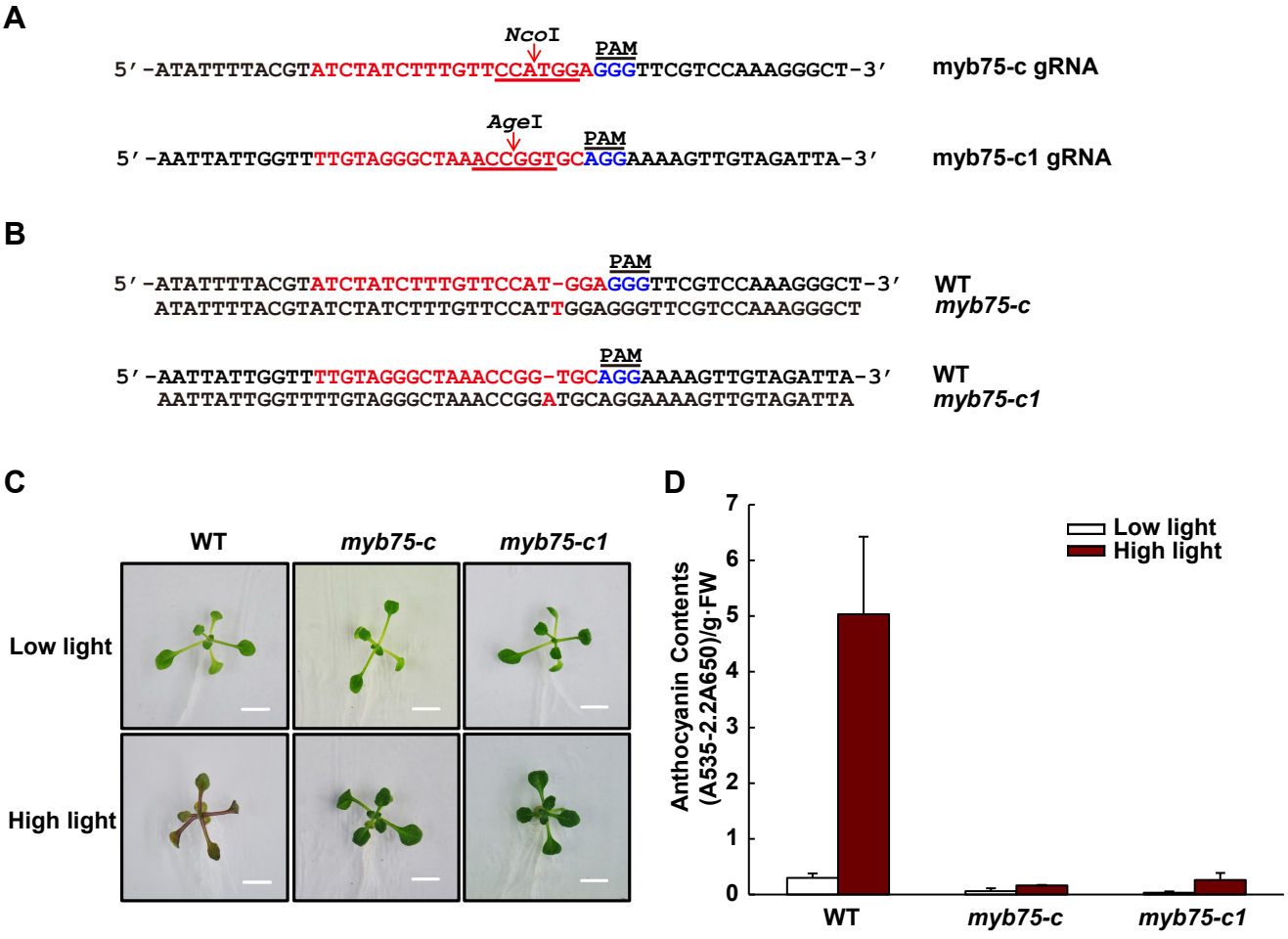
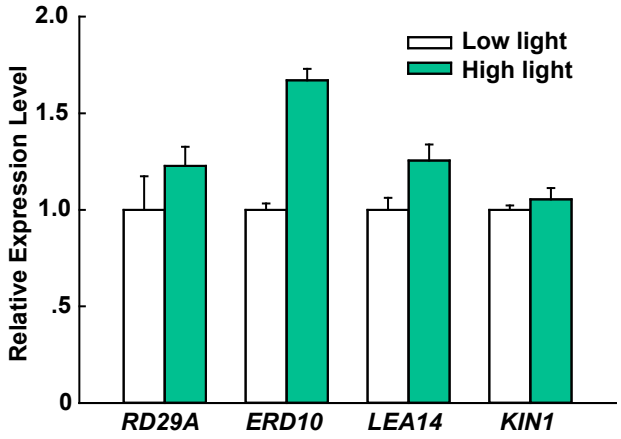
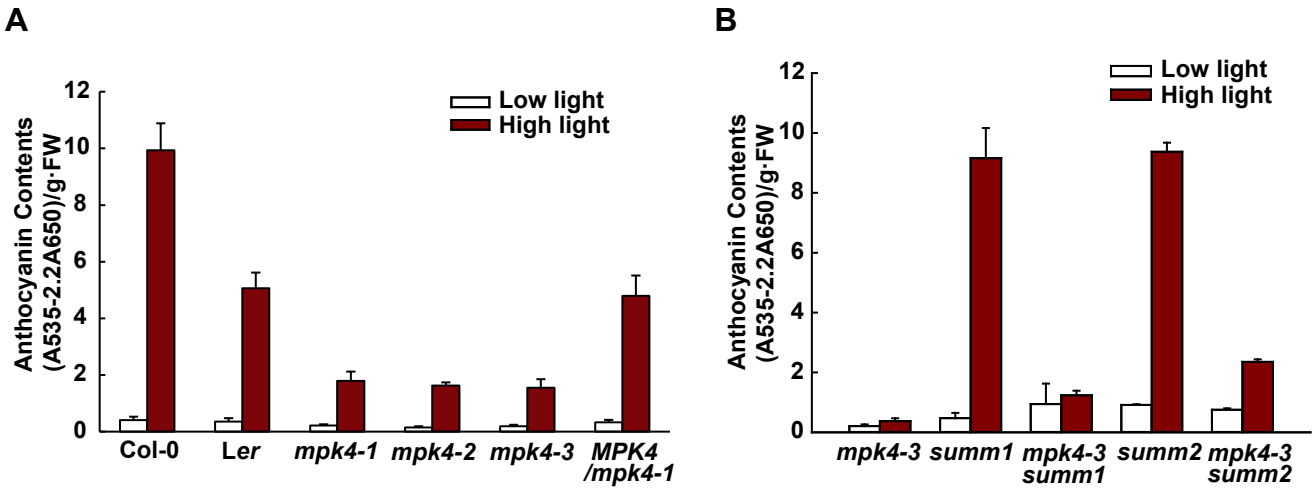


Supplemental Figure 1. Characterization of the *myb75-c* Mutants Generated Using the CRISPR-Cas9 System.
(A) Schematic illustrating the two sgRNA:Cas9 targets (red) and corresponding PAMs (blue) of *MYB75* gene. The *Nco*I and *Age*I sites are underlined. PAM: protospacer-adjacent motif sequence.
(B) Sequencing of the sgRNA:Cas9-induced *MYB75* mutations in two independent transgenic lines of Arabidopsis.
(C) Twelve-day-old Arabidopsis seedlings of wild type (WT), *myb75-c*, and *myb75-c1* grown on plates under low light and moderate high light (high light). Bars = 0.5 cm.
(D) Anthocyanin contents of the seedlings in **(C)**. FW, fresh weight. Error bars represent SD of three replicates (as described in Figure 2B).

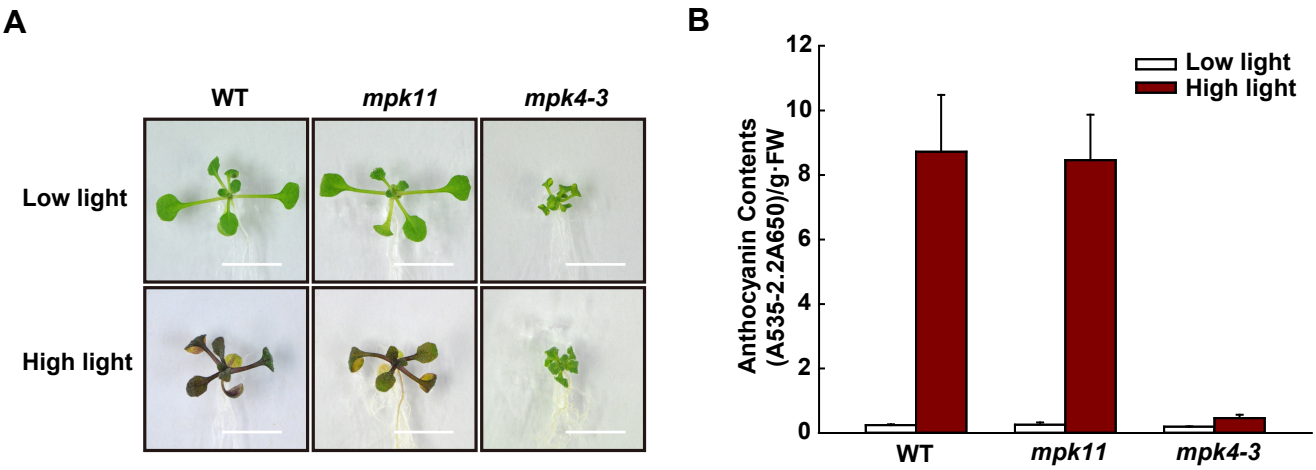


Supplemental Figure 2. Expression Levels of General Stress Genes under Low Light and Moderate High Light Conditions.

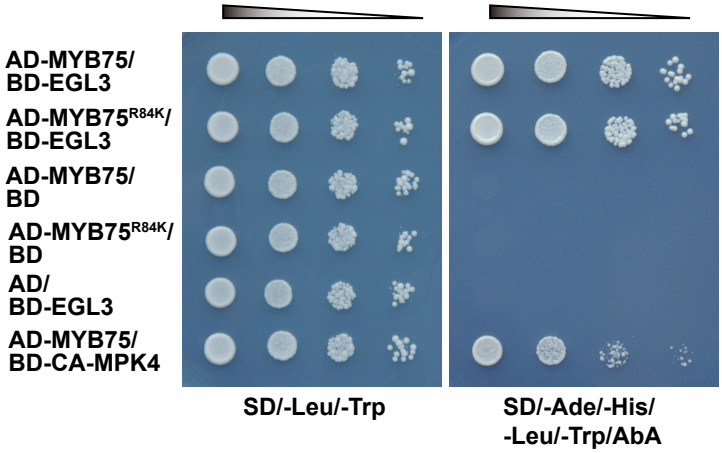
Quantitative real-time PCR analysis showing the expression of general stress responsive genes, *RD29A*, *ERD10*, *LEA14*, and *KIN1* in Arabidopsis under low light (40 μmol m^{-2} s^{-1}) and moderate high light (175 μmol m^{-2} s^{-1}) condition. Results were normalized to *ACTIN8* and expression levels of the genes under low light condition were set at one unit. Error bars indicate SD of three replicates (as described in Figure 2B).



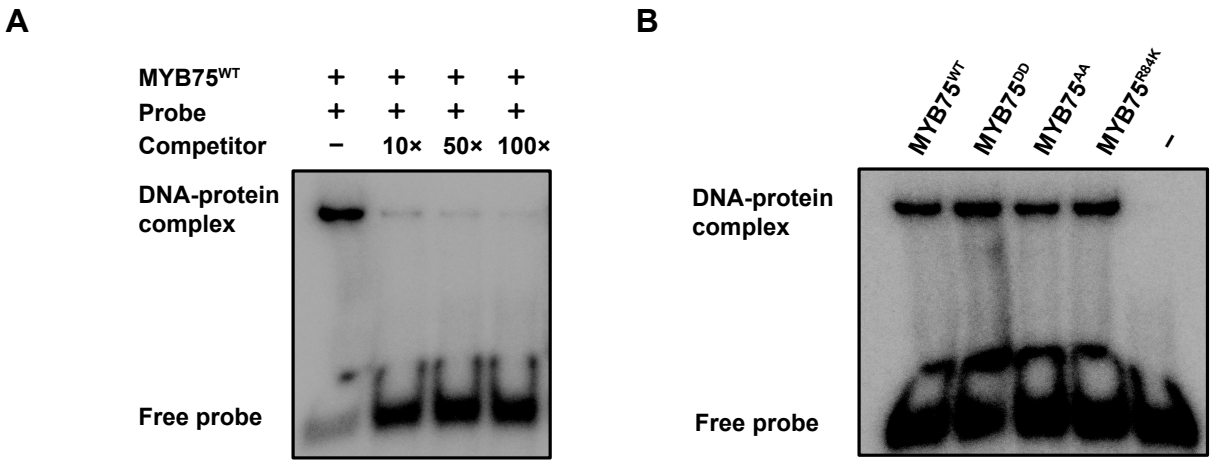
Supplemental Figure 3. Mutations of *MPK4* Lead to Compromised Anthocyanin Accumulation.
(A) Anthocyanin contents of twelve-day-old seedlings of Col-0, L*er*, *mpk4-1* (L*er*), *mpk4-2* (Col), *mpk4-3* (Col), and the complemented line of *mpk4-1* grown on plates under low light and moderate high light (high light). FW, fresh weight. Error bars represent SD of three replicates (as described in Figure 2B).
(B) Anthocyanin contents of twelve-day-old seedlings of *mpk4-3*, *summ1*, *mpk4-3 summ1*, *summ2*, and *mpk4-3 summ2* grown on plates under low light and moderate high light (high light). FW, fresh weight. Error bars represent SD of three replicates (as described in Figure 2B).



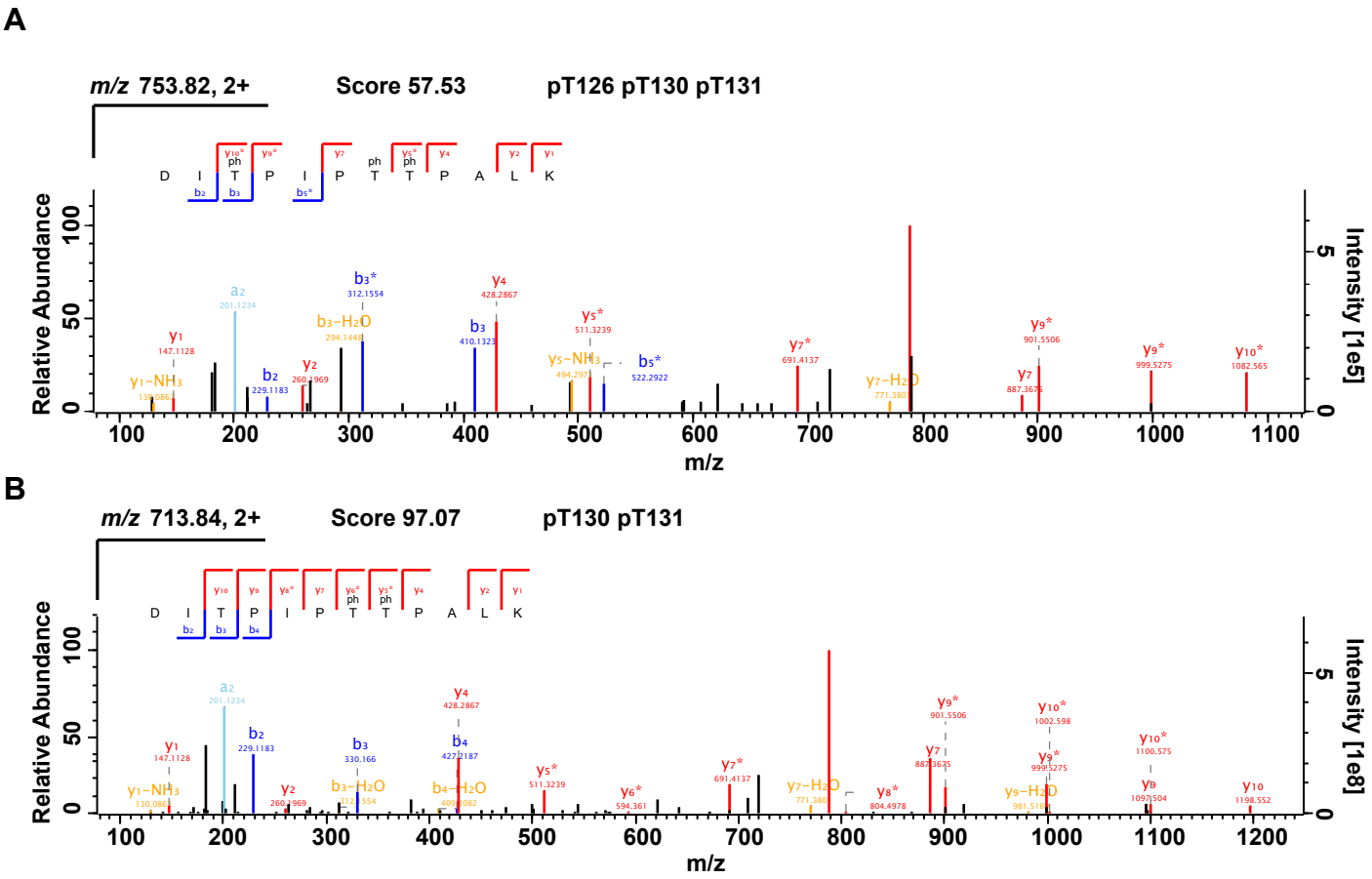
Supplemental Figure 4. MPK11 Is Not Involved in High Light-Induced Anthocyanin Accumulation.
(A) Twelve-day-old seedlings of wild type (Col-0), *mpk11*, and *mpk4-3* grown on plates under low light or moderate high light (high light). Bars = 1 cm.
(B) Anthocyanin contents of the seedlings in **(A)**. FW, fresh weight. Error bars represent SD of three replicates (as described in Figure 2B).



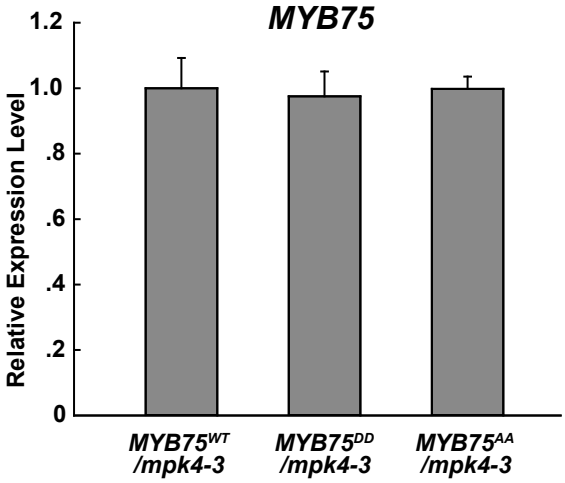
Supplemental Figure 5. R84K Mutation of MYB75 Does Not Change Its Interaction with EGL3 in Yeast.
MYB75^{R84K} interacts with EGL3 in the yeast two-hybrid system. Serial dilutions of transformed yeast cells were spotted on the indicated amino acid dropout agar plates. Co-transformation of MYB75 and CA-MPK4 was used as a positive control. AD, GAL4 activation domain; BD, GAL4 DNA binding domain. SD, synthetically defined medium; AbA, Aureobasidin A.



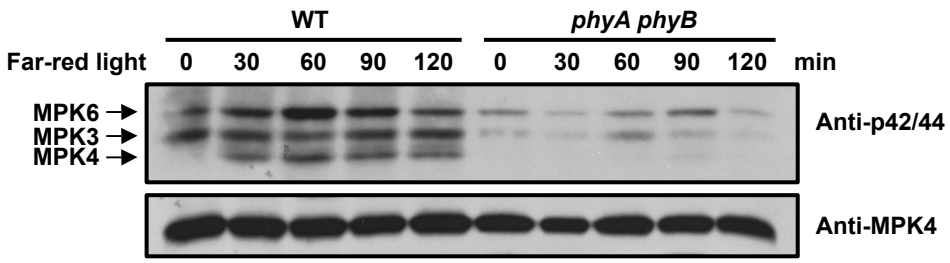
Supplemental Figure 6. Specific Mutations of MYB75 Do Not Affect Its DNA Binding Activity.
(A) EMSA showing that MYB75^{WT} specifically binds to a probe containing MYB75/PAP1 *cis*-regulatory element (PCE) from the promoter of the *DFR* gene. Freshly prepared recombinant MYB75^{WT} was incubated with labeled DNA probe containing PCE for 30 min. The indicated amounts of unlabeled probe were used in competition assay.
(B) MYB75 variants display similar DNA binding activities. The DNA binding activities of the MYB75 variants were determined by EMSAs as in **(A)**.



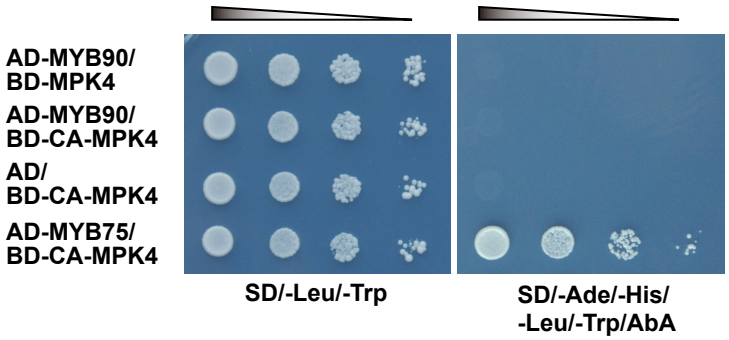
Supplemental Figure 7. LC-MS/MS Analysis of *in vitro* Phosphorylation of MYB75.
(A) LC-MS/MS analysis showing that MYB75 Thr126, T130, and Thr131 are phosphorylated. The sequence of a doubly-charged peptide ion at m/z 753.82, score 57.53, matches DIpTPIpTpTPALK of MYB75. “b” and “y” denote peptide fragment ions retaining charges at the N and C terminus, respectively. The subscript numbers indicate their positions in the identified peptide. pT indicates phosphorylated Thr.
(B) LC-MS/MS analysis showing that MYB75 Thr130 and Thr131 are phosphorylated. The sequence of the doubly-charged peptide ion at m/z 713.84, score 97.07, matches DITPIPpTpTPALK of MYB75. “b” and “y” denote peptide fragment ions retaining charges at the N and C terminus, respectively. The subscript numbers indicate their positions in the identified peptide. pT indicates phosphorylated Thr.



Supplemental Figure 8. Expression Levels of *MYB75* Variant Transgenes in the *mpk4-3* Mutant.
Quantitative real-time PCR analysis showing comparable *MYB75* expression levels in *35S:MYB75^{WT}*, *35S:MYB75^{DD}*, and *35S:MYB75^{AA}* transgenic seedlings in the *mpk4-3* background. Primers were designed to detect both transgenic and endogenous *MYB75* transcripts. Results were normalized to *ACTIN8* and expression levels of the genes in the *35S:MYB75^{WT}*/*mpk4-3* transgenic seedlings were set at one unit. Error bars indicate SD of three replicates (as described in Figure 2B).



Supplemental Figure 9. Far-Red Light Does Not Activate MAPKs in the *phyA phyB* Mutant.
Four-day-old dark-grown wild-type (WT) and *phyA phyB* seedlings were exposed to far-red light (10 μmol m^{-2} s^{-1}) for the indicated times. MAPK activity was analyzed by immunoblotting with Phospho-p44/42 MAPK (Erk1/2) antibody (top panel), and the level of MPK4 was determined by immunoblotting with anti-MPK4 antibody (bottom panel).



Supplemental Figure 10. MPK4 Does Not Interact with MYB90/PAP2 in Yeast.
MPK4 does not interact with MYB90/PAP2 in the yeast two-hybrid system. Serial dilutions of transformed yeast cells were spotted on the indicated amino acid dropout agar plates. Co-transformation of MYB75 and CA-MPK4 was used as a positive control. AD, GAL4 activation domain; BD, GAL4 DNA binding domain. SD, synthetically defined medium; AbA, Aureobasidin A.

Supplemental Table 1. Phosphopeptides Identified in MYB75 by Mass Spectrometric Analysis

Peptide[a]	Phosphosites	Phospho (STY) Probabilities[b]	PEP[c]	Score[d]	Freq.[e]
124-DIpTPIPTTPALK-135	T126	DIT(1)PIPTTPALK	1.40E-07	69.258	2
124-DITPIPpTTPALK-135	T130	DITPIPT(0.892)T(0.108)PALK	4.77E-07	77.185	1
124-DITPIPTpTPALK-135	T131	DITPIPT(0.082)T(0.918)PALK	4.75E-159	144.88	59
124-DIpTPIPTpTPALK-135	T126,T131	DIT(1)PIPT(0.031)T(0.969)PALK	6.82E-23	106.6	11
124-DITPIPpTpTPALK-135	T130,T131	DIT(0.011)PIPT(0.992)T(0.997)PALK	5.53E-11	97.073	9
124-DIpTPIPpTpTPALK-135	T126,T130, T131	DIT(1)PIPT(1)T(1)PALK	2.26E-06	57.525	2

[a]The positions of the peptides in the MYB75 sequence are indicated by the numbers before and after the peptides. pT denotes phosphorylated residues.
[b]Sequence representation of the peptide including PTM positioning probabilities for Phospho (STY).
[c]Posterior Error Probability of the identification. This value essentially operates as a p-value, where smaller is more significant.
[d]Andromeda score for the best associated MS/MS spectrum.
[e]The number of peptide matches to the same peptide sequence with the same modifications.

Supplemental Table 2. Sequences of the Primers Used in This Work.

Cloning and mutation primers

Gene	Forward Primer	Reverse Primer
MPK4	GGAATTCATGTCGGCGGAGAGTTGTTTC	CGGGATCCCACTGAGTCTTGAGGATTGAAC
MPK4^{AEF}	CTGACTTTATG**GCT**GAA**TTT**GTTGTTACAC	TCTCGGATTTGGTCCTCGCAAG
CA-MPK4 (MPK4$^{D198G/E202A}$)	CGAGACTGGCTTTATGACTGCATATGTTG	GATTGGTCCTCGCAAGCCC
MKK1^{DD}	AAGC**GAA**AGTAGTCTTGCTAAT**G** **AT**TTCGTGGGCAC	GTCAAGATCTTGCTGACACCAAAG
MYB75 genomic	TAGGTACCATACCTTTTACAATTTGTTTATATATTTTACG	ACCTGTCGACATCAAATTTCACAGTCTCTCCATC
MYB75 CDS	ACGGATCCATGGAGGGTTCGTCCAAAG	TAAATGCGGCCGCTAATCAAATTTCACAGTCTCTC
MYB75^{R84K}	CTAGGGAAT**AAG**TGGTCTTTAATTGCTG	AAGCCTATGAAGGCGAAGAAGAAG
MYB75^{W85A}	CTAGGGAATAGG**GCT**TCTTTAATTGCTG	AAGCCTATGAAGGCGAAGAAGAAG
MYB75^{T126A}	GAGAGACATT**GCT**CCCATTCCTAC	TTTTTCATCTTTATCTTACAACACGGTTCATG
MYB75^{T131A}	CATTCCTACA**GCA**CCGGCACTAAAAAAC	GGCGTAATGTCTCTCTTTTTCATCTTTATC
MYB75^{AA} (MYB75$^{T126A/T131A}$)	GAGAGACATT**GCT**CCCATTCCTACA**GCA**CCGGCACTAAAAAAC	TTTTTCATCTTTATCTTACAACACGGTTCATGTTTC
MYB75^{DD} (MYB75$^{T126D/T131D}$)	GAGAGACATT**GAT**CCCATTCCTACA**GAT**CCGGCACTAAAAAAC	TTTTTCATCTTTATCTTACAACACGGTTCATGTTTC
MYB75ΔN1	GGAATTCATGCACCAAGTTCCTGTAAGAGCTG	CGGGATCCCTAATCAAATTTCACAGTCTCTCCATC
MYB75ΔN2	GGAATTCATGAGCTCTGATGAAGTCGATCTTCTTC	CGGGATCCCTAATCAAATTTCACAGTCTCTCCATC
MYB75ΔN3	GGAATTCATGGTCAAGAATTACTGGAACACTCATCTG	CGGGATCCCTAATCAAATTTCACAGTCTCTCCATC
MYB75ΔN4	GGAATTCATGCGCCTTCATAGGCTTCTAGGG	CGGGATCCCTAATCAAATTTCACAGTCTCTCCATC
MYB75ΔN5	GGAATTCATGAGGTGGTCTTTAATTGCTGGAAG	CGGGATCCCTAATCAAATTTCACAGTCTCTCCATC
MYB75ΔN6	GGAATTCATGTTACCTGGTCGGACCGCAAATG	CGGGATCCCTAATCAAATTTCACAGTCTCTCCATC
MYB75ΔN7	GGAATTCATGTCTTTAATTGCTGAAGATTACCTG	CGGGATCCCTAATCAAATTTCACAGTCTCTCCATC

MYB75ΔN8	GGAATTCATGATTGCTGGAAGATTACCTGGTCG	CGGGATCCCTAATCAAATTTCACAGTCTCTCCATC
MYB75ΔN9	GGAATTCATGGGAAGATTACCTGGTCGGAC	CGGGATCCCTAATCAAATTTCACAGTCTCTCCATC
MYB75ΔC1	GGAATTCATGGAGGGTTCGTCCAAAGG	CGGGATCCGCTTTCCTCTAGGAATTTCTCTAAC
MYB75ΔC2	GGAATTCATGGAGGGTTCGTCCAAAGG	CGGGATCCCATGGAGGATTAACGTCAACTTTTG
MYB75ΔC3	GGAATTCATGGAGGGTTCGTCCAAAGG	CGGGATCCGTGCCGGTGTTGTAGGAATG

Note: The restriction enzyme sites are underlined. For point-mutation primers, the mutation sites are in bold.

RT-qPCR primers

Gene	Forward Primer	Reverse Primer
MYB75	AGATAAGAAGAAAGACCAACTAGTG	CCAAGGTGTCCCCCTTTTC
MYB75-EGFP	TTCCTGAAGCGACGACAACAG	GTCCAGCTCGACCAGGATG
DFR	TGGTGTCGGTCCATTCAT	GAGAGAGCGCGGTGATAAGG
LDOX	TCCGGGTTTGCAGCTTTTC	ATCAGGAACACATTTTGCAGTGA
UF3GT	TGGAGGTGGCGGTTGAA	CTTTGCCGCGAGAACCA
RD29A	ACGTCGAGACCCCGATAAC	CAATCTCCGGTACTCCTCCA
ERD10	CTCTGAACCAGAGTCGTTTGTG	TTGTCGAGGAGACTTGGCTTG
LEA14	GGACTTCGTGGCGGATAAAC	GCCAAGTACTCAACTGAGTCAC
KIN1	ATCTCTTCTCATCATCACTAACC	AACATTGCTCTTCTCCTCAG
ACTIN8	TCAGCACTTTCCAGCAGATG	CTGTGGACAATGCCTGGAC