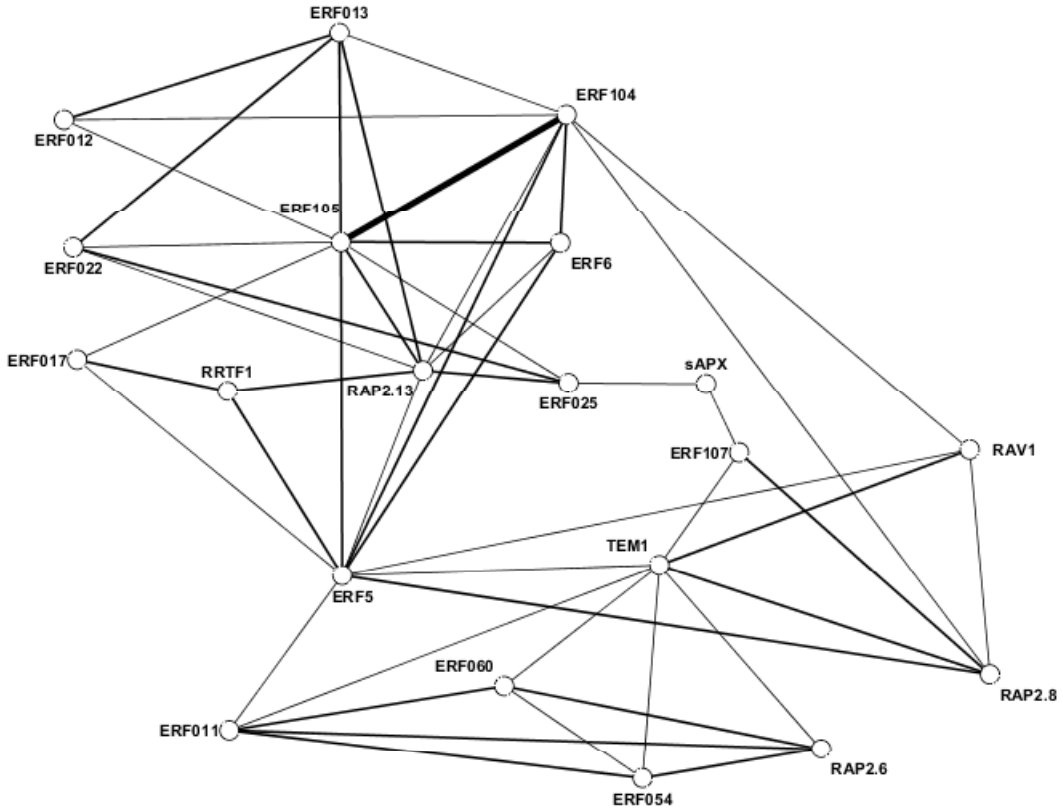
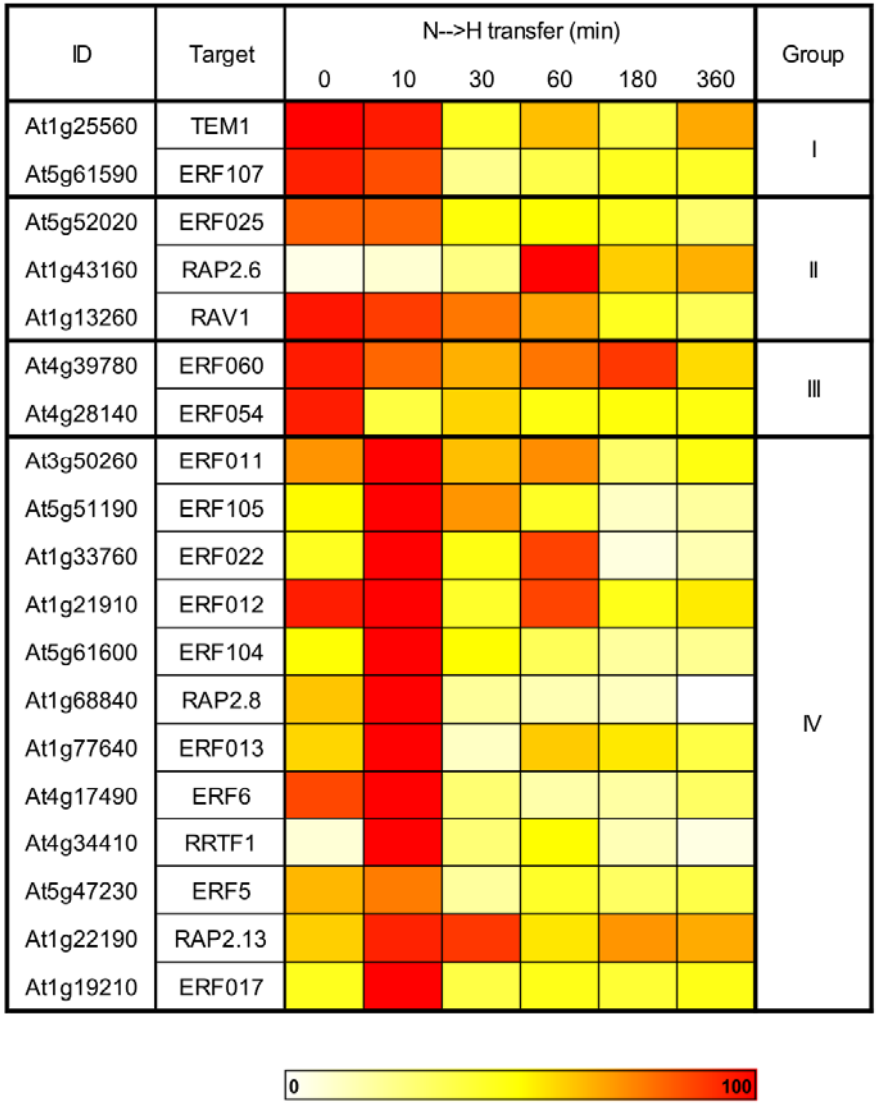
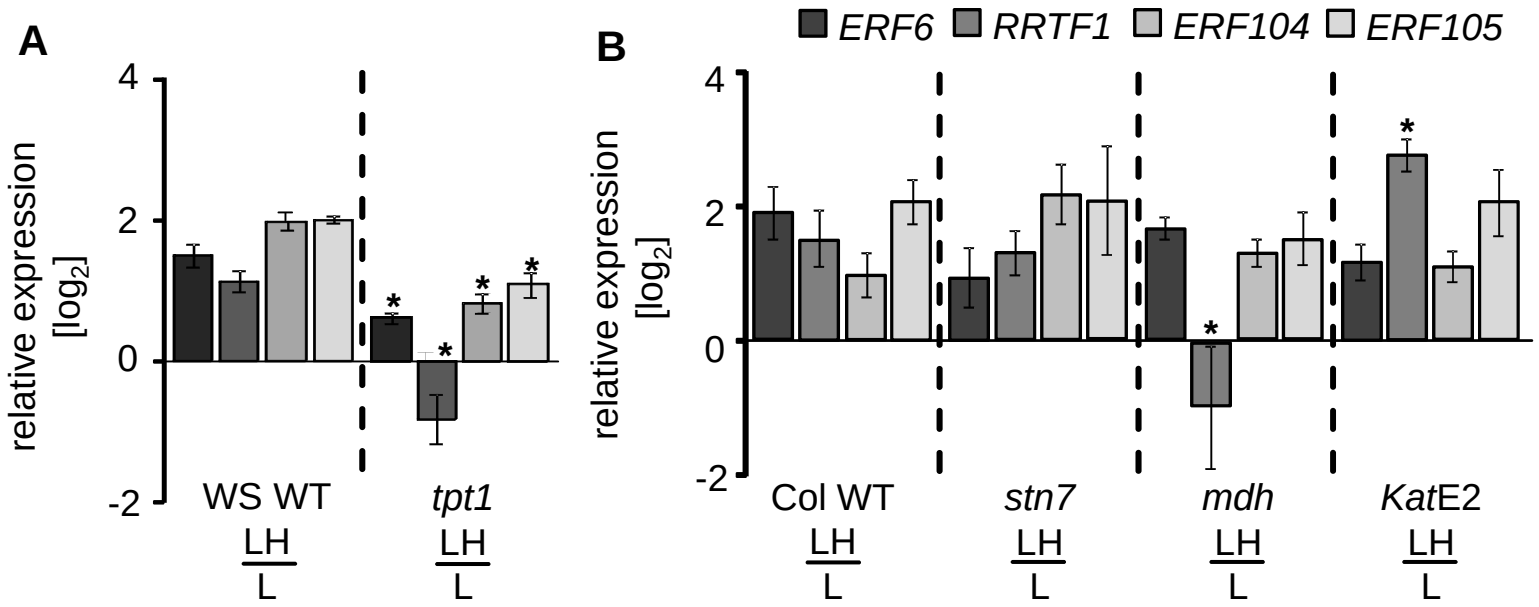


Supplemental Figure 1: Potential H-light responsive co-expression network of AP2/ERF-TFs.

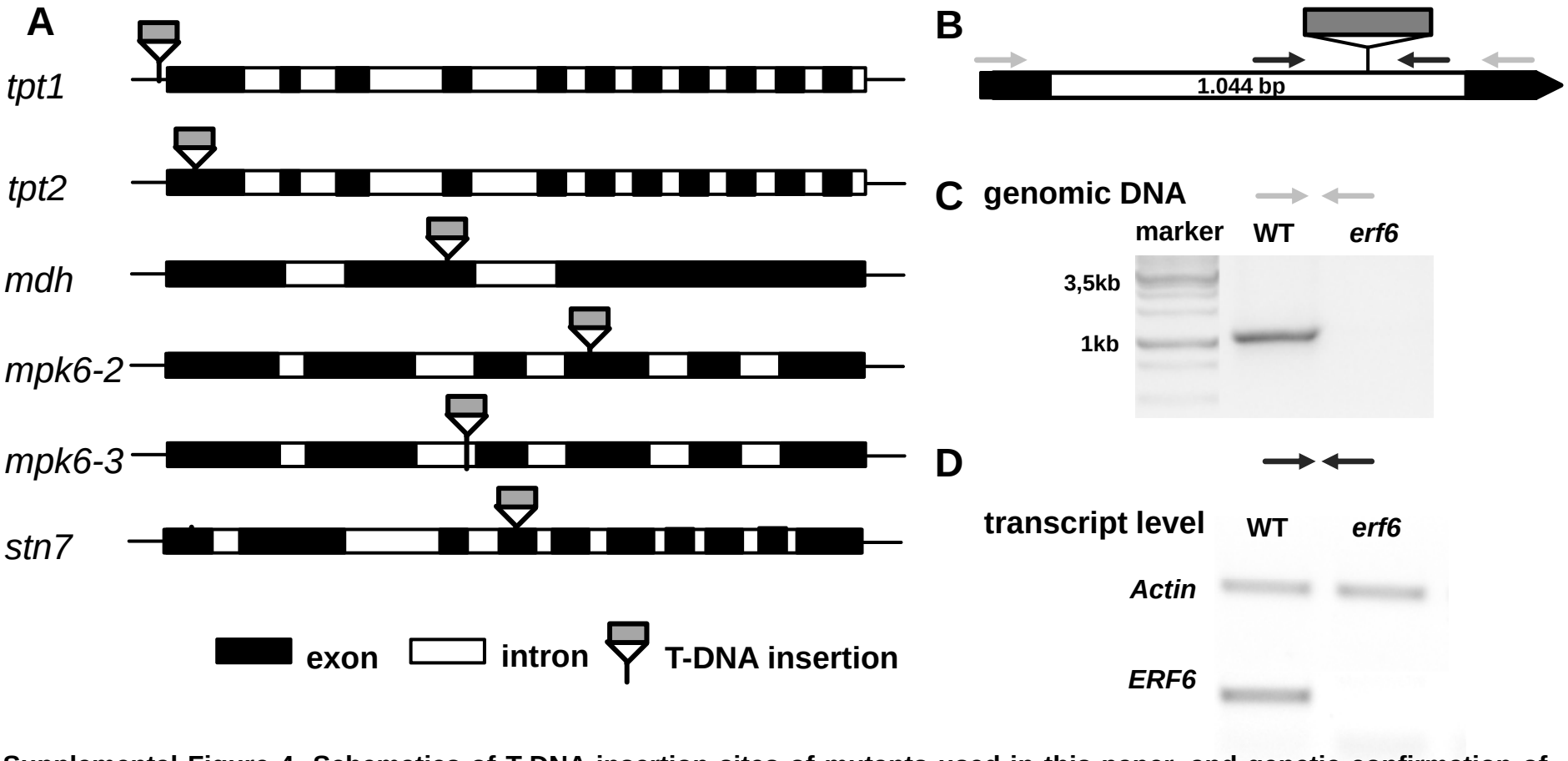
The co-expression network of AP2/ERF-TFs was constructed with two co-expression tools, ACT (Manfield *et al.*, 2006) and ExpressionAngler (Toufighi *et al.*, 2005). The network consists of 19 AP2/ERF-TFs and the *sAPX* as HL-responsive gene. The thickness of the lines corresponds to the degree of co-expression. The cut-off of interaction was set to Pearson value r=0.4. Overall 29 interactions were medium (0.5>r>0.7) or strong (r>0.7) and 21 weak (0.4>r<0.5).



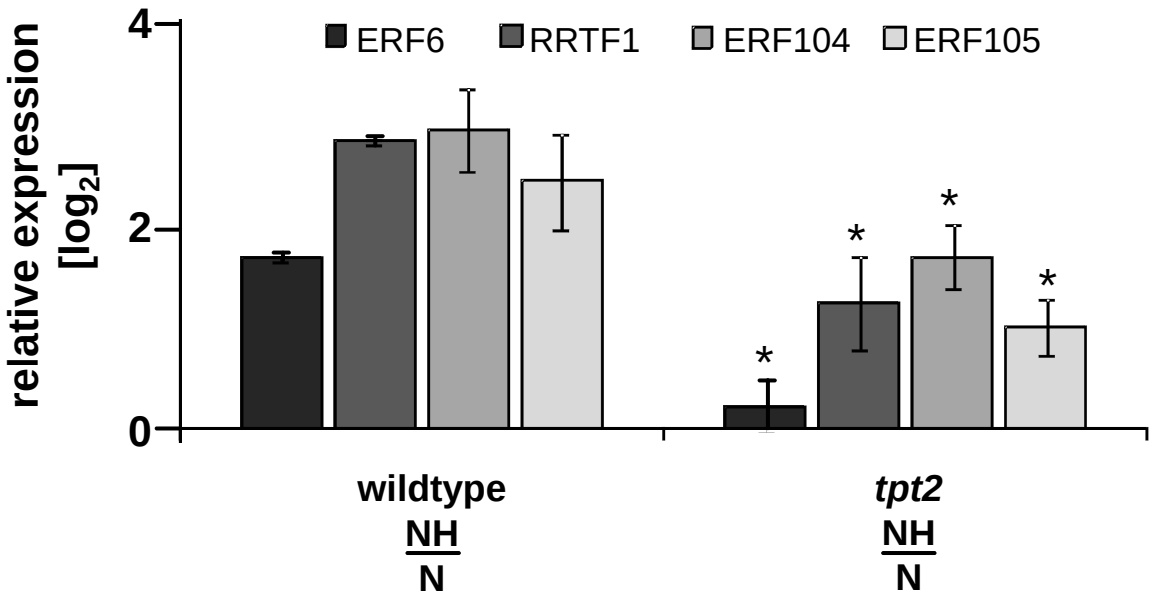
Supplemental Figure 2: Transcript regulation of AP2/ERF-TFs in N-light grown plants in response to H-light treatment. The network members as classified above in Fig. 1A were analyzed for transcript levels in dependence on time after the N→H shift. The data are means of 3 independent experiments with duplicate determinations by RT-PCR.



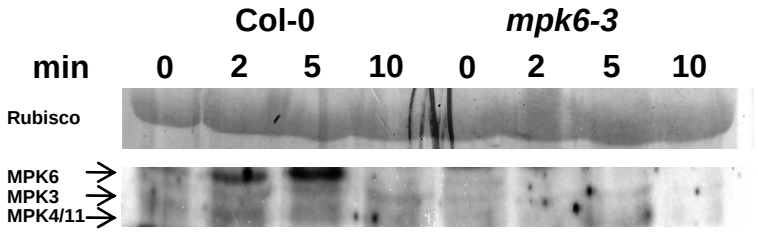
Supplemental Figure 3: Comparison of AP2/ERF-TF transcript levels in wildtype plants and mutants. *ERF6*, *RRTF1*, *ERF104* and *ERF105* transcript levels were quantified in wildtype plants and mutants defective in retrograde signalling pathways 10 min following the L→H-transfer. (A) Comparison between *tpt1* (Wassilewskija background) with Wassilewskija wildtype (WS WT) (B) Comparison between Columbia wildtype (Col WT), *stn7*, *mdh* and *KatE2*. and Col WT. Data represent ratios of transcript levels in L→H-plants relative to L-light-samples. (qPCR, n=3 independent experiments with duplicate determinations, mean±SE, asterisks indicate significant difference to the wildtype transcript level, Student`s t-test $p<0.05$).



Supplemental Figure 4: Schematics of T-DNA insertion sites of mutants used in this paper, and genetic confirmation of the *erf6* insertion mutant. (A) Schematics of T-DNA insertion sites in *tpt1*, *tpt2*, *mdh*, *mpk6-2*, *mpk6-3* and *stn7*. These mutants have been characterized in the respective publications as cited in the text. (B) Schematic view of the *ERF6* gene and position of used primers for confirmation PCRs. (C) Genomic DNA was used as template for PCR. The expected band of ~1 kb was detected in wildtype (WT) but not in the mutant. (D) A product could not be amplified in the *erf6* mutant following RNA isolation, cDNA-synthesis and subsequent RT-PCR with gene specific primers.

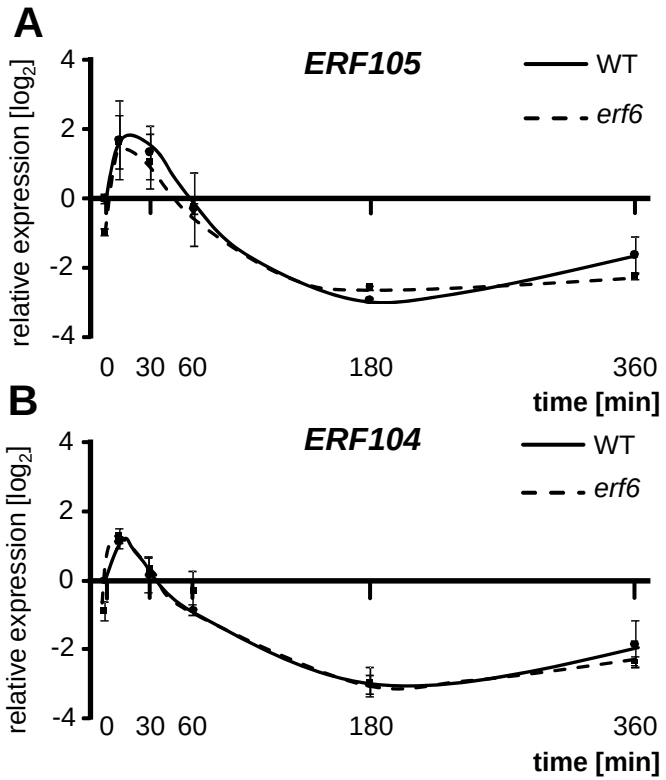


Supplemental Figure 5: Transcript abundances of AP2/ERF-TFs after 10 min of N→H in wildtype and *tpt2* mutant. To exclude possible starvation effects in L-light, transcript levels of the selected AP2/ERF-TFs were analyzed at t=10 min of N→H shift in the wildtype and the *tpt2* mutant. Deregulation as detected upon the L→H shift was observed for all selected TFs also in N→H shifted plants (qPCR, n=3 independent experiments with duplicate determinations, mean±SE, asterisks indicate significant difference, Student`s t-test $p<0.05$).



Supplemental Figure 6: Comparison of phosphorylation state of different MAPKs in wildtype and *mpk6* mutant plants. A representative immunoblot shows the assessment of phosphorylated MPK3, 4, 6 and 11 at different time points of L→H treatment. An increase of the phosphorylation state was observed for the MPK6 in wildtype but not in the *mpk6-3* mutant. Furthermore, no distinct activation was seen for the other detected MAPKs in both types of plants.

SFigure 7: Vogel et al.



Supplemental Figure 7: L→H-light response of ERF104 and ERF105 transcript level in *erf6* mutant. *ERF104* and *ERF105* display high Pearson co-regulation coefficients to *ERF 6* (r=0.665 and r=0.704). The RNA-levels of both AP2/ERF-TFs were similar in WT and *erf6* mutant during 6 hours of L→H stress (n=3 and 4 independent experiments with duplicate determinations, mean±SE).

Supplemental Table 1: Results of the single Chip hybridization. Hybridization was done with WT Col0 and *erf6* mutants at t=30 min of L→H shift.

Affymetrix Probeset ID	AT ID (gene locus)	Normalized log_2 value WT	Normalized log_2 value *erf6* mutant	Log_2 fold change	Annotation
256940_at	At3g30720	7.673209	10.29516	2.621949	unknown protein
248668_at	At5g48720	5.671278	7.119067	1.447788	unknown protein
255500_at	At4g02390	6.272786	7.667199	1.394413	NAD+ ADP-ribosyltransferase
261065_at	At1g07500	5.232255	6.622111	1.389856	hypothetical protein
252539_at	At3g45730	5.767702	6.991127	1.223426	putative protein
255872_at	At2g30360	5.712693	6.913678	1.200985	CBL inter. protein kinase 11
262719_at	At1g43590	4.496756	5.583848	1.087092	hypothetical protein
247615_at	At5g60250	4.382606	5.444821	1.062216	putative protein
246884_at	At5g26220	5.886007	4.880385	-1.005622	putative protein cation transport
254832_at	At4g12490	6.373779	5.358045	-1.015734	pEARLI 1-like protein
250296_at	At5g12020	9.075039	7.99411	-1.080929	heat shock protein 17.6-II
260556_at	At2g43620	5.521255	4.399725	-1.12153	putative endochitinase
261838_at	At1g16030	7.815173	6.682122	-1.13305	heat shock protein hsp70
260978_at	At1g53540	8.936294	7.593398	-1.342896	17.6 kDa heat shock protein
264960_at	At1g76930	5.201322	3.808407	-1.392915	extensin1
252265_at	At3g49620	6.457196	4.425243	-2.031953	putative protein SRG1 protein
266385_at	At2g14610	7.313099	5.247048	-2.066051	pathogenesis-related PR-1-like
250824_at	At5g05200	10.32994	8.023967	-2.305968	chloroplast protein kinase-like

Supplemental Table 2: Primers

Target gene	ID number	Forward Sequence (5' – 3')	Reverse Sequence (5' – 3')	T_A (°C)
RAV1	At1g13260	GATTCAGAGAACGGCGTAGA	CTTCGTCCATCTTCACGTCT	61
ERF013	At1g77640	GATCACCATCCATCTGCTTC	CATCGTTGCCTCTGAGCTAT	61
ERF017	At1g19210	GACGTAACTTGTCGCGATCT	AACGATCACCGGAGTATTCA	58
ERF012	At1g21910	AACCATTTTGCCCCTACTTC	GCATCGTCGTCGAGTTTAGT	61
RAP2.13	At1g22190	TTCCCTGATCTCCGTCATAA	ATCTCCTCCTCCGTATCACC	58
TEM1	At1g25560	CCGATGAGTTTGAGCAGAGT	TAATCAAAACGCCTTTCGTC	63
RAP2.6	At1g43160	ATGGTGTCTATGCTGACTAATGTTG	AGACTGAAGTTGTATTGGGACAGAA	61
ERF022	At1g33760	TGTCCTACAGAGGCATTCGT	TGTGCTCCGAACTAGAGCTT	62
HSP20-like	At1g53540	ATTTACCGGGACTGAGGAAG	AACCGACAACACACCATTTT	68
RAP2.8	At1g68840	CGGCGATTTAGCTTTTCTTG	CACGAGACGGTTTAGCTTCC	58
EXT1	At1g76930	CACCACCCAAGAAGCACTAC	AATTCTCCCGTCAACGATCT	61
PR1	At2g14610	CCTTACGGGGAAAACTTAGC	CATAATTCCCACGAGGATCA	56
CIPK	At2g30360	CCGTGAAAATCCTCAACAAG	CTTCGCTAAGACGTCCATGT	56
CHFP	At2g43620	TGGCTACCCTAAGAGCAATG	GTGGGATAGGTGTGGTTGAG	58
MPK6	At2g43790	GCTCATGGAGCTCATAGGAA	GCCAATGCGTCTAAAACTGT	58
Actin2	At3g18780	TTGGTAGGCCAAGACATCAT	GGAGCCTCGGTAAGAAGAAC	58
CEJ1	At3g50260	ACAAGCGTTCAAGACTTTGG	CCCCTATCGCATCTACTTGA	63
ERF6	At4g17490	TGAAACCAAACCGGAAATAA	TCTCCTCTGCTGCTACAACC	58
ERF054	At4g28140	TCGTTAGAGGCTTTCCCTTT	CTTCGTTGCGATGTAAGGTT	61
RRTF1	At4g34410	GAAGGATGTCTCGGCTGTAA	ACACGTGTGGCTCTTTTAGG	61
ERF060	At4g39780	CATGACCGCTCAGAAACTCT	CCGTAGTATCCATCCTCGTG	61
ChlPK-like	At5g05200	GAACGCATGGGAGCTACTTA	ATTGGCGTAGGGTCAACATA	56
ERF5	At5g47230	CCGATGAAGGTGAGAAGAAA	CAACTGGGAATAACCAAACG	61
ERF105	At5g51190	TTAGACACCTTTGCCTCCAC	CCTAACCAGACACGAACACC	61
ERF025	At5g52020	AATTTGGCTCGGGACTTATC	ACCGGTTCCAATACCTTCTC	60
ERF107	At5g61590	TGAGGAAAGCTCTGATTTGG	ACCTCAGGTGACGTTGTTGT	61
ERF104	At5g61600	TACAGGGGAGTGAGACGAAG	ACCCTTATCTCGCTTTCGTT	61
SAIL_1236_H11	At4g17490	GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC	CAAACTAGGATAAATTATCGCGCGCGGTGTC	58

References from supplemental materials:

Manfield IW, Jen CH, Pinney JW, Michalopoulos I, Bradford JR, Gilmartin PM, Westhead DR (2006) Arabidopsis Co-expression Tool (ACT): web server tools for microarray-based gene expression analysis. Nucleic Acids Res 34:W504–W509

Toufighi K, Brady SM, Austin R, Ly E, Provart NJ (2005) The Botany Array Resource: e-Northerns, Expression Angling, and promoter analyses. Plant J. 43: 153-63.