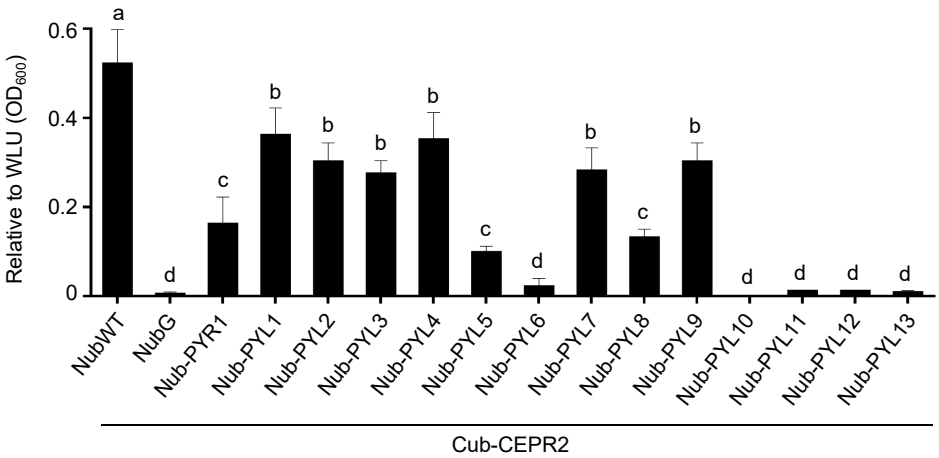
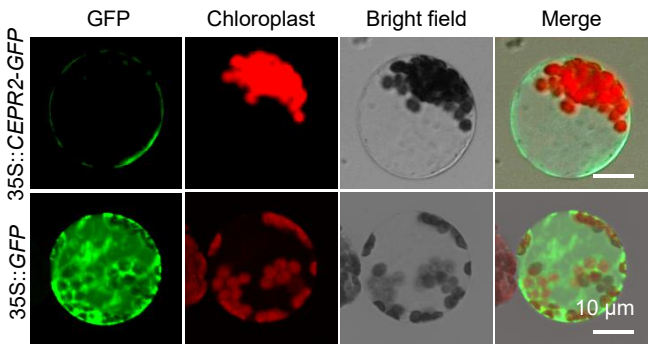
Supplementary Figure S1



Supplementary Figure S1. CEPR2 interacts with PYR/PYLs in yeast.

The interaction of CEPR2 with all PYLs were detected in yeast, and then the absorbance values of yeast cultured in -WLUAH liquid medium were measured by spectrophotometer at OD_{600}. Three replicates were conducted. Error bars indicate SD (n = 18), $p < 0.05$. One-way ANOVA Duncan's test was used for statistical analysis. Statistical differences are indicated by lowercase letters and different letters represent different significance. WLUAH: Trp, Leu, Ura, Ade and His.

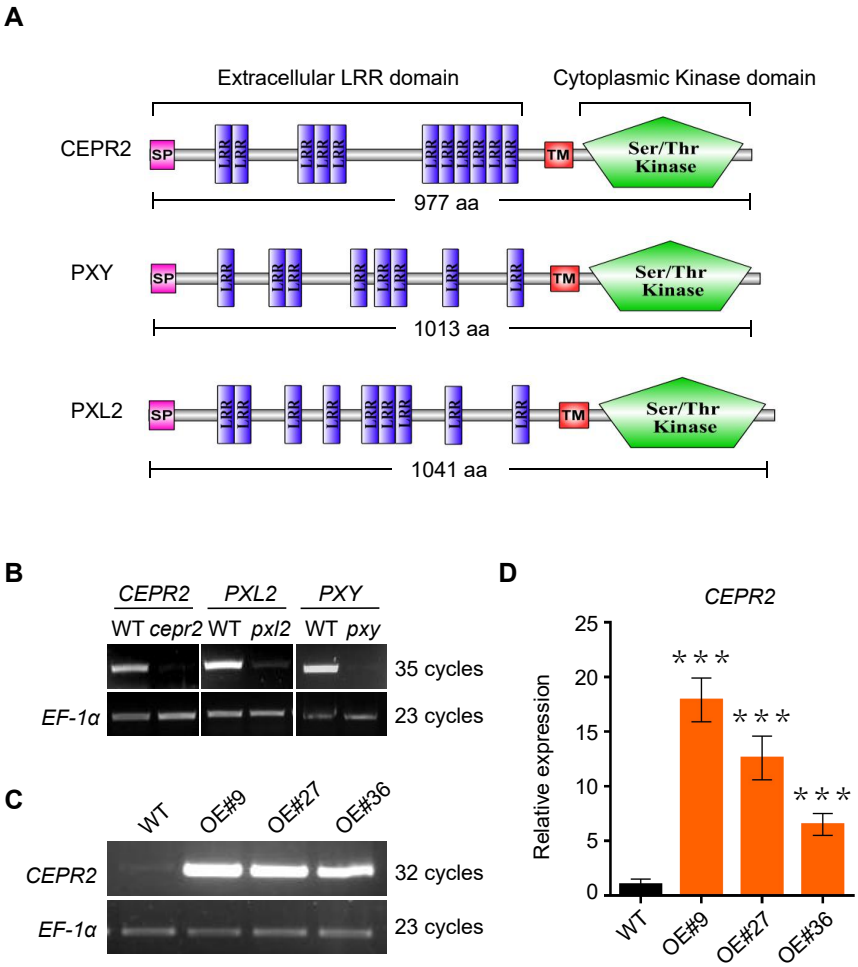
Supplementary Figure S2



Supplementary Figure S2. CEPR2 is localized in plasma membrane.

The GFP fluorescence of 35S::*CEPR2-GFP* transgenic protoplast was imaged by confocal microscopy at 488 nm. 35S::*GFP* was used as control.

Supplementary Figure S3



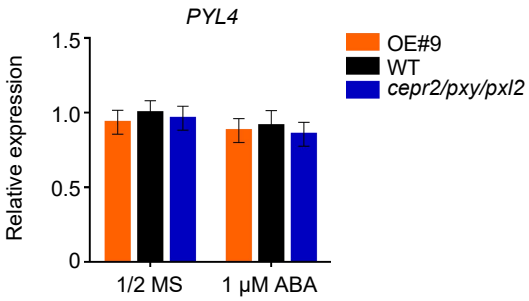
Supplementary Figure S3. Identification of different mutants and *CEPR2*-OE lines.

(A) The protein structures of CEPR2, PXY and PXL2. SP, signal peptide; TM, transmembrane.

(B) Identification of the different T-DNA insertion mutants by RT-PCR.

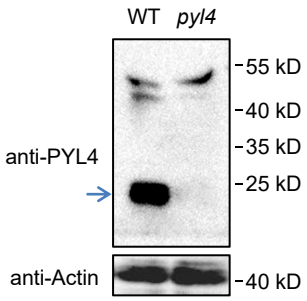
(C and **D)** The expression levels of *CEPR2* in different OE lines were detected by RT-PCR and qRT-PCR. Error bars in **(D)** indicate SEM ($N = 3$). ***$P < 0.001$ (Student's *t*-test).

Supplementary Figure S4



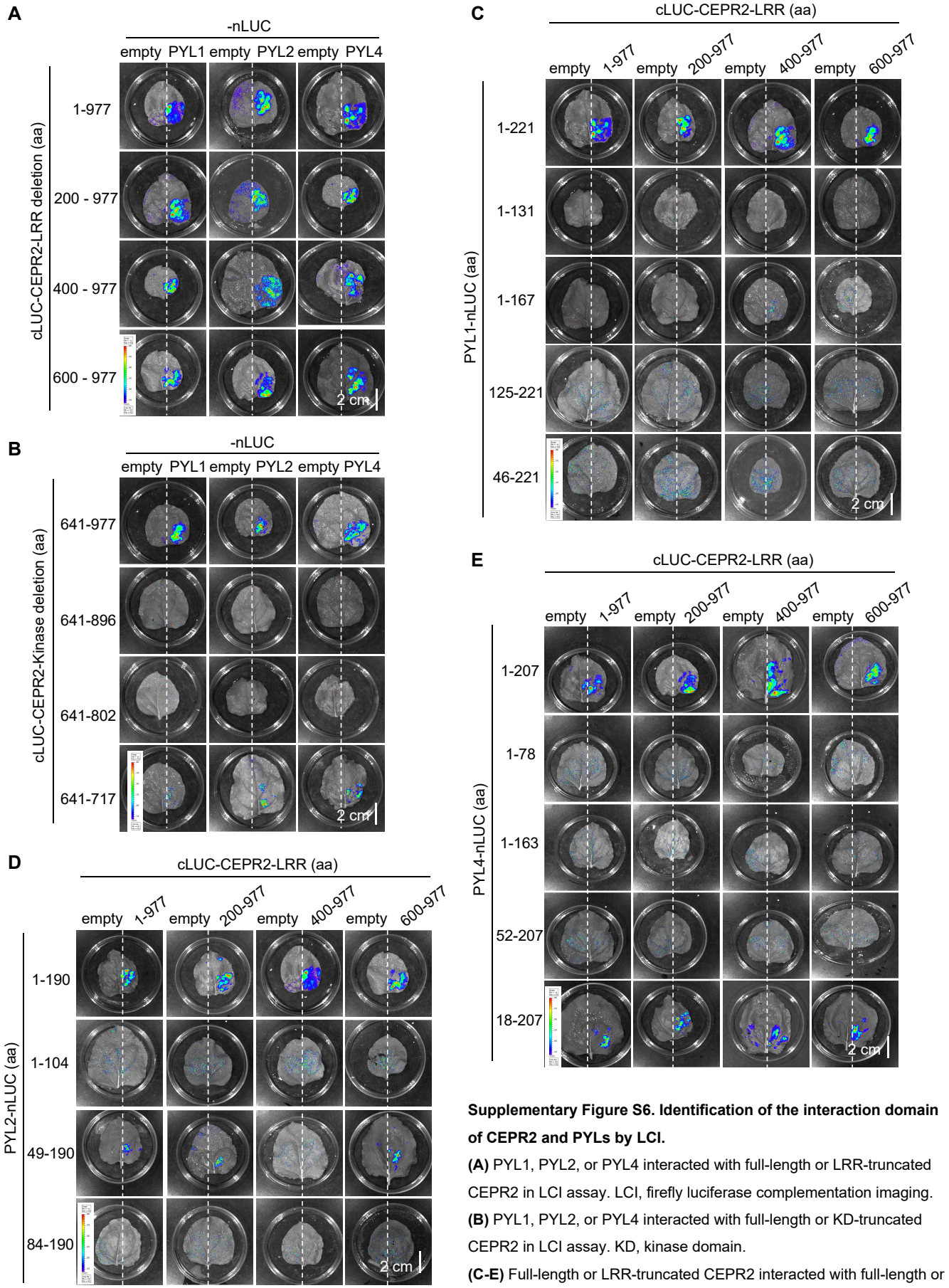
Supplementary Figure S4. CEPR2 does not regulate the transcript levels of *PYL4*.
The expression levels of *PYL4* in OE#9, WT and *cepr2/pxy/pxl2* lines grown on 1/2 MS or 1 μM ABA for 7 d were analyzed by qRT-PCR.

Supplementary Figure S5



Supplementary Figure S5. Anti-PYL4 antibody can specifically recognize PYL4.
The specificity of anti-PYL4 provided by Dr. Xie was examined by western blot with 7-day-old seedlings of *pyl4* and WT grown on 1/2 MS.

Supplementary Figure S6



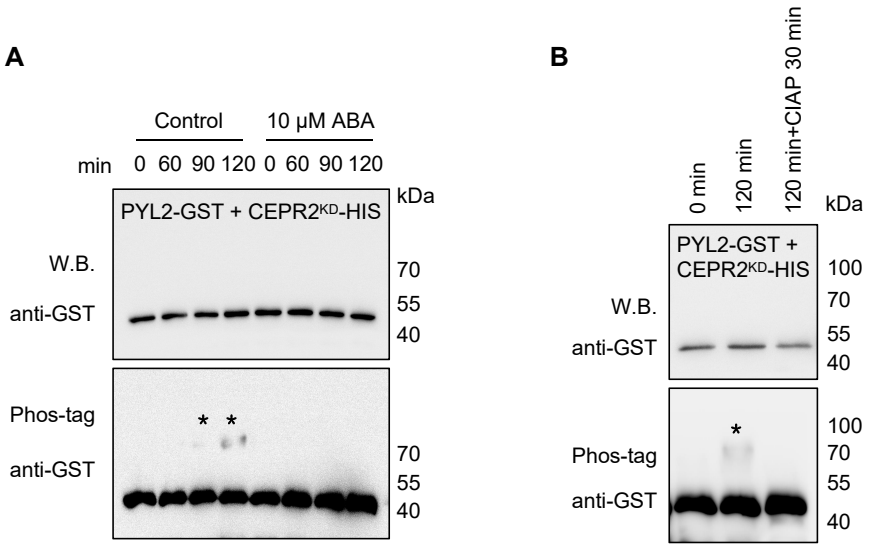
Supplementary Figure S6. Identification of the interaction domain of CEPR2 and PYLs by LCI.

(A) PYL1, PYL2, or PYL4 interacted with full-length or LRR-truncated CEPR2 in LCI assay. LCI, firefly luciferase complementation imaging.

(B) PYL1, PYL2, or PYL4 interacted with full-length or KD-truncated CEPR2 in LCI assay. KD, kinase domain.

(C-E) Full-length or LRR-truncated CEPR2 interacted with full-length or truncated PYL1, PYL2 or PYL4 in LCI assay.

Supplementary Figure S7



Supplementary Figure S7. CEPR2 phosphorylates PYL2 *in vitro*.

(A) *In vitro* kinase assays showed that PYL2 was phosphorylated by CEPR2^{KD}, while the phosphorylated PYL2 was disappeared under the ABA treatment condition. The W.B. assay was used to shown the loading control and un-phosphorylated PYL2. 50 μM phos-tag was used to isolate the phosphorylated forms of PYL2 in this kinase assay. W.B., western blot.

(B) CIAP successfully removed the phosphoryl group of PYL2 in this kinase assay. CIAP, Calf Intestinal Alkaline Phosphatase.

Supplementary Figure S8

The phosphorylation mass spectrometry protocol

Protein digestion was performed using FASP method with modifications (*Nature Methods* 6, 359 - 362 (2009). Briefly, 100 μg protein was dissolved with 50 mM ABC (NH_4HCO_3), reduced with DTT (dithiothreitol) at 56℃ for 45 min, and alkylated with IAM (iodoacetamide) at room temperature for 30 min in the dark. The solution was transferred into a 10K ultrafiltration tube (Vivacon 500, Satrorius), centrifuged at 14,000 g for 20 min. 50 mM ABC solution was used to wash the protein for 3 times. 2 μg trypsin was added in 50 μL 50 mM ABC and incubated at 37℃ overnight. The ultrafiltration tube was centrifuged at 14,000 g for 20 min with a new collection tube to collect digested peptides. ABC solution was added into the ultrafiltration tube to wash the digested peptide into the collection tube. The collected solution was diluted with 0.1% FA for nanoLC-MS analysis.

NanoLC separation was achieved with a Waters (Milford, MA, USA) nanoAcquity nanoHPLC. The trap column was Thermo Acclaim PepMap 100 (75 μm×2 mm, C18, 3 μm). The analytical column was homemade with 100 μm I.D. fused silica capillary (Polymicro) filled with 20 cm of C18 stationary phase (Phenomenex, Aqua 3 μm C18 125A). A gradient elution program was used, with mobile phase increases linearly from 1% B to 35% B in 65 min. Mobile phase A: 0.1% FA in water, B: 0.1% FA in acetonitrile.

Nanospray ESI-MS was performed on a Thermo Q-Exactive high resolution mass spectrometer (Thermo, Waltham, MA, USA) with 70,000 MS scan resolution and 17,500 MS/MS scan resolution and top-10 MS/MS selection.

Raw data from the mass spectrometer were preprocessed with Mascot Distiller 2.4 for peak picking. The resulted peak lists were searched against database using Mascot 2.5 search engine. The search parameters are: Fixed modifications: Carbamidomethyl (C), Variable modifications: Oxidation (M) and Phosphorylation (S, T, Y). Enzyme: Trypsin, Maximum missed cleavages: 2, MS mass tolerance: 10 ppm, MSMS mass tolerance: 0.02 Da. Scaffold PTM was used to evaluated phosphorylation sites of the Mascot search results using Ascore algorithm.

Phosphorylation mass spectrometry

Protein View: AT2G38310.1

| Symbols: PYL4, RCAR10 | PYR1-like 4 | chr2:16050251-16050874 FORWARD LENGTH=207

Database: TAIR10
Score: 34253
Nominal mass (M_r): 22706
Calculated pI: 6.43

Sequence similarity is available as **an NCBI BLAST search of AT2G38310.1 against nr**.

Search parameters

MS data file: G:\UserData\Public\Data\2018\201803\20180328-Q1\shandong-4.raw
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M), Phospho (ST), Phospho (Y)

Protein sequence coverage: 98%

Matched peptides shown in ***bold red***.

```
  1 MLAVHRPSSA VSDGDSVQIP MMIASFQKRF PSLSRDSTAA RFHTHEVGPN
 51 QCCSAVIQEI SAPISTVWSV VRRFDNPQAY KHFLKSCSVI GGDGDNVGSL
101 RQVHVVSGLP AASSTERLDI LDDERHVISF SVVGGDHRLS NYRSVTTLHP
151 SPISGTVVVE SYVVDVPPGN TKEETCDFVD VIVRCNLQSL AKIAENTAAE
201 SKKKMSL
```

Query	Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Score	Expect	Rank	U	Peptide
30199	42 – 72	1196.9181	3587.7325	3587.6691	17.7	0	66	6e-007	1	U	R.FHTHEVGPNQCCSAVIQEISAPISTVWSVVR.R + Phospho (ST)
12258	82 – 101	733.6701	2197.9885	2196.9987	450	1	47	4.5e-005	1	U	K.HFLKSCSVIGGDGDNVGSLR.Q + Phospho (ST)
22569	82 – 101	550.5055	2197.9928	2196.9987	452	1	19	0.017	1	U	K.HFLKSCSVIGGDGDNVGSLR.Q + Phospho (ST)

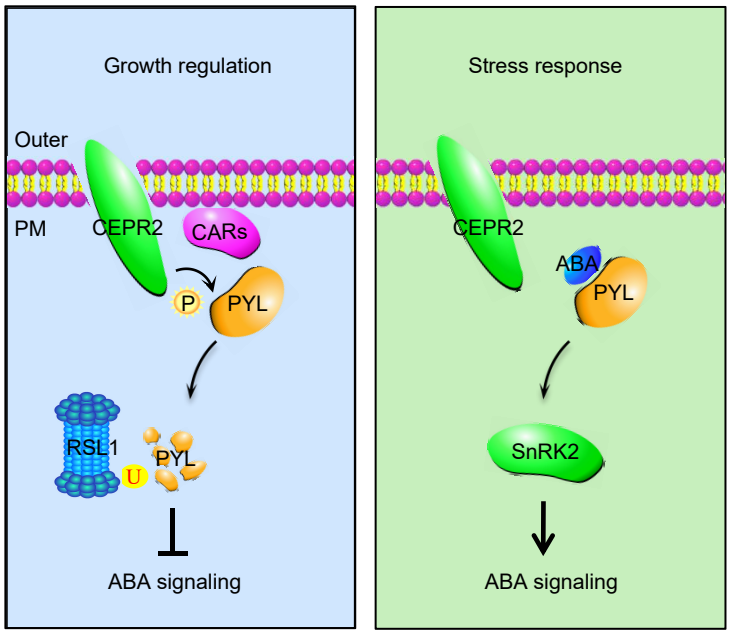
The final result,
the phosphorylation sites are marked in red

```
                                                    54
      MLAVHRPSSAVSDGDSVQIPMMIASFQKRFPSLSRDSTAARFHTHEVGPNQCCSAVIQEISAPISTVWSVVRRFDNPQA
            86 88
PYL4  YKHFLKSCSVIGGDGDNVGSLRQVHVVSGLPAASSTERLDILDDERHVISFSVVGGDHRLSNYRSVTTLHPSPISGTVVV

      ESYVVDVPPGNTKEETCDFVDVIVRCNLQSLAKIAENTAAESKKKMSL
```

Supplementary Figure S8. Identification of the phosphorylation sites of PYL4 in phosphorylation mass spectrometry.
The protein samples incubated in kinase buffer for 1 h were separated by SDS-PAGE to isolate the phosphorylated PYL4. Subsequently, the target proteins were cut and analyzed by phosphorylation mass spectrometry, three putative phosphorylation sites, S54, S86 and S88, were finally identified.

Supplementary Figure S9



Supplementary Figure S9. CEPR2-mediated phosphorylation optimizes the balance of growth regulation and stress response in Arabidopsis.

The phosphorylation of PYR/PYLs by CEPR2 promotes the ubiquitination of PYR/PYLs by RSL1, resulting in the repressed ABA signaling. However, ABA-bound PYLs successfully prevent this process and activate ABA signaling during times of stress. Taken together, plants utilize this phospho-regulatory mechanism to optimize the balance of growth and stress responses.

Supplementary Table S1. Primers used in this study

Purpose	Name	Sequence (5'-3')
Co-IP	CEPR2-LRR F	TCTAGAATGACCGTTGAGAAACAAGCTCT
	CEPR2-LRR R	CTCGAGTGTTCCATCGAGTGAACTATTCCTC
	CEPR2-KD F	CTCGAGCGTTACAGAGTTGTGAAGATACGTG
	CEPR2-KD R	GGTACCTACTGTAATCTTTCCAGTTGTGTC
	CEPR2-FL F	GGTACCATGACCGTTGAGAAACAAGCTCT
	CEPR2-FL R	CCCGGGTACTGTAATCTTTCCAGTTGTGTC
	RSL1 F	CACCATGGAGGAAGATGACCTAAACCC
	RSL1 R	ACAGCAGCACGAACCACAACATT
	CAR4 F	CACCTAAAGGAAATGACAACGGCGTGTC
	CAR4 R	TAGACCCTTGGAGCCAGGGA
	PYL2 F	CACCATGAGCTCATCCCCGGCC
	PYL2 R	TTCATCATCATGCATAGGTGCAGATG
	PYL4 F	CACCATGCTTGCCGTTCACCGT
	PYL4 R	CAGAGACATCTTCTTCTTGCTCT
BIFC	YFP^C-PYL1 F	CACCATGGCGAATTCAGAGTCCTC
	YFP^C-PYL1 R	CCTAACCTGAGAAGAGTTGTTG
	YFP^C-PYL4 F	CACCATGCTTGCCGTTCACCGT
	YFP^C-PYL4 R	CAGAGACATCTTCTTCTTGCTCT
	YFP^C-PYL9 F	CACCATGATGGACGGCGTTGAAG
	YFP^C-PYL9 R	CTGAGTAATGTCCTGAGAAGCC
	YFP^N-CEPR2 F	CACCATGTCGAGAAGACCAGACC
	YFP^N-CEPR2 R	TACTGTAATCTTTCCAGTTGTGTC
LCI	cLUC-CAR4 F	GGTACCATGACAACGGCGTGTCCG
	cLUC-CAR4 R	CTGCAGTCATAGACCCTTGGAGCCAG
	cLUC-PYL2 F	GGTACCATGAGCTCATCCCCGGCC
	cLUC-PYL2 R	GTCGACTTATTCATCATCATGCATAGGTGCAG
	cLUC-PYL4 F	GGTACCATGCTTGCCGTTCACCGTC
	cLUC-PYL4 R	GTCGACTCACAGAGACATCTTCTTCTTGCTC
	cLUC-RSL1 F	GGTACCATGGAGGAAGATGACCTAAACCC
	cLUC-RSL1 R	GTCGACTTACGAGAACCGTCTTACGAGT
	nLUC-RSL1 F	GGTACCATGGAGGAAGATGACCTAAACCC
	nLUC-RSL1 R	GTCGACCGAGAACCGTCTTACGAGT
	nLUC-CEPR2 F	GGTACCATGTCGAGAAGACCAGACCTC
	nLUC-CEPR2 R	GTCGACACTGTAATCTTTCCAGTTGTGTC
MbSUS	Nub-CEPR2 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGTCGAGAAGACCAGACCT
	Nub-CEPR2 R	tccgccaccaccaaccactttgtacaagaaagctgggtaCTATACTGTAATCTTTCCAGTTGTGTC
	Cub-CEPR2 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGTCGAGAAGACCAGACCT
	Cub-CEPR2 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTACTGTAATCTTTCCAGTTGTGTC
	Nub-PYR1 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGCCTTCGGAGTTAACACCAG
	Nub-PYR1 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTCACGTCACCTGAGAACCAC
	Nub-PYL1 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGGCGAATTCAGAGTCCTC
	Nub-PYL1 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTACCTAACCTGAGAAGAGT
	Nub-PYL2 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGAGCTCATCCCCGGCC
	Nub-PYL2 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTATTCATCATCATGCATAGGTGCAGA
	Nub-PYL3 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGAATCTTGCTCCAATCCATGA
	Nub-PYL3 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTCAGGTCGGAGAAGCCGT
	Nub-PYL4 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGCTTGCCGTTCACCGTC
	Nub-PYL4 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTCACAGAGACATCTTCTTCT
	Nub-PYL5 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGAGGTCACCGGTGCAAC
	Nub-PYL5 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTATTGCCGGTTGGTACTTC
	Nub-PYL6 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGCCAACGTCGATACAGTTTCA
	Nub-PYL6 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTACGAGAATTTAGAAGTGTTCTCG
	Nub-PYL7 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGGAGATGATCGGAGGAGA
	Nub-PYL7 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTCAAAGGTTGGTTTCTGTATGATTC
	Nub-PYL8 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGGAAGCTAACGGGATTGA
	Nub-PYL8 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTAGACTCTCGATTCTGTCG
	Nub-PYL9 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGATGGACGGCGTTGAA
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	Nub-PYL10 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGAACGGTGACGAAACAAAGAA
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	Nub-PYL11 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTACAACTTTAGATGAGCCA
	Nub-PYL12 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGAAAACATCTCAAGAACAGC
	Nub-PYL12 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTAAGTGAGCTCCATCATCT
	Nub-PYL13 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGGAAAGTTCTAAGCAAAAACG
	Nub-PYL13 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTACTTCATCATTTTCTTTGTGAGC
	Nub-ABI1 F	ACAAGTTTGTACAAAAAAGCAGGCTCTCCAACCACCATGGAGGAAGTATCTCCGG
	Nub-ABI1 R	TCCGCCACCACCAACCACTTTGTACAAGAAAGCTGGGTATCAGTTCAAGGGTTTGCTCT
	Nub-ABI2 F	ACAAGTTTGTACAAAAAAGCAGGCTCTCCAACCACCATGGACGAAGTTTCTCCTG
	Nub-ABI2 R	TCCGCCACCACCAACCACTTTGTACAAGAAAGCTGGGTATCAATTCAAGGATTTGCTCT

MbSUS	Nub-SnRk2.2 F	ACAAGTTTGTACAAAAAAGCAGGCTCTCCAACCACCATGGATCCGGCGACTAATTC
	Nub-SnRk2.2 R	TCCGCCACCACCAACCACTTTGTACAAGAAAGCTGGGTATCAGAGAGCATAAACTATCTCTCC
	Nub-SnRk2.3 F	ACAAGTTTGTACAAAAAAGCAGGCTCTCCAACCACCATGGATCGAGCTCCGGTGA
	Nub-SnRk2.3 R	TCCGCCACCACCAACCACTTTGTACAAGAAAGCTGGGTATTAGAGAGCGTAAACTATCTCTCCGC
	Nub-SnRk2.6 F	ACAAGTTTGTACAAAAAAGCAGGCTCTCCAACCACCATGGATCGACCAGCAGT
	Nub-SnRk2.6 R	TCCGCCACCACCAACCACTTTGTACAAGAAAGCTGGGTATCACATTGCGTACACAATCT
	Nub-ABI4 F	ACAAGTTTGTACAAAAAAGCAGGCTCTCCAACCACCATGGACCCTTTAGCTTCCCA
	Nub-ABI4 R	TCCGCCACCACCAACCACTTTGTACAAGAAAGCTGGGTATTAATAGAATTCCCCCAAGATGGG
	Nub-ABI5 F	ACAAGTTTGTACAAAAAAGCAGGCTCTCCAACCACCATGGTAACTAGAGAAACGAAG
	Nub-ABI5 R	TCCGCCACCACCAACCACTTTGTACAAGAAAGCTGGGTATTAGAGTGGACAACTCGG
	Nub-CAR1 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGGAGAATCTTGTAGGTCTTCTTCG
	Nub-CAR1 R	tccgccaccaccaaccactttgtacaagaaagctgggtaCTAAATACCCCTTGAACCCGG
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	Nub-CAR8 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGGAGAATCTGGTGGGACT
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	Nub-CAR10 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTAGGTAGAGGAAGAGCCTCCA
	Nub-PYL1-1~131aa F	acaagtttgtacaaaaaagcaggctctccaaccaccATGGCGAATTCAGAGTCCTC
	Nub-PYL1-1~131aa R	tccgccaccaccaaccactttgtacaagaaagctgggtaTCTCCGATCATCGTCCAA
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	Nub-PYL1-46~221aa F	acaagtttgtacaaaaaagcaggctctccaaccaccATGGAGTTCCACACGTACCAACT
	Nub-PYL1-46~221aa R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTACCTAACCTGAGAAGAGTTGTTG
	Nub-PYL2-1~104 aa F	acaagtttgtacaaaaaagcaggctctccaaccaccATGAGCTCATCCCCGGCC
	Nub-PYL2-1~104 aa R	tccgccaccaccaaccactttgtacaagaaagctgggtaATCGACGAACTCAAGCCGCT
	Nub-PYL2-49~190 aa F	acaagtttgtacaaaaaagcaggctctccaaccaccATGGTGGTTTGGCCTCTTATCCG
	Nub-PYL2-49~190 aa R	tccgccaccaccaaccactttgtacaagaaagctgggtaTTATTCATCATCATGCATAGGTGCAGA
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	Nub-CAR8-74-165 aa R	tccgccaccaccaaccactttgtacaagaaagctgggtaTCAAAAATCGCTTGAACCAG
	Cub-CEPR2-LRR 200 - 621 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGTTAGCTCGCTCCAACTTGACC
	Cub-CEPR2-LRR 200 - 621 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTACTGTAATCTTTCCAGTTGTGTC
	Cub-CEPR2-LRR 400 - 621 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGCAAGTTGTTGAAGGATTCTGGTCT
	Cub-CEPR2-LRR 400 - 621 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTACTGTAATCTTTCCAGTTGTGTC
	Cub-CEPR2-LRR 600 - 621 F	acaagtttgtacaaaaaagcaggctctccaaccaccATGTTGGGGTTGAGTATTTGCAGT
	Cub-CEPR2-LRR 600 - 621 R	tccgccaccaccaaccactttgtacaagaaagctgggtaTACTGTAATCTTTCCAGTTGTGTC
	Cub-CEPR2-KD 642-650 aa F	acaagtttgtacaaaaaagcaggctctccaaccaccATGTCGAGAAGACCAGACCTC
	Cub-CEPR2-KD 642-650 aa R	tccgccaccaccaaccactttgtacaagaaagctgggtaACGTATCTTCACAACTCTGTAACGC
	Cub-CEPR2-KD 642-717 aa F	acaagtttgtacaaaaaagcaggctctccaaccaccATGTCGAGAAGACCAGACCTC
	Cub-CEPR2-KD 642-717 aa R	tccgccaccaccaaccactttgtacaagaaagctgggtaCTTCAACCACTTAACCGCCA
	Cub-CEPR2-KD 642-802 aa F	acaagtttgtacaaaaaagcaggctctccaaccaccATGTCGAGAAGACCAGACCTC
	Cub-CEPR2-KD 642-802 aa R	tccgccaccaccaaccactttgtacaagaaagctgggtaTGCGATTCCTTTTGCCGCT
	Cub-CEPR2-KD 642-896 aa F	acaagtttgtacaaaaaagcaggctctccaaccaccATGTCGAGAAGACCAGACCTC
	Cub-CEPR2-KD 642-896 aa R	tccgccaccaccaaccactttgtacaagaaagctgggtaCTCTCCAAACTCGTCTTCCA

Deletion analysis for LCI assay	cLUC-PYL1-1~131aa F	GGTACCATGGCGAATTCAGAGTCCTC
	cLUC-PYL1-1~131aa R	GTCGACTTATCTCCGATCATCGTCCAA
	cLUC-PYL1-1~167aa F	GGTACCATGGCGAATTCAGAGTCCTC
	cLUC-PYL1-1~167aa R	GTCGACTTAGGTCCAGATCCTTTCTTC
	cLUC-PYL1-125~221aa F	GGTACCATGCTGTTGGACGATGATCG
	cLUC-PYL1-125~221aa R	GTCGACTTACCTAACCTGAGAAGAGTTGTTG
	cLUC-PYL1-46~221aa F	GGTACCATGGAGTTCCACACGTACCAAC
	cLUC-PYL1-46~221aa R	GTCGACTTACCTAACCTGAGAAGAGTTGTTG
	cLUC-PYL2-1~104 aa F	GGTACCATGAGCTCATCCCCGGCC
	cLUC-PYL2-1~104 aa R	GTCGACTTAATCGACGAACTCAAGCCGCTC
	cLUC-PYL2-49~190 aa F	GGTACCATGGTGGTTTGGCCTCTTATCCG
	cLUC-PYL2-49~190 aa R	GTCGACTTATTCATCATCATGCATAGGTGCAGA
	cLUC-PYL2-84~190 aa F	GGTACCATGGAAGTGACCGTAATCTCCGG
	cLUC-PYL2-84~190 aa R	GTCGACTTATTCATCATCATGCATAGGTGCAGA
	cLUC-PYL4-1~78 aa F	GGTACCATGCTTGCCGTTCACCGTC
	cLUC-PYL4-1~78 aa R	GTCGACTCATTGTGGGTTATCAAAGCGGC
	cLUC-PYL4-1~163 aa F	GGTACCATGCTTGCCGTTCACCGTC
	cLUC-PYL4-1~163 aa R	GTCGACTCAGACGTAAGACTCGACAACGA
	cLUC-PYL4-52~207 aa F	GGTACCATGTGTTGCTCCGCCGTTATTCA
	cLUC-PYL4-52~207 aa R	GTCGACTCACAGAGACATCTTCTTCTTGCTC
	cLUC-PYL4-18~207aa F	GGTACCATGCAGATTCCGATGATGATCGC
	cLUC-PYL4-18~207 aa R	GTCGACTCACAGAGACATCTTCTTCTTGCTC
	nLUC-CEPR2-LRR 200 - 621 F	GGTACCATGTTAGCTCGCTCCAACTTGACC
	nLUC-CEPR2-LRR 200 - 621 R	GTCGACTACTGTAATCTTTCCAGTTGTGTC
	nLUC-CEPR2-LRR 400 - 621 F	GGTACCATGCAAGTTGTTGAAGGATTCTGGTCT
	nLUC-CEPR2-LRR 400 - 621 R	GTCGACTACTGTAATCTTTCCAGTTGTGTC
	nLUC-CEPR2-LRR 600 - 621 F	GGTACCATGTTGGGGTTGAGTATTTGCAGT
	nLUC-CEPR2-LRR 600 - 621 R	GTCGACTACTGTAATCTTTCCAGTTGTGTC
	nLUC-CEPR2-KD 642-650 aa F	GGTACCATGTCGAGAAGACCAGACCTC
	nLUC-CEPR2-KD 642-650 aa R	GTCGACACGTATCTTCACAACTCTGTAACGC
	nLUC-CEPR2-KD 642-717 aa F	GGTACCATGTCGAGAAGACCAGACCTC
	nLUC-CEPR2-KD 642-717 aa R	GTCGACCTTCAACCACTTAACCGCCA
	nLUC-CEPR2-KD 642-802 aa F	GGTACCATGTCGAGAAGACCAGACCTC
	nLUC-CEPR2-KD 642-802 aa R	GTCGACTGCGATTCCTTTTGCCGCT
	nLUC-CEPR2-KD 642-896 aa F	GGTACCATGTCGAGAAGACCAGACCTC
	nLUC-CEPR2-KD 642-896 aa R	GTCGACCTCTCCAAACTCGTCTTCCA
Pull down and *in vitro* kinase assays	CEPR2-pET30a F	GGATCCCGTTACAGAGTTGTGAAGATACGT
	CEPR2-pET30a R	GTCGACTACTGTAATCTTTCCAGTTGTGTC
	PYL2-pGEX 4t-1 F	GGATCCATGAGCTCATCCCCGGCC
	PYL2-pGEX 4t-1 R	GAATTCTTATTCATCATCATGCATAGGTGCAGA
	PYL4-pGEX 4t-1 F	GGATCCATGCTTGCCGTTCACCGTC
	PYL4-pGEX 4t-1 R	GAATTCTCACAGAGACATCTTCTTCTTGCTC
T-DNA	*cepr2* LP	TCACAACTCTGTAACGCAACG
	cepr2 RP	AACTCGGAGTTTTGAAGGAGC
	pxy LP	AATCTCGATTCGTGCAACATC
	pxy RP	GTTTCGGAGTCAAAACAATCG
	pxl2 LP	TCGAACGAATCAGTTTATCGG
	pxl2 RP	AATGGCCTTGGAGATTAATGG
	LB	TCAAACAGGATTTTCGCCTGCT
qRT (60℃)	qRT-ABI1 F	TCCATTATCCGTTGACCATA
	qRT-ABI1 R	CATCTTCTTTTACTCTCTTCACA
	qRT-ABI2 F	AGATACCTTAAACCGTCAGT
	qRT-ABI2 R	CGTTCTTCTTATGCCATAGTAA
	qRT-PYL1 F	TAGATTTGAGAAAGAAGAAGAAGAA
	qRT-PYL1 R	AGAGTTGTTGTTGTTGTTGT
	qRT-PYL4 F	TCTAACTACCGATCCGTAAC
	qRT-PYL4 R	GACATCTTCTTCTTGCTCTC
	qRT-SnRK2.2 F	TCAAGTCTTCTGTTCTTCATTC
	qRT-SnRK2.2 R	GCTCCAACCAACATTACATAT
	qRT-SnRK2.3 F	AGTCTTCTGTTCTTCATTCAC
	qRT-SnRK2.3 R	GATAGTCTCTTGGCTCTTCT
	qRT-SnRK2.6 F	CTAATGAACGATAACACGATGA
	qRT-SnRK2.6 R	TCTCTAAGTCTTCCTCCATATC
	qRT-ABI4 F	CAACACCAACAGTATCAGAAT
	qRT-ABI4 R	ACTATTATTATTACACCCACTTCC
	qRT-ABI5 F	GTAGTAGTAGTAGTAATGGACAGA
	qRT-ABI5 R	CGGGTTTGGATTAGGTTTAG
	qRT-RAB18 F	GCAGCAGTATGACGAGTA
	qRT-RAB18 R	AGTTCCAAAGCCTTCAGT
	qRT-LUC F	CAGGTATCAGGCAAGGATAT
	qRT-LUC R	TAATCATAGGACCTCTCACAC

RT	RT-CEPR2 F	ACAATTCTTGCTCGCCTTGCAGA
	RT-CEPR2 R	GGATTTCACCTGTTAGCCTATTCCCT
	RT-PXL2 F	CATGATCGGAATGGGAGCAACC
	RT-PXL2 R	CGGCGACCATTGAAACGGTT
	RT-PXY F	CTCTCAACCAATTTCTTCCACAGGA
	RT-PXY R	CAATATCCAAACAATAGCTCCGGCTG
	RT-EF-1α F	gtatggttgttacctttgctcccacag
	RT-EF-1α R	catcatttggcacccttcttcactgc