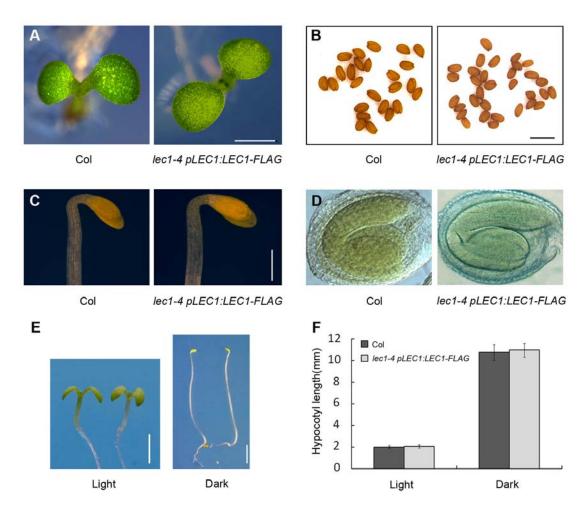


Supplemental Figure 1. Characterization of the *lec1-4* Mutant.

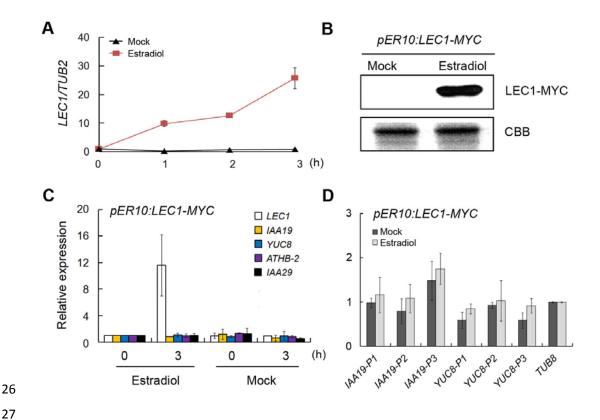
- **(A)** The *lec1* mutants exhibit mature seeds with abnormal morphologic characters in comparison to the wild type. Bar=1 mm.
- **(B)** Dark-grown *lec1-4* mutant exhibits abnormal apical hook formation. Red arrowheads indicate trichomes. Bar=1 mm.
- **(C)** The *lec1-4* mutant develops a varying degree of trichomes on cotyledons in comparison to the wild type. 5-day-old seedlings grown in the light were used for investigation. Red arrowheads indicate trichomes. Bar=1 mm.



Supplemental Figure 2. *pLEC1:LEC1-FLAG* Complements Growth Defects of *lec1-4*.

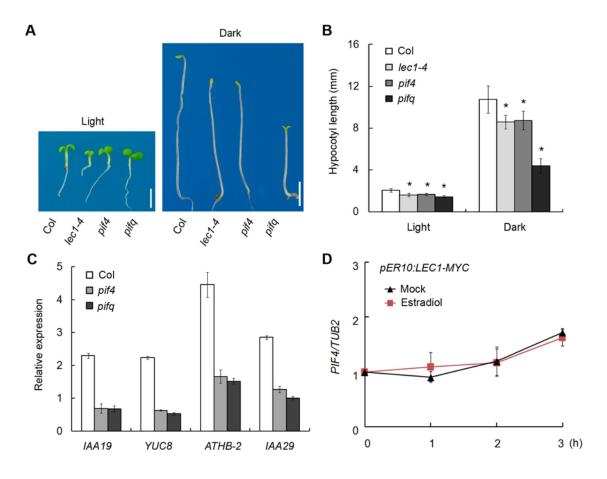
(A) lec1-4 pLEC1:LEC1-FLAG exhibits normal cotyledon. Bar=1 mm.

- (B) lec1-4 pLEC1:LEC1-FLAG exhibits normal mature seeds. Bar=1 mm.
- **(C)** Dark-grown *lec1-4 pLEC1:LEC1-FLAG* exhibits normal apical hook. Bar=1 mm.
- **(D)** *lec1-4 pLEC1:LEC1-FLAG* exhibits normal embryo development.
- **(E)** *lec1-4 pLEC1:LEC1-FLAG* has similar hypocotyl length with the wild type in both light and dark condition. Bar=2 mm.
- **(F)** Hypocotyl length statistics of the wild type and *lec1-4 pLEC1:LEC1-FLAG* seedlings shown in **(E)**. Data represent mean ±SD of at least 30 seedlings.



Supplemental Figure 3. Characterization of *pER10:LEC1-MYC* Transgenic Line.

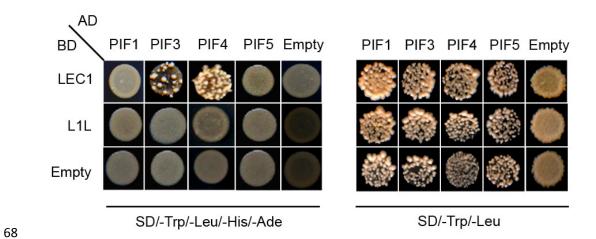
- (A) Quantitative RT-PCR analysis of *LEC1* expression in *pER10:LEC1-MYC*. 3-day-old *pER10:LEC1-MYC* seedlings were treated with 10 μ M estradiol or mock-treated for the indicated times and harvested for RNA extraction. Relative gene expression was calculated by comparing to the values at 0 h.
- **(B)** Immunoblot analysis of estradiol-induced LEC1-MYC protein. 3-day-old pER10:LEC1-MYC seedlings were treated with 10 μ M estradiol or mock-treated for 2 days and harvested for detection of LEC1-MYC using anti-MYC antibody.
- **(C)** Overexpression of *LEC1* has no effect on the expression of downstream genes in the light. 3-day-old *pER10:LEC1-MYC* seedlings were treated with 10 µM estradiol or mock-treated for 3 h in the light.
- (D) ChIP analysis of LEC1-MYC binding in *IAA19* and *YUC8* genes in the light. 3-day-old pER10:LEC1-MYC seedlings were treated with 10 μ M estradiol or mock-treated and kept in continuous light for an additional two days and harvested for ChIP assay. Data represent mean \pm SD of triplicates. Asterisks indicate significant changes in ChIP-enrichment fold in estradiol-treated sample compared with mock-treated sample (p < 0.05, by Student's *t*-test).



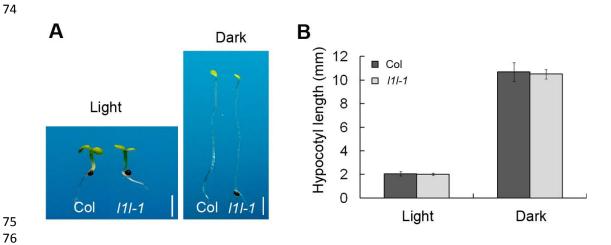
Supplemental Figure 4. Hypocotyl Length and Gene Expression Analysis in *lec1-4*, *pif4*, *pifq*, and *pER10:LEC1-MYC* Transgenic Plants.

(A) Hypocotyl lengths of 5-day-old Col wild type, *lec1-4*, *pif4*, and *pifq* seedlings grown in the light or the dark. *pifq*, *pif1 pif3 pif4 pif5* quadruple mutant. Bar=2 mm.

- **(B)** Hypocotyl length statistics of the wild-type, *lec1-4*, *pif4*, and *pifq* seedlings shown in **(A)**. Data represent mean \pm SD of at least 30 seedlings. Asterisks indicate significant differences of mutants compared with the wild type (p < 0.05, by Student's *t*-test).
- **(C)** Expression of hypocotyl elongation-related genes was impaired in *pif4* and *pifq* mutants. 3-day-old seedlings in the light were transferred to darkness for 6 h and harvested for RNA extraction. Relative gene expression levels were normalized against the expression of *TUB2*.
- (D) Overexpression of *LEC1* has no effect on *PIF4* expression. 3-day-old pER10:LEC1-MYC seedling were treated with 10 μ M estradiol or mock-treated and immediately transferred to darkness for the indicated time. The relative gene expression was calculated by comparing the values at different time points to that at 0 h.



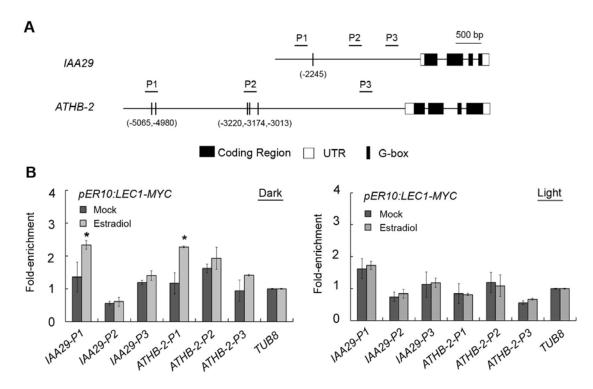
Supplemental Figure 5. Yeast Two-Hybrid Assays Showing the Interactions between LEC1, L1L, and PIFs. Transformed yeast cells were grown on SD/-Trp/-Leu/-His/-Ade and SD/-Trp/-Leu medium.



Supplemental Figure 6. Hypocotyl Phenotype of the *I1I-1* Mutant.

- **(A)** 5-day-old *I1I-1* seedlings grown in the light or darkness show similar hypocotyl length with the wild type. Bar=2 mm.
- **(B)** Hypocotyl length statistics of the wild type and *I1I-1* mutant shown in **(A)**. Data represent mean ±SD of at least 30 seedlings.





Supplemental Figure 7. ChIP Analysis of LEC1-MYC Binding in *IAA29* and *ATHB-2* Genes in the Dark and Light.

(A) Schematic diagram of *IAA29* and *ATHB-2* genomic regions. P1 to P3 indicate fragments for ChIP-quantitative PCR amplification. Numbers indicate the positions of G-box elements in *IAA29* and *ATHB-2* promoters relative to ATG.

(B) ChIP analysis of LEC1-MYC binding to the G-box containing region in *IAA29* and *ATHB-2* genes upon precipitation with anti-MYC antibody. 3-day-old of pER10:LEC1-MYC seedlings were treated with $10\mu\text{M}$ estradiol or mock and immediately transferred to darkness or continuous light for additional two days and harvested for ChIP assay. Data represent mean $\pm\text{SD}$ of triplicates. Asterisks indicate significant changes in ChIP-enrichment fold in estradiol-treated sample compared with mock-treated sample (p < 0.05, by Student's t-test).

A

Biotinylated probe:

gaagactttagatatcaaatgactc CACGTG tcgatattggattggttttcattgg

Cold competitor:

gaagactttagatatcaaatgactc CACGgG tcgatattggattggttttcattgg

B

IAA19 gene promoter region (1958bp)

TTGAGATGAAAACCAAACACTGCTCCCACTCAAAATTTGTAAAAAATGGAATTTATAAATATTTGGTGCTACAAATGTCGTTTGGTAGCCTTTGGAAA CATTAAAGGTAAACTAGAGATATGGGAGTATGGAACTTAATCTCTTTATGTGGTTGTATTTCATATAATTTCACGTGGCCCAACTTGTTTCTGTCAATC AACCCCATCATTATACTTCTTGTGTTTTATTGGTATGCTGAGCTAGAGATAGTTAACAACTACCCAACAATGCGGGTCTGGCTTAGTTTGAACCTATT CGAAACTAGTTATACTCCGCTTGAAGTCATTGGTTCGAGACTAACTTTGGAGATGAGTATCATAAACAGCTCTAACTTAAGATTACAATACATCCTCT TGTTAGTCTAAGTTGAGAGGTGTTGCCATTGACTATATTTCTTTGGGAATTTGGTTTACCAGGATGTTGCAAAGAAGATTTAAATATTAAAATT TATATAATTGAATCCCTAAGTAAAATTCAACCCAATACTTGAGAAGGTAGTTATATTCTTATAAATTATGGATATGATTTGATTAAAACTCAAACCTGAA CCCAAAACATACTAGAATATACGTTTTTACTTTGTAACTATTTGTCACATTCCAAAACTAAACTCGGTACTATTTTGATTCTGATCCATACAAATTTTG AAGCCAATCCAAAAAAACTGATGCAAAGAGAGATAAACGAACATATCCCAAAATGGTAGGATTTGATTTAATATTCCCATCCTCTTATTAGAAATGC AAACAAATAGACTATAGTTTTATTTATTTTATTTTCACTATAAAATAACTAAATAACATGAACTTATTGAAGAAAAAAGTATACTATAGTTGTGATTCTGTG AGACTTTAGATATCAAATGACTCCACGTGTCGATATTGGATTGGTTTTCATTGGTTGTATCGTGTGGACCAACGAAGCAACATATAAAAAAGCACGAC

mpIAA19:GUS: CACGTG → CACGgG

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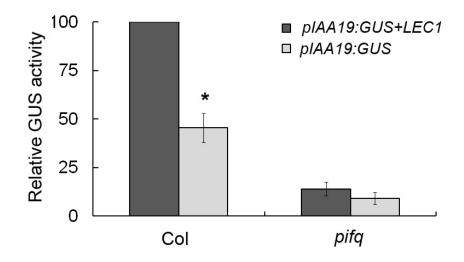
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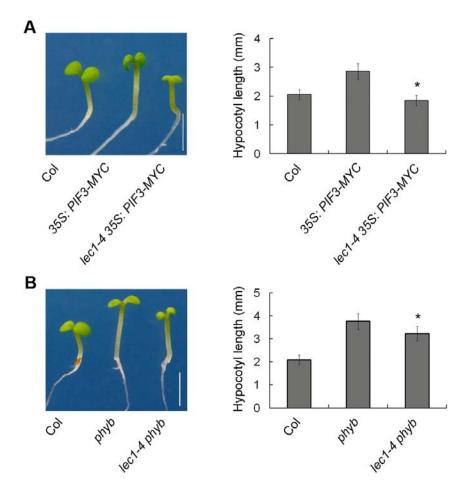
Supplemental Figure 8. Mutated Versions of the *IAA19* Sequence Used in EMSA and Transient Expression Assays.

- (A) Biotinylated probe and cold competitor used in EMSA assay. Red lower case indicates mutated base from T to G.
- **(B)** *IAA19* promoter sequence and its mutated version in *pIAA19:GUS* and *mpIAA19:GUS* used in transient expression assay, respectively. For *mpIAA19:GUS*, two G-box elements in *IAA19* promoter were mutated to CACGgG.



Supplemental Figure 9. Transient Expression Assays of *IAA19* Transcriptional Activity Modulated by LEC1. *Arabidopsis* mesophyll protoplasts were isolated from wild type or *pifq* mutant. *LEC1*, *35S:LEC1-EYFP^C*. Values are mean ±SD of three biological replicates.



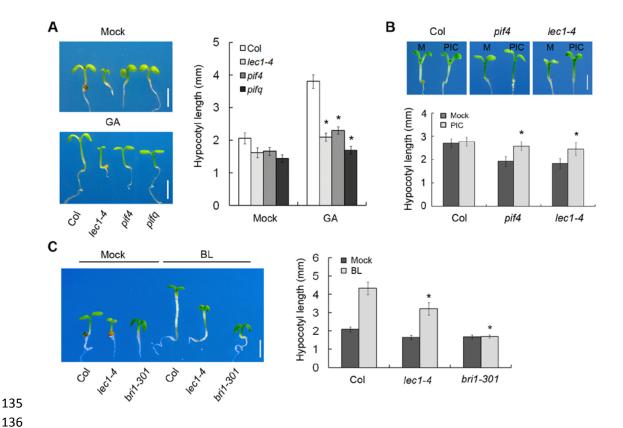


Supplemental Figure 10. *lec1-4* Suppresses the Long Hypocotyl Phenotype of *35S:PIF3-MYC* and *phyb*.

(A) Hypocotyl photograph (left) and length statistics (right) of 5-day-old light-grown wild-type, 35S:PIF3-MYC, and lec1-4 35S:PIF3-MYC seedlings. Data represent mean $\pm SD$ of at least 30 seedlings. Asterisks indicate significant difference of hypocotyl length of lec1-4 35S:PIF3-MYC compared with 35S:PIF3-MYC (p < 0.05, by Student's t-test). Bar=2 mm.

(B) Hypocotyl photograph (left) and length statistics (right) of 5-day-old light-grown wild type, *phyb* and *lec1-4 phyb* seedlings. Data represent mean \pm SD of at least 30 seedlings. Asterisks indicate significant difference of hypocotyl length of *lec1-4 phyb* compared with *phyb* (p < 0.05, by Student's test). Bar=2 mm

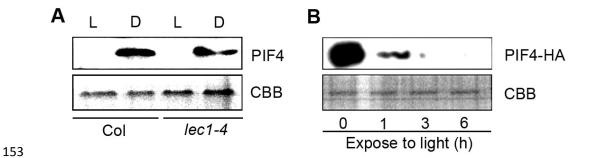
t-test). Bar=2 mm.



Supplemental Figure 11. Effects of GA, Auxin and BR on Hypocotyl Elongation of *lec1-4* and *pif4*.

- (A) GA effect on hypocotyl length of wild type, *lec1-4* and *pif4*. Seedlings were grown on 1/2 MS in the light with 10 µM GA or mock treatment for 5 days.
- **(B)** Auxin effect on hypocotyl length of wild type, *lec1-4*, and *pif4* at high temperature. Seedlings were grown on 1/2x MS with $0.1~\mu M$ synthetic auxin picloram (PIC) or mock treatment (M) at the 28 °C for 5 days.
- **(C)** Effect of brassinosteroids on hypocotyl length of wild type, *lec1-4*, and *bri1-301*. Seedlings were grown on 1/2x MS with $0.1~\mu$ M exogenous brassinolide (BL, the most active form of brassinosteroids) or mock-treated for 5 days. The *bri1-301* was used as a negative control. Data represent mean \pm SD of at least 30 seedlings. Asterisks indicate significant differences of relative hypocotyl length calculated by comparing the values of GA, PIC, or BL treatment to those of mock treatment between Col and mutants (p < 0.05, by Student's *t*-test). Bar=2 mm.





Supplemental Figure 12. Immunoblot Analysis of PIF4 Protein.

- **(A)** Immunoblot analysis of PIF4 protein expressed in 3-day-old Col and *lec1-4* seedlings grown in the light (L) or the dark (D). Anti-PIF4 antibody (Abiocode, USA) was used to examine the PIF4 protein level.
- **(B)** Immunoblot analysis of PIF4-HA protein expressed in 3-day-old 35S:PIF4-HA seedlings grown in the dark and then exposed to light for indicated time. Coomassie blue staining (CBB) was used as a loading control.

Supplemental Table 1. List of Primers Used in This Study.

Primers for quantitative real-time PCR

Gene name	Primers (5'-3')	
LEC1	F:AAACCTATGGAGGAAATGG	
	R:TAATGGAAGACGAAGAGCC	
PIF4	F: CAACCCATCACAGAACGA	
	R: GCAACCAGAGGAGCCACC	
IAA19	F: AAATGGAGAAGGAC	
	R: ACCACCAGATGAAACGAC	
IAA29	F: TTGCGACAGAGAAGATAC	
	R: CAAAATAAAAAATAATGG	
ATHB-2	F: CGGAGATGCTGCGAGAAT	
	R: GTCAAAGTAGTGGGTGGG	
YUC8	F: ACAACCCACGAAACGCTC	
	R: AAAACACGCACAACACCC	
TUB2	F: ATCCGTGAAGAGTACCCAGAT	
	R: AAGAACCATGCACTCATCAGC	

166

163164

165

167 Primers for RT-PCR

Gene name	Primers (5'-3')	
LEC1	F: CCAAAATCCATCTCTGAAT	
	R: CATAGCCCAAAGGATATC	
TUB2	F: ATCCGTGAAGAGTACCCAGAT	
	R: TCACCTTCTTCATCCGCAGTT	

168 169

Primers for constructs in plant transformation

Construct name	Primers (5'-3')
pLEC1:LEC1-FLAG	F:AAA <u>CTGCAG</u> GAAGTAAATTATGATGCTTGTTGCGTG
•	R:CGCGGATCCCTTATACTGACCATAATGGTCAAAAGC
pLEC1: GUS	F: AAA <u>CTGCAG</u> GAAGTAAATTATGATGCTTGTTGCGTG
	R: CGC <u>GGATCC</u> TGTTTCTCTGCCGTCTTTTTTTTTTTG

170171

Primers for constructs in yeast two-hybrid assays

1 Timers for constructs in yeast two hybrid assays	
Construct name	Primers (5'-3')
BD-LEC1	F:AATT <u>CATATGATG</u> GAACGTGGAGCTCCCT
	R: CGC <u>GGATCC</u> TCACTTATACTGACCATA
BD-LEC1N	F:AATT <u>CATATG</u> ATGGAACGTGGAGCTCCCT
	R:CGC <u>GGATCC</u> CATAGCCCAAAGGATATC
BD-LEC1C	F:AATT <u>CATATG</u> AAGCTTGGGTTCGATAAC
	R:CGC <u>GGATCC</u> TCACTTATACTGACCATA
BD-L1L	F:GGAATT <u>CATATG</u> ATGGAACGTGGAGGCTTC
	R:CGC <u>GGATCC</u> TCAGTACTTATGTTGTTG

Supplemental Data. Huang et al. (2015). Plant Cell 10.1105/tpc.15.00750

AD-PIF4	F:CTC <u>GAATTC</u> ATGGAACACCAAGGTTGG
	R:CAG <u>GAGCTC</u> CTAGTGGTCCAAACGAGA
AD-PIF4N1	F:CTC <u>GAATTC</u> ATGGAACACCAAGGTTGG
	R:CAG <u>GAGCTC</u> GTTTGATCCTGATCGTTG
AD-PIF4N2	F:CTC <u>GAATTC</u> ATGGAACACCAAGGTTGG
	R:CAG <u>GAGCTC</u> CATCACTTGAAGCTGTAAC
AD-PIF4C	F:CTC <u>GAATTC</u> ATGGGGAGTGGAATGGCG
	R:CAG <u>GAGCTC</u> CTAGTGGTCCAAACGAGA
AD-PIF1	F: CTC <u>GAATTC</u> ATGCATCATTTTGTCCCTG
	R:CAG <u>GAGCTC</u> TTAACCTGTTGTGTGGTT
AD-PIF3	F: CTC <u>GAATTC</u> ATGCCTCTGTTTGAGCTTTTC
	R: CAG <u>GAGCTC</u> TCACGACGATCCACAAAAC
AD-PIF5	F:CTC <u>GAATTC</u> ATGGAACAAGTGTTTGCTG
	R:CAG <u>GAGCTC</u> TCAGCCTATTTTACCCATAT

172173

Primers for constructs in pull-down assays

Construct name	Primers (5'-3')
GST-PIF4	F: CCG <u>GAATTC</u> ATGGAACACCAAGGTTGGAG
	R: CGA <u>CTCGAG</u> CTAGTGGTCCAAACGAGAA
His-LEC1	F: CGC <u>GGATCC</u> ATGGAACGTGGAGCTCCCTT
	R: ACGC <u>GTCGAC</u> CTTATACTGACCATAATGGT

174 175

Primers for ChIP assays

Gene name	Primers (5'-3')
IAA19	P1 F:GATGAAAACCAAACACTGCTCC
	P1 R: CCAAAGGCTACCAAACGAC
	P2 F: CAAACCTGAACCCAAAACATAC
	P2 R: CCGCTTTAATCTCACATGGAG
	P3 F: CCCCACTTTGTCTCCCCACA
	P3 R: CACCGCGTCGTGCTTTT
YUC8	P1 F: CAACTCCCAATAAAAGAC
	P1 R: TTTTCTGGTTTCCTCAAT
	P2 F: ATTCTGCATTTGGTTCCA
	P2 R: GGGTGATTCTTTGTGGGAC
	P3 F: TAAGCAATCATACTCACA
	P3 R: TTTTCCACTCGACGATAT
IAA29	P1 F: GCAAGACTAAGTGTAAAGTGG
	P1 R: TCGTGGCGTAATGTCGGGTC
	P2 F: GTCAAATAGGGGAGGAGGTACT
	P2 R: TACGGTTTGCCTATCCTGAG
	P3 F: ATAAATAGTAGCGTGTTGG
	P3 R: TATAGTAAAAGGAAATGGG
ATHB-2	P1 F: ATGTCACGCGGGTAATGGT
	P1 R: AGGGCTCGTGGCATGTTTT

Supplemental Data. Huang et al. (2015). Plant Cell 10.1105/tpc.15.00750

P2 F: TTAGGGAAGAACAAGAAGTA
P2 R: GATATTATGAGCCAGTGAGA
P3 F: AGAGTCATCAAGAAGGGTAATC
P3 R: GCACATCCAACAATAGTAAAATC

176177

Primers for constructs in BiFC assays

Construct name	Primers (5'-3')
35S:LEC1-EYFP ^C	F: CCG <u>CTCGAG</u> GAATGGAACGTGGAGCTCCCTT
	R: CGC <u>GGATCC</u> GCTTATACTGACCATAATGGT
35S:PIF4-EYFP ^N	F:CCGCTCGAGGAATGGAACACCAAGGTTGGAG
	R:CGC <u>GGTACC</u> GGTGGTCCAAACGAGAACC

178179

Primers for transient transactivation assays

Gene name	Primers (5'-3')
pIAA19-GUS	F: CTG <u>CTGCAG</u> AAGAAACATGAGACATGTCA
	R: CTG <u>GGATCC</u> TTCTTGAACTTCTTTTTTCC
mpIAA19-GUS	F1: ATTTCATATAATTTCACGgGGCCCAACTTG
	R1: CAAGTTGGGCCcCGTGAAATTATATGAAAT
	F2: GATATCAAATGACTCCACGgGTCGATATTG
	R2: CAATATCGACcCGTGGAGTCATTTGATATC

180 181

Oligos for EMSA probes

Probe name	Primers (5'-3')
IAA19 wt probe	gaagactttagatatcaaatgactcCACGTGtcgatattggattggttttcattgg
IAA19 mut probe	gaagactttagatatcaaatgactcCACGgGtcgatattggattggttttcattgg

182

183 Primers for Arabidopsis mutant genotyping

Mutant name	Primers (5'-3')
lec1-4	P1: AGAGTAAGTTTGTGGGGTCTA
	P2: ATCTACGGTTCATGTGATTCA
pif4-2	P1: TAAATCTCAACATCTCCAT
	P2: AGAACTAATACCTCACTGC
T-DNA left border primer	LB1.3: ATTTTGCCGATTTCGGAAC