

Supplementary Information for

C-TERMINAL DOMAIN PHOSPHATASE-LIKE 1 protein promotes flowering with TAF15b by repressing the floral repressor gene *FLOWERING LOCUS C*

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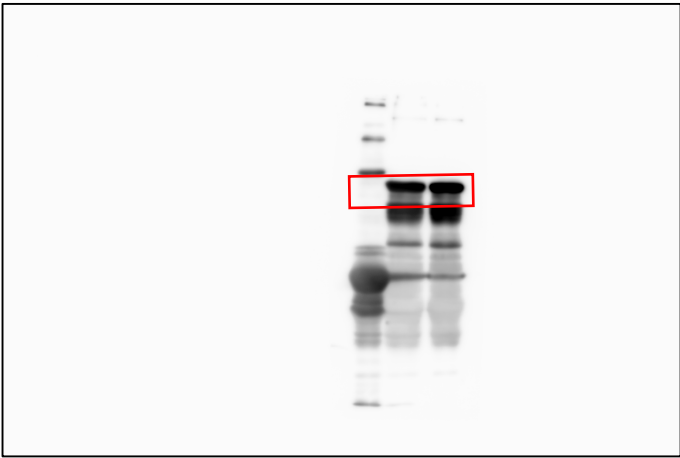
This document file includes:

Supplementary Figures. S1 to S4

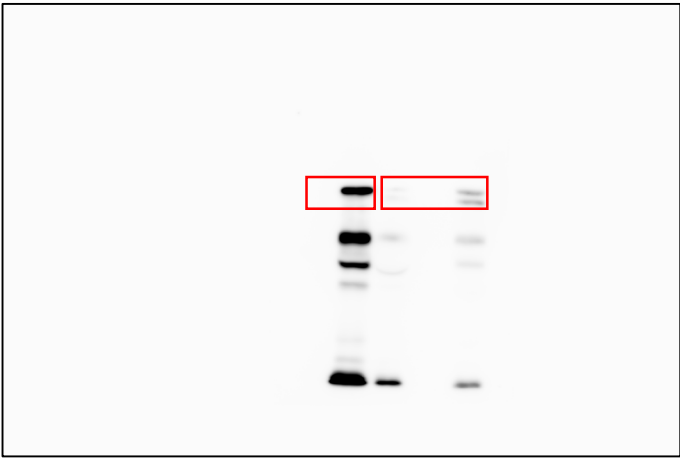
Supplementary Tables S1 and S2

a

α -MBP	input		
TAF15b-GFP	+	-	+
MBP-CPL1 ^{RBD}	-	+	+



α -MBP	input		IP		
TAF15b-GFP	-	+	+	-	+
MBP-CPL1 ^{RBD}	+	+	-	+	+

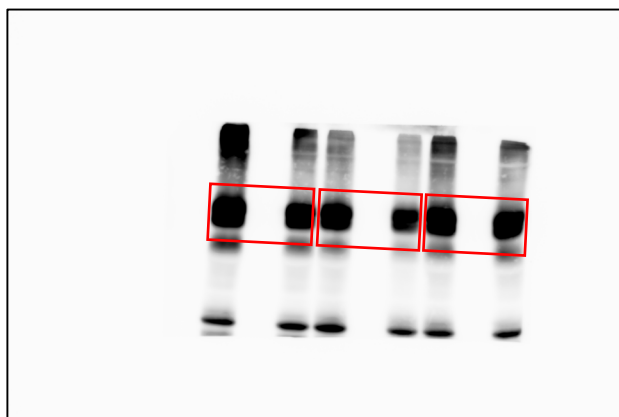


Supplementary Figure S1. Original images of representative immunoblot of semi-*in vivo* pull-down assay products

Original images used for representative immunoblot figures in **Fig. 1c** were displayed. Red boxes denote MBP-CPL1^{RBD} (**a**) and TAF15b-GFP (**b**) proteins.

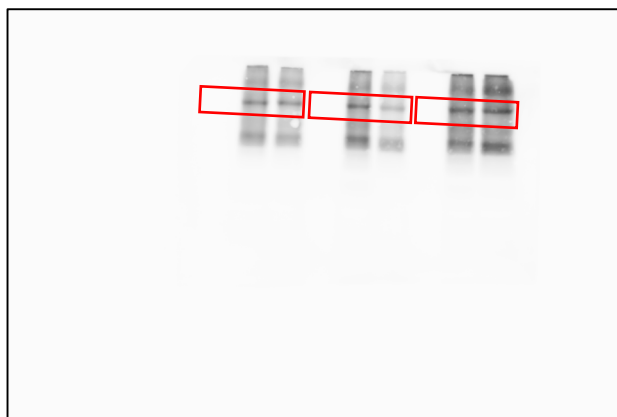
a

input α -GFP	replicate #1			replicate #2			replicate #3		
TAF15b-GFP	+	-	+	+	-	+	+	-	+
Myc-CPL1	-	+	+	-	+	+	-	+	+



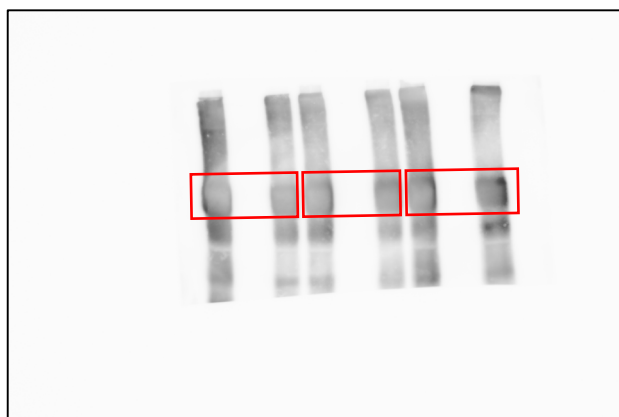
b

input α -Myc	replicate #1			replicate #2			replicate #3		
TAF15b-GFP	+	-	+	+	-	+	+	-	+
Myc-CPL1	-	+	+	-	+	+	-	+	+



c

IP α -GFP	replicate #1			replicate #2			replicate #3		
TAF15b-GFP	+	-	+	+	-	+	+	-	+
Myc-CPL1	-	+	+	-	+	+	-	+	+



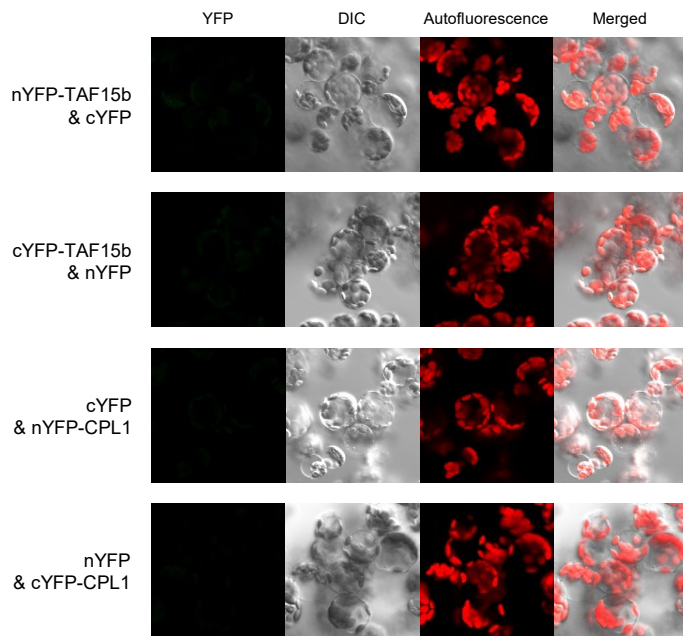
d

IP α -Myc	replicate #1			replicate #2			replicate #3		
TAF15b-GFP	+	-	+	+	-	+	+	-	+
Myc-CPL1	-	+	+	-	+	+	-	+	+



Supplementary Figure S2. Original images of co-immunoprecipitation products.

Original images used for representative immunoblot figures in **Fig. 1d** were displayed. Red boxes denote TAF15b-GFP (**a**, **c**) and Myc-CPL1 (**b**, **d**) proteins.

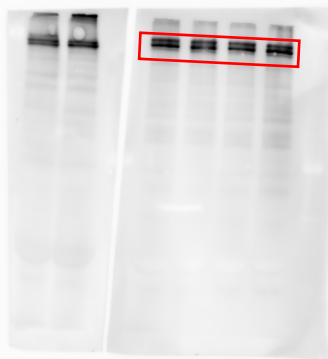


Supplementary Figure S3. Negative control of the BiFC between TAF15b and CPL1.

BiFC analysis result of each construct used in **Figure 1e** and empty vector (nYFP or cYFP) were shown. *A. thaliana* mesophyll protoplasts were transfected with the indicated plasmid constructs. No YFP signal is observed in all represented sets.

a

α -Pol II				
Col	<i>cpl1</i>	<i>taf1 5b</i>	<i>taf1 5b</i>	<i>cpl1</i>



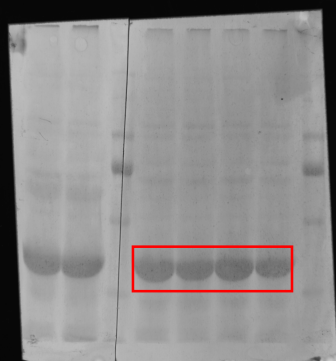
b

α -Pol II Ser5P				
Col	<i>cpl1</i>	<i>taf1 5b</i>	<i>taf1 5b</i>	<i>cpl1</i>

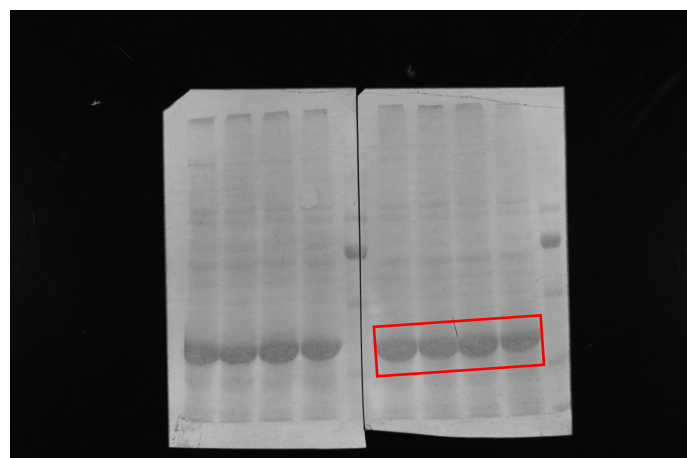
α -Pol II Ser2P				
Col	<i>cpl1</i>	<i>taf1 5b</i>	<i>taf1 5b</i>	<i>cpl1</i>



c



d



Supplementary Figure S4. Original images of representative Pol II proteins

Original images used for representative immunoblot figures in **Fig. 5a** were displayed. Red boxes denote total Pol II (**a**), Pol II Ser5P (**b**), Pol II Ser2P (**b**), and Rubisco (**c**, **d**)

Supplementary Table S1. Gene ontology enriched in common targets of TAF15b and CPL1.

Gene ontology analysis was performed using the upregulated genes or downregulated genes in both *taf15b-1* and *cpl1-7*. x, the number of genes in the cluster annotated to a particular GO class; X, the total number of genes in the cluster; n, the number of genes in the reference set annotated to a particular GO class; N, the total number of genes in the reference set.

up-regulated in cpl1-7 and taf15b-1

corr p-value	x	n	X	N	Description
7.72E-03	12	3207	25	22304	response to stimulus
1.51E-02	2	21	25	22304	response to oxygen levels
2.69E-02	8	1853	25	22304	response to stress
4.52E-02	7	1710	25	22304	response to chemical stimulus
4.52E-02	1	2	25	22304	regulation of defense response to virus by host
4.52E-02	1	2	25	22304	response to anoxia
4.52E-02	1	3	25	22304	regulation of defense response to virus
4.52E-02	1	3	25	22304	arsenite transport
4.52E-02	1	3	25	22304	regulation of immune effector process

down-regulated in cpl1-7 and taf15b-1

corr p-value	x	n	X	N	Description
1.84E-04	4	30	66	22304	S-glycoside biosynthetic process
1.84E-04	4	30	66	22304	glycosinolate biosynthetic process
1.84E-04	4	30	66	22304	glucosinolate biosynthetic process
4.14E-04	5	86	66	22304	sulfur compound biosynthetic process
4.14E-04	4	45	66	22304	S-glycoside metabolic process
4.14E-04	4	45	66	22304	glycosinolate metabolic process
4.14E-04	4	45	66	22304	glucosinolate metabolic process
1.15E-03	4	60	66	22304	glycoside biosynthetic process
4.06E-03	4	87	66	22304	glycoside metabolic process
4.06E-03	5	166	66	22304	sulfur metabolic process
1.07E-02	7	455	66	22304	response to light stimulus
1.21E-02	7	471	66	22304	response to radiation
1.80E-02	2	14	66	22304	syncytium formation
2.79E-02	2	18	66	22304	leaf vascular tissue pattern formation
3.13E-02	4	173	66	22304	cellular carbohydrate biosynthetic process
3.13E-02	2	21	66	22304	regulation of timing of meristematic phase transition
3.13E-02	2	21	66	22304	regulation of timing of transition from vegetative to reproductive phase
4.10E-02	5	330	66	22304	secondary metabolic process
4.10E-02	1	1	66	22304	glucosinolate biosynthetic process from homomethionine
4.10E-02	1	1	66	22304	cellular sodium ion homeostasis
4.10E-02	1	1	66	22304	sodium ion homeostasis
4.10E-02	1	1	66	22304	regulation of membrane potential

Supplementary Table S2. Primers used in the study

qRT-PCR		
gene	strand	sequence
UBC	F	TTGTGCCATTGAATTGAACCC
UBC	R	CATCCTAATGTTCAATTCAAGACAG
FT	F	GATACGAGTAACGAACGGTGAT
FT	R	CCCCCTCTCATTTTTATTACAC
SOC1	F	ATGAATTCGCCAGCTCCAAT
SOC1	R	GCTTCATATTTCAAATGCTGCA
FLC	F	AGCCAAGAAG^ACCGAACTCA
FLC	R	TTTGTCCAGCAGGTGACATC
FCA	F	GGTCAGAATGCTCAG GATTATG
FCA	R	TTCTTGGGGAGATTGACGGCT
FLD	F	AAGCGGAAGATGATCAG AAGG
FLD	R	ATTTGCCATTACCTAAAGACTCTG
FLK	F	GCTTGTATAGTCAGAGTTCTTGG
FLK	R	CAAGAACTTTCTGAGATGTGACG
FPA	F	GGGATTGAAACTAAACT GCCTG
FPA	R	AACGATCTCACATCCAATGGC
FVE	F	GGTGGAACATTGCAG ATATGG
FVE	R	TTAAGGCTTGGAGGCACAAGT
FY	F	TGGCGGACCCCAAATGTATC
FY	R	GTGGCTGCTGCTG CTGTTG
LD	F	GTCTCTCAAATGGAAAGTCAGAG
LD	R	TCATCAGCAGACATTGGGCG
TAF15b	F	TAGAGGAAATCGAGGCGGTG
TAF15b	R	CTGGGGTTGGGACAACGC
CPL1	F	AGATGAATTACATGCTCAGGTTG
CPL1	R	GCTCTCTCAGCAGCCTGC
ChIP		
gene	strand	sequence
FLC -2320 F	F	ATCCAGAAAAGGGCAAGGAG
FLC -2267 R	R	CGAATCGATTGGGTGAATG
FLC -1599 F	F	TGGAGGGAACAACCTAATGC
FLC -1530 R	R	TCATTGGACCAAACCAAACC
FLC -392 F	F	ACTATGTAGGCACGACTTTGGTAAC
FLC -272 R	R	TGCAGAAAGAACCTCCACTCTAC
FLC -49 F	F	GCCCGACGAAGAAAAAGTAG
FLC 53 R	R	TCCTCAGGTTTGGGTTCAAG
FLC 157 F	F	CGACAAGTCACCTTCTCCAAA
FLC 314 R	R	AGGGGGAACAAATGAAAACC
FLC 416 F	F	GGCGGATCTCTTGTGTTTC
FLC 502 R	R	CTTCTTCACGACATTGTTCTTCC
FLC 3197 F	F	GGGGCTGCGTTTACATTTTA
FLC 3333 R	R	GTGATAGCGCTGGCTTTGAT
FLC 5643 F	F	TGGTTGTTATTTGGTGGTGTG
FLC 5758 R	R	ATCTCCATCTCAGCTTCTGCTC
FLC 6057 F	F	CGTGTGAGAATTGCATCGAG
FLC 6175 R	R	AAAAACGCGCAGAGAGAGAG
FLC 6877 F	F	TTGTAAAGTCCGATGGAGACG
FLC 6947 R	R	ACTCGGCGAGAAAGTTTGTG
AtSN1	F	CCAGAAATTCATCTTCTTTGGAAAAG
AtSN1	R	GCCCAGTGGTAAATCTCTCAGATAGA
TA3	F	TGGAATCTCAGGGTCAAGG
TA3	R	CCTTCTGAGGTGAGGGACA
ACT7	F	GTATCGGGTGACAATGCAGCTATTATGT
ACT7	R	TGCTGGAGTAAAACATAAGCCACTCAC
FUS3	F	GTGGCAAGTGTTGATCATGG
FUS3	R	AGTTGGCACGTGGGAAATAG