



## Supplementary Material

**Table S1.** Proteins differentially accumulated in *Pinus halepensis* EMs induced under different temperatures treatments, according to the Kruskal-Wallis test ( $p < 0.05$ ) and Dunn's test of multiple comparisons (Benjamini-Hochberg  $p$ -value adjustment): Cond1 = 23 °C; Cond2: 40 °C (4 h); Cond3: 50 °C (30 min); Cond4: 60 °C (5 min).

Protein	Uniprot Accession	Species	Dunn's Test of Multiple Comparisons			Kruskal-Wallis
			Cond2/Cond1	Cond3/Cond1	Cond4/Cond1	$p$ - value
Citrate synthase, mitochondrial	O80433	<i>Daucus carota</i>	0.350	0.056	0.003	0.004
Aconitate hydratase, cytoplasmic	P49608	<i>Cucurbita maxima</i>	0.017	0.002	0.081	0.006
NADP-dependent malic enzyme 3	Q9XGZ0	<i>Arabidopsis thaliana</i>	0.069	0.478	0.056	0.006
Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1	Q9SYM5	<i>Arabidopsis thaliana</i>	0.275	0.061	0.021	0.009
Agglutinin	P06750	<i>Ricinus communis</i>	0.026	0.018	0.006	0.011
Protein kinase G11A	Q0DCT8	<i>Oryza sativa</i> subsp. <i>japonica</i>	0.080	0.017	0.007	0.014
Polyadenylate-binding protein RBP47	Q9LEB3	<i>Nicotiana glauca</i>	0.009	0.015	0.056	0.015
Molybdenum cofactor sulfurase	Q8LGM7	<i>Solanum lycopersicum</i>	0.116	0.010	0.014	0.016
Actin-depolymerizing factor 10	Q9LQ81	<i>Arabidopsis thaliana</i>	0.188	0.017	0.015	0.017
40S ribosomal protein S15a-1	P42798	<i>Arabidopsis thaliana</i>	0.129	0.118	0.116	0.018
20 kDa chaperonin, chloroplastic	O65282	<i>Arabidopsis thaliana</i>	0.011	0.025	0.028	0.018
NADPH--cytochrome P450 reductase 1	Q9SB48	<i>Arabidopsis thaliana</i>	0.181	0.006	0.072	0.019
Eukaryotic translation initiation factor 2 subunit beta	Q41969	<i>Arabidopsis thaliana</i>	0.016	0.015	0.144	0.019
Histone H4 variant TH091	P62786	<i>Triticum aestivum</i>	0.352	0.061	0.033	0.023
Histone H2A.2.2	P02277	<i>Triticum aestivum</i>	0.139	0.020	0.015	0.023
Dynamitin-related protein 12A	Q39821	<i>Glycine max</i>	0.139	0.015	0.020	0.023
Probable fructokinase-7	Q9FLH8	<i>Arabidopsis thaliana</i>	0.027	0.025	0.017	0.024

Pyruvate dehydrogenase E1 component subunit beta-4. chloroplastic	Q10G39	<i>Oryza sativa</i> subsp. <i>japonica</i>	0.403	0.048	0.033	0.025
Chaperonin CPN60. mitochondrial	P35480	<i>Brassica napus</i>	0.007	0.130	0.097	0.025
6-phosphogluconate dehydrogenase. decarboxylating 1	Q9LI00	<i>Oryza sativa</i> subsp. <i>japonica</i>	0.401	0.129	0.018	0.026
60S ribosomal protein L18-3	Q940B0	<i>Arabidopsis thaliana</i>	0.380	0.049	0.069	0.028
Chalcone synthase	P30079	<i>Pinus sylvestris</i>	0.075	0.162	0.012	0.031
Diacylglycerol O-acyltransferase 1	Q9SLD2	<i>Arabidopsis thaliana</i>	0.021	0.038	0.037	0.032
Glutathione reductase. cytosolic	P48642	<i>Oryza sativa</i> subsp. <i>japonica</i>	0.071	0.043	0.455	0.032
Pyruvate dehydrogenase E1 component subunit beta-1. mitochondrial	Q6Z1G7	<i>Oryza sativa</i> subsp. <i>japonica</i>	0.060	0.064	0.015	0.034
Glutamyl-tRNA(Gln) amidotransferase subunit B. chloroplastic/mitochondrial	Q2R2Z0	<i>Oryza sativa</i> subsp. <i>japonica</i>	0.160	0.021	0.032	0.036
25.3 kDa vesicle transport protein	Q94AU2	<i>Arabidopsis thaliana</i>	0.056	0.024	0.029	0.036
Ubiquitin carboxyl-terminal hydrolase 13	Q84WU2	<i>Arabidopsis thaliana</i>	0.045	0.287	0.171	0.037
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A gamma isoform	Q38951	<i>Arabidopsis thaliana</i>	0.093	0.162	0.204	0.038
3-isopropylmalate dehydrogenase. chloroplastic	P29696	<i>Solanum tuberosum</i>	0.385	0.061	0.049	0.038
Alcohol dehydrogenase	P17648	<i>Fragaria ananassa</i>	0.321	0.097	0.056	0.041
Carbamoyl-phosphate synthase large chain. chloroplastic	B9EXM2	<i>Oryza sativa</i> subsp. <i>japonica</i>	0.401	0.072	0.040	0.042
Transcription factor TGA5	Q39163	<i>Arabidopsis thaliana</i>	0.058	0.098	0.520	0.042
40S ribosomal protein S12	Q9XHS0	<i>Hordeum vulgare</i>	0.031	0.049	0.162	0.049

**Table S2.** One-way analysis of variance for expression of different transcripts detected in *P. halepensis* embryonal masses induced under different temperature conditions (23 °C, 9 weeks; 40 °C, 4 h; 50 °C, 30 min; 60 °C, 5 min).

Kruskal-Wallis	df	X <sup>2</sup> test	p Value
20 KDA CHAPERONIN (CPN20)	3	0.5245	n.s. <sup>1</sup>
CHAPERONIN CPN60 (CPN60)	3	0.0745	n.s.
CITRATE SYNTHASE (PDHB)	3	0.2167	n.s.
PYRUVATE DEHYDROGENASE E1 COMPONENT SUBUNIT BETA- 1	3	0.1841	n.s.
6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING 1 (G6PGH1)	3	0.2401	n.s.
PYRUVATE DEHYDROGENASE E1 COMPONENT SUBUNIT BETA-4	3	0.8395	n.s.
TRIFUNCTIONAL UDP-GLUCOSE 4,6-DEHYDRATASE/UDP-4-KETO-6DEOXY-D-GLUCOSE 3,5-EPIMERASE/UDP-4-KETO-L-RHAMNOSE-REDUCTASE RHM1 (RHM1)	3	0.5921	n.s.
NADPH-CYTOCHROME P450 REDUCTASE 1 (ATR1)	3	0.5959	n.s.
PROBABLE FRUCTOKINASE-7	3	0.6958	n.s.

<sup>1</sup> not statistically significant.**Table S3.** One-way analysis of variance for concentration of sugars (μmol g<sup>-1</sup> FW) detected in *P. halepensis* embryonal masses induced under different temperature conditions (23 °C, 9 weeks; 40 °C, 4 h; 50 °C, 30 min; 60 °C, 5 min).

Sugars	df	F value	p value
Sucrose	3	3.7320	0.0330
Glucose	3	1.1930	n.s. <sup>1</sup>
Fructose	3	1.8890	n.s.
Mannitol	3	0.9782	n.s.
Sorbitol	3	0.1167	n.s.

<sup>1</sup> not statistically significant.

**Table S4.** One-way analysis of variance for concentration of amino acids ( $\mu\text{mol g}^{-1}$  FW) detected in *P. halepensis* embryonal masses induced under different temperature treatments (23 °C, 9 weeks; 40 °C, 4 h; 50 °C, 30 min; 60 °C, 5 min).

Amino acids			
ANOVA	df	F value	p value
Aspartic acid	3	0.4546	n.s. <sup>1</sup>
Glutamic acid	3	0.5485	n.s.
Asparagine	3	1.6030	n.s.
Serine	3	0.8004	n.s.
Glutamine	3	4.4920	0.0181
Histidine	3	0.5378	n.s.
Glycine	3	3.9470	0.0277
Threonine	3	0.8126	n.s.
Arginine	3	0.3369	n.s.
Alanine	3	1.8050	n.s.
Tyrosine	3	0.5632	n.s.
Cysteine	3	4.2780	0.0213
Valine	3	0.3568	n.s.
Metionine	3	0.5148	n.s.
Tryptophan	3	0.2859	n.s.
Phenilalanine	3	0.0708	n.s.
Isoleucine	3	0.2505	n.s.
Leucine	3	0.3126	n.s.
Lysine	3	0.5958	n.s.
Proline	3	0.4094	n.s.

<sup>1</sup> not statistically significant.