Supplementary Table S5. Functional classification according to gene ontology (GO) of proteins that were significantly differentially expressed between isogenic embryonal mass (EM) and non-embryogenic callus (NEC) of all three Douglas-fir genotypes. Total number of proteins annotated to each GO term indicated in the first column and corresponding percentage in the second column.

	EM		NEC	
_	No	%	No	%
Biological regulation (GO:0065007)	7	2.0	5	2.5
Cellular component organization or biogenesis				
(GO:0071840)	24	6.9	8	4.0
Cellular process (GO:0009987)	83	24.0	33	16.7
Cellular component movement (GO:0006928)	4	1.2	2	1.0
Cytokinesis (GO:0000910)	2	0.6	0	0.0
Cell cycle (GO:0007049)	7	2.0	3	1.5
Chromosome segregation (GO:0007059)	4	1.2	2	1.0
Cell communication (GO:0007154)	4	1.2	3	1.5
Developmental process (GO:0032502)	3	0.9	3	1.5
Localization (GO:0051179)	34	9.4	5	2.5
Protein localization (GO:0008104)	4	1.2	0	0.0
Transport (GO:0006810)	34	9.8	5	2.5
Metabolic process (GO:0008152)	106	30.6	72	36.4
Phosphate-containing compound metabolic process				
(GO:0006796)	24	6.9	2	1.0
Biosynthetic process (GO:0009058)	21	6.1	13	6.6
Vitamin metabolic process (GO:0006766)	0	0.0	3	1.5
Primary metabolic process (GO:0044238)	102	29.5	59	29.8
Catabolic process (GO:0009056)	26	7.5	11	5.6
Sulfur compound metabolic process (GO:0006790)	6	1.7	8	4.0
Coenzyme metabolic process (GO:0006732)	1	0.3	6	3.0
Nitrogen compound metabolic process (GO:0006807)	36	10.4	14	7.1
Generation of precursor metabolites and energy				
(GO:0006091)	5	1.4	12	6.1
Secondary metabolic process (GO:0019748)	1	0.3	3	1.5
Response to stimulus (GO:0050896)	8	2.3	9	4.5
Response to stress (GO:0006950)	6	1.7	8	4.0
response to abiotic stimulus (GO:0009628)	1	0.3	0	0.0
Response to endogenous stimulus (GO:0009719)	1	0.3	0	0.0
Immune response (GO:0006955)	1	0.3	0	0.0
Immune system process (GO:0002376)	1	0.3	0	0.0
Unclassified	80	23.1	63	31.8