

Supplementary Table S2. Analysis of *lPT* and *DPT* promoters. One kb regions upstream of the ATG were examined for the presence of cis elements.

SAGE tag ID	GenBank Accession	Gene	Cis element [†]	GCC box GCCGCC	G box CACGTG	DRE box CCGAC	MYB binding site 1 ² : GTTAGTT	MYB binding site 2 ² : (C/A)TCC-(T/A)ACC	MYB binding site 3 ² : TAAC(C/G)GTT	W box TTGACC	as-1 element TGACG
Environmental/pathogen response (PR and antimicrobial genes, and drought and salt responsive genes)											
65	T04323	antifungal protein PDF1.2		310		666	965				445
212	U42724	chloroplast stromal cyclophilin ROO4				674(-)		121			
243	X78584	drought induced D119						766			
356	X98189	peroxidase ATP1a		981			221		783		
523	AF003728	salt-induced plasma membrane intrinsic protein SIMIP								845	752
617	AV527586	putative protein, disease resistance protein family (LRR)			662			611		648	655(-), 712(-)
634	BE038927	major latex protein (MLP)-related			948						114(-)
642	AA395048	thylakoid lumen rotamase				166	309(-), 377(-), 404(-), 469				832(-), 943(-)
854	U01880	hevein-like protein precursor (PR-4)		616						533	
Signal transduction (transcription factors, kinases, signaling molecules)											
347	AB013886	transcription factor RAV1			582			736(-)		303	
352	X91259	similar to putative lectin								146	649
423	U27698	putative calreticulin ALCRTL			282	175(-)					181
427	AJ242970	general transcription factor BTF3b homolog			535	293(-)					
503	AF285106	CBL-interacting protein kinase CIPK6		159 (-), 487	527	162 (-), 213(-), 345					633(-), 520(-)
844	AA598125	receptor-protein kinase-like protein					729(-)				518(-)
636	AV556265	putative M-type thioredoxin					171, 266				438(-), 672
842	U37697	glutathione reductase				786	94				
Fatty acid, phospholipid, and isoprenoid metabolism											
645	AB007799	NADH-cytochrome b5 reductase					925				246(-)
Energy metabolism and photosynthesis											
318	S74719	sedoheptulose-1,7-bisphosphatase			130						
321	L44582	vacuolar H ⁺ -pumping ATPase ava-p2				125					352(-)
422	X97484	putative phosphate transporter					657(-)				781(-)

640	Z29881	putative fructose 1,6-bisphosphatase		194	413, 408					301, 326(-)
834	AA598190	similar to rubisco activase		251						276
Ribosomal proteins										
275	A1100025	putative ribosomal protein L18								
317	AA728511	60S ribosomal protein L10A	424							354(-), 780(-)
355	AV549039	50S ribosomal protein L27							567(-)	133, 166
357	BE038325	ribosomal protein S13 -like				297(-), 368(-)				608
419	Y09635	50S ribosomal protein L24, chloroplast precursor	711(-)		686(-)					
506	T43594	60S ribosomal protein L38-like protein			636(-)					920
511	AA597822	putative 60S ribosomal protein L21								
Protein processing/rate										
635	AA712419	ATP-dependent Clp protease ATP-binding subunit (ClpC1)		685	695(-), 748(-), 891					
Membrane proteins										
210	Y08061	endomembrane-associated protein						992(-)		984, 882
242	AA728495	water channel - like protein						430(-)	850	
Other categories										
512	AF017074	RNA polymerase I, II and III 16.5 kDa subunit					533			710
Unknown proteins										
425	R90105	unknown protein	733	150	436(-), 839					130(-), 138, 958

¹The presence of a cis-element in a promoter is indicated by its distance in bp from the ATG site. Cis-elements found in the reverse orientation are shown with a (-).

²The nomenclature MYB binding sites 1, 2 and 3 has been used here to distinguish between the different sequences (see also Table 3).