## Houyin Deng, Dehuo Hu, Ruping Wei, Shu Yan, Runhui Wang, Huiquan Zheng Global transcriptome analysis reveals genes associated with seedling advance growth traits in a selfed family of Chinese fir (Cunninghamia lanceolata)

## Supplementary Material

Databases	Number of annotated unigenes	Number of unannotated unigenes	Proportion of annotated unigenes
Non-redundant (Nr)	33,447	50,296	39.94%
Pfam	23,402	60,341	27.95%
Swiss-Prot	19,440	64,303	23.21%
Gene Ontology (GO)	19,091	64,652	22.80%
EuKaryotic Orthologous Groups (KOG)	16,606	67,137	19.83%
Clusters of Orthologous Groups (COG)	9,455	74,288	11.29%
Kyoto Encyclopedia of Genes and Genomes (KEGG)	6,593	77,150	7.87%

Table S1. The number and proportion of unigenes in databases

Table S2. The number of overlapped differentially expressed genes (DEGs) for significant modules (MEhoneydew1, MElavenderblush3, and MEorangered3) corresponding to group I, group II, and group III

Group	Number of DEGs in MEhoneydew1	Number of DEGs in MElavenderblush3	Number of DEGs in MEorangered3	Total number of DEGs
group I	118	4	30	152
group II	36	2	43	81
group III	147	2	19	168

Table S3. The annotation information of 23 overlapped differentially expressed genes (DEGs) all belonging to three groups

Gene ID	Gene name	Description
c161494.graph_c0	ERF071	Ethylene-responsive transcription factor ERF071
c93428.graph_c0	MYB-related 305	MYB-related protein 305-like
c162854.graph_c0	WRKY31	WRKY transcription factor 31
c129205.graph_c0	WRKY6	WRKY transcription factor 6
c167222.graph_c0	CESA8	Cellulose synthase A catalytic subunit 8
c159724.graph_c4	CESA9	Cellulose synthase A catalytic subunit 9
c157800.graph_c0	LAC4	Laccase-4
c140599.graph_c0	PER3	Peroxidase 3
c150189.graph_c0	GMPP	Probable mannose-1-phosphate guanylyltransferase 3
c168594.graph_c0	NRT	High-affinity nitrate transporter 2.2
c169030.graph_c1	GAMT2	Gibberellic acid methyltransferase 2
c161342.graph_c1	GID1	Gibberellin receptor GID1 [EC:3] (A)
c142768.graph_c0	PR1	Pathogenesis-related protein 1
c156848.graph_c0	PR10	Pathogenesis-related protein 10
c166470.graph_c3	TIR/NBS/LRR	Putative TIR/NBS/LRR disease resistance protein
c174736.graph_c0 c171750.graph_c0 c149953.graph_c0	CYP707A1 CYP716B1 CYP76B10	Cytochrome P450 716B1 Geraniol 8-hydroxylase
c168337.graph_c0	CYP77A1	Cytochrome P450 77A1
c160195.graph_c0	CYP77A3	Cytochrome P450 77A3
c149389_graph_c0	CYP82C4	Cytochrome P450 82C4
c170705.graph_c0	CYP86B1	Cytochrome P450 86B1
c162370.graph_c0	CYP86B1-2	Cytochrome P450 86B1

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Fig. S1. Radial barchart visualizing the seedling height of cx569 selfed family (n=210) at 5 months old. Gray barcharts represent seedling height from each of samples. The inside of the circle shows the legend with a specific seedling height value. The number outside the barcharts indicate the sample number. The AD (A1, A2, and A3) and DE (D1, D2, and D3) are selected by using the random function of Microsoft Excel. These variants displayed in the corresponding sample number. Seedlings with the same mean seedling height are also marked. The arrow represents AD and DE variants with the corresponding sample number







Fig. S3. The number of annotated and unannotated differentially expressed genes (DEGs) in different groups







