

S3 Table. Significantly enriched GO-term associated with the genes terminally connected to hubs associated with *PtaJAZ3* and *PtaRAP2.6* as shown in Fig 4.

Hubs	GO Ontology	Corrected p-values
<i>PtaCYCB2;3</i> (54 Genes)	GO:0043687: post-translational protein modification	0.017
	GO:0060255: regulation of macromolecule metabolic process	0.018
	GO:0010468: regulation of gene expression	0.021
	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.021
	GO:0044260: cellular macromolecule metabolic process	0.042
<i>PtaSAUR37</i> (94 Genes)	GO:0010467: gene expression	0.00029
	GO:0034645: cellular macromolecule biosynthetic process	0.0005
	GO:0051726: regulation of cell cycle	0.002
	GO:0051171: regulation of nitrogen compound metabolic process	0.0005
	GO:0019222: regulation of metabolic process	0.0012
<i>PtaARFA1F</i> (117 Genes)	GO:0009059: macromolecule biosynthetic process	0.0043
	GO:0080090: regulation of primary metabolic process	0.0029
	GO:0019222: regulation of metabolic process	0.0029
	GO:0048527: lateral root development	0.029
	GO:0045449: regulation of transcription	0.029
	GO:0031323: regulation of cellular metabolic process	0.031
<i>PtaGH16</i> (59 Genes)	GO:0050789: regulation of biological process	0.37
	GO:0008152: metabolic process	0.025
	GO:0019219: regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.025
	GO:0010468: regulation of gene expression	0.025
	GO:0007049: cell cycle	0.039
<i>PtaGRF</i> (70 Genes)	GO:0045449: regulation of transcription	0.045
	GO:0080090: regulation of primary metabolic process	0.029
	GO:0019222: regulation of metabolic process	0.029
	GO:0031326: regulation of cellular biosynthetic process	0.029
	GO:0031323: regulation of cellular metabolic process	0.029
	GO:0044249: cellular biosynthetic process	0.029
<i>PtaEBF1</i> (49 Genes)	GO:0045449:regulation of transcription	0.029
	GO:0031326: regulation of cellular biosynthetic process	6.20E-05
	GO:0031323: regulation of cellular metabolic process	6.20E-05
	GO:0045449: regulation of transcription	6.50E-05
	GO:0010468: regulation of gene expression	6.50E-05
	GO:0019219: regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	6.50E-05
<i>PtaCDC2</i> (270 Genes)	GO:0051171: regulation of nitrogen compound metabolic process	0.00015
	GO:0044249: cellular biosynthetic process	0.00069
	GO:0055114: oxidation reduction	0.00078
	GO:0043687: post-translational protein modification	0.0046
	GO:0009059: macromolecule biosynthetic process	0.0046
	GO:0006950: response to stress	0.0046
	GO:0009987: cellular process	0.007
		0.007

<i>PtaXTH23</i> (31 Genes)	GO:0031326: regulation of cellular biosynthetic process	0.009
	GO:0031323: regulation of cellular metabolic process	0.017
	GO:0006807: nitrogen compound metabolic process	0.017
	GO:0045449: regulation of transcription	0.027
	GO:0006139: nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	

The number of genes connected to each hub is shown in the parenthesis. The agriGO tool (<http://bioinfo.cau.edu.cn/agriGO/>) was used to perform the enrichment analysis using SEA (Singular Enrichment Analysis) coupled with available background data of *Populus trichocarpa* genome data (V 3.0). Abbreviations for the eight hubs connected to *PtaJAZ3* and *PtaRAP2.6* are as follows: 1. *PtaCYCB2;4* (Cycline B2;4, Potri.005G251400); 2. *PtaSAUR37* (Small Auxin Upregulated RNA 37, Potri.006G278100); 3. *PtaARFA1F* (ADP-Ribosylation Factor A1F, Potri.008G100000); 4. *PtaGHI6* (Glycosyl Hydrolases family 16, Potri.006G071200); 5. *PtaGRF* (Gibberellin-Regulated Family protein, Potri.014G020100); 6. *PtaEBF1* (EIN3-Binding F-box protein1, Potri.006G068500); 7. *PtaCDC2* (Cell Division Control 2, Potri.004G133500) and 8. *PtaXTH23* (Xyloglucan Endotransglucosylase/Hydrolase 23, Potri.018G095100).