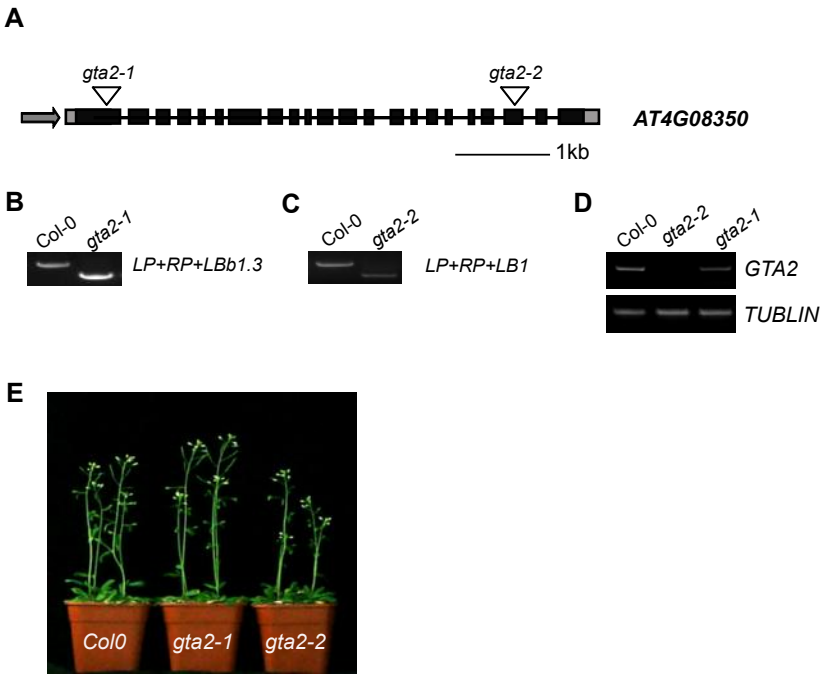
Supplemental Figure 1



Supplemental Figure 1. Phenotypic analysis of *gta2* mutants.

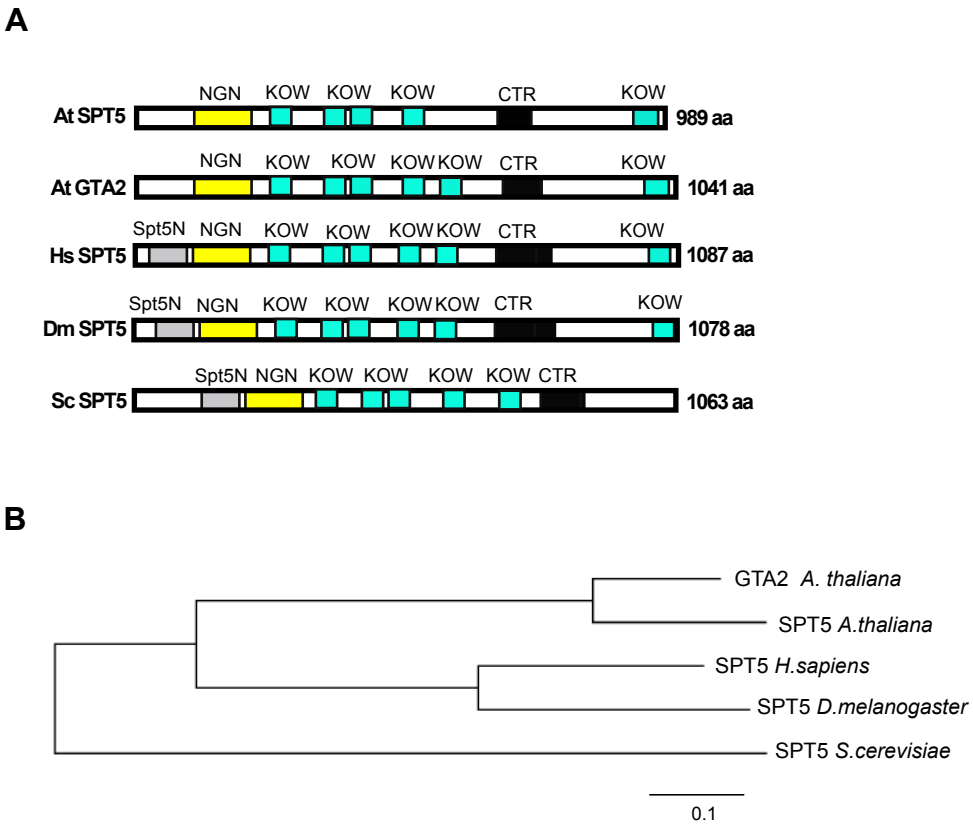
(A) Gene structure of *GTA2*. Exons are shown as boxes and introns are indicated as lines.

(B) and (C) Genotypic analysis of *gta2* mutants with left genomic primer (LP), right genomic primer (RP), and the vector primer (LBb1.3 or LB1)

(D) The transcripts of *GTA2* were tested in Col-0 and *gta2* mutants.

(E) The flowering time of Col-0 and *gta2* mutants.

Supplemental Figure 2



Supplemental Figure 2. Phylogenetic analysis of SPT5 proteins from Arabidopsis humans, *Drosophila*, and yeast.

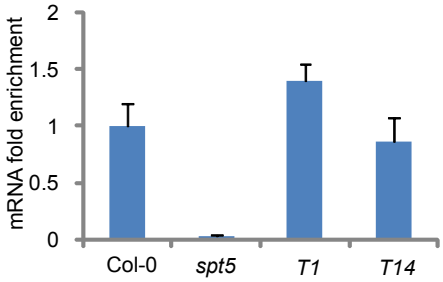
(A) Diagram of the domain structures of SPT5 proteins from Arabidopsis, humans, *Drosophila*, and yeast. Proteins all contain NGN (yellow boxes), KOW (blue boxes), and CTR (black boxes) domains. aa = amino acids.

(B) The SPT5 proteins from Arabidopsis, human, *Drosophila*, and yeast were aligned with ClustalW. The relationships of those sequences were examined with MEGA5. The evolutional scar bar was indicated in bottom.

Supplemental Figure 3

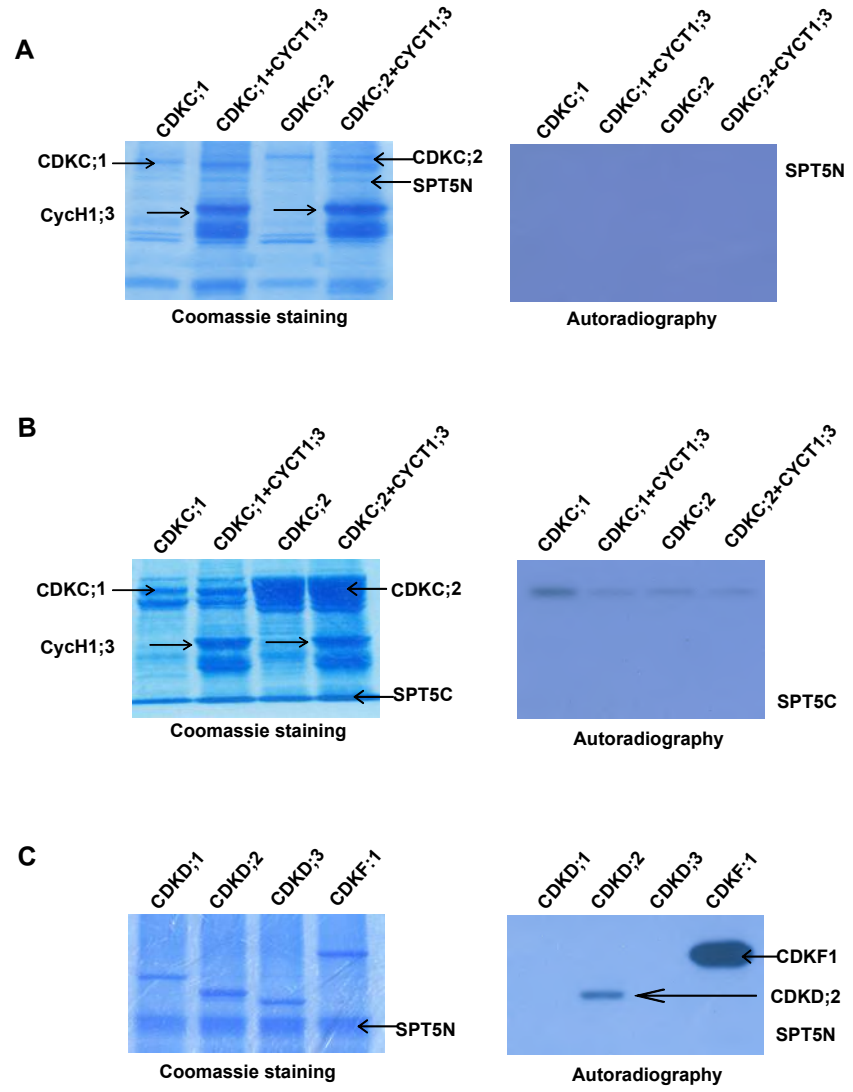
A

B



Supplemental Figure 3. Complementation of *spt5* with *ProSPT5::FLAG-SPT5.*
(A) Phenotypic analysis of flowering time in 4-week-old plants. Over 40 independent transgenic lines were generated, and two representative transgenic plants are shown.
(B) Transcript analysis of *SPT5* in the Col-0, *spt5* mutant, and two transgenic lines (*T1* and *T14*). Experiments were repeated at least three times, and each experiment included three replicates, the representative experiments shown indicate the mean ±SE, n = 3 replicates.

Supplemental Figure 4

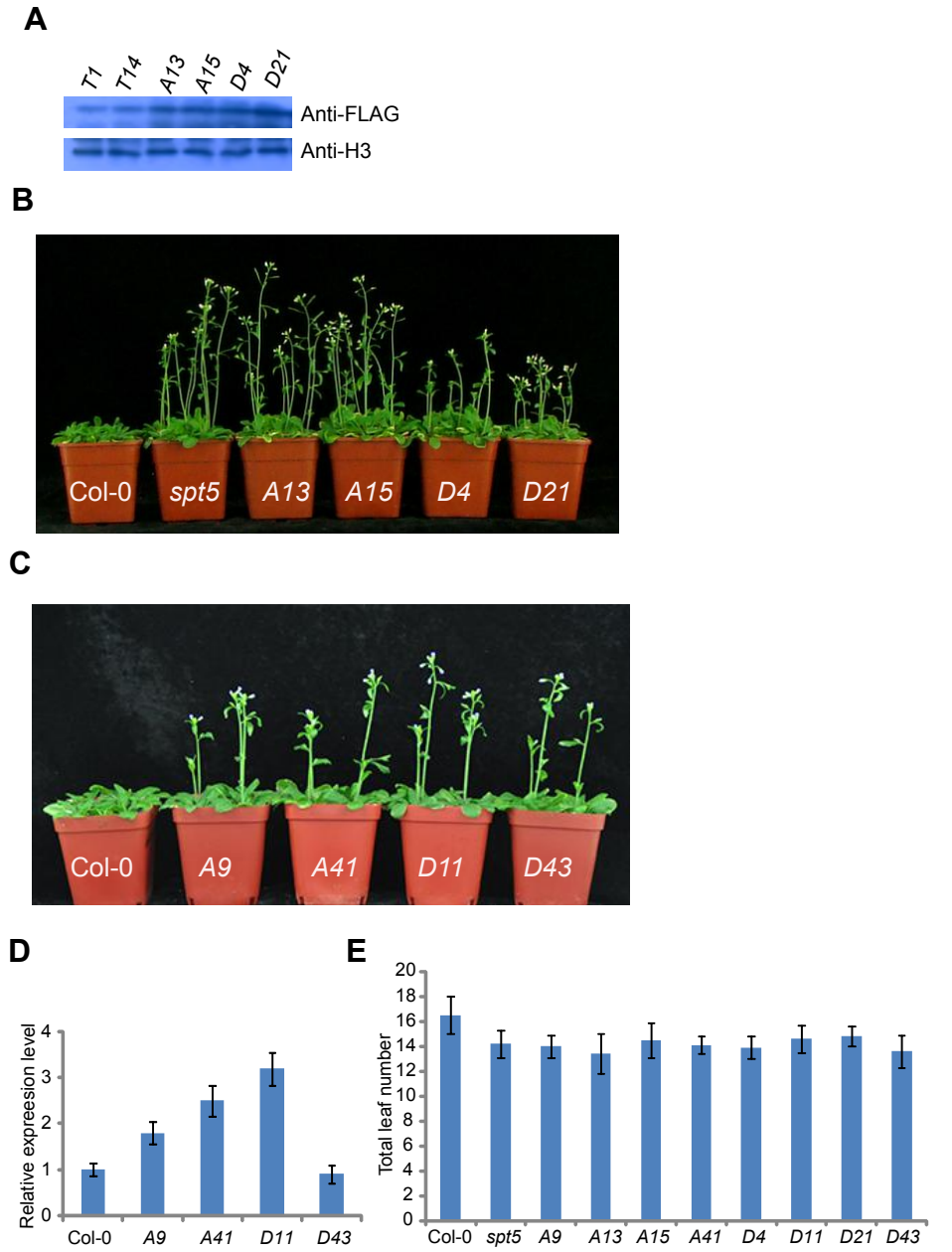


Supplemental Figure 4. The phosphorylation activity of CDKC and CDK proteins

(A) and (B) CDKC;1 and CDKC;2 were tested for their ability to phosphorylate the N-terminus of SPT5 (SPT5N) or C-terminus of SPT5 (SPT5C). Cyclin T1;3 was used to enhance the CDKC;1 and CDKC;2 phosphorylation activity. The left panel shows the Coomassie blue-stained gel. The positions of different proteins are indicated on the right. Autoradiography in the right panel shows the activity and specificity of the kinase. The positions of the proteins are indicated by arrows.

(C) CDKD;1, CDKD;2, CDKD;3, and CDKF;1 were tested for their ability to phosphorylate the N-terminus of SPT5 (SPTN). The left panel shows the Coomassie blue-stained gel. The positions of different CDK proteins and SPT5 are indicated on the right. Autoradiography in the right panel shows the activity and specificity of the kinase.

Supplemental Figure 5



Supplemental Figure 5. Complementation of *spt5* with mutated *SPT5*

(A) SPT5 accumulation in different transgenic plants. The *spt5* mutant was complemented by genomic *SPT5* with mutations that encoded nonphosphorylatable ($SPT5^{TA}$; transgenic lines *A13* and *A15*) or phospho-mimic (SPT^{TD}; transgenic lines *D4* and *D21*) forms of SPT5. *T1* and *T14* are indicated in Supplemental Figure 3. The amount of SPT5 was determined by immunoblot analysis with a FLAG antibody (anti-FLAG). H3 was used as the internal control (anti-H3).

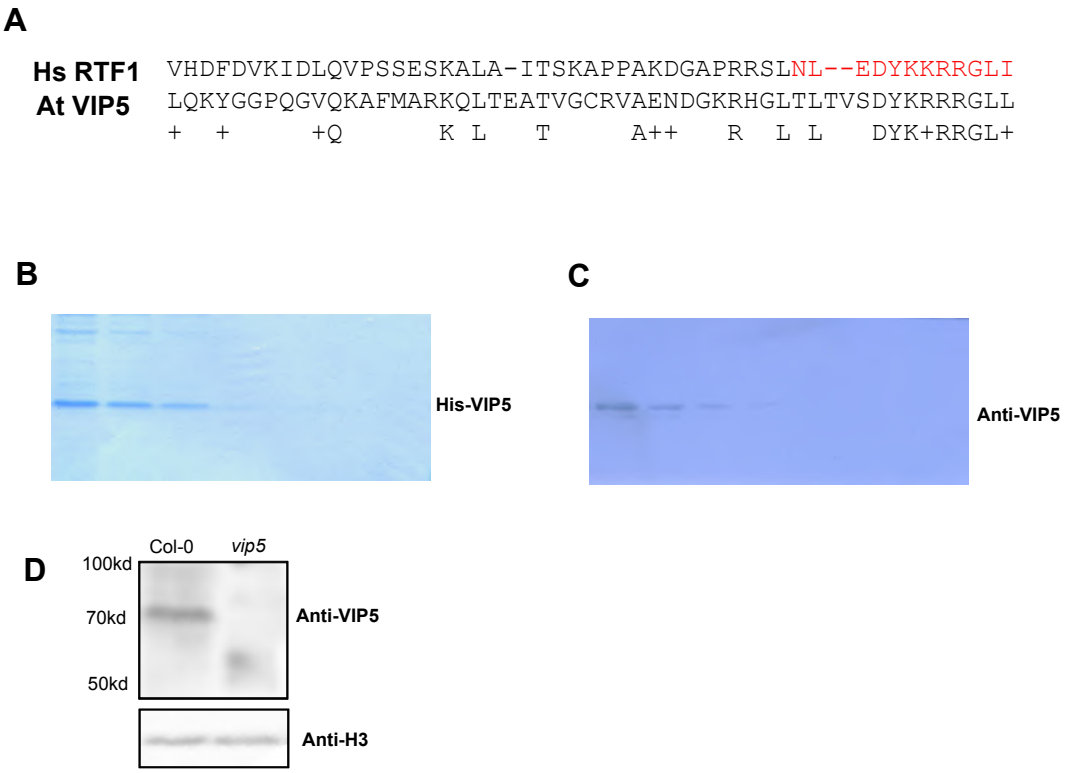
(B) The flowering time of Col-0, *spt5*, and transgenic plants (transgenic lines *A13*, *A15*, *D4* and *D21*) in a long-day photoperiod.

(C) The flowering time of Col-0 and nonphosphorylatable (transgenic lines *A9* and *A41*) or phospho-mimic (transgenic lines *D11* and *D43*) forms of SPT5 in a long-day photoperiod.

(D) The transcripts of *SPT5* in transgenic plants (*A9*, *A41*, *D11*, and *D43*). Experiments were repeated at least three times, and each experiment included three replicates, and the representative experiments shown indicate the mean ±SE, n = 3 replicates.

(E) Flowering time was assessed by counting the total leaf number at bolting under long-day photoperiod.

Supplemental Figure 6



Supplemental Figure 6. Commercial antibody to mammalian RTF1 recognizes Arabidopsis VIP5.

(A) The amino acid sequences of human RTF1 (660-710 amino acids) and Arabidopsis VIP5 (590-643 amino acids) were aligned by ClustalW2, with the sequence of the human antigen peptide used to make antibodies shown in red.

(B) The cDNA for the C-terminus of VIP5 was expressed in *E. coli* as a N-terminal fusion to His. The His-purified fusion proteins (His-VIP5C) produced were visualized on a Coomassie-stained protein gel.

(C) The same purified samples were analyzed by immunoblot using a commercially available antibody to human RTF1 (Abcam ab52887). The antibody is specific to the C-terminus of human RTF1 and recognizes Arabidopsis VIP5.

(D) The cell extracts from wild-type and *vip5* plants were blotted with anti-RTF1 antibody (top panel) using H3 as a control (anti-H3; bottom panel).

Supplemental Table 1

GST-CDKC;1
To generate *GST-CDKC;1*, the *CDKC;1* was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CGGAATTCATGGCGATGGCATCATTCGG-3') and reverse primer (5'- GCGTCGACCTGTTGCCATCCGTATTGCT-3'), and cloned into pGEX-6p-1 with EcoRI/ SalI

GST-CDKC;2
To generate *GST-CDKC2*, the *CDKC;2* was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CGGAATTCATGGCGGCTGCGGCTTTTGG-3') and reverse primer (5'- GCGTCGACCGGTTGCCATCCATATTGTT-3'), and cloned into pGEX-6p-1 with EcoRI/ SalI

GST- CYCT1;3
To generate *GST- CYCT1;3*, the *CYCT1;3* was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- GGAATTCATGGGAGAGGAGCATCCGAGAAAG -3') and reverse primer (5'- GACGTCGACCCAGATGCCAGCCTGTCTATAGGA -3'), and cloned into pGEX-6p-1 with EcoRI/ SalI

GST-CDKF;1
To generate *GST-CDKF;1*, the *CDKF;1* was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'-TCCCCCGGG TTTAAAGGAGATGGATAAACAA-3') and reverse primer (5'- ACGCGTCGAC ATGAAAAATAGGGTAAAGAATGGC-3'), and cloned into pGEX-6p-1 with SmaI/ SalI

GST-CDKD;1
To generate *GST-CDKD;1*, the *CDKD;1* was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'-"CGGGATCC CTAAAAATGTCGATTCCTTCTGTA-3') and reverse primer (5'- "CGGAATTCTCAAGAAGAAGCCTGTTACGCGAT-3'), and cloned into pGEX-6p-1 with BamHI/EcoRI

GST-CDKD;2
To generate *GST-CDKD;2*, the *CDKD;2* was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- "CGGGATCC GCCCTCGTACTTCCTCGAAGTGTA-3') and reverse primer (5'- TCCCCCGGG AATCCTTCAGGACCCATCACTCTC-3'), and cloned into pGEX-6p-1 with BamHI/ SmaI

GST-CDKD;3
To generate *GST-CDKD;3*, the *CDKD;3* was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- "CGGGATCC ATTATTGAGTGGGTTCTGAAAAAC-3') and reverse primer (5'- ACGCGTCGAC ATAACCAACAGTCTTACTGGAACT-3'), and cloned into pGEX-6p-1 with BamHI/ SalI

pGEX6p-1-SPT5 N

To generate *pGEX6p-1-SPT5 N*, the *SPT5 N* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'-CGCGGATCCATGCTTTTCAAAGATGGTTTTC-3') and reverse primer (5'-CGGAATTCTTGGCTTCCCATATTATACTGCGG -3'), and cloned into pGEX-6p-1 with BamHI/EcoRI.

GST-SPT5 C

To generate *GST-SPT5 C*, the C fragment from *SPT5* cDNA was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CGGGATCCGTCGCAACCCCGCAGTAT AATAT -3') and reverse primer (5'- CGGAATTC TCACTCATGAACTAACTTGGCTAA -3'), and cloned into pGEX-6p-1 with BamHI/EcoR I

pGEX6p-1-SPT5 CTR

To generate *pGEX6p-1-SPT5 CTR*, the *SPT5 CTR* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CGGGATCC GTCGCAACCCCGCAGTATAATAT-3') and reverse primer (5'- CGGAATTC GAGACATGACATCGAGATCGGTTC -3'), and cloned into pGEX-6p-1 with BamHI/EcoRI.

PET30a-SPT5 KOW

To generate *pGBKT7-SPT5 KOW6*, the *KOW6* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'-CGGGATCCAACAAAGTGAGCCTAGTTTGTC-3') and reverse primer (5'- CGGAATTC TCACTCATGAACTAACTTGGCTAA-3'), and cloned into PET30a with BamHI/EcoRI.

pGEX6p-1-SPT5 KOW

To generate *pGEX6p-1-SPT5 KOW6*, the *KOW6* fragment was digested from *PET30a-SPT5 KOW6* by BamHI/EcoRI, cloned into pGEX6p-1.

PET- SPT5 CTR

To generate *PET- SPT5 CTR4* repeat, the *CTR4* repeat was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CGGGATCCGGAAGCCAAACTCCTATGCATCCTT-3') and reverse primer (5'-CGGAATTCGATAGGTGTAGCTCCAGAATGCCGC -3'), and cloned into PET-30a with BamHI/EcoRI

PET- SPT5 CTR^{SA}

To generate *PET- SPT5 CTR^{SA}*, the *SPT5 CTR^{SA}* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CCGGAATTC GAAACACCTATGCATCCTG -3') and reverse primer (5'- CCGCTCGAG CCTCATTCCATCATGGATTGGTGTAGCTCCAGC -3'), and cloned into PET-30a with EcoRI/XhoI

PET-SPT5 CTR^{TA}

To generate *PET-SPT5 CTR^{TA}*, the *CTR^{TA}* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'-

CGGGATCCGGAAGCCAAGCTCCTATGCATCCTTCCCGGGCTCCACTT-3') and reverse primer (5'- CGGAATTCGATAGGTGCAGCTCCAGAATGCCGCATTGGAGCCATACA -3'), and cloned into PET-30a with EcoRI/BamHI

PET-SPT5 CTR ^{TD}

To generate *PET-SPT5 CTR ^{TD}*, The *CTR ^{TD}* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CATGCCATGG GGAAGCCAAGATCCTATGCATCCTTCCCGGGATCCACTT-3') and reverse primer (5'- CGGAATTC GATAGGATCAGCTCCAGAATGCCGCATTGGATCCATACA -3'), and cloned into PET-30a with NcoI/BamHI

PET- SPT5 CTR ^{TE}

To generate *PET- SPT5 CTR ^{TE}*, the *CTR ^{TE}* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CGGGATCC GGAAGCCAAGAACCTATGCATCCTTCCCGGGAACCACTT-3') and reverse primer (5'- CGGAATTC GATAGGTTCAGCTCCAGAATGCCGCATTGGTTCCATACA -3'), and cloned into PET-30a with BamHI/EcoRI

ProSPT5::*SPT5-1300FLAG/N*

To generate *ProSPT5*::*SPT5-1300Flag/N*. The *SPT5* promoter was amplified from an Arabidopsis genomic using forward primer (5'- TGCCTGCAGG AGAGACACTCACCAACAGAGACCT-3') and reverse primer (5'-CGGGGTACC TGGTTCGATTACAGAGAAACTAGG-3'), and cloned into pCAMBIA1300Flag/N with SbfI/KpnI. The *SPT5* was amplified from an Arabidopsis genomic using forward primer (5'- TCAGC AGTCGAAGAGC ATGTCTCAGTACTCAGACGACGAT-3') and reverse primer (5'- TTAGCGTGTGAAGA GC CTCCTGAACTAACTTGGCTAA-3'), cloned into *ProSPT5*:: pCAMBIA1300FLAG/N by Gateway.

ProSPT5::SPT5-1300FLAG/N CTR ^{TA}

To generate *ProSPT5::SPT5-1300FLAG/N CTR ^{TA}*. The CTR T mutant to A was amplified from *ProSPT5*::*SPT5-1300Flag/N* using forward primer 1 (5'- GCTCCTATGCATCCTTCCCGGGCTCCACTTCATCCCTGTATGGCTCCAATGCGGCATTCT G-3'), reverse 1 primer (5'- CCATACAGGGATGAAGTGGAGCCCGGGAAGGATGCATAGGAGCTTGGCTTCCCATAT TA
-3'), forward primer 2 (5'- GCACCTATCCATGATGGAATGAGGGCACCTATGCGTGGt-3'), reverse primer 2 (5'- TGCCCTCATTCCATCATGGATAGGTGCAGCTGAATTTTT-3'), forward primer 3 (5'- AGATTGGGGTAGTAGTGCTCCTGGTCGTA-3'), and reverse primer 3 (5'- AGCACTACTACCCCAATCTGATCCAGGCG-3')

ProSPT5::SPT5-1300FLAG/N CTR ^{TD}

To generate ProSPT5::SPT5-1300FLAG/N *CTR ^{TD}*. The CTR T mutant to D was amplified from *ProSPT5*::*SPT5*-1300FLAG/N using forward primer 1 (5'- GATCCTATGCATCCTTCCCGGGATCCACTTCATCCCTGTATGGATCCAATGCGGCATTC

-3'), reverse 1 primer (5'-ATCCATACAGGGATGAAGTGGATCCCGGGAAGGATGCATAGGATCTTGGCTTCCCATAt -3'), forward primer 2 (5'- GATCCTATCCATGATGGAATGAGGGATCCTATGCGTGGt -3'), reverse primer 2 (5'-ATCCCTCATTCCATCATGGATAGGATCAGCTGAATTTTT-3'), forward primer 3 (5'- AGATTGGGGTAGTAGTGATCCTGGTCGTA-3'), and reverse primer 3 (5'- ATCACTACTACCCCAATCTGATCCAGGCG -3')

pGBKT7-SPT5 N

To generate *pGBKT7-SPT5 N*, the *SPT5 N* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CATGCCATGGAGGATGAGGACGAAGAAGAC -3') and reverse primer (5'- CGGAATTCTAACCCACGAGTCACGGGATAAAT -3'), and cloned into pGBKT7 with NcoI/EcoR I.

pGBKT7-SPT5 KOW

To generate *pGBKT7-SPT5 KOW*, the *KOW* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CATGCCATGGCTGCTGTTCTTTCTGTCGAG-3') and reverse primer (5'- CGGAATTCTTGGCTTCCCATATTATACTGCGG-3'), and cloned into pGBKT7 with NcoI/EcoR I.

PET-SPT5 C

To generate *PET-SPT5 C*, the C fragment from SPT5 cDNA was digested from *pGEX6p-1-SPT5 C* by BamHI/EcoRI, and cloned into PET30a.

pGBKT7-SPT5 C

To generate *pGBKT7-SPT5 C*, the *SPT5 C* fragment was digested from *PET30a-SPT5 C* by NcoI/EcoR I, and cloned into pGBKT7.

PET-SPT5 CTR

To generate *PET-SPT5 CTR*, the *SPT5 CTR* fragment was digested from pGEX6p-1-SPT5 CTR by BamHI/EcoRI, and cloned into PET30a.

pGBKT7-SPT5 CTR

To generate *pGBKT7-SPT5 CTR*, the *CTR* fragment was digested from *PET3a-SPT5 CTR* by NcoI/EcoR I, and cloned into pGBKT7.

pGBKT7-SPT5 KOW

To generate *pGBKT7-SPT5 KOW6*, the *KOW6* fragment was digested from *PET30a-SPT5 KOW6* by NcoI/EcoR I, and cloned into pGBKT7.

PET-VIP5

To generate *PET-VIP5*, the *VIP5* was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CGCGGATCC ATGGGTGATTTAGAGAACTTGCTT-3') and reverse primer (5'- CCGGAATTC AATGCAAATAAATCCGAGAAGA-3'), and cloned into PET-30a with BamHI/EcoRI

pGADT7-VIP5
To generate *pGADT7-VIP5*, the *VIP5* cDNA was digested from *PET30a-VIP5* by NcoI/ EcoRI, and cloned into pGADT7

pGADT7-VIP5 PLUS3
To generate *pGADT7-VIP5 plus3*, the *plus3* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'-CATGCCATGGTTGAGTAGTTCCAGCCAAAGTGACA-3') and reverse primer (5'-CCGCTCGAGAACATTCATTGGCCTGACTGACGCA-3'), and cloned into pGADT7 with NcoI/XhoI

PUC-spYNE-VIP5
To generate PUC-spYNE-VIP5. The VIP5 cDNA was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CGCGGATCC ATGGGTGATTTAGAGAACTTGCTT-3') and reverse primer (5'- TCCCCCGGG AATGCAAATAAATCCGAGAAGA-3'), and cloned into PUC-spYNE with BamHI/ SmaI

PUC-spYNE-CDKD2
To generate *PUC-spYNE-CDKD2*, the *CDKD2* cDNA was digested from pGEX6p-1-CDKD2 by BamHI/SmaI, and cloned into PUC-spYNE.

PUC-spYCE-SPT5 C
To generate *PUC-spYCE-SPT5 C*, the *SPT5 C* fragment was digested from *pGEX6p-1-SPT5 C* by BamHI/Xho1, and cloned into PUC-spYCE.

PET-VIP5 C
To generate *PET-VIP5 C*, the *VIP5 C* fragment was amplified from an Arabidopsis first strand cDNA pool using forward primer (5'- CCGGAATTC GAAGCAGCTTTAGAAGCAGCTG-3') and reverse primer (5'- TCCCCCGGG AATGCAAATAAATCCGAGAAGA-3'), and cloned into PET-30a with BamHI/SmaI.

Genotyping primers

SALK_062223
Forward primer: GTCTCTTGCCATCGTTCTCTG
Reverse primer: ATGTGCCTACGTTTGAGGATG

SALKseq_9711
Forward primer: ATTCAACATTCAGCAACCAGC
Reverse primer: AGGGTAATATAACGCATGGGG

SALK_065163
Forward primer: GATGGTTTGTTTTTGGTGTGG
Reverse primer: CTCAGCAAAAATACAGCCTGC

SALK_ 063929
Forward primer: TTTCCGGATAGCATTTTGTTG
Reverse primer: AAGCTGGAATCTGAAGCTTCC

SALK_ 126891
Forward primer: GGAATTCTGAAACCTCCGAAG
Reverse primer: AAGGTCCGTTCCATTATCCAC

CS813305
Forward primer: AGGAAATCAAGCCAAACCATG
Reverse primer: TGGTGGTAGTTACTCGGATGC

flc-3
Forward primer: TATCGCCGGAGGAGAAGC
Reverse primer: TAGAAAGAAATAAAGCGAGAAAAGGA

FRIGIDA
Forward primer: GGGGTACCATGGTGAGCAAGGGCGAGGAGCTGTT
Reverse primer: GGGGTACCACTTGTACAGCTCGTCCATGCCGAGA

SALK_126891
Forward primer: GGAATTCTGAAACCTCCGAAG
Reverse primer: AAGGTCCGTTCCATTATCCAC

CS 813305
Forward primer: AGGAAATCAAGCCAAACCATG
Reverse primer: TGGTGGTAGTTACTCGGATGC

RT-PCR primer

SPT5
Forward primer: CGGTGAAAGATGTTGTCAGG
Reverse primer: AAGGTTATGCCGGTCATGTAT

VIP5
Forward primer: GAAATGAAACCTCGGCGGCT
Reverse primer: TCATTGGCCTGACTGACGCA

CDKD;2
Forward primer: GATTAGTCTTGTTCTTGATG

Reverse primer: CTACAGAACTAATCAATTGC

FLC
Forward primer: CGGTCTCATCGAGAAAGCTC
Reverse primer: CCACAAGCTTGCTATCCACA

GTA2
Forward primer: GAGTCCTCAATATCAGCCGG
Reverse primer: TCACGGTTGCACAAACTTGG

UBIQUITIN 10
Forward primer: AGGATGGCAGAACTCTTGCT
Reverse primer: TCCCAGTCAACGTCTTAACG

Primers for ChIP-PCR

FLC
Region 1
Forward primer: TGGAGGGAACAACCTAATGC
Reverse primer: TCATTGGACCAAACCAAACC

Region 2
Forward primer: CGACAAGTCACCTTCTCCAAA
Reverse primer: AGGGGGAACAAATGAAAACC

Region 3
Forward primer: GGCGGATCTCTTGTTGTTTC
Reverse primer: CTTCTTCACGACATTGTTCTTCC

Region 4
Forward primer: GGGGCTGCGTTTACATTTTA
Reverse primer: GTGATAGCGCTGGCTTTGAT

Region 5
Forward primer: CTTTTTCATGGGCAGGATCA
Reverse primer: TGACATTTGATCCCACAAGC

Region 6
Forward primer: CTTTTTCATGGGCAGGATCA
Reverse primer: TGACATTTGATCCCACAAGC

Region 6
Forward primer: CGTGTGAGAATTGCATCGAG

Reverse primer: AAAAACGCGCAGAGAGAGAG

UBIQUITIN 10
Forward primer: AGGATGGCAGAACTCTTGCT
Reverse primer: TCCCAGTCAACGTCTTAACG