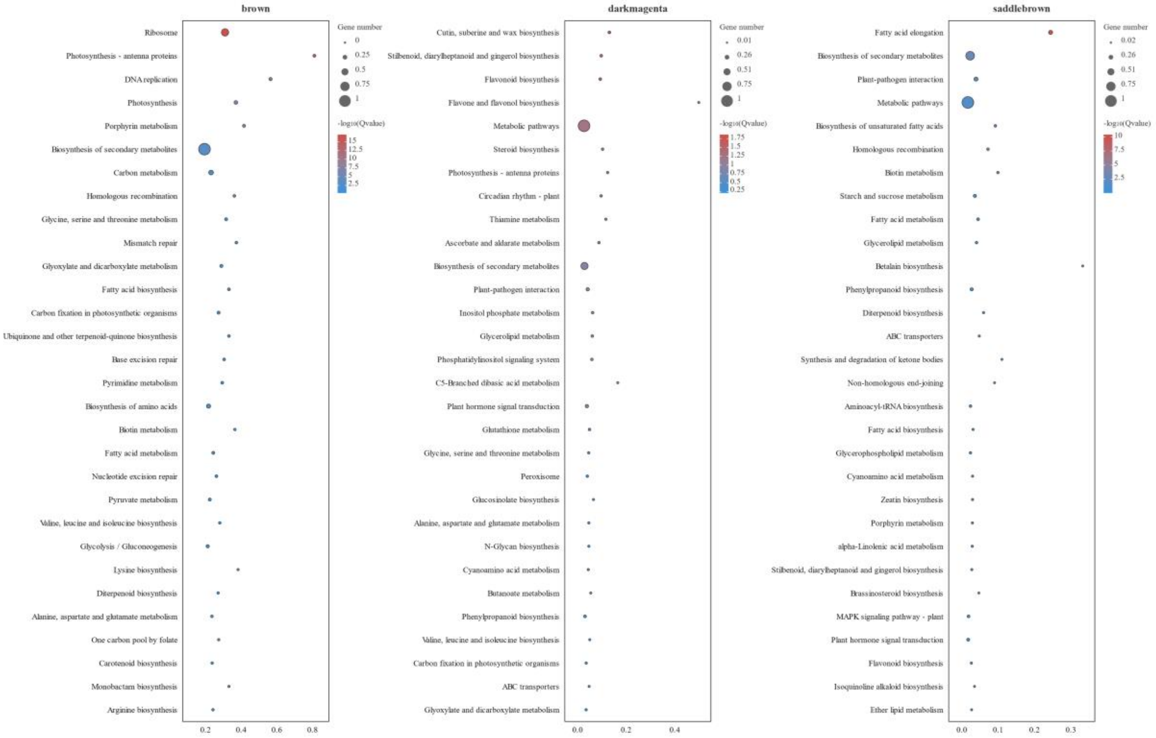

Fig. 2 Suppl. TOP-30 KEGG pathway enrichment in WGCNA with axillary bud length significantly enriched modules DEGs (brown; left panel) (darkmagenta; middle panel) (saddlebrown; right panel).The size circle corresponds to the number of DEGs and is color coded according to the value of g. x-axisDisplays the enrichment factor value.

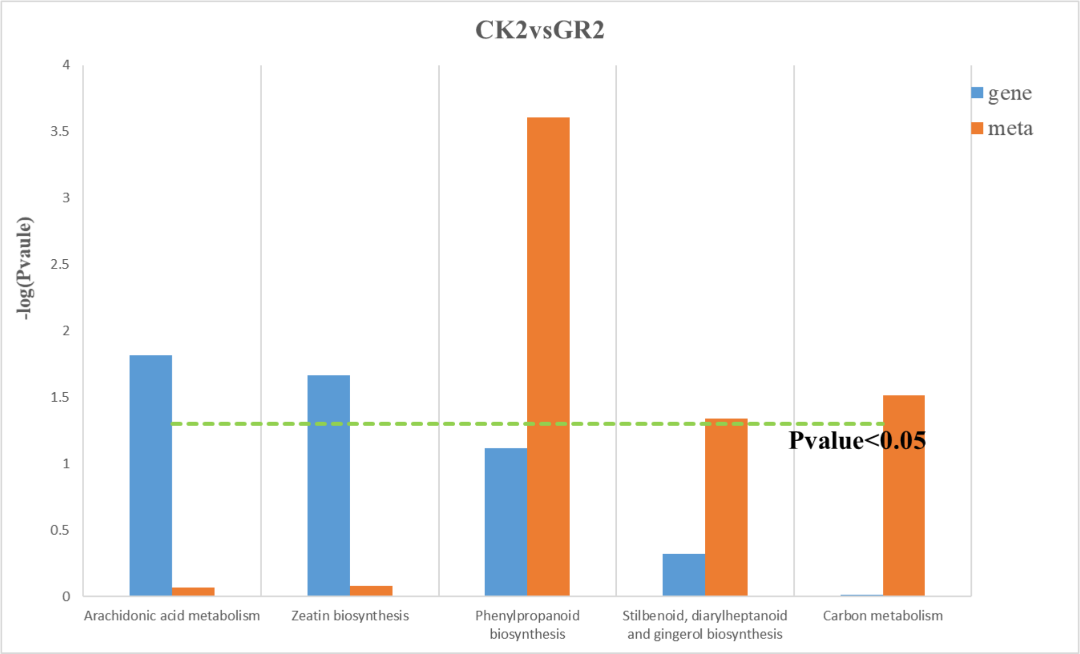

Fig. 3 Suppl. The expression of KEGG enrichment pathway was shared between the axillary bud transcriptome and the metabolome at 2 days after GR24 treatment.

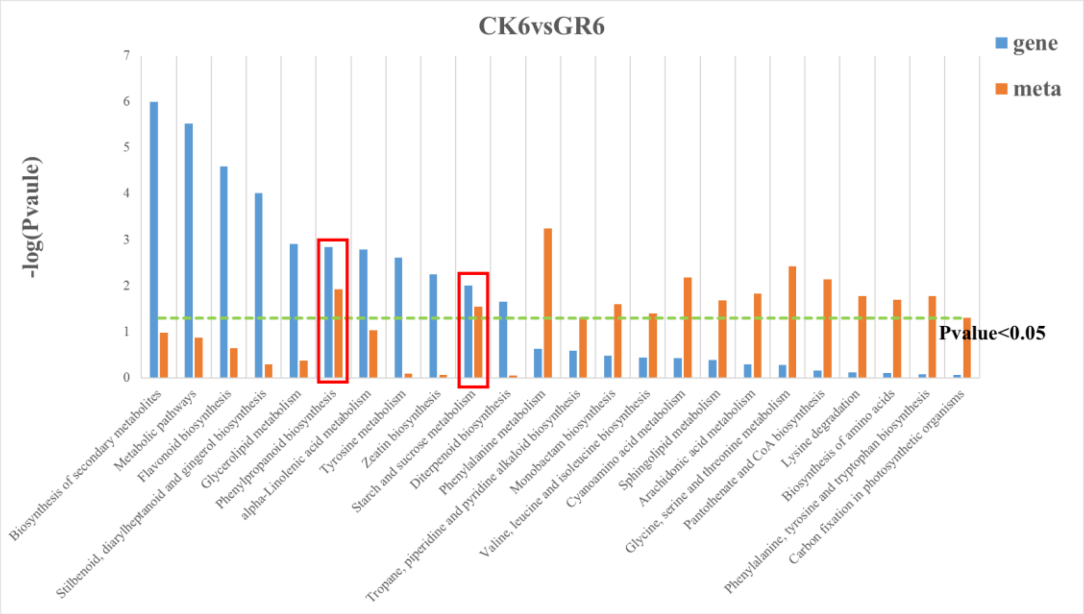

Fig. 4 Suppl. The expression of KEGG enrichment pathway was shared between the axillary bud transcriptome and the metabolome at 6 days after GR24 treatment.