

**Gene expression and proteomic analysis of shoot apical meristem transition from dormancy to activation in  
*Cunninghamia lanceolata* (Lamb.) Hook.**

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Table S1 Differentially expressed proteins identified by LC-MS<sup>E</sup>

Accession no.	Protein name	Log R/D bud	P value	Log A/ D bud	P value	Log A/ R bud	P value
<b>Amino acid metabolism</b>							
ABK24266.1	Putative uncharacterized protein	inf	0.31	#N/A	#N/A	-1.87	0.29
ABR17712.1	Putative uncharacterized protein	inf	0.18	inf	0.21	-1.75	0.10
ABK22122.1	Putative uncharacterized protein	1.03	0.00	1.31	0.19	0.28	0.63
ACN39946.1	Putative uncharacterized protein	-0.77	0.56	0.84	0.21	1.61	0.17
CAA53078.1	3-ketoacyl-coa thiolase B	0.73	0.65	-1.30	0.41	-2.03	0.40
Q9FVG7.1	S-adenosylmethionine synthetase 2	2.31	0.01	2.27	0.00	-0.04	0.88
<b>Carbon metabolic process</b>							
AAM81204.1	Fructose-1,6-diphosphate aldolase	1.74	0.09	1.77	0.02	0.03	0.95
ACU23111.1	Fructose-bisphosphate aldolase	-1.60	0.13	0.17	0.58	1.77	0.10
ACU21446.1	Fumarylacetoacetase	1.06	0.06	-0.54	0.68	-1.60	0.15
CAC80374.1	Glyceraldehyde-3-phosphate dehydrogenase	1.87	0.17	2.27	0.00	0.40	0.49
AAA34077.1	Glyceraldehyde-3-phosphate dehydrogenase	2.63	0.10	1.48	0.43	-1.15	0.30
ABP68613.1	Malic enzyme	-3.34	0.09	-inf	0.13	#N/A	#N/A
AAP68889.1	Putative glyoxysomal malate dehydrogenase	inf	0.24	#N/A	#N/A	-1.48	0.41
BAF46028.1	Putative Adomet decarboxylase	2.09	0.01	1.98	0.00	-0.12	0.68
XP_002520198.1	Pyruvate dehydrogenase, putative	-1.30	0.11	-1.49	0.06	-0.19	0.87
XP_002520198.1	Pyruvate dehydrogenase, putative	-1.30	0.11	-1.49	0.06	-0.19	0.87
AAT80327.1	UDP-D-glucuronate decarboxylase	3.58	0.01	3.27	0.04	-0.31	0.52
<b>Cytoskeleton</b>							
O81982.1	Profilin	-2.14	0.33	-inf	0.37	#N/A	#N/A
EEC74344.1	Tubulin beta-2 chain	0.96	0.11	1.31	0.12	0.34	0.57
XP_002283198.1	Putative uncharacterized protein	1.57	0.00	1.64	0.05	0.07	0.86
<b>Energy production and conversion</b>							
XP_001771011.1	Phosphoribulokinase	1.79	0.27	2.18	0.03	0.39	0.64
BAD45421.1	Putative cytosolic phosphoglycerate kinase 1	0.98	0.07	1.30	0.00	0.32	0.29
XP_002321126.1	Aconitate hydratase	inf	0.00	#N/A	#N/A	-2.37	0.01
Q43130.1	Enolase	-1.61	0.04	-1.62	0.04	0.00	0.99
CAF21946.1	ATP synthase beta subunit	-3.17	0.27	-inf	0.39	#N/A	#N/A
BAH73398.1	ATP synthase CF1 alpha subunit	1.26	0.35	1.60	0.34	0.35	0.78

Accession no.	Protein name	Log R/D bud	P value	Log A/ D bud	P value	Log A/ R bud	P value
<b>P31541.1</b>	ATP-dependent Clp protease ATP-binding subunit clpa homolog CD4A, chloroplastic	2.55	0.19	3.03	0.04	0.49	0.55
<b>AAC06385.1</b>	Early fruit mrna	inf	0.15	inf	0.17	-2.33	0.21
<b>CAJ42303.1</b>	VDAC-like porin	-1.42	0.31	-1.46	0.30	-0.04	0.97
<b>AAD03393.1</b>	ATPase beta subunit	-1.30	0.01	-1.11	0.01	0.18	0.48
<b>ABR16190.1</b>	Cyt_c_oxidase_su6a	-1.48	0.29	-1.11	0.40	0.37	0.76
<b>AAP80659.1</b>	Dynammin like Pr6(ADL6)	inf	0.19	#N/A	#N/A	-1.62	0.33
<b>AAR27291.1</b>	Peptidyl-prolyl cis-trans isomerase	-1.47	0.01	-1.03	0.03	0.44	0.32
<b>XP_002320625.1</b>	Succinyl-coa ligase beta-chain family protein	-3.09	0.01	-2.44	0.03	#N/A	#N/A
<b>XP_001765853.1</b>	Predicted protein	0.14	0.90	-1.29	0.40	-1.43	0.22
<b>Hormone metabolism</b>							
<b>AAP31311.2</b>	ABI3-interacting protein 1	-inf	0.01	-1.54	0.14	#N/A	#N/A
<b>AAP31312.2</b>	ABI3-interacting protein 2	-1.69	0.34	-1.92	0.29	#N/A	#N/A
<b>Nucleosome assembly</b>							
<b>ABK24519.1</b>	Putative uncharacterized protein	-inf	0.47	-3.43	0.43	#N/A	#N/A
<b>ABK26056.1</b>	Histone H2B	1.17	0.10	1.34	0.14	0.18	0.72
<b>BAE92289.1</b>	Putative histone H1	4.27	0.40	#N/A	#N/A	-inf	0.38
<b>Photosynthesis</b>							
<b>AAB41553.1</b>	6-phosphogluconate dehydrogenase, decarboxylating	inf	0.18	#N/A	#N/A	-3.30	0.05
<b>A4QK31.1</b>	Cytochrome f	3.37	0.10	2.68	0.21	-0.68	0.51
<b>BAH73335.1</b>	Cytochrome f	1.29	0.11	1.93	0.03	0.64	0.18
<b>CAB60127.1</b>	Cytosolic phosphoglucomutase	2.97	0.22	1.94	0.05	-1.03	0.47
<b>XP_002273783.1</b>	Lyceraldehyde-3-phosphate dehydrogenase B, chloroplastic isoform 2	1.41	0.29	1.80	0.01	0.39	0.56
<b>ACM51422.1</b>	Mg-protoporphyrin IX chelatase	2.21	0.03	1.70	0.32	-0.51	0.48
<b>XP_002307234.1</b>	O2 evolving complex 33kd family protein	-0.87	0.12	-1.91	0.06	-1.04	0.22
<b>NP_042469.1</b>	Photosystem II 44 kda protein	3.24	0.30	1.58	0.40	-1.67	0.37
<b>BAH73339.1</b>	Photosystem II CP47 chlorophyll apoprotein	4.10	0.26	2.86	0.08	-1.24	0.40
<b>AAx76828.1</b>	Photosystem II subunit A	inf	0.30	inf	0.20	-1.36	0.46
<b>ACA30289.1</b>	Putative ribulose-1,5-bisphosphate carboxylase/oxygenase activase alpha 2	5.34	0.04	5.16	0.38	-0.18	0.89
<b>AAA63163.1</b>	Ribulose 1,5-bisphosphate carboxylase activase isoform 1	3.28	0.00	2.78	0.41	-0.50	0.65

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AAG22772.1	Ribulose-1,5-biphosphate carboxylase/oxygenase large subunit	-0.08	0.96	#N/A	#N/A	-3.09	0.11
AAN71862.1	Ribulose-1,5-bisphosphate carboxylase	3.94	0.22	3.49	0.02	-0.45	0.65
AAW29427.1	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	inf	0.15	#N/A	#N/A	-2.47	0.16
AAL11902.1	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	3.11	0.28	1.62	0.33	-1.48	0.42
AAS88137.1	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	1.86	0.07	1.65	0.17	-0.21	0.76
<b>Redox regulation</b>							
ABK23157.1	Putative uncharacterized protein	2.68	0.05	1.32	0.61	-1.36	0.27
XP_002283310.1	Mitochondrial-processing peptidase subunit alpha	-2.81	0.03	-1.93	0.09	#N/A	#N/A
CAB71293.1	Chloroplast ferredoxin-NADP+ oxidoreductase	1.26	0.10	1.35	0.01	0.09	0.81
AAQ14591.1	Copper/zinc superoxide dismutase	-2.42	0.20	-2.18	0.21	0.24	0.73
XP_002528162.1	Glycine cleavage system h protein, putative	-inf	0.14	-2.52	0.15	#N/A	#N/A
CAN63539.1	Hypothetical protein VITISV_016625	2.47	0.07	1.73	0.14	-0.75	0.26
AAA96137.1	Peroxidase	#N/A	#N/A	0.16	0.94	1.47	0.58
ACD56608.1	Putative protein disulfide	-1.78	0.36	-1.93	0.34	-0.16	0.89
ACN39940.1	Putative uncharacterized protein	-1.60	0.32	-1.12	0.41	0.49	0.10
ABK24614.1	Putative uncharacterized protein	-1.40	0.01	-1.22	0.01	0.18	0.66
ABR16663.1	Putative uncharacterized protein	2.28	0.01	2.13	0.04	-0.16	0.70
ABR16034.1	Putative uncharacterized protein	-1.50	0.56	#N/A	#N/A	-inf	0.18
ABK21331.1	Putative uncharacterized protein	-1.35	0.03	-1.52	0.04	-0.17	0.69
ABR16661.1	Putative uncharacterized protein	#N/A	#N/A	1.35	0.40	inf	0.30
XP_001785162.1	Putative uncharacterized protein	0.73	0.28	-0.56	0.62	-1.29	0.06
EEE62118.1	Glutathione_s-trfase_n	-4.60	0.44	#N/A	#N/A	-inf	0.30
AAK27264.1	Isoflavone reductase-like protein CJP-6	-1.43	0.13	-1.81	0.11	-0.38	0.07
<b>Ribosome assembly</b>							
ACN40331.1	Cyanate hydratase	-1.52	0.37	-2.17	0.29	-0.65	0.52
XP_002510412.1	Protein yrdA, putative	-2.05	0.01	-3.05	0.01	-1.00	0.53
ABB87125.1	Ribosomal_S11	1.21	0.17	1.49	0.08	0.28	0.47
ABR17947.1	Putative uncharacterized protein	2.48	0.03	2.65	0.01	0.18	0.59
EEH59263.1	Predicted protein	inf	0.27	#N/A	#N/A	-3.21	0.25
<b>Stress response</b>							
AAR12193.1	Heat shock protein 90	2.21	0.23	0.27	0.90	-1.93	0.26
XP_002517727.1	Cationic peroxidase 1 precursor, putative	-4.18	0.35	-5.26	0.33	-1.08	0.49

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ACT82479.1	Chloroplast stromal ascorbate peroxidase 12	-1.42	0.13	-1.85	0.06	-0.44	0.57
XP_001760558.1	Cysteine_dsase	-2.01	0.09	-3.61	0.02	-1.60	0.12
ACN60402.1	Flavanone 3-beta-hydroxylase	#N/A	#N/A	1.79	0.45	2.34	0.38
ABQ96600.1	Glutathione peroxidase	-0.89	0.12	-2.39	0.03	-1.50	0.21
ABJ80949.1	Hsp90	inf	0.10	inf	0.26	-2.01	0.11
Q9STX5.1	Endoplasmin homolog	1.50	0.07	1.57	0.15	0.07	0.90
XP_002447413.1	Hypothetical protein SORBIDRAFT_06g000660	2.10	0.06	2.13	0.12	0.03	0.96
BAA93024.1	Putative phosphogluconate dehydrogenase	inf	0.18	inf	0.20	-2.04	0.22
ABK25734.1	Putative uncharacterized protein	inf	0.18	#N/A	#N/A	1.99	0.54
ABK24283.1	Putative uncharacterized protein	2.10	0.04	2.68	0.13	0.59	0.51
ACN39800.1	Unknown	2.41	0.00	2.25	0.06	-0.15	0.72
ABK26682.1	Putative uncharacterized protein	0.56	0.40	1.62	0.16	1.06	0.29
<b>Translation</b>							
AAK85129.1	Elongation factor	1.62	0.01	1.60	0.24	-0.02	0.98
CAA11705.1	Elongation factor 1 alpha subunit	2.84	0.02	2.88	0.21	0.04	0.96
XP_002312029.1	Elongation factor 1-alpha	2.45	0.07	2.77	0.22	0.32	0.72
BAD26337.1	Elongation factor 2	2.31	0.08	1.37	0.01	-0.94	0.13
AAS58429.1	Elongation factor Tu	3.26	0.02	2.77	0.01	-0.49	0.30
BAD07825.1	Putative 60S ribosomal protein L9	4.54	0.00	4.52	0.00	-0.02	0.95
BAE92290.1	Putative elongation factor	-2.00	0.28	-2.41	0.24	-0.41	0.75
CAC27139.1	Translation elongation factor-1 alpha	3.16	0.01	3.08	0.17	-0.07	0.93
<b>Transporter activity</b>							
NP_001065986.1	Non-specific lipid-transfer protein 2B	0.64	0.43	1.82	0.34	1.18	0.44
1109190A	Calmodulin	-2.61	0.37	-2.55	0.38	0.06	0.91
P02662.2	Antioxidant peptide	-inf	0.06	-1.59	0.18	#N/A	#N/A
XP_002528311.1	Clathrin heavy chain, putative	inf	0.21	#N/A	#N/A	-1.74	0.33
BAF08021.2	Os02g0184200	3.31	0.34	#N/A	#N/A	-2.36	0.34
XP_002456080.1	Putative uncharacterized protein Sb03g030060	-0.81	0.27	-1.50	0.17	-0.69	0.67
XP_002310404.1	Uncharacterized protein	inf	0.27	#N/A	#N/A	-1.49	0.44
ABR17902.1	Putative uncharacterized protein	-2.83	0.03	-2.55	0.03	0.29	0.26
<b>Unknown</b>							
XP_002276912.1	Hypothetical protein isoform 2	2.09	0.04	2.98	0.15	0.89	0.43

Accession no.	Protein name	Log R/D bud	P value	Log A/ D bud	P value	Log A/ R bud	P value
<b>XP_002531232.1</b>	Transcription factor, putative	-inf	0.19	-1.78	0.29	#N/A	#N/A
<b>ACN40912.1</b>	Uncharacterized protein	inf	0.01	#N/A	#N/A	-2.33	0.02
<b>ACN40697.1</b>	Unknown	-1.40	0.12	-1.56	0.07	-0.16	0.83
<b>ACU20577.1</b>	Unknown	-1.85	0.15	-1.65	0.11	0.20	0.78
<b>ACN40685.1</b>	Unknown	-1.79	0.20	-2.52	0.20	-0.73	0.45
<b>ACN40755.1</b>	Unknown	3.98	0.21	#N/A	#N/A	-inf	0.30
<b>ACN41066.1</b>	Unknown	-2.82	0.01	-inf	0.04	#N/A	#N/A
<b>ACJ85785.1</b>	Unknown	2.63	0.00	2.88	0.05	0.25	0.64
<b>ACN40584.1</b>	Unknown	2.19	0.17	2.40	0.28	0.21	0.84
<b>ACU23974.1</b>	Unknown	1.10	0.42	1.50	0.29	0.40	0.72
<b>ABR18217.1</b>	Putative uncharacterized protein	1.28	0.38	1.47	0.47	0.19	0.90
<b>ABK26810.1</b>	Unknown	1.48	0.07	1.45	0.24	-0.03	0.96
<b>ACN40726.1</b>	Unknown	-2.15	0.16	-1.49	0.21	0.66	0.67
<b>ACN40616.1</b>	Unknown	-0.96	0.02	-1.51	0.05	-0.55	0.45
<b>CAO65998.1</b>	Unnamed protein product	2.56	0.01	2.13	0.21	-0.42	0.56
<b>CAV26532.1</b>	Unnamed protein product	1.60	0.02	1.48	0.26	-0.12	0.87
<b>CAY34137.1</b>	Unnamed protein product	-2.89	0.31	-2.08	0.37	0.81	0.73
<b>CAO43976.1</b>	Unnamed protein product	-2.05	0.42	-2.19	0.42	-0.13	0.86
<b>CAW84864.1</b>	Unnamed protein product	-5.04	0.01	-3.92	0.00	1.12	0.39
<b>CAY38961.1</b>	Unnamed protein product	3.30	0.00	2.76	0.40	-0.54	0.62
<b>CAV26040.1</b>	Unnamed protein product	3.58	0.04	2.69	0.22	-0.89	0.34
<b>CAV25021.1</b>	Unnamed protein product	-2.87	0.42	-3.80	0.39	-0.93	0.19

Note: R, reactivating bud; D, dormant bud; A, active bud. The fold-change of different stages of bud described by log scale (1.3-fold-change). The positive and negative value represents that the fold-change of up-regulated and down-regulated differential proteins, respectively.