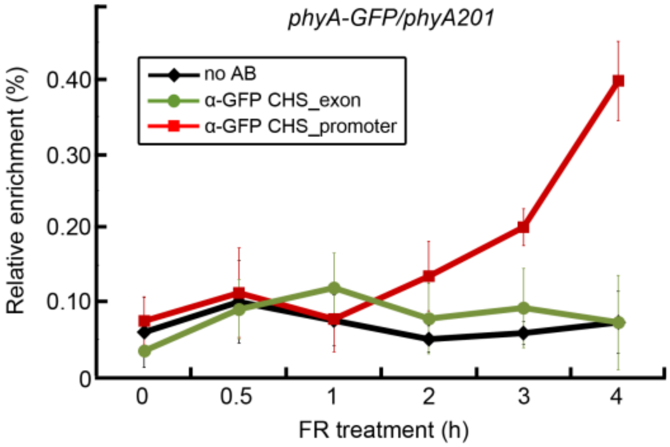
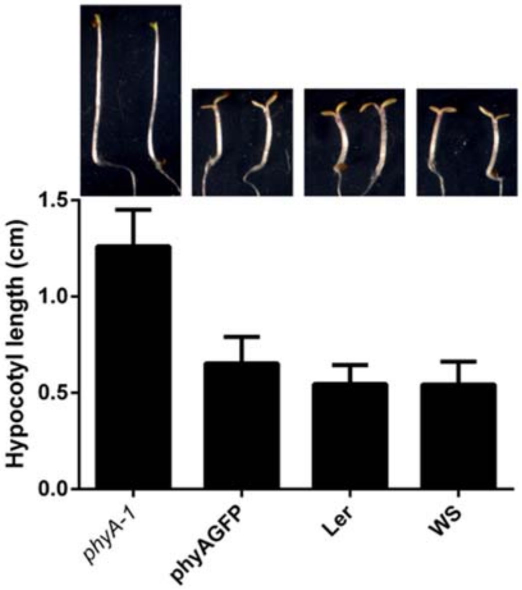


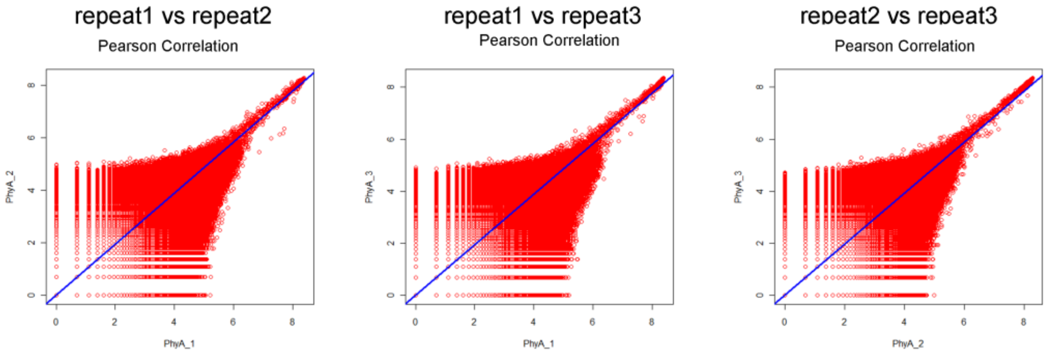
Supplemental Figure 1. Time Course of phyA Association with Its Known Direct Target Gene *CHS* by ChIP-qPCR.

Four-day-old etiolated *phyA-GFP/phyA201* seedlings were irradiated with FR as indicated, followed by ChIP-qPCR using anti-GFP antibody or without antibody (no AB). ChIP-DNA was amplified on *CHS* promoter region and exon region (as negative control). Primer information is as reported in Chen et al., 2012.



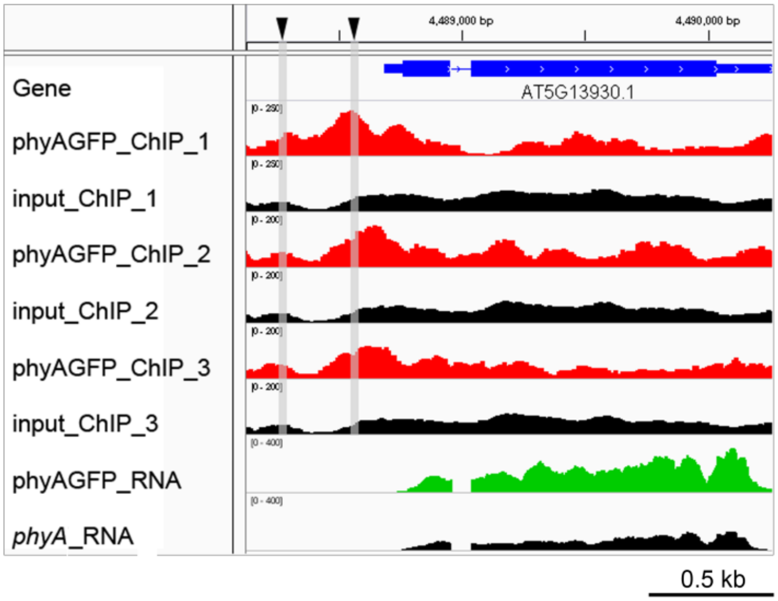
Supplemental Figure 2. Phenotype of 5-day-old FR-grown phyA-GFP Line, *phyA-1* Null Mutant and WT Seedlings (of Ler and WS ecotype).

Error bars represent SD of three biological experiments (n>20 for each biological repeat).



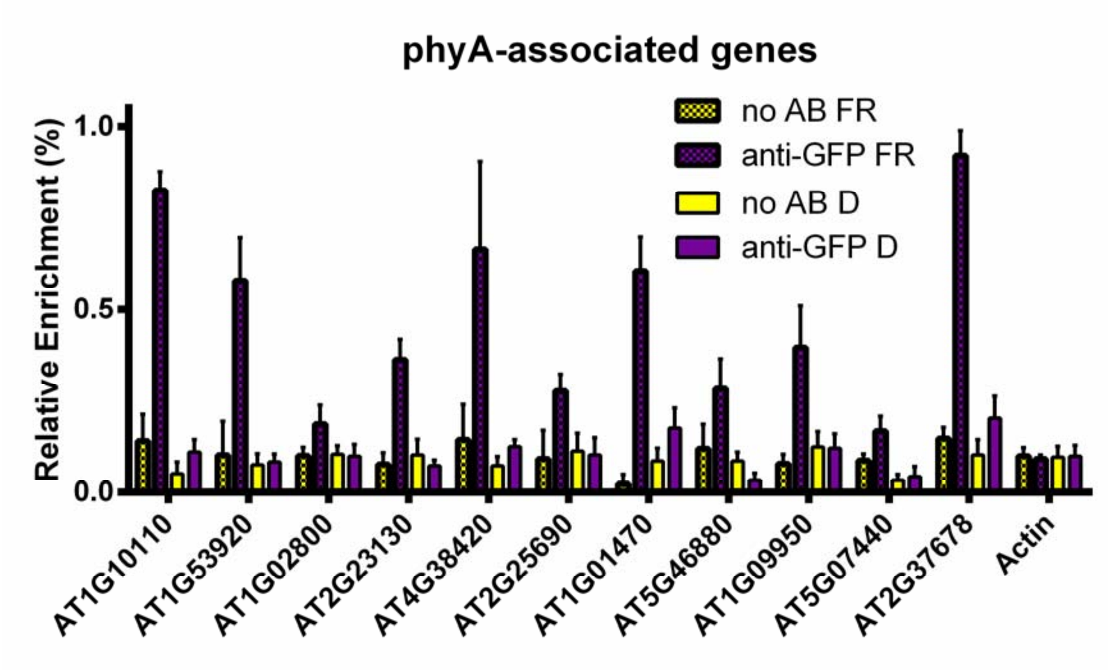
Supplemental Figure 3. Scatter Plot of Pearson Correlation of Three phyA ChIP-seq Replicates.

The coefficients between replicate 1 and 2, 1 and 3, and 2 and 3 are 0.9747149, 0.9724806, and 0.980623, respectively.

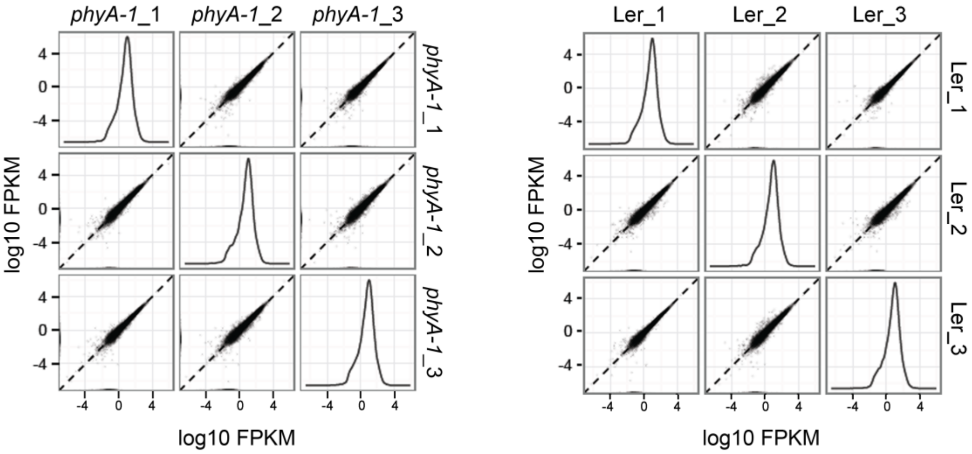


Supplemental Figure 4. phyA ChIP-seq and RNA-seq Peaks on Its Known Direct Target Gene *CHS*.

phyA ChIP-seq peaks (in red) of all three biological replicates are mainly located on *CHS* promoter region. The input controls are shown in black. Representative RNA-seq peaks are indicated in green. Schematic diagram of the *CHS* gene structure is shown at the top. Triangles represent the positions of the two G-boxes on the *CHS* promoter, which are experimentally-proved binding sites of phyA and FHY1 (Chen et al., 2012). The grey bars indicate the positions of the two G-boxes in phyA ChIP-seq peaks.

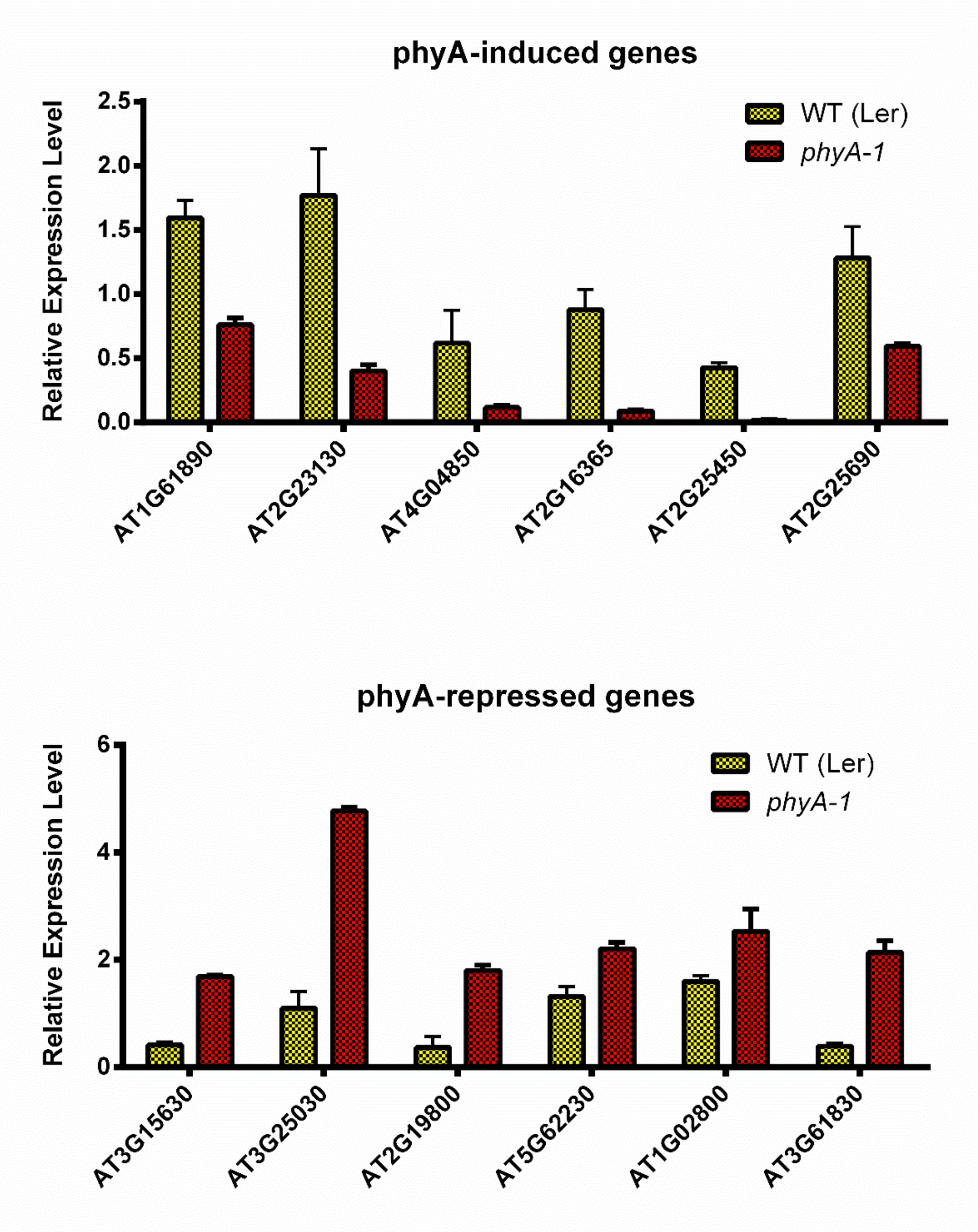


Supplemental Figure 5. Validation of Several phyA-associated Genes by ChIP-qPCR Analysis. Four-day-old etiolated phyA-GFP transgenic lines were treated without (D) or with 3 h FR (FR), followed by ChIP-qPCR analysis using anti-GFP antibody. Data were normalized with corresponding input samples. Error bars represent SD of three biological experiments.

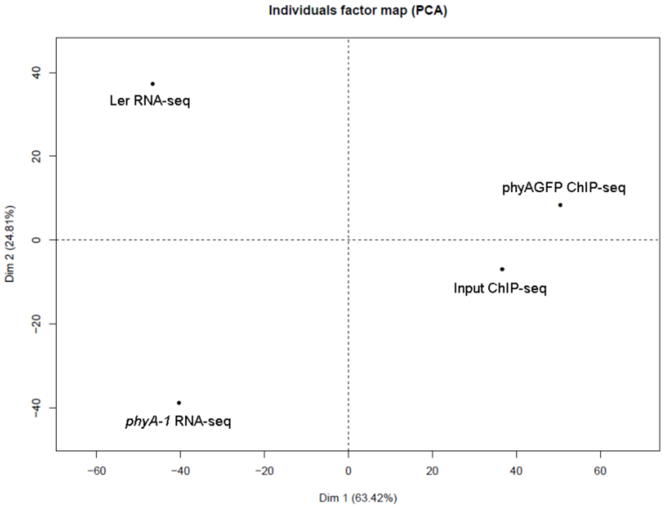


Supplemental Figure 6. Scatter Plot of Pearson Correlation of Three RNA-seq Replicates for wild-type (Ler) and *phyA* Mutant.

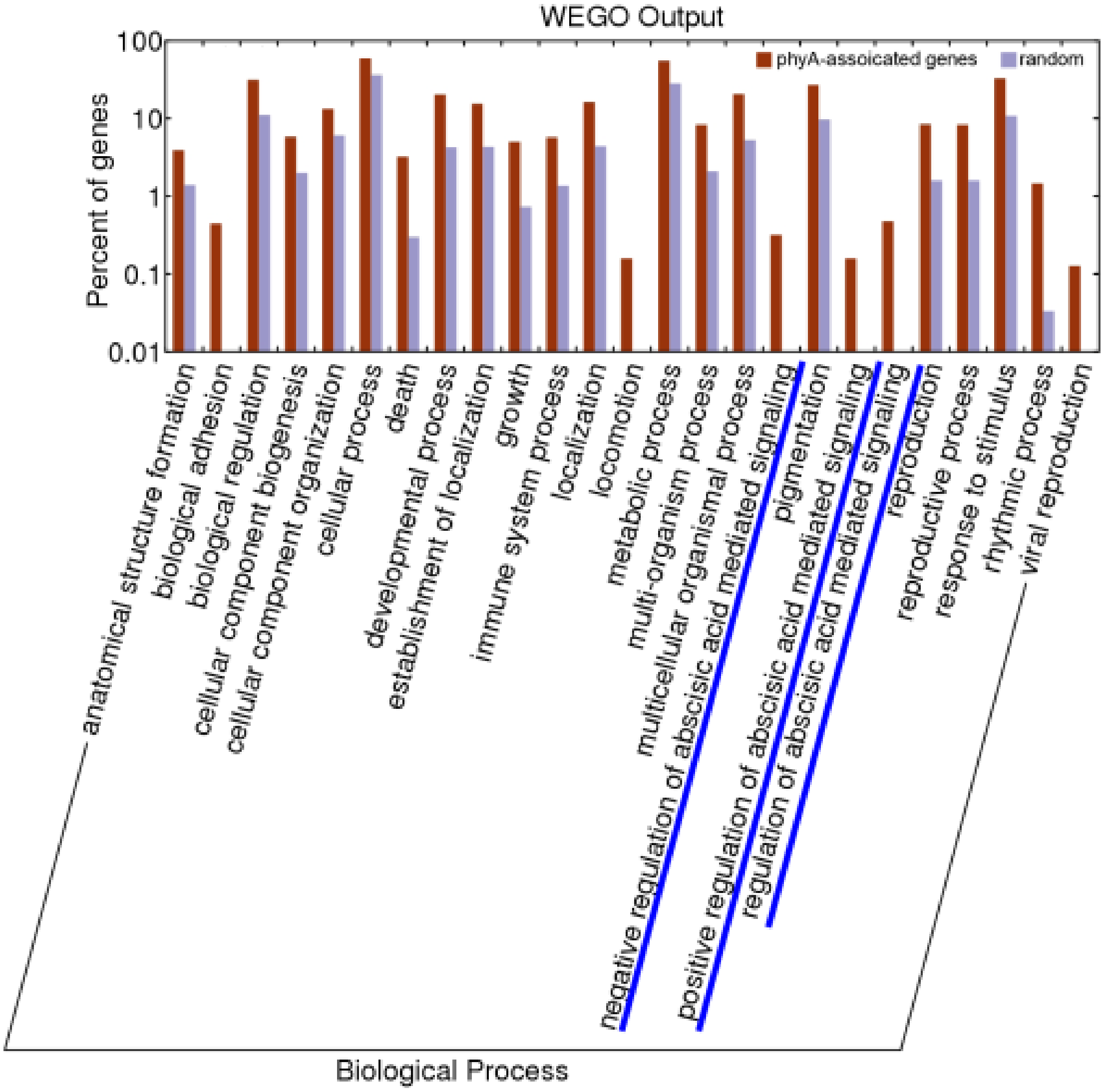
The coefficients between replicate 1 and 2, 2 and 3, and 1 and 3 are 0.9997498, 0.9961875, and 0.9942736, respectively, for phyA-1 and 0.9985142, 0.9972821, 0.9994166, respectively, for Ler. The peaks represent distribution of normalized gene expression value in each sample.



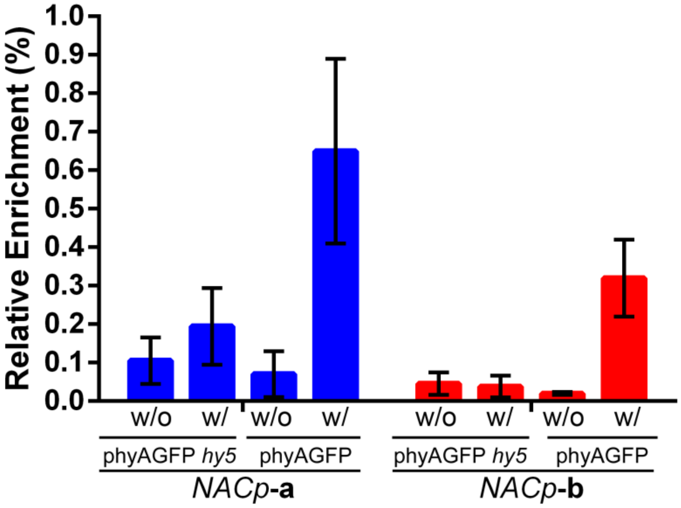
Supplemental Figure 7. Validation of Several phyA-induced Genes (top) and phyA-Repressed Genes (bottom) by RT-qPCR Analysis. WT (of Ler ecotype) and *phyA-1* mutant lines were treated as same as the samples used for RNA-seq, followed by RT-qPCR analysis. *Gene/Actin* is expressed as relative expression level. Error bars represent SD of three biological experiments.



Supplemental Figure 8. Principal Components Analysis of 448 phyA Direct Target Genes. phyA ChIP-seq and RNA-seq data are distinguishable by the first dimension (Dim 1, 63.42% of the total variation). On the other hand, mRNA-seq data from Ler is closest to the ChIP-seq data from the phyA-GFP line on the second dimension (Dim 2, 24.81% of the total variation). The PCA analysis was performed in R using the “prcomp” command. The quantity of phyA binding signals and gene expression levels were calculated using FPKM values (Fragments Per Kilobase of exon or promoter/5’ UTR per Million).

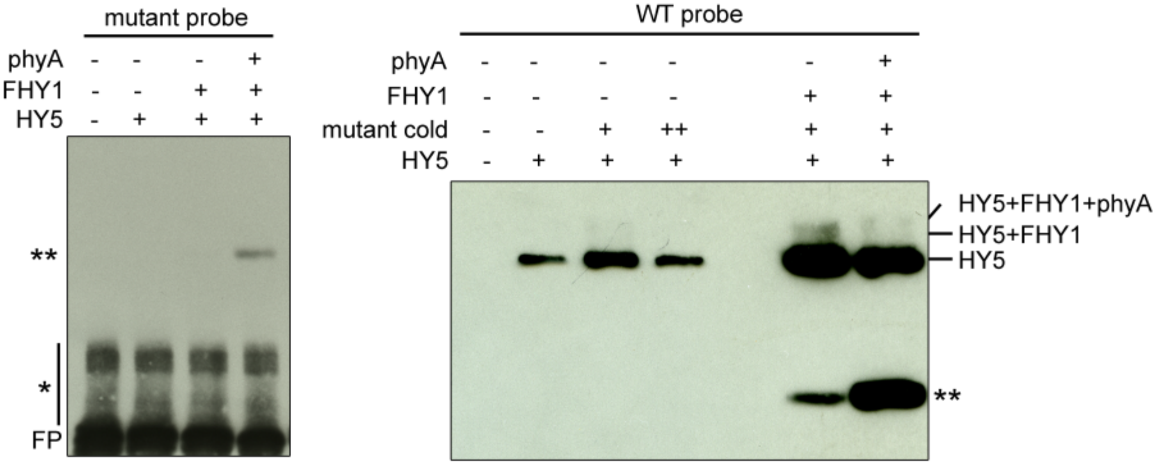


Supplemental Figure 9. WEGO Analysis of phyA-associated Genes Compared with Random. The occurrence of ABA-related genes in phyA-associated genes is much higher than random genes. More detailed information (Biological function, level 4) were provided for ABA-related genes, while brief information (Biological function, level 2) were provided for other groups to make the figure more compact.



Supplemental Figure 10. PhyA Fails to Associate with Two G-box Containing Regions on *NAC019* Promoter in Absence of HY5.

The homozygous crossed line phyA-GFP/*phyA201 hy5-ks50* were grown in dark for four days and exposed to FR for 3 hours. Then the materials were collected for anti-GFP ChIP-PCR. w/o, without antibody; w/, with antibody. Error bars represent SD of triplicate experiments.



Supplemental Figure 11. Super-shifted EMSA Assay Shows That the HY5 Binding Site G-box Is Critical to the Recruitment of the phyA-FHY1-HY5 Complex. The G-box which is positioned at -159 on *NAC019* promoter was mutated to AAAAAA. Left, neither HY5 nor FHY1-phyA complex binds to the mutant probe. Right, the HY5-DNA band is still super-shifted in presence of mutant cold sequence. The bands are separated on gels for longer time compared to that on the left panel to distinguish supershifted bands. The EMSA reactions contained indicated proteins and labeled probes, without (-) or with 200-folds (+), or 1000-folds (++) cold sequence (unlabelled probes). * represents non-specific bands, ** represents an unknown band. FP, free probe.

Supplemental Table 1. The Correspondence between phyA Peaks and phyA-associated Genes.

Total phyA peaks	intergenic	One peak assigned to multiple genes	Multiple peaks reside in one gene	One peak resides in one gene
3798	811	944	997	1183

Supplemental Table 2. List of Motifs Enriched in Promoters of phyA-associated or phyA-regulated Genes.

Motifs enriched in phyA-associated genes	
name	**sequence**
ABADESI1	RTACGTGGCR
ABRE2HVA22	CGCACGTGTC
ABRE3HVA1	GCAACGTGTC
ABREA2HVA1	CCTACGTGGC
ABREATCONSENSUS	YACGTGGC
ABREATRD22	RYACGTGGYR
ABREAZMRAB28	GCCACGTGGG
ABREBNNAPA	CGCCACGTGTCC
ABREBZMRAB28	TCCACGTCTC
ABRECE1HVA22	TGCCACCGG
ABREMOTIFAOSOSEM	TACGTGTC
ABREOSRAB21	ACGTSSSC
ABRETAEM	GGACACGTGGC
ABREZMRAB28	CCACGTGG
ACEATCHS	GACACGTAGA
ACGTABREMOTIFA2OSEM	ACGTGKC
ACGTROOT1	GCCACGTGGC
AGL1ATCONSENSUS	NTTDCCWWWWNNGGWAAN
AUXRETGA2GMGH3	TGACGTGGC
B2GMAUX28	CTTGTCGTCA
BOXIIPCCHS	ACGTGGC
CACGTGMOTIF	CACGTG
CE3OSOSEM	AACGCGTGTC
CPRFPCCHS	CCACGTGGCC
CPRFPCCHS	CCACGTGGCC
CTRMCAMV35S	TCTCTCTCT
DR5GMGH3	CCTTTTGTCTC
EMBP1TAEM	CACGTGGC
EREGCC	TAAGAGCCGCC
GADOWNAT	ACGTGTC
GARE2	RTAACARANTCYGG
GBOXLERBCS	MCACGTGGC
GBOXPC	ACCACGTGGC
GBOXRELOSAMY3	CTACGTGGCCA
GCBP2ZMGAPC4	GTGGGCCCG
HEXAT	TGACGTGG
HY5AT	TGACACGTGGCA
LREBOXIIPCCHS1	TCCACGTGGC

LRENPCABE	ACGTGGCA
MREATCHS	TCTAACCTACCA
MSACRCYM	AGACCGTTG
NONAMERATH4	AGATCGACG
O2F1BE2S1	TCCACGTCGA
OPAQUE2ZMB32	GATGAYRTGG
PALBOXPPC	YTYYMMCMAMCMMC
PALINDROMICCBOXGM	TGACGTCA
PE2FNTRNR1A	ATTCGCGC
SGBFGMGMAUX28	TCCACGTGTC
SITEIIATCYTC	TGGGCY
SITEIIBOSPCNA	TGGTCCCAC
SORLIP2AT	GGGCC
UP1ATMSD	GGCCCAWWW
UPRE2AT	CCACGTCATC
UPRMOTIFIAT	CCACGTCA
UPRMOTIFIIAT	CCNNNNNNNNNNNNCCACG
VOZATVPP	GCGTNNNNNNNACGC

Motifs enriched in phyA-induced genes

name	**sequence**
ABADESI1	RTACGTGGCR
ABRE2HVA22	CGCACGTGTC
ABRE3HVA1	GCAACGTGTC
ABREA2HVA1	CCTACGTGGC
ABREATCONSENSUS	YACGTGGC
ABREATRD22	RYACGTGGYR
ABREBNNAPA	CGCCACGTGTCC
ABRETAEM	GGACACGTGGC
ABREZMRAB28	CCACGTGG
ACGTABREMOTIFA2OSEM	ACGTGKC
ACGTROOT1	GCCACGTGGC
AUXRETGA2GMGH3	TGACGTGGC
BOXIIPCCHS	ACGTGGC
CPRFPCCHS	CCACGTGGCC
CPRFPCCHS	CCACGTGGCC
DR5GMGH3	CCTTTTGTCTC
EMBP1TAEM	CACGTGGC
EREGCC	TAAGAGCCGCC
GARE2	RTAACARANTCYGG
GBOXLERBCS	MCACGTGGC
GBOXRELOSAMY3	CTACGTGGCCA
HEXAT	TGACGTGG

HY5AT	TGACACGTGGCA
LREBOXIIPCCHS1	TCCACGTGGC
LRENPCABE	ACGTGGCA
MREATCHS	TCTAACCTACCA
PE2FNTRNR1A	ATTCGCGC
SGBFGMGMAUX28	TCCACGTGTC
SITEIIBOSPCNA	TGGTCCCAC
UPRE2AT	CCACGTCATC
UPRMOTIFIAT	CCACGTCA
ABRE3HVA22	GCCACGTACA
ABRECE3ZMRAB28	ACGCGCCTCCTC
ABREDISTBBNNAPA	GCCACTTGTC
ABREMOTIFIIIOSRAB16B	GCCGCGTGGC
ACGTSEED3	GTACGTGGCG
ACIPVPAL2	CCCACCTACC
AMMORESVDCRNIA1	GGCCCCGGG
AS1LIKECSHPRA	AAATGACGAAAATGC
C1MOTIFZMBZ2	TAACTSAGTTA
CGF1ATCAB2	GATAAAGATTACTTCAGATATAACAAACGTTAC
CONSERVED11NTZMATP1	ACGTATTAAAA
D2GMAUX28	ATTTATATAAAT
ELRE2PCPAL1	ATTCTCACCTACCA
GBOX10NT	GCCACGTGCC
GBOXSORBCS1	TCCACGTGGT
GCAACREPEATZMZEIN	GCAACGCAAC
GLUTECOREOS	CTTTCGTGTAC
GRAZMRAB28	CATGCCGCC
HDZIPIIIAT	GTAATSATTAC
HSELIKENTGLN2	AGGAATTCCT
MEJARELELOX	GATACANNAATNTGATG
OBP1ATGST6	TACACTTTTGG
PIIATGAPB	TTGGTTTTGATCAAAACCAA
POLLEN2LELAT52	TCCACCATA
PR2GCNT	TAARAGCCGCC
RSEPVGRP1	CAACTTTCATAT
S2FSORPL21	CCATACATT
SORLIP3AT	CTCAAGTGA
UPRE1AT	ATTGGTCCACG
Motifs enriched in phyA-repressed genes	
name	**sequence**
ABADESI1	RTACGTGGCR
ABREA2HVA1	CCTACGTGGC

ABREAZMRAB28	GCCACGTGGG
ABRETAEM	GGACACGTGGC
ABREZMRAB28	CCACGTGG
ACGTROOT1	GCCACGTGGC
CACGTGMOTIF	CACGTG
GBOXPC	ACCACGTGGC
GBOXRELOSAMY3	CTACGTGGCCA
SGBFGMGMAUX28	TCCACGTGTC
SITEIIBOSPCNA	TGGTCCCAC
ABASEED1	TGTTACGTGCC
ACGTSEED2	ACACACGTCAA
ACGTSEED3	GTACGTGGCG
AGL3ATCONSENSUS	TTWCYAWWWWTRGWAA
AMMORESVDCRNIA1	GGCCCCGGG
AUXRETGA1GMGH3	TGACGTAA
BOXBPSAS1	AAACGACACCGTTT
CONSERVED11NTZMATP1	ACGTATTAAAA
D4GMAUX28	TAGTGCTGT
GLUTAACAOS	AACAAACTCTAT
HDZIPIIIAT	GTAATSATTAC
LS7ATPR1	ACGTCATAGA
O2F3BE2S1	TCCACGTACT
OCTAMOTIF2	CGCGGCAT
OPAQUE2ZM22Z	TCCACGTAGA
PIATGAPB	GTGATCAC
PR2GCNT	TAARAGCCGCC
RBENTGA3	TCCAACTTGGA
SORLREP3AT	TGTATATAT
SRENTTTO1	TGGTAGGTGAGAT

Supplemental Table 3. List of Motifs Enriched in both phyA-associated and –regulated Promoters.

motif	species	motif sequence	signal-ing	motif Annota-tion	possible TF	reported target gene	reference
GBOXPC	parsley	ACCACGTGGC	light	G-box	GBFs		Plant Cell 6: 545-559 (1994)
CPRFPCCHS	parsley	CCACGTGGCC	light	Box II	CPRFs	*CHS*	EMBO J 10: 1777-1786 (1991)
LREBOXIIPCCHS1	parsley	TCCACGTGGC	light	LRE		*CHS-1*	EMBO J 8: 651-656 (1989)
MREATCHS	arabidopsis	TCTAACCTACCA	light	MRE	MYB	*CHS*	Plant Mol Biol (1998) 36: 741-754
PE2FNTRNR1A	tobacco	ATTCGCGC	light	pE2F		*RNR1a*	Nucleic Acids Res. 32: 1430-1438 (2004)
BOXIIPCCHS	parsley	ACGTGGC	light	LRE		*CHS*	EMBO J 8:651 (1989)
GBOXLERBCS	arabidopsis	MCACGTGGC	light	G-box		*rbcS-1A*	EMBO J 9:1717 (1990)
HY5AT	arabidopsis	TGACACGTGGCA	light	G-box	HY5		Plant Cell 10:673 (1998)
LRENPCABE	tobacco	ACGTGGCA	light	LRE		*CAB-E*	EMBO J 7:1929 (1988)
ABREAZMRAB28	maize	GCCACGTGGG	ABA	ABRE-A		*RAB28*	Plant Cell 9:2261 (1997)
ABREZMRAB28	arabidopsis	CCACGTGG	ABA	ABRE	CBF2	*Adh*	Plant Physiol.139:437 (2005)
ABREATCONSENSUS	arabidopsis	YACGTGGC	ABA	ABRE	ABFs		Plant Physiol 138:341 (2005)
EMBP1TAEM	arabidopsis	CACGTGGC	ABA	ABRE	ABFs		Science 250:267 (1990)
ABREA2HVA1	barley	CCTACGTGGC	ABA	ABRE		*HVA1*	Plant Cell 8:1107-1119 (1996)
ABRETAEM	wheat	GGACACGTGGC	ABA	ABRE	EMBP-1		Science 250:267-270 (1990)
ABRE2HVA22	barley	CGCACGTGTC	ABA	ABRE		*HVA22*	Plant Cell 7:295-307 (1995)
ABRE3HVA1	barley	GCAACGTGTC	ABA	ABRE		*HVA1*	Plant Mol Biol 26:617-630 (1994)
ABREBNNAPA	Brassica napus	CGCCACGTGTCC	ABA	ABRE		*napA*	Planta 199:515-519 (1996)
ACGTABREMOTIFA2OSEM	arabidopsis	ACGTGKC	ABA	ABRE		*rd29A*	Plant J. 34: 137-148 (2003)
ABADESI1	rice	RTACGTGGCR	ABA	ABRE	TAF-1	*rab21*	PNAS 87:1406 (1990); EMBO J 10:1793 (1991)
ACGTROOT1	tobacco	GCCACGTGGC	ABA	ACGT motif	TAF-1		Plant Cell 4:1485 (1992)
ABREATRD22	arabidopsis	RYACGTGGYR	ABA	ABRE		*RD22*	Mol Gen Genet 247:391 (1995)
SGBFGMGMAUX28	soybean	TCCACGTGTC	auxin	G-box	SGBF-1/-2	*AUX28*	Plant J 8:199 (1995)
AUXRETGA2GMGH3	soybean	TGACGTGGC	auxin	AUXRE	SGBF-2	*GH3*	Plant Physiol 115:397 (1997)

DR5GMGH3	soybean	CCTTTTGTCTC	auxin	AUXRE	ARF1	*GH3*	Plant Cell 9:1963 (1997)
GARE2	rice	RTAACARANTCYGG	GA	GARE			Plant Mol Biol 14:655-668 (1990)
EREGCC	arabidopsis	TAAGAGCCGCC	ethylene	GCC-box	AtEBP		PNAS 94: 5961-5966 (1997)
HEXAT	arabidopsis	TGACGTGG	defense	Hex motif	TGA1/GBF1		TPC 4: 1309 (1992);MPMI 25:1459 (2012)
CACGTGMOTIF	arabidopsis	CACGTG	Em	G-box	GBF4	*β-phaseolin*	Plant Mol Biol 39:1299-1310 (1999)
UPRE2AT	arabidopsis	CCACGTCATC	UPR	UPRE	XBP1		Biochem Biophys Res Commun 301:225 (2003)
UPRMOTIFIAT	arabidopsis	CCACGTCA	UPR	UPRE			Plant Cell 15:561 (2003)
GBOXRELOSAMY3	rice	CTACGTGGCCA	SS	G-box		*Amy3D*	Plant Mol Biol 36:331 (1998)
SITEIIBOSPCNA	rice	TGGTCCCAC	ME	Site IIb	PCF1/2	*PCNA*	Plant J 7:877 (1995)

LRE: Light-responsive element; MRE: MYB responsive element; ABRE: ABA responsive element; AUXRE: auxin-resonsive element; EIRE: Elicitor-responsive element; UPRE: unfolded protein responsive element.

Em: embryogenesis; UPR: unfolded protein response; SS: sugar starvation; ME: meristematic tissue-specific expression.

N=A,T,C,G; M=A,C; Y=C,T; W=A,T; R=A,G; X, unknown base.

Supplemental Table 4. List of Primers Used in This Study.

For ChIP-PCR verification	
name	**sequence**
actin-F	CACAATGTTTGGCGGGATTGGTGA
actin-R	TGTACTTCCTTTCCGGTGGAGCAA
NAC-a-F	GGTTCAATGAACTCAAGGGAT
NAC-a-R	ACGCAGTGTATAGGTGAATCCA
NAC-b-F	GTGGACACGTGTCGTCAT
NAC-b-R	ATGTGAACTGGTAAAGGAAGAG
AT2G23130-pro-R	GATCTGGACCGTTGAAGGGAC
AT2G23130-pro-F	CGGAATATGCCAACTCTCCA
AT4G38420-pro-R	CGAGAAATATTGATTGAACGC
AT4G38420-pro-F	ATGAAAGTGAAGGGAAAAGGAGA
AT5G07440-pro-R	TGTAGGGGAAAGAAGAGAAAGC
AT5G07440-pro-F	AACTTTCCAACTCAAGCCAATA
AT5G46880-pro-R	TAACGCTCGTCTAACTCTTCCGT
AT5G46880-pro-F	AACGCGTGGTGAATAAAAGTTTG
AT1G53920-pro-R	GAAGCAGAACTGTCCAGAAGAG
AT1G53920-pro-F	AAAGTGATTGCCTAGAGAAGTGC
AT1G10110-pro-R	CGATGCTTATTCAGTTATTTGGTT
AT1G10110-pro-F	CGAGATCGCATCATTTTCCA
AT1G01470-pro-R	AAGTCGTGAATCTTCTTCTCTTA
AT1G01470-pro-F	GACTTCTTAACATAAATGCTGACTC
AT1G09950-pro-R	CCGACACATGTTGGTAAAATAAG
AT1G09950-pro-F	GAACTGTTGGTTTATTTGGTTTCTA
AT1G02800-pro-R	TGCATATGCTTTGTCAGACCAA
AT1G02800-pro-F	ACTGAAAGGAATAAATGAAGGTGC
AT2G37678-pro-R	GAGAGAGAGAGATAGAGAGAGTTCAA
AT2G37678-pro-F	ACGCGCCAAATCAAACA
AT2G25690-pro-R	GGATCTATGGGCGGGTCAAG
AT2G25690-pro-F	CACAAAACAGAGTGGGAACAGTG
AT4G34000-pro-R	TTGAGAAATAAAAGATACCTGAAAGG
AT4G34000-pro-F	GGTGGGAAACGCAAATGTAT
AT5G05440-pro-R	TGATTGTGGTAAATTTTAAGATAGACAT
AT5G05440-pro-F	TAATATAAAAATGGGCAACAAGAACA
AT5G57050-pro-R	CCATTATTGTCGGAAAACAGAC
AT5G57050-pro-F	GTAAATAAATAAAACAGACACCAAATAA
AT1G67080-pro-R	AGAAATTGGATGGAGTAGGAAGA
AT1G67080-pro-F	TTTTTGTACCATTTAATCTCAAGAAT

AT1G71960-pro-R	CTTGAGAGAGACGAGGAGATGAATC
AT1G71960-pro-F	TCCTTTCAGCAGTCGCCAGC
AT4G26080-pro-R	CTCTCTTTTTCCTCTCCTCATTA
AT4G26080-pro-F	CCATCATCCAAAGCCCACTT
AT4G27410-pro-R	CTTCGATTCCTCAGCAACCAA
AT4G27410-pro-F	CAGTATCTAAATGGTTAAACGGGTC
AT5G13630-pro-R	TGATATAAGAGTACCGCTTCATTCTC
AT5G13630-pro-F	GTTGATTTCATTAATTAGTCTGCGT
AT5G52570-pro-R	TTTTCTAGGATTTTCCCAAGTCA
AT5G52570-pro-F	TCATGTCAAGCAATACCTCATTTA
AT5G66880-pro-R	ATATTCGGTTGCGTTATTCCGTTA
AT5G66880-pro-F	CATGGTGGGATTGGGCTGG

For reverse transcription-PCR verification

name	sequence
AT2G25450-R	TCAGATCCTTAAATGGTCCAAC
AT2G25450-F	GACCCATTAAAGAGCTTCTGTCT
AT1G61890-R	AGCGGCTCACGGCTCTCTT
AT1G61890-F	GAATATGGACTGGGATGATTGG
AT5G66052-R	TTAAGACAAAGATGAAGCGGC
AT5G66052-F	TCGTCCGGTATTGATGGCTTT
AT5G62230-R	TTATATGCTACTTTTGGAGATGAC
AT5G62230-F	TCCCATCTCTGCAAGTAGCAA
AT5G46880-R	CTAGCTGACTTCTTGATTGGAC
AT5G46880-F	GTAACGTCCCAACAGCGAAAC
AT5G07440-R	TTAAGCTTCCCAACCACGCAA
AT5G07440-F	GAACTTGGAGCTGCAAAAATACA
AT5G02490-R	GACTTCCTCGATCTTGGGACC
AT5G02490-F	TGGTGGTGAAGCTGGTGGTC
AT4G31805-R	TCTAGAAAAACTGGTGCGGTGTA
AT4G31805-F	CCTGCTTGCCCAGCGTG
AT4G04850-R	TTAATCTTGAGCTTTATCAGC
AT4G04850-F	CTGCAGCAGAGATTCTTC
AT3G61830-R	TCACCCCCTACTACGATTTTC
AT3G61830-F	GTGATGATCCGTGGAATGAGTT
AT3G25030-R	TTGTGGTATTACAGAGAGGACAG
AT3G25030-F	ACGGCGGCGGAGATAAG
AT3G15630-R	GCAGCTGCTTAGCCTTCTCC
AT3G15630-F	CATGGTGGGCTCCTCTTTTTG
AT2G25690-R	ATCTATCATCATCTCCTCTGAACG
AT2G25690-F	ATAACTTCCTCGGCATCTGC
AT2G23130-R	CGGAGCAGGCGGGCTTA
AT2G23130-F	CACCTTCAGCTGATGTTCCG

AT2G19800-R	AATACTTGTTGATGAGTGAAATGTAG
AT2G19800-F	GAGCCTACACACACTTGATGAAC
AT2G16365-R	GAACTCCTTGTGACTCTCTGGCT
AT2G16365-F	GAGGAGATGACATTACACTTCTGC
AT1G10110-R	TTATTCACCAGCACCGAAACAA
AT1G10110-F	GTGCTTATGAGATTCCTACGCA
AT1G10090-R	GGGAATTACGAATTGGGGAAG
AT1G10090-F	TGCTCAGATCAGGAGTTACCAG
AT1G09950-R	GAGGTGAAGCTGTCCGATTGT
AT1G09950-F	GGAGGCGATGGAGGTGCTTA
AT1G02800-R	TTAGGATCGAGCAAGATAAGCC
AT1G02800-F	GGTGCAGTAGTCGGTGGTCC
AT1G15520-R	GCTTCACACTCATATTACTATCTGC
AT1G15520-F	CTTTCTACGGCATCTGGAATCTC
AT4G27410-R	ACGTCGTCAAGCTGTGATGAAG
AT4G27410-F	TGGATTATGCACGAGTATCGCTTA
AT3G15500-R	TCAAATAAACCCGAACCCACTA
AT3G15500-F	CTGAGTCATAACGTTCCGAGTATTC
AT1G01360-R	TCACTGAGTAATGTCCTGAGAAGC
AT1G01360-F	GGAGATAATCGAGGGAAGAGC
AT2G40330-R	GGCGAGTTTAGCCAGCGATTG
AT2G40330-F	ACGGTGCATGAGTCGGAGGA
AT2G38310-R	AACGTCAACGAAGTCACAAGTCTCT
AT2G38310-F	CTCGACGACGAACGCCAC
AT2G29090-R	ATTCGGAGGAGTGATGGATTC
AT2G29090-F	GATACAAGAAAAATGCCACTGACC
AT1G52400-R	CACAGTTTCCAACCTCCAAGC
AT1G52400-F	CAAAGTGAACGTTACGGGATACT
AT5G67030-R	TTATCGTTGTTACTCTCATTCTTCC
AT5G67030-F	ACGGAACCTATGTGACCGAT
AT5G57050-R	CTTCAAATCAACCACTACCACACTTA
AT5G57050-F	TTTACTATGGCATAAGAAGAACGC
AT4G26080-R	TTCCTCCGAGGCTTCAAATCA
AT4G26080-F	ACAAGAAAAACGCGGTGGCT
AT5G13630-R	CGATCTTGTCTTCCACCTGC
AT5G13630-F	GAGGAGATGCTGAACCGTCT
AT4G19230-R	GGCAATTCTGTCATTCTACACTTC
AT4G19230-F	GATTCATCATCTCACCACCAAG
AT3G14440-R	TCACACGACCTGCTTCGC
AT3G14440-F	ATGGAAATCGGAGTTACAGATAGTTA
For EMSA	
name	**sequence**

NAC-988-F-BIO	TTCTACGATAGACACGTGGACACGTGTCGTCATGATGTAGTTTTGT
NAC-988-F	TTCTACGATAGACACGTGGACACGTGTCGTCATGATGTAGTTTTGT
NAC-988-R	ACAAAACTACATCATGACGACACGTGTCCACGTGTCTATCGTAGAA
NAC-159-F-BIO	TCACGACGATCTAACTGACACACGTGTCAGAATTCAAAAGTG
NAC-159-F	TCACGACGATCTAACTGACACACGTGTCAGAATTCAAAAGTG
NAC-159-R	CACTTTTGAATTCTGACACGTGTGTCAGTTAGATCGTCGTGA

For yeast assays and tobacco assay

name	sequence
NACpA-F	ATTGGTACCACGTGGACACGTGTC (tobacco also)
NACpA-R	actgtcgacGAAATATGTGAACTGGTAA
NACpB-F	agggtaccTTACCAGTTCACATATTTC
NACpB-R	actgtcgacACATGAGTAGATTTAGCTC
NACpC-F	attggtaccGAGCTAAATCTACTCATGT
NACpC-R	actgtcgacTTGACAATAATGTTTGG (tobacco also)
NACp-mG1-F	CGATCTAACTGACAAAAAAATCAGAATTC
NACp-mG1-R	GAATTCTGATTTTTTTGTCAGTTAGATCG
NACp-mACE-F	CCATATTCAGTACACAAAATAATCAGCG
NACp-mACE-R	CGCTGATTATTTTGTGTACTGAATATGG
NACp-mG2-F	ATTGGTACCACGTGGAAAAAAATCGTCATGA
NACp-mG3-F	GTCAACAAAAAAAAAAAAAAATAAAATATC
NACp-mG3-R	GATATTTTATTTTTTTTTTTTTTTGTTGAC