

Table S7. GO and KEGG enrichment analysis of differentially expressed genes in spines and leaves together. BP: biological process. Q-value less than 0.01 (for GO) and 0.05 (for KEGG) represented significant enrichment.

GO enrichment					
Category	GO ID	Description	P-value	Q-value	Ratio
BP	GO:0032502	developmental process	4.85E-11	1.16E-08	0.081
BP	GO:0006355	regulation of transcription, DNA-templated	0.000136	0.003324	0.015
BP	GO:0051252	regulation of RNA metabolic process	0.000136	0.003324	0.015
BP	GO:1903506	regulation of nucleic acid-templated transcription	0.000136	0.003324	0.015
BP	GO:2001141	regulation of RNA biosynthetic process	0.000136	0.003324	0.015
BP	GO:0019219	regulation of nucleobase-containing compound metabolic process	0.000145	0.003324	0.015
BP	GO:0009889	regulation of biosynthetic process	0.000147	0.003324	0.015
BP	GO:0010556	regulation of macromolecule biosynthetic process	0.000147	0.003324	0.015
BP	GO:0031326	regulation of cellular biosynthetic process	0.000147	0.003324	0.015
BP	GO:2000112	regulation of cellular macromolecule biosynthetic process	0.000147	0.003324	0.015
BP	GO:0051171	regulation of nitrogen compound metabolic process	0.000153	0.003324	0.015
BP	GO:0010468	regulation of gene expression	0.000168	0.003346	0.015
BP	GO:0031323	regulation of cellular metabolic process	0.00023	0.004089	0.014
BP	GO:0080090	regulation of primary metabolic process	0.00024	0.004089	0.014
BP	GO:0060255	regulation of macromolecule metabolic process	0.000272	0.004337	0.014
BP	GO:0019222	regulation of metabolic process	0.000381	0.005684	0.014
BP	GO:0006351	transcription, DNA-templated	0.000579	0.007416	0.013
BP	GO:0097659	nucleic acid-templated transcription	0.000579	0.007416	0.013
BP	GO:0032774	RNA biosynthetic process	0.00059	0.007416	0.013
BP	GO:0007275	multicellular organism development	0.00074	0.008838	0.041
BP	GO:0044707	single-multicellular organism process	0.000796	0.009054	0.040
KEGG enrichment					
Pathway	Ko ID	P-value	Q-value	Ratio	
Valine, leucine and isoleucine degradation	ko00280	0.000247	0.011111	0.056	
Fatty acid elongation	ko00062	0.001133	0.024237	0.062	
Limonene and pinene degradation	ko00903	0.001616	0.024237	0.143	
Biosynthesis of secondary metabolites	ko01110	0.002483	0.027938	0.008	