

Table 1 KEGG pathway enrichment of the target genes with differential expression

KEGG pathway	Gene number (percentage)	Predicted protein
Metabolic pathways	69(53.49%)	No annotation
Biosynthesis of secondary metabolites	56(43.41%)	No annotation
Plant hormone signal transduction	17(13.18%)	AUX1, CRE1, SAUR, TIFY, PP2C, BZR1/2, COI1, PIF3, MYC2, NPR1, TGA, PR1
Carbon metabolism	14(10.85%)	HK, G6PD, PGD, ALDO, glpX-SEBP, GLDC, SHMT, aceB, ENO, aceE, ACAT, MDH1, OGDH
Plant-pathogen interaction	13(10.08%)	CDPK, CML, FLS2, PR1, RPS2, MYB, SLC45A3
Phenylpropanoid biosynthesis	10(7.75%)	COMT, F5H, CCOAMT, CCR, Prx2540

Note: * represent significantly enriched KEGG pathway; The values in brackets represent the proportion of the number of target genes enriched in the metabolic pathway in all the target genes enriched