



**Figure S1.** GUS-mediated *PAO3* expression pattern during heat stress. Representative images of histochemical GUS-stained transgenic plants harboring the constructs pVB765PAO3p, pVB479PAO3p and pVB252PAO3p. Shoot and root tissues (differentiation and meristematic zones) of control and heat treated 8-day-old seedlings showed similar expression levels, while root tips displayed a slight decrease in GUS staining.

**Supplementary Table S1:** Primers used in this study.

Primer name	Sequence
AtPAO3pdaF1-Sal	ATAGTCGACGGCATATAGTTTTCTCCGA
AtPAO3pdaF2-Sal	ATAGTCGACAGGATAGACTAGGCCTGCAT
AtPAO3pdaF3-Sal	ATAGTCGACGTACGTAACGACTAGCGAGT
AtPAO3pdaF4-Sal	ATAGTCGACGTAGGTTTCCGATTAAAGCGA
AtPAO3pdaF5-Sal	ATAGTCGACTTCGTTGATCTCTGTGGAAG
AtPAO3pdaR1-Bam	ATAGGATCCGATTCAACAATGAACGGAGT

**Table S2:** Putative TFBs identified within the regulatory sequence of the *AtPAO3* gene locus

Category	Motif	Consensus Sequence	Function	Position
ABA, Dehydration and Salinity responsive	MYBCORE	CNGTTR	Binding site for ATMYB1 and ATMYB2. ATMYB2 is involved in regulation of genes that are responsive to water stress in Arabidopsis.	-973, -863
	MYCCONSENSUSAT	CANNTG	MYC recognition site found in the promoters of the dehydration-responsive gene rd22 and many other genes in Arabidopsis. Binding site of ATMYC2 (previously known as rd22BP1)	-973, -919, -863, -842, -816, -743, -526
	MYCATERD1	CATGTG	MYC recognition sequence necessary for expression of erd1 (early responsive to dehydration) in dehydrated Arabidopsis.	-816
	MYB2CONSENSUSAT	YAACKG	MYB recognition site found in the promoters of the dehydration-responsive gene rd22 and many other genes in Arabidopsis.	-566
	GT1GMSCAM4	GAAAAA	"GT-1 motif" found in the promoter of soybean (Glycine max) CaM isoform, SCaM-4; Plays a role in pathogen- and salt-induced SCaM-4 gene expression.	-776, -449, -344
	WRKY71OS (WRKY TF interacts with ABAR which binds ABA)	TGAC	"A core of TGAC-containing W-box" of, e.g., Amy32b promoter; Binding site of rice WRKY71, a transcriptional repressor of the gibberellin signaling pathway. WRKYs are positive and negative regulators of abscisic acid signaling in aleurone cells.	-740, -529
	DPBFCOREDCDC3	ACACNNG	A novel class of bZIP transcription factors, DPBF-1 and 2 (Dc3 promoter-binding factor-1 and 2) binding core sequence; Found in the carrot (D.c.) Dc3 gene promoter; Dc3 expression is normally embryo-specific, and can be induced by ABA.	-527
	ABRE	ACGTG	ABA responsive elements	-643, -523
	DRE	A/GCCGAC/G or TACCGACAT	Dehydration responsive elements	-549, -331

Cell type/organ specific expression	GTGANTG10	GTGA	"GTGA motif" found in the promoter of the tobacco late pollen gene g10.	-969, -563, -530, -415
	TAAAGSTKST1	TAAAG	Target site for trans-acting StDof1 protein controlling guard cell-specific gene expression.	-828, -533, -462
	ROOTMOTIFTAPOX1	ATATT	Root specific expression	-800, -692
	SITEIIATCYTC	TGGGCY	"Site II element" found in the promoter regions of cytochrome genes (CytC-1, CytC-2) in Arabidopsis; Involvement of TCP-domain RT protein-binding elements in anther- and meristem-specific RT expression of the CytC-1 gene.	-729
	POLLEN1LELAT52	AGAAA	Pollen specific expression.	-778, -451, -346, -229, -216, -194
Phytohormone responsive	GT1CONSENSUS	GRWAAW	Consensus GT-1 binding site. Binding of GT-1-like factors to the PR-1a promoter influences the level of SA-inducible gene expression.	-776, -654, -449, -344
	WBOXATNPR1	TTGAC	"W-box" found in promoter of Arabidopsis thaliana (A.t.) NPR1 gene. They were recognized specifically by salicylic acid (SA)-induced WRKY DNA binding proteins.	-741
	T/GBOXATPIN2	AACGTG	"T/G-box" involves in jasmonate (JA) induction; bHLH-Leu zipper JAMYC2 and JAMYC10 proteins specifically recognize this motif.	-644
Conserved promoter motifs	CAATBOX1	CCAAT	CAAT-box	-397
	TATABOX3	TATTAAT	TATA-box	-351
Others	LTRE1HVBLT49	CCGAAA	"LTRE-1" (low-temperature-responsive element) in barley.	-991
	ANAERO1CONSENSUS	AAACAAA	One of 16 motifs found in silico in promoters of 13 anaerobic genes involved in the fermentative pathway	-772, -364



ACGTATERD1	ACGT	ACGT sequence required for etiolation-induced expression of <i>erd1</i> (early responsive to dehydration) in <i>Arabidopsis</i> .	-672, -643, -619, -527, -426
ABRERATCAL	MACGYGB	"ABRE-related sequence" or "Repeated sequence motifs" identified in the upstream regions of 162 $\text{Ca}^{(2+)}$ -responsive upregulated genes.	-644, -525
ABRELATERD1	ACGTG	ABRE-like sequence required for etiolation-induced expression of <i>erd1</i> (early responsive to dehydration) in <i>Arabidopsis</i> .	-643, -526
CURECORECR	GTAC	GTAC is the core of a CuRE (copper-response element) found in <i>Cyc6</i> and <i>Cpx1</i> genes in <i>Chlamydomonas</i>	-621
GADOWNAT	ACGTGTC	Sequence present in 24 genes in the GA-down regulated d1 cluster (106 genes) found in <i>Arabidopsis</i> seed germination; This motif is similar to ABRE. Common sequence found in the 5'-non-coding regions of eukaryotic genes; "CCAAT box" found in the promoter of heat shock protein genes; Located immediately upstream from the most distal HSE of the promoter; "CCAAT box" act cooperatively with HSEs to increase the hs promoter activity.	-522
CCAATBOX1	CCAAT	"CCAAT box" found in the promoter of heat shock protein genes; Located immediately upstream from the most distal HSE of the promoter; "CCAAT box" act cooperatively with HSEs to increase the hs promoter activity.	-397
AACACOREOSGLUB1	AACAAAC	Core of AACA motifs found in rice (O.s.) glutelin genes, involved in controlling the endosperm-specific expression.	-363
CANBNNAPA	CNAACAC	Core of "(CA) <sub>n</sub> element" in storage protein genes in <i>Brasica napus</i> (B.n.); embryo- and endosperm-specific transcription of napin (storage protein) gene, <i>napA</i> ; seed specificity; activator and repressor.	-361
SURE1STPAT21	AATAGAAAA	Sucrose Responsive Element (SURE); A motif conserved among genes regulated by sucrose.	-345
LTRECOREATCOR15	CCGAC	Core of low temperature responsive element (LTRE) of <i>cor15a</i> gene in <i>Arabidopsis</i> (A.t.); A portion of repeat-C (C-repeat), TGGCCGAC, which is repeated twice in <i>cor15a</i> promoter (Baker et al., 1994); ABA responsiveness.	-331

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