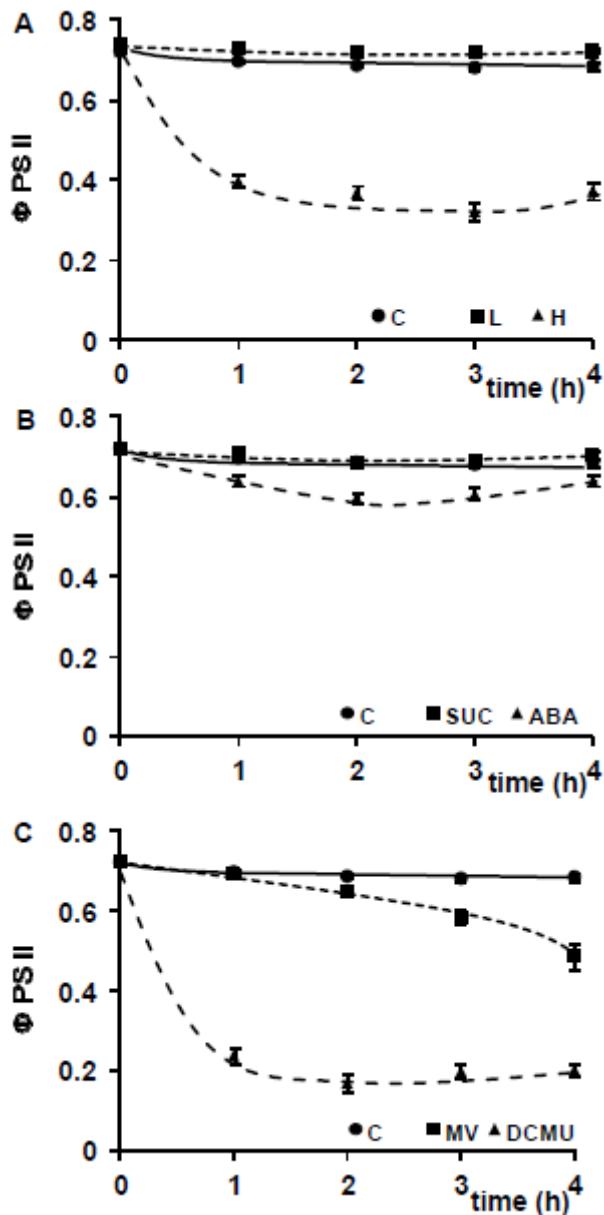
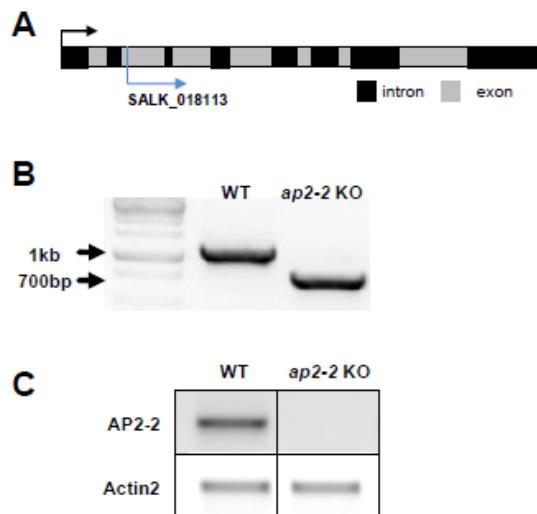


## Supplementary Information

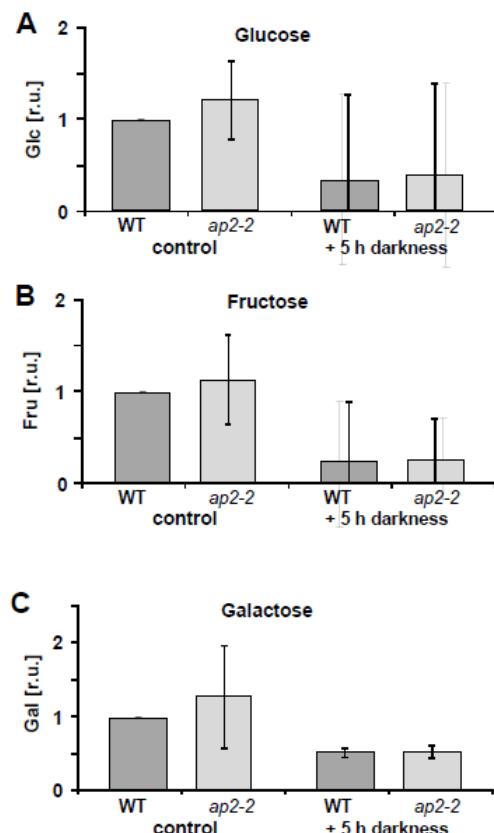
**Figure S.1.** Effective photosynthetic quantum yield of leaf discs.  $\Phi_{PSII}$  in H-light decreased to about half within 1 h. No significant effect was observed in low light (A). Sucrose had no effect, while ABA slightly decreased  $\Phi_{PSII}$  (B). Application of 10  $\mu$ M DCMU strongly decreased  $\Phi_{PSII}$  within 1 h. Methylviologen led to a slow but progressive decrease in  $\Phi_{PSII}$  (C).  $n = 3$  with 6 leaf discs each,  $\pm$ SE.



**Figure S.2.** Characterization of the *ap2-2* (At1g79700) KO-mutant. (A) The T-DNA insertion is located in the second exon of *ap2-2*. (B) The presence of the T-DNA insertion and homozygosity were confirmed by PCR with combinations of gene-specific and T-DNA insertion-specific primers (Table S.1) that generated a 1 kbp band in wild type or a 700 bp in *ap2-2* background. (C) Transcript analysis by RT-PCR gave the expected 220 bp product in the wild type and no products in *ap2-2*.



**Figure S.3.** Metabolite analysis of *ap2-2* and wild type measured in an extended darkness of 5 h. Metabolite profiles determined by GC-MS analysis were in three experiments. Significant differences were not observed.



**Table S.1.** Primers for RT-PCR and SALK-T-DNA line of AP2-2.

Target Gene	ID Number	Forward Sequence (5' – 3')	Reverse Sequence (5' – 3')	T <sub>A</sub> (°C)
ERF023	At1g01250	CAGCTGAATTCCCTGAAGA	ACCCACCTCCACTCATCATA	52
RAV1	At1g13260	GATTCAAGAGAACGGCGTAGA	CTTCGTCCATCTCACGTCT	61
ADAP	At1g16060	TGGGTTTACAGAGGTGTAT	CGGCTGATGTCAAAGTTAGT	55
ERF017	At1g19210	GACGTAACTTGTGCGGATCT	AACGATCACCGGAGTATTCA	58
ERF012	At1g21910	AACCATTGCCCCCTACTTC	GCATCGTCGAGTTAGT	61
RAP2.13	At1g22190	TTCCCTGATCTCCGTATAA	ATCTCCTCCCTCCGTATCACC	58
ERF019	At1g22810	CGACGTTGTTCTTCTGTGTT	CCGCCAGATAATCATACAC	61
TEM1	At1g25560	CCGATGAGTTGAGCAGAGT	TAATCAAACGCCCTTCGTC	63
ERF11	At1g28370	GCCTACGACAACGTCCTAT	CACTCCTTCATCGAACACC	58
RAP2.6	At1g43160	ATGGTGTCTATGCTGACTAATGTTG	AGACTGAAGTTGATTGGACAGAA	61
ERF3	At1g50640	CAGATTCAAGGGCTAAGGA	GGGAACCTGTTGTTGATGGTC	58
ERF8	At1g53170	GACCAATTCCGGTGTTCATCG	CAGATCTAACGGCGGAGATA	58
RAP2.12	At1g53910	ATTCGACGTCGGTGATGTT	TTCTAGCACCTCCCTTGGGA	61
CRF10	At1g68550	TAGGAAGAACGCTGTTGGTG	CAGGTGAAGAACGAGAGCAT	61
RAP2.8	At1g68840	CGGCGATTAGCTTTCTTG	CACGAGACGGTTAGCTTCC	58
HRE1	At1g72360	GAGCAGTCGGTACAAAGGAA	TCAGCCTCATGATTCTCC	61
MSCP	At1g72820	AGCTCTTATCCTGCGTTT	CAGCAGCTTACGCCCTGTC	56
DREB2D	At1g75490	CGAGATGTCATCATGGAA	AGTGGGAATGAAAGGAATC	58
ERF013	At1g77640	GATCACCATCCATCTGCTC	CATCGTTGCCCTTGAGCTAT	61
RAP2.4	At1g78080	GCGTTTCTCCCTCCTCT	CTTTGGGCTGAGAAGATTG	56
AP2-2	At1g79700	GTACTGGGACGAGAACAC	CCCTTCCAATTCTAGCTTCC	61
DEAR3	At2g23340	GGAGGAAGAGGTGGTATT	CATCATCACCATCCGAATT	58
ERF112	At2g33710	CTTCCCATGATCGCATTATC	TGTTCTTCACGTTTACCA	58
AP2-like	At2g41710	TGGAGAAGATAACGGAAG	TCTCTGTGGGAGGTAGCTG	62
ERF034	At2g44940	ACCAACGGTGGAGATAAAC	CGGCTTGAATGTTAGGA	52
CRF5	At2g46310	GGAAAGCGAAGAAAAAGTCC	CAACTGGGAATAACCAAACG	52
RAP2.5	At3g15210	ACCCACAATAATGCAAGGA	GGACCTCTGGTCACTCAGC	56
RAP2.3	At3g16770	GTGAAGAAGGAGCAGGCAAC	TATCACCACGGATCTGCTT	61
Actin2	At3g18780	TTGGTAGGCCAAGACATCAT	GGAGCCTCGGTAAGAAGAAC	58
ARF14	At3g25730	TTAAAACGGCGGAGTTACTG	CTCCAACCTTGGTCAACAC	61
CRF11	At3g25890	CAGATTCTGAAATGGGTT	GTGGTCCAATGAGACCAAG	58
ASN1	At3g47340	TTGCTGACACACGAGATAA	CTCATAAGCGTTGAAGGAA	56
PKRP	At3g49160	TTAAAACCTGGTCCGTGT	ACAAACCCGGTACTGTTGAA	58
CEJ1	At3g50260	ACAAGCGTCAAGACTTGG	CCCCTATCGCATTACTTGA	63
WR11	At3g54320	ATCAGAATCTCGCGAATGAG	ACCGAGGTTGTTGTTGTTG	61
SMZ	At3g54990	AAAATGCACCCAATTCAAAA	TGGACGATTGACATCCCTTA	52
ERF035	At3g60490	ATTATCGGTTGCTTCCTC	TCTTCGTTGCTTCTTGTGTC	61
AP2-like	At4g13040	TTCCAAATCTAATGCCAGA	TCGCTTCTTCTATGCTGCT	61
B-Amylase	At4g15210	TTCTGGGATTCACTGGTGT	GTTCTCACCGCAACTCTA	56
ERF6	At4g17490	TGAAACAAACCGGAAATAA	TCTCCTCTGCTGCTACAACC	58
ERF1A	At4g17500	GGAGCTAGGGTTGGTAGG	ACCGTCAATCCCTTATCCAT	58
CRF2	At4g23750	CACTCACCAAACCGGATT	AACTCTCTCTCCCGTCGT	61
ERF054	At4g28140	TCGTTAGAGGTTTCCCTT	CTTCGTTGCGATGTAAGGTT	61
ERF015	At4g31060	GCCTATGATGCTGCTTGT	CAGAGGAAGCAGGAACCTCA	58
RRTF1	At4g34410	GAAGGATGTCGGCTGTAA	ACACGTGTCGCTTTAGG	61
FLO2	At4g36920	CAGACCCATAACCCACTG	ACTCTTTCAACGGCTGTG	56
ERF060	At4g39780	CATGACCCTCAGAAACTCT	CCGTAGTATCCATCCTCGT	61
ERF106	At5g07580	TGACCCCCATCTAAACCA	CCAAATCAGAGCTTCCCTCA	61
AIL6	At5g10510	GGAGGAAGAGTAGCGGTT	AAGACGTTAGCTGCACCAAC	58
TINY2	At5g11590	TATCGCGGAGTAAGGATGAG	CTGAATGTCGAGGGCTTA	63
RAP2.6L	At5g13330	AAAGGCACCAAGGCTAAACT	AAGAAGGCAGTTGAAAAAGGT	58
LEP	At5g13910	TACAAGGTTCTGGGGTGA	GATCATTGCTAGGAGGAGCA	61
DIN10	At5g20250	GGAGAGTTATGCAAGCTGA	TTAGCAAGCTGACACCATCA	61
AKIN $\beta$ 1	At5g22170	TACCAAGCCGAGAACGATTAC	GAGCGGTTGAGGAGACAA	58
ERF003	At5g25190	CGCTAAACTCCACAAATGCT	CGCTAAACTCCACAAATGCT	63
ERF5	At5g47230	CCGATGAAGGTGAGAACAAA	CAACTGGGAATAACCAAACG	61
BXL1	At5g49360	CAAGATACCGAGGACACTT	CGGGTCACTAGGTCTTGTG	58
RD29a	At5g52310	GTGGAGTAGAGGAGCAACGA	CCGAACCATCCTTAATCCT	58
ERF107	At5g61590	TGAGGAAAGCTCTGATTG	ACCTCAGGTGACGTTGTTG	61
ERF104	At5g61600	TACAGGGAGTGAGACGAAG	ACCCCTATCTCGCTTTCGTT	61
TOE3	At5g67180	TTAACGACTCACCCGATCAT	TGATATCTCCGGCTTTCTG	58
ERF010	At5g67190	CACGGCGTTTCTATCTTA	CCGTTTGATAATTCCGATG	61
SALK TDNA	Insertion	ATTTGCCGATTTCGGAAC	-	58
SALK TDNA AP2-2	SALK_018113	CGTGACAGTGGACTAGACACG	AATTGCATTGGATTGGACC	58

**Table S.2.** Co-expression data for AP2-2. The data were obtained from *Expression Angler* [S-1] and *Arabidopsis Co-expression data mining tool* [S-2].

ID	r-Value Expression Angler	r-Value Arabidopsis Co-expression Tool	Annotation
At3g15450	0,773	0,78543	Aluminium induced protein
At5g21170	0,754	0,795346	AKINBETA1
At5g22920	0,748	0,760928	CHY-type Zinc finger protein
At5g20250	0,692	0,693651	DIN10
At3g15630	0,687	0,68728	unknown protein
At4g35770	0,682	0,682269	ATSEN1
At2g17880	0,674	0,643799	Chaperone DnaJ-domain
At3g47340	0,672	0,685696	ASN1
At1g56220	0,652	0,658175	Dormancy/auxin associated family protein
At5g19120	0,649	0,699898	Eukaryotic aspartyl protease family protein
At1g80920	0,648	0,651041	Chaperone DnaJ-domain superfamily protein
At1g72820	0,646	0,728021	Mitochondrial substrate carrier family protein
At5g49360	0,645	0,682814	ATBXL1
At5g28770	0,644	0,666374	AtbZIP63
At1g03090	0,639	0,656148	MCCA
At2g25900	0,62	0,63037	ATCTH
At1g13700	0,615	0,606129	PGL1_6-phosphogluconolactonase 1
At3g02540	0,613	0,646452	Rad23 UV excision repair protein family
At3g26510	0,612	0,610532	Octicosapeptide family protein
At2g31810	0,612	0,620013	small subunit of acetolactate synthase protein
At2g20670	0,611	0,630448	unknown protein
At3g23050	0,599	0,588006	indole-3-acetic acid 7
At1g01620	0,596	0,606231	plasma membrane intrinsic protein 1C
At1g21830	0,596	0,653546	unknown protein
At5g24490	0,595	0,576504	30S ribosomal protein, putative
At3g60530	0,593	0,577982	GATA transcription factor 4
At1g25230	0,592	0,597163	Calcineurin-like metallo-phosphoesterase superfamily protein
At1g22740	0,592	0,603202	ATRABG3B
At1g68190	0,591	0,598229	B-box zinc finger family protein
At2g05540	0,588	0,607264	Glycine-rich protein family
At3g15450	0,773	0,78543	Aluminium induced protein

## References

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- S-2. Manfield, I.W.; Jen, C.H.; Pinney, J.W.; Michalopoulos, I.; Bradford, J.R.; Gilmartin, P.M.; Westhead, D.R. Arabidopsis Co-expression tool (ACT): Web server tools for microarray based gene expression analysis. *Nucleic Acids Res.* **2006**, *34*, W504–W509.

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