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SUPPLEMENTARY INFORMATION

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A group of receptor kinases are essential for CLAVATA signalling to maintain stem cell homeostasis

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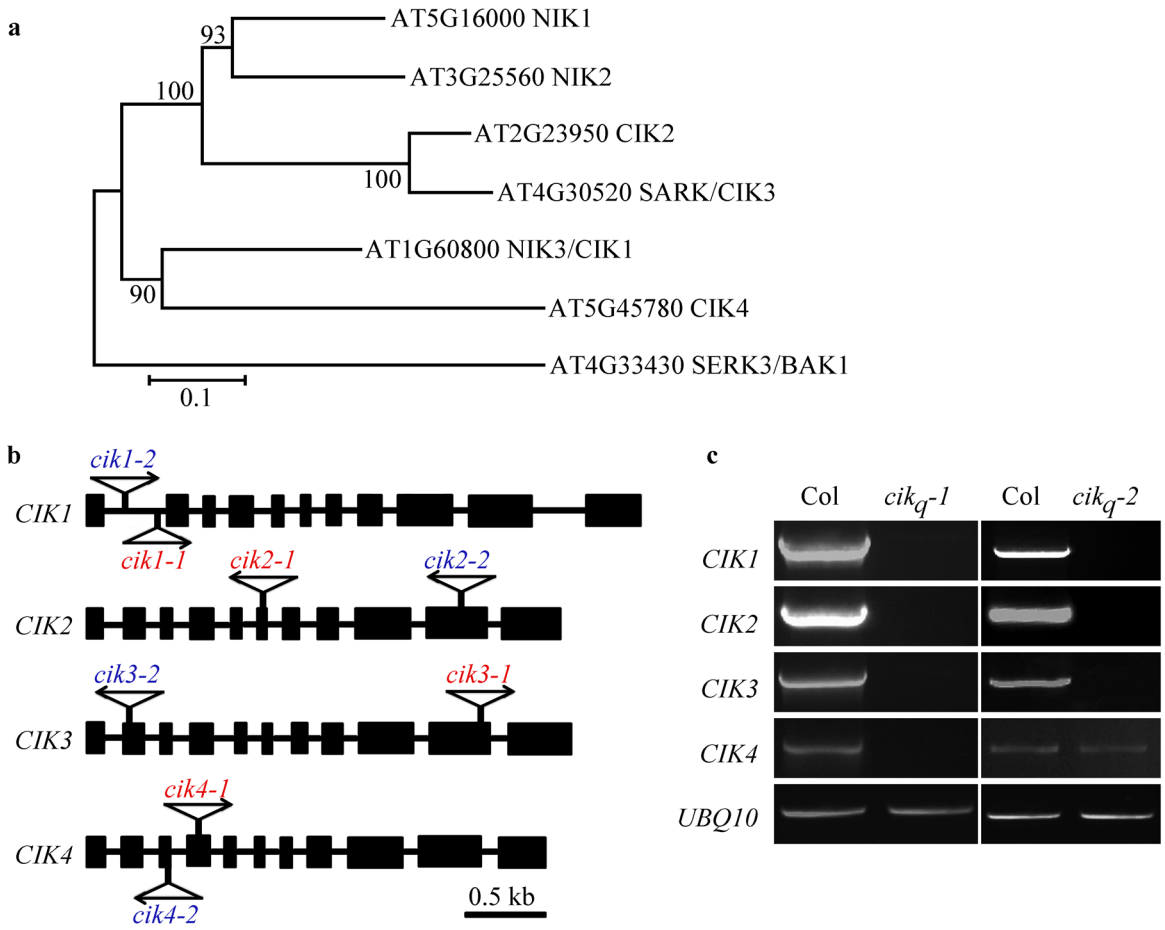
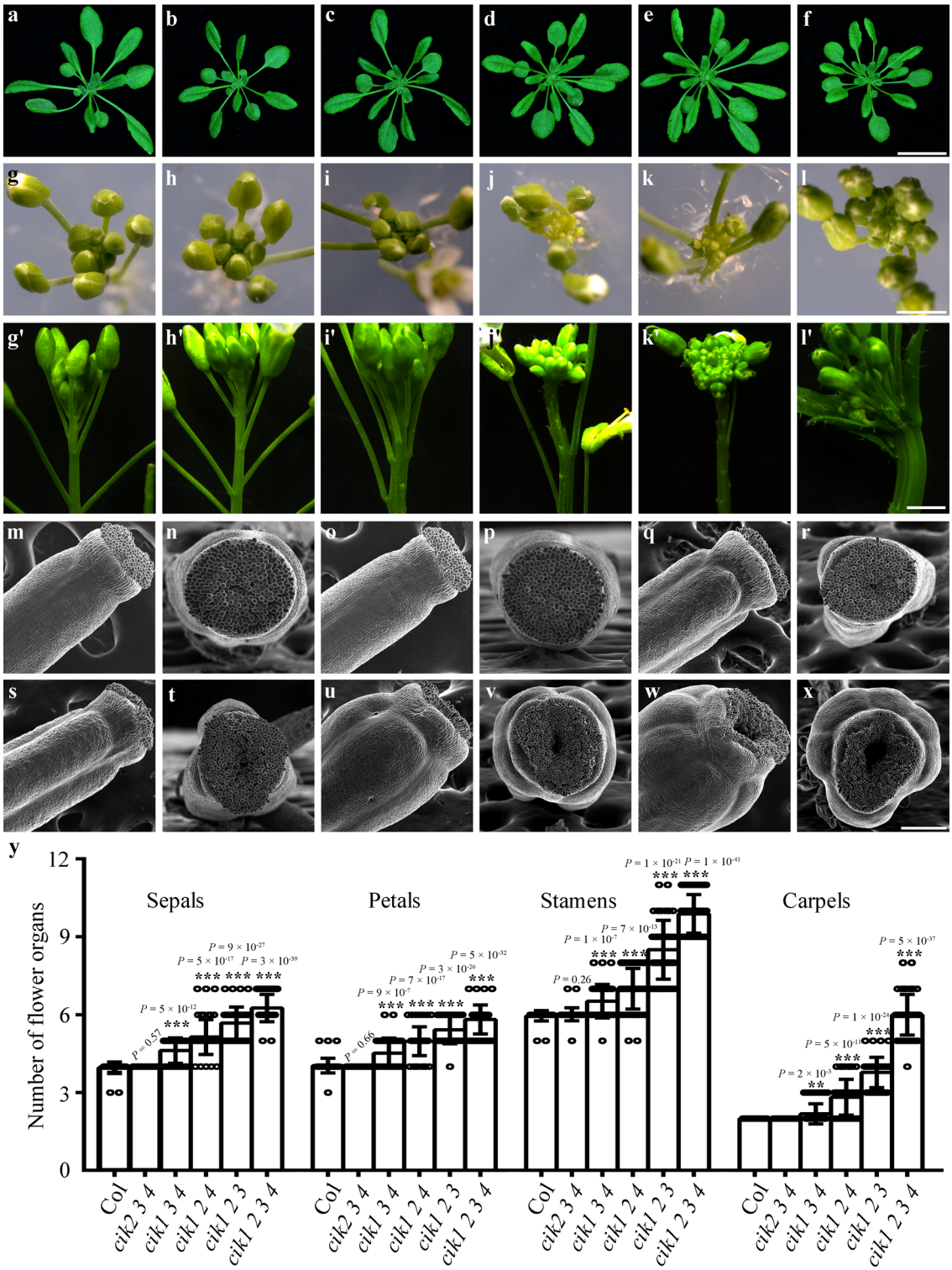
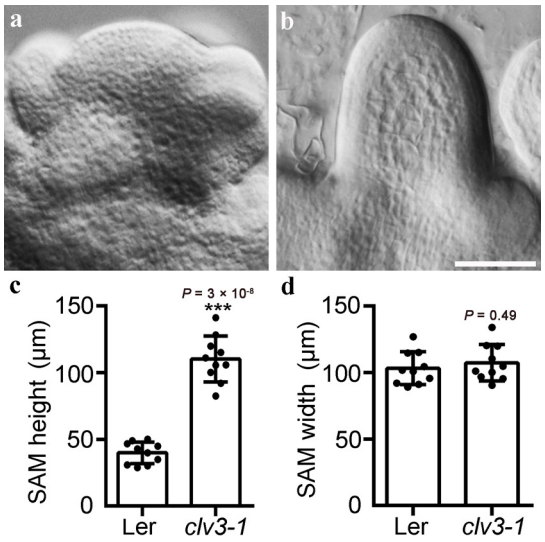


Supplementary Figure 1 | Information of *CIK* gene family and the corresponding T-DNA insertion lines. a, Phylogenetic analysis of CIKs based on their full-length amino acid sequences. SERK3/BAK1 was used as an out-group control. **b,** Insertion information of the used *CIK* T-DNA lines. The lines in red or in blue were respectively used to generate two independent quadruple mutants. **c,** RT-PCR analyses confirmed that *cik* quadruple mutants cannot produce full-length transcripts of *CIKs* except for *cik4-2*. *UBQ10* was used as a control. *cikq-1*, *cik1-1 cik2-1 cik3-1 cik4-1*; *cikq-2*, *cik1-2 cik2-2 cik3-2 cik4-2*. The experiment was repeated for at least three times independently with similar results.

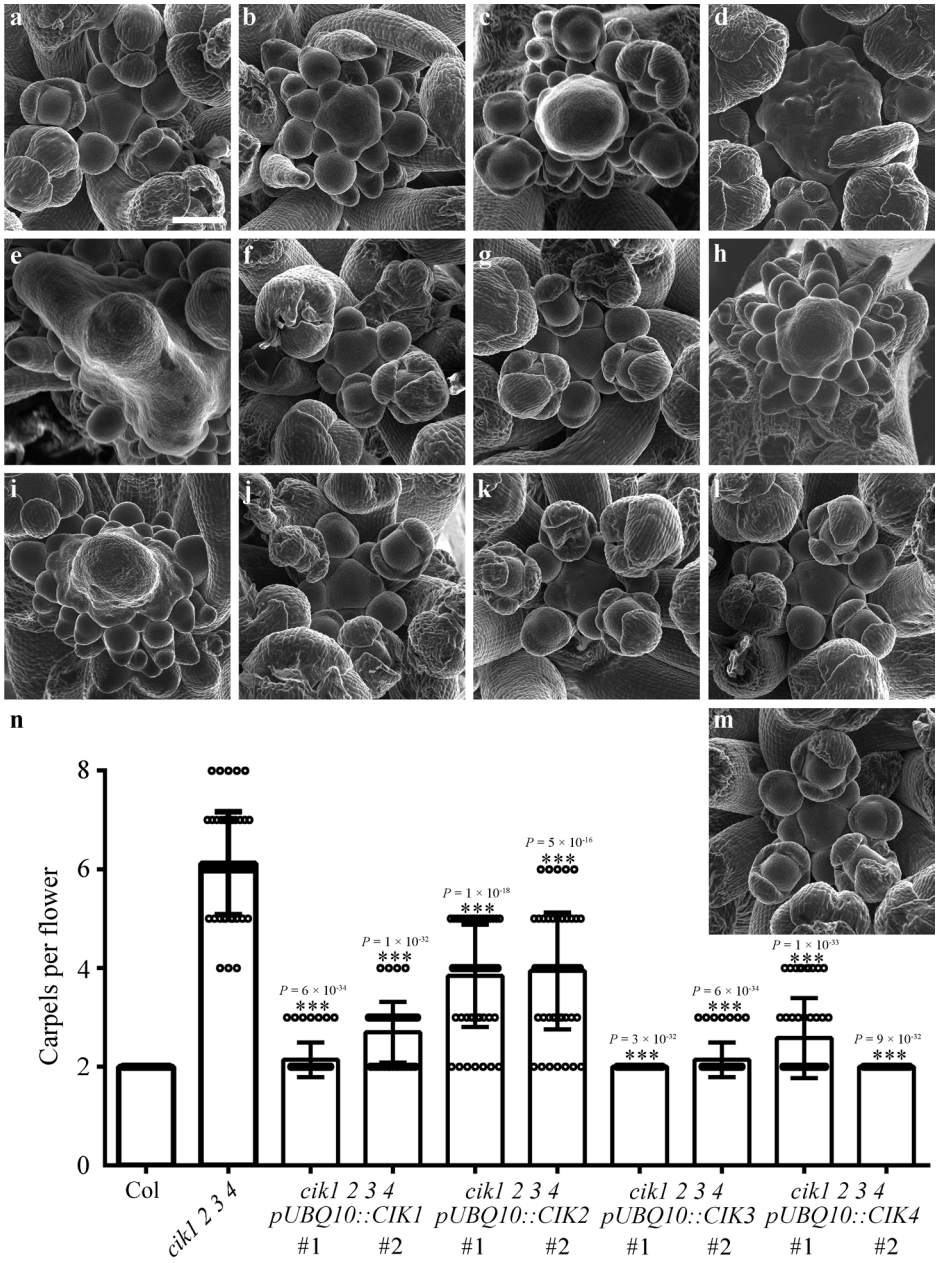


Supplementary Figure 2 | Triple and quadruple *cik* mutants produce more rosette leaves, flowers, and floral organs. a-f, Four-week-old plants of wild type (Col; **a**), *cik2 3 4* (**b**), *cik1 3 4* (**c**), *cik1 2 4* (**d**), *cik1 2 3* (**e**) and *cik1 2 3 4* (**f**). Scale bar, 2 cm. **g-l',** Inflorescences of wild type (Col; **g, g'**), *cik2 3 4* (**h, h'**), *cik1 3 4* (**i, i'**), *cik1 2 4* (**j, j'**), *cik1 2 3* (**k, k'**) and *cik1 2 3 4* (**l, l'**). **g-l,**

top view; **g'-l',** side view. Scale bars, 2 mm. **m-x,** SEM images of pistils of wild type (Col; **m, n**), *cik2 3 4* (**o, p**), *cik1 3 4* (**q, r**), *cik1 2 4* (**s, t**), *cik1 2 3* (**u, v**) and *cik1 2 3 4* (**w, x**). Scale bar, 200 μm. These experiments were repeated for at least three times independently with similar results. **y,** Statistical analysis of floral organ numbers. Data shown are mean ± s.d. (n=50 biologically independent samples). *P* values calculated using two-tailed *t*-test.

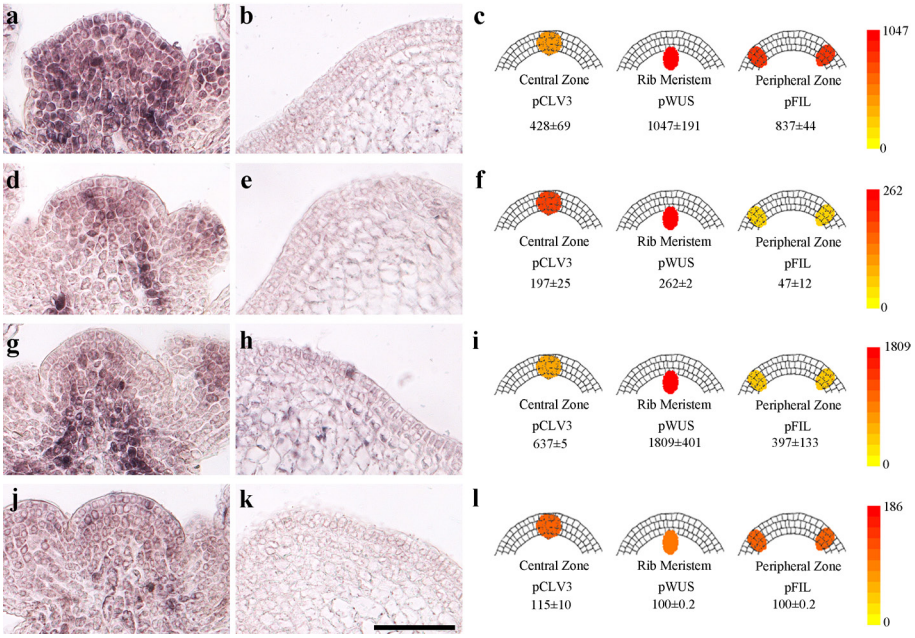


Supplementary Figure 3 | *clv3-1* displays enlarged inflorescence meristems. a,b, DIC images of the IMs from 15-day-old seedlings. Wild-type (Ler, **a**) and *clv3-1* (**b**) are shown. Scale bar, 100 μm. These experiments were repeated for three times independently with similar results. **c,d,** Quantitative analysis of SAM height (**c**) and width (**d**). Data are shown as mean ± s.d. (n=10 biologically independent samples). *P* values calculated using two-tailed *t*-test.

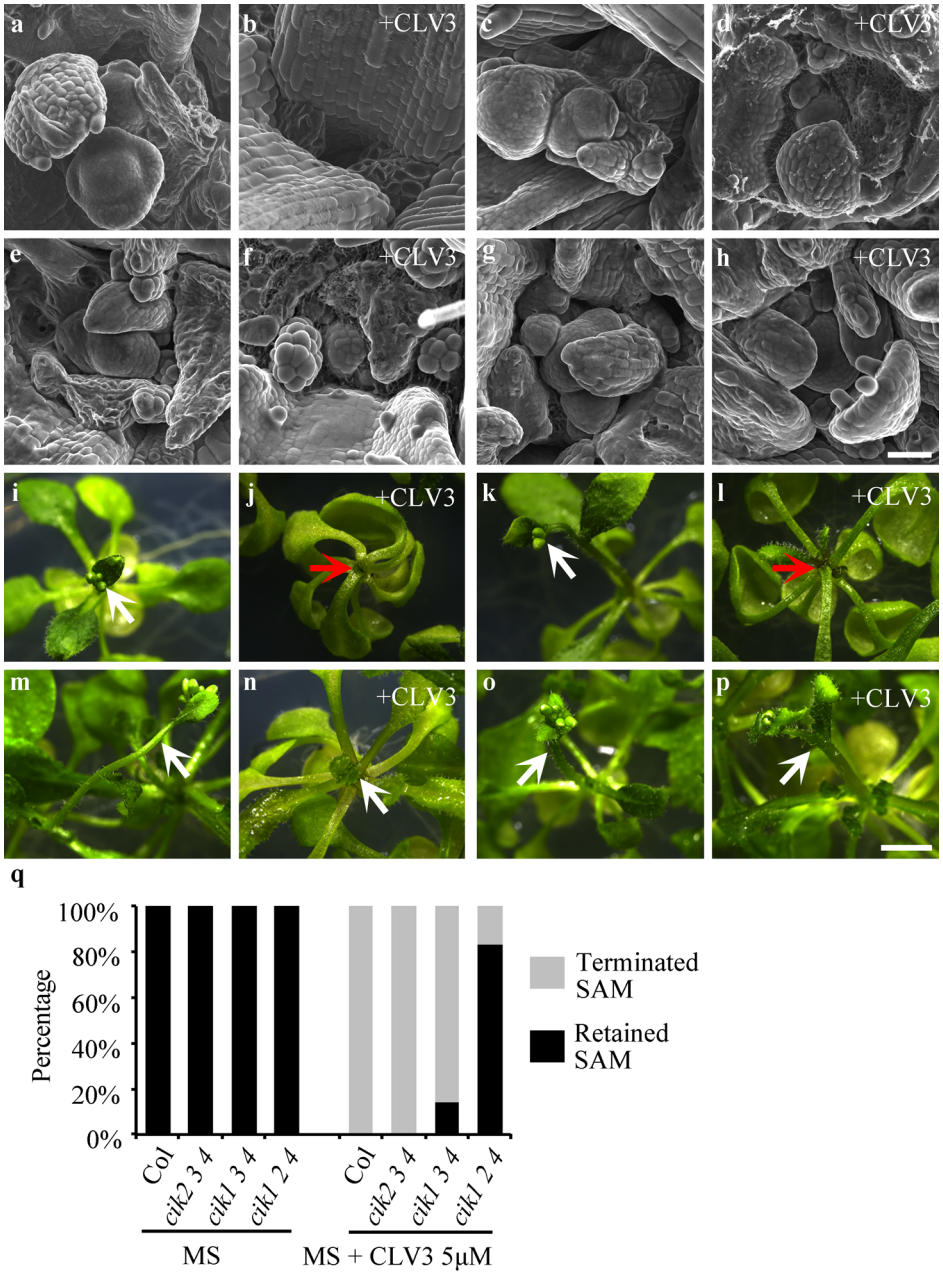


Supplementary Figure 4 | *CIKs* are responsible for the mutant phenotypes. a-d, The second set of *cik* mutants show similar defective SAMs. SEM images of the IMs are shown for wild type (Col; **a**), *cik1-2 2-2 4-2* (**b**), *cik1-2 2-2 3-2* (**c**) and *cik1-2 2-2 3-2 4-2* (**d**). Scale bar, 100 μm. **e-m,** Defective SAM of *cik1 2 3 4* can be rescued by overexpressed *CIKs*. SEM images of the IMs are shown for *cik1 2 3 4* (**e**) and two independent transgenic lines that overexpressing *CIK1* (**f, g**), *CIK2* (**h, i**), *CIK3* (**j, k**) and *CIK4* (**l, m**) in the quadruple mutant. These experiments were repeated for three times independently with similar results. **n,** Statistical analysis of carpel numbers. Data are

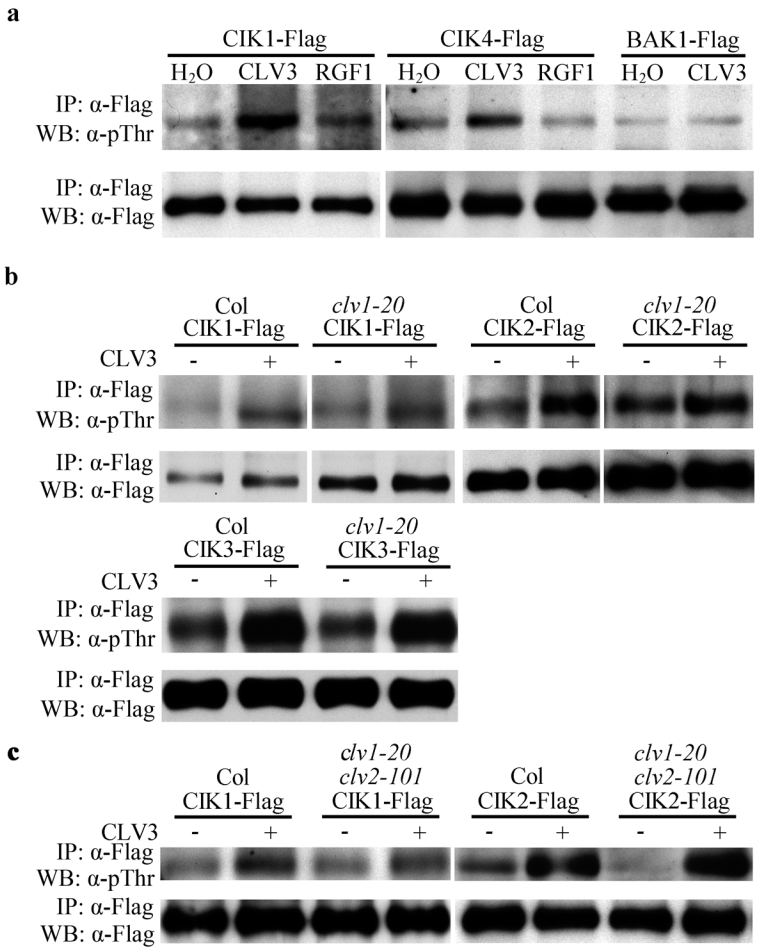
shown as mean ± s.d. (n=50 biologically independent samples). *P* values calculated using two-tailed *t*-test.



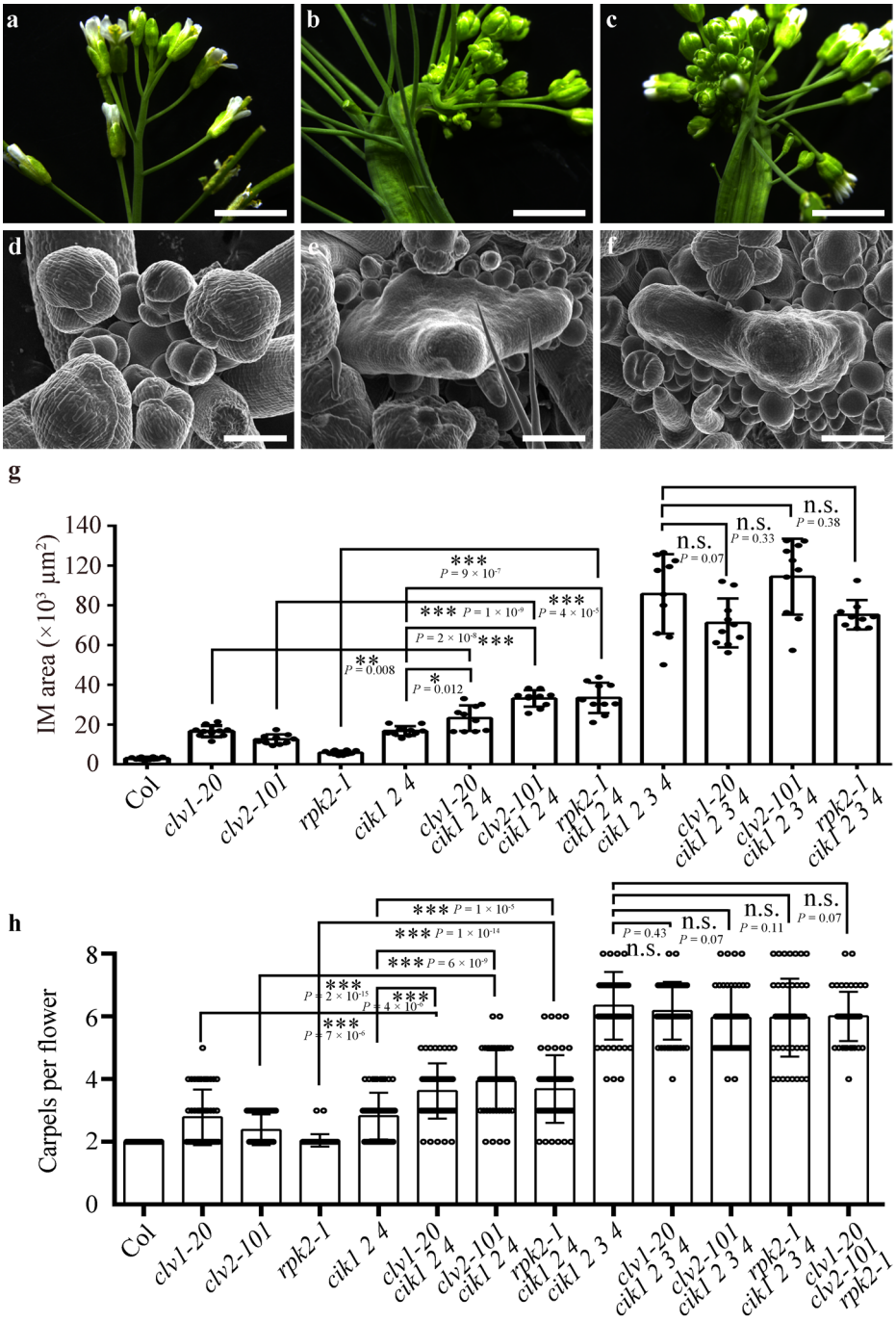
Supplementary Figure 5 | Expression patterns of *CIKs* in the IMs. a,b, d,e, g,h, j,k, RNA in situ hybridization showed the expression patterns of *CIK1* (**a, b**), *CIK2* (**d, e**), *CIK3* (**g, h**) and *CIK4* (**j, k**) in the IMs of wild type (**a, d, g, j**) and *cik1 2 3 4* (**b, e, h, k**). This experiment was repeated for three times, and similar results were obtained. Scale bar, 50 μm. **c, f, i, l,** Expression patterns of *CIK1* (**c**), *CIK2* (**f**), *CIK3* (**i**) and *CIK4* (**l**) shown by Arabidopsis eFP browser (http://bbc.botany.utoronto.ca/efp/cgi-bin/efpWeb.cgi?).



Supplementary Figure 6 | Triple *cik* mutants show reduced sensitivity to CLV3 treatment. a-p, Plants were grown on MS medium without (**a, c, e, g, i, k, m, o**) or with (**b, d, f, h, j, l, n, p**) 5μM CLV3. **a-h,** SEM images of 12-day-old SAMs from wild type (Col; **a, b**), *cik2 3 4* (**c, d**), *cik1 3 4* (**e, f**) and *cik1 2 4* (**g, h**). Scale bar, 50 μm. **i-p,** 20-day-old seedlings of wild type (Col; **i, j**), *cik2 3 4* (**k, 1**), *cik1 3 4* (**m, n**) and *cik1 2 4* (**o, p**). Scale bar, 5 mm. White arrows indicate the bolting inflorescences, and red arrows indicate the terminated SAMs. These experiments were repeated for three times independently with similar results. **q,** Quantification of 20-day-old seedlings showing terminated SAMs or bolting inflorescences (n=50 biologically independent samples).

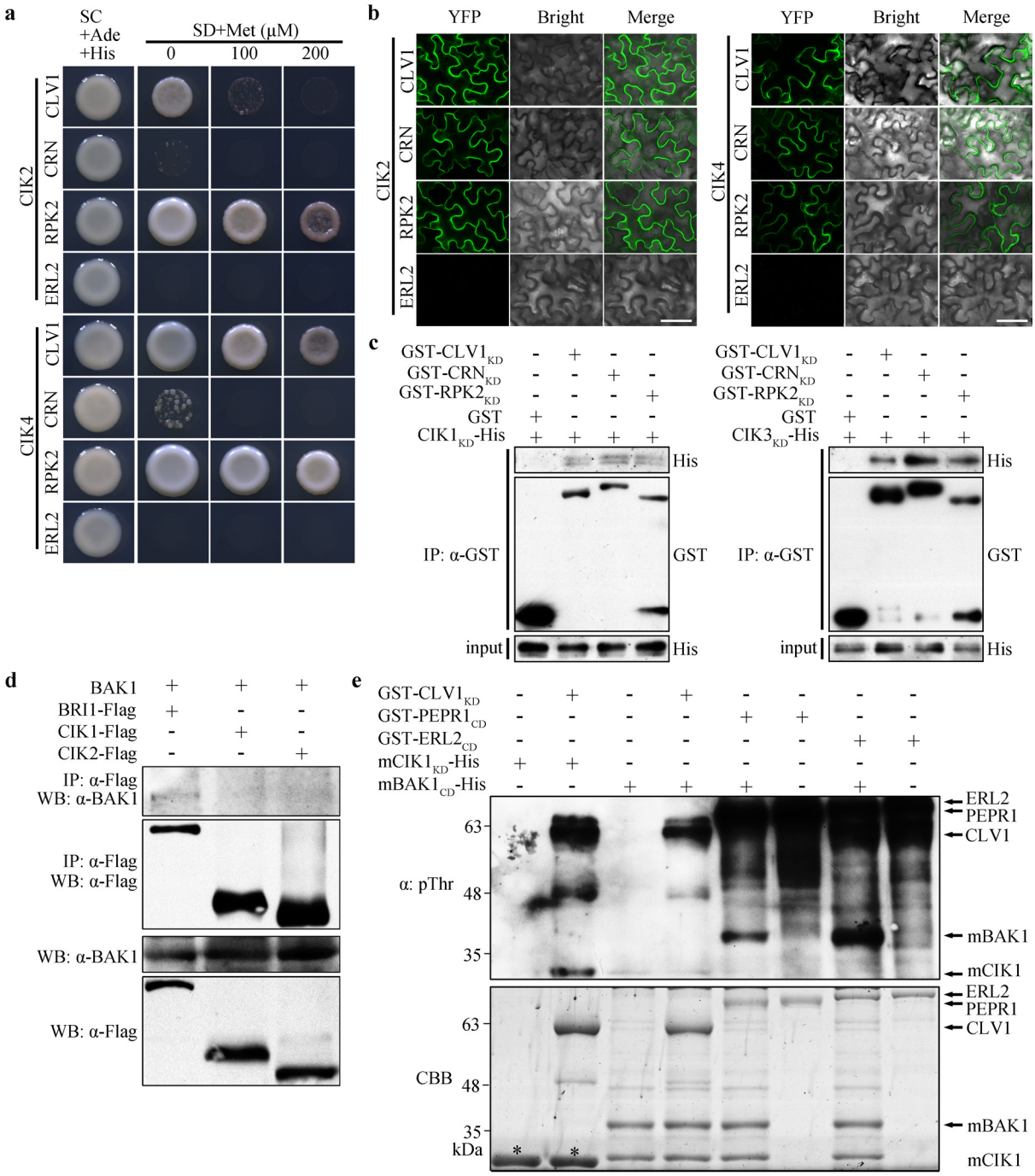


Supplementary Figure 7 | Phosphorylation responses of CIKs to CLV3 treatment in different background. a, CLV3 but not RGF1 treatment enhanced the phosphorylation level of CIK1 and CIK4. The phosphorylation level of BAK1 cannot be enhanced by CLV3 treatment. **b,** CIK1, CIK2 and CIK3 show enhanced phosphorylation level upon CLV3 treatment in the *clv1-20* mutant. **c,** CIK1 and CIK2 show enhanced phosphorylation level upon CLV3 treatment in the *clv1-20 clv2-101* mutant. These experiments were repeated for at least three times with similar results, and one representative data set is shown.



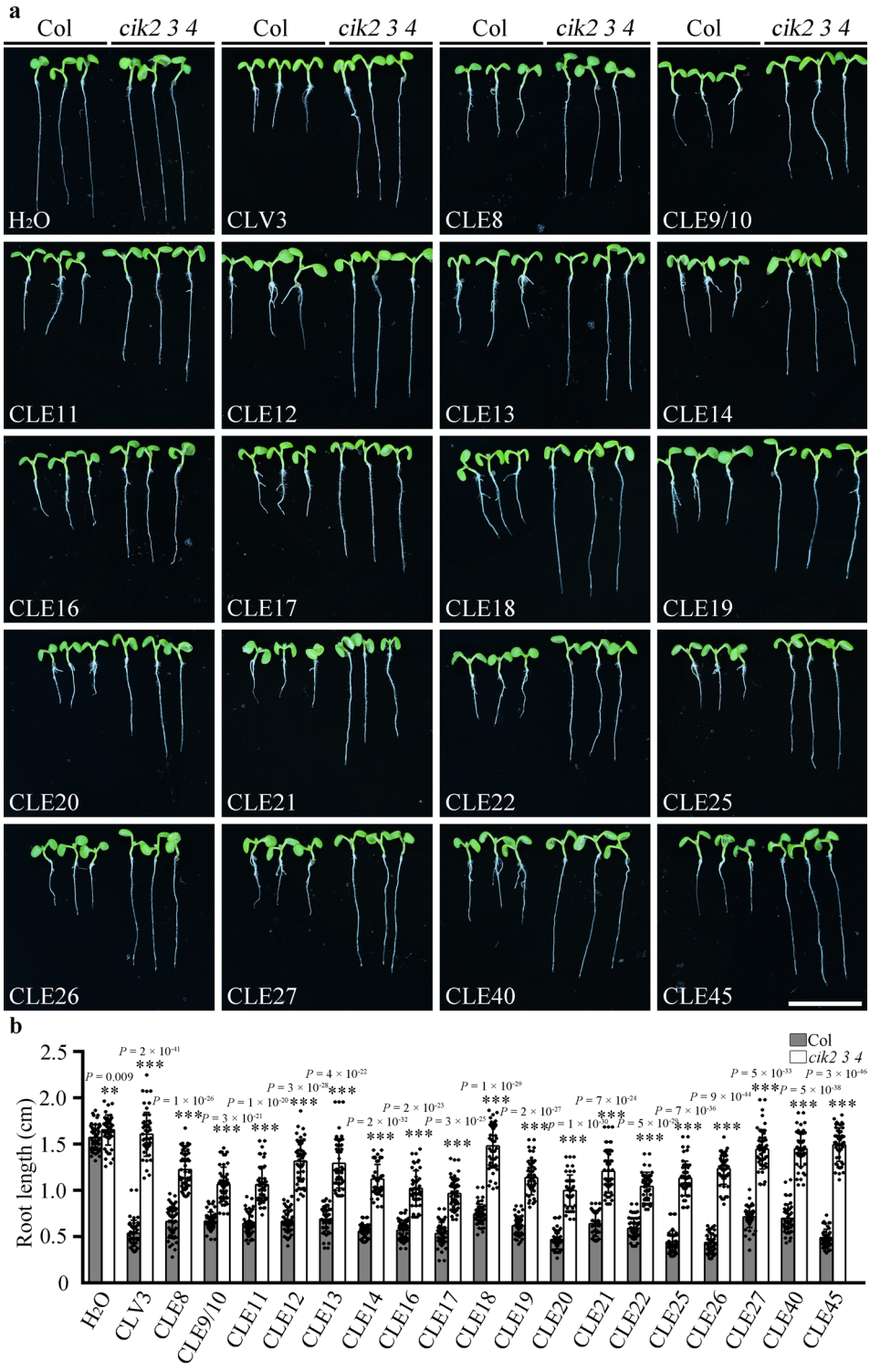
Supplementary Figure 8 | CIKs function as common regulators involved in CLV1-, CLV2/CRN- and RPK2-mediated CLV3 signalling. a-c, Inflorescences of wild type (Col; **a**), *cik1 2 3 4* (**b**) and *clv1-20 clv2-101 rpk2-1* (**c**). Scale bars, 4 mm. **d-f,** SEM images of the IMs of wild type (Col; **d**), *cik1 2 3 4* (**e**) and *clv1-20 clv2-101 rpk2-1* (**f**). Scale bars, 100 μm. These experiments were repeated for three times independently with similar results. **g,** IM area of the indicated genotypes (n=10 biologically independent samples). **h,** Carpel numbers per silique were

measured for the indicated genotypes (n=50 biologically independent samples). Data are shown as mean ± s.d. (**g, h**). *P* values calculated using two-tailed *t*-test. n.s., not significant.



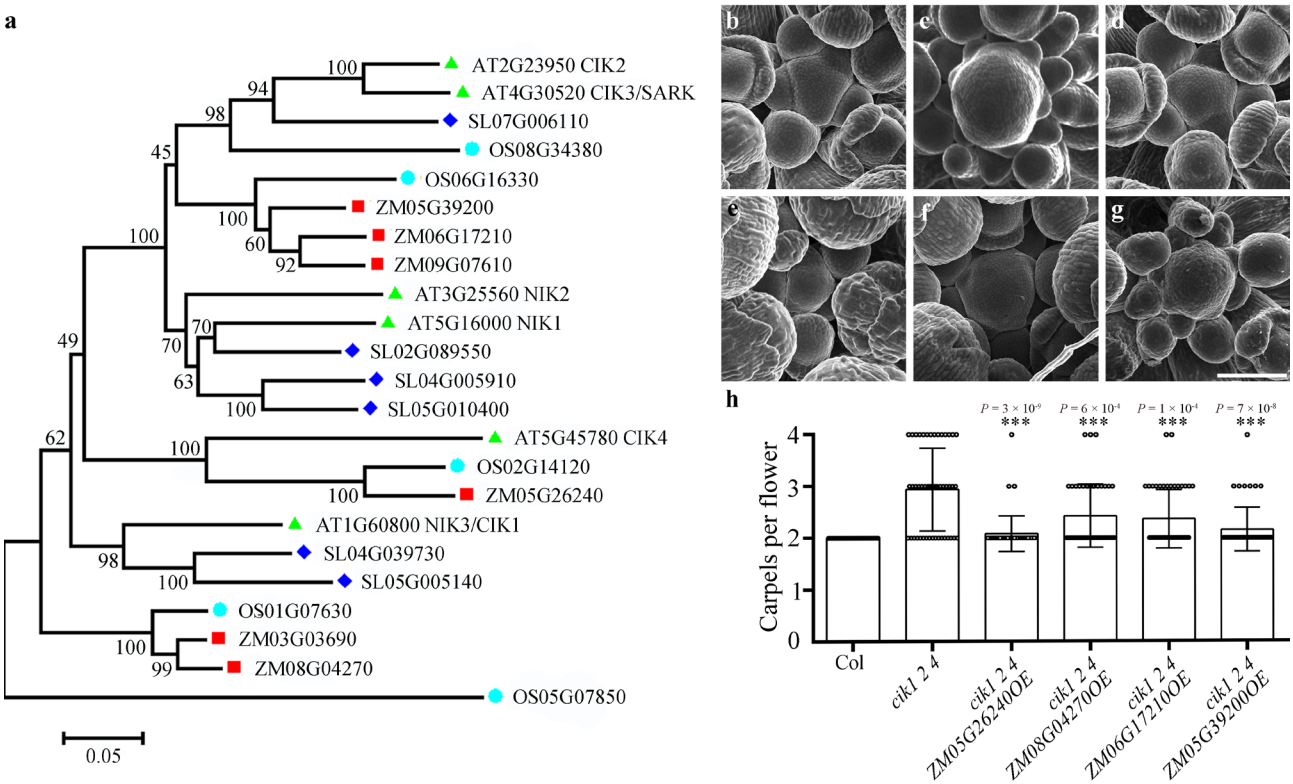
Supplementary Figure 9 | CIKs interact with CLV1, CRN and RPK2, respectively. a, Interactions of CIK2, CIK4 with CLV1, CRN and RPK2 were detected by an mbSUS yeast two-hybrid system. CIK proteins were fused to the N-terminal part of ubiquitin; CLV1, CRN,

RPK2 and ERL2 were fused to the C-terminal part of ubiquitin. Yeast was grown on medium selecting for diploid cells (SC+Ade+His) or detecting interactions (SD, with three different methionine concentrations). **b,** BiFC assay in *N. benthamiana* to show interactions between CIK2, CIK4 and CLV1, CRN and RPK2. CIKs were fused to the N-terminal part of YFP; CLV1, CRN, RPK2 and ERL2 were fused to the C-terminal part of YFP. Scale bars, 50 μm. **c,** $CIK1_{KD}$ and $CIK3_{KD}$ interact with $CLV1_{KD}$, CRN_{KD} and $RPK2_{KD}$ in vitro, respectively. **d,** BAK1 cannot be co-immunoprecipitated by CIK1-Flag and CIK2-Flag in stable transgenic plants. In vivo co-immunoprecipitation of BAK1 with BRI1-Flag was used as a positive control. **e,** $CLV1_{KD}$ can phosphorylate $mCIK1_{KD}$ but not $mBAK1_{CD}$. $mBAK1_{CD}$ can be phosphorylated by $PEPR1_{CD}$ and $ERL2_{CD}$, which is used as a positive control. Asterisks indicate mCIK1. These experiments were repeated for three times independently with similar results.



Supplementary Figure 10 | The *cik2 3 4* triple mutant plants show resistance to different CLE peptides that can consume Arabidopsis RAM. a, Five-day-old seedlings of wild type (Col; left) and *cik2 3 4* (right) grown on medium without or with 200 nM of various CLE peptides. Scale bar, 1 cm. These experiments were repeated for at least three times independently with similar results. **b,**

Quantitative analysis of root length. Data are shown as mean ± s.d. (n=50 biologically independent samples). *P* values calculated using two-tailed *t*-test.



Supplementary Figure 11 | CIKs are widespread in other species and may be functionally conserved. a, Phylogenetic analysis of homologous CIKs from Arabidopsis, maize (*Zea mays*), tomato (*Solanum lycopersicum*) and rice (*Oryza sativa*). The protein sequences of putative CIKs were retrieved from the Plaza database (http://bioinformatics.psb.ugent.be/plaza/), and those without either extracellular LRR domain or intracellular kinase domain were excluded. The sequences were aligned with CLUSTAL W and the phylogenetic reconstruction was performed with MEGA6. **b-g,** Defective SAM of *cik1 2 4* can be rescued by overexpression of maize *CIKs* driven by an Arabidopsis *UBQ10* promoter. SEM images of the IMs from wild type (Col; **b**), *cik1 2 4* (**c**) and transgenic lines overexpressing *ZM05G26240* (**d**), *ZM08G04270* **(e)**, *ZM06G17210* **(f)** and *ZM05G39200* (**g**). Scale bar, 100 µm. These experiments were repeated for three times

independently with similar results. **h,** Statistical analysis of carpel numbers. Data are shown as mean ± s.d. (n=50 biologically independent samples). *P* values calculated using two-tailed *t*-test.

Supplementary Table 1 | Primers used in this study.

Primers	Sequences	Note
bam1-LP	CGGTATCTCGCCGTGAAGTT	For mutant genotyping.
bam1-RP	CCTTTCCGGTCTTCGTCACT	
bam2-LP	AAATTTATCAGAGCTTGTTCGG	
bam2-RP	AATACGGACCACAAAGATGAG	
cik1-1 LP	GAAGGGATATGGAAGGTG	
cik1-1 RP	TAGGTGAGGTTTCCGATT	
cik2 -1 LP	GGTTCTACGTCCTACACATCCC	
cik2-1 RP	CGGTAAAATCCCACCGGAGA	
cik3-1 LP	TCAGGGGATTCACAGTTT	
cik3-1 RP	GCGTCAAGCCTTGAGACA	
cik4-1 LP	ATTGTAGTGGCTGCGTTAA	
cik4-1 RP	AGTTGGTCCGCTTAGATTG	
cik1-2 LP	GGTGTGGAATTAGAAGCAAACC	
cik1-2 RP	TAGCCATCAGTGCAAGAAACC	
cik2-2 LP	AACAAAAATTGAAGTCATGGGG	
cik2-2 RP	TCGGTTAATCGGTTATTGTGC	
cik3-2 LP	GAGAGGTGAGGAATTTGGGAC	
cik3-2 RP	TTTTGCTTTGTTTGCTTTTGC	
cik4-2 LP	GGGAATCGGTTTAGTGGTGA	
cik4-2 RP	TGACTCTGTTTCTGCCATGG	
clv1-20 LP	ATAACTGGTGCCGTTGACAAG	
clv1-20 RP	GAGACCGTGTCCTTTAGGACC	
clv2-101 LP	CGGATTACGTACTGAATCAAACC	
clv2-101 RP	ACTAAGAGACGGACGAGAGGC	
rpk2-1 LP	CCCAGTAAACTGATCCGGCA	
rpk2-1 RP	AAGGGTCGAGCTTGGGATTG	
wus-101 LP	AAAACCTTCTTTTTGGGTCCC	
wus-101 RP	TAGATGCAAATTTGGTTTGCC	
LBo8409	ATATTGACCATCATACTCATTGC	
LBb1.3	ATTTTGCCGATTTCGGAAC	
LB3	TAGCATCTGAATTTCATAACCAATCTCGATACAC	
spm32	TACGAATAAGAGCGTCCATTTTAGAGTGA	
BAK1-BF	AAAAAGCAGGCTTCATGGAACGAAGATTAATGATCCCT	For CDS gateway cloning. Partial *att*B1 and *att*B2 sequences are underlined.
BAK1-BR	AGAAAGCTGGGTCTCTTGGACCCGAGGGGTATTCGT	
BRI1-BF	AAAAAGCAGGCTTCATGAAGACTTTTTCAAGCTTCT	
BRI1-BR	AGAAAGCTGGGTCTAATTTTCCTTCAGGAACTTCT	
CIK1-BF	AAAAAGCAGGCTTCATGGAAGGTGTGAGATTTGTGGTGT	
CIK1-BR	AGAAAGCTGGGTCTCGAGGACCCGAGAGCTCAATGG	
CIK2-BF	AAAAAGCAGGCTTCATGGTGGTGATGAAGTTAATAACAA	
CIK2-BR	AGAAAGCTGGGTCCCTTGGACCAGATAGTTCCATGG	
CIK3-BF	AAAAAGCAGGCTTCATGGTAGTAGTAACAAAGAAGACCA	

CIK3-BR	AGAAAGCTGGGTCTCTTGGACCGGATAGTTCCATGG	
CIK4-BF	AAAAAGCAGGCTTCATGGAGATTTCTTTGATGAAGTTTC	
CIK4-BR	AGAAAGCTGGGTCTCGTGGTCCAGAGAGCTCAATGG	
CLV1-BF	AAAAAGCAGGCTTCATGGCGATGAGACTTTTGAAGACT	
CLV1-BR	AGAAAGCTGGGTCTCAGAACGCGATCAAGTTCGCCA	
CRN-BF	AAAAAGCAGGCTTCATGAAGCAAAGAAGAAGAAGA	
CRN-BR	AGAAAGCTGGGTCAAAGCTGTGCAGTTGTGTAAGC	
ERL2-BF	AAAAAGCAGGCTTCATGGCGATAAAGGCTTCATTCAGCA	
ERL2-BR	AGAAAGCTGGGTCTAAGCTACTTTTGGAGATATCTTCACG	
RPK2-BF	AAAAAGCAGGCTTCATGACTTCTTTGCCTTCTTCAG	
RPK2-BR	AGAAAGCTGGGTCACACGACGGAGGTTGTAGCTGC	
$BAK1_{CD}$*-BF*	AAAAAGCAGGCTTCTTTAGCAACAAGAACATATTGGG	For kinase domain cloning. Partial *att*B1 and *att*B2 sequences are underlined.
$BAK1_{CD}$*-BR*	AGAAAGCTGGGTCTTATCTTGGACCCGAGGGGTATTC	
$CIK1_{KD}$*-BF*	AAAAAGCAGGCTTCTTCAAAGAGCTTAGATCTGCCACC	
$CIK1_{KD}$*-BR*	AGAAAGCTGGGTCTCAACCAGTACCGTTCTGCGTCG	
$CIK3_{KD}$*-BF*	AAAAAGCAGGCTTCAGCTTCACATTCAGAGAACTCC	
$CIK3_{KD}$*-BR*	AGAAAGCTGGGTCTCAATGGTAGAAATGTGAATGGTT	
$CLV1_{KD}$*-BF*	AAAAAGCAGGCTTCTCTGAAGACGTTCTCGAGTG	
$CLV1_{KD}$*-BR*	AGAAAGCTGGGTCTCAAGGAGGGTTAGTGAGCATGTG	
CRN_{KD}*-BF*	AAAAAGCAGGCTTCGTGTTAGCTTTCTTGGTTCGTAG	
CRN_{KD}*-BR*	AGAAAGCTGGGTCCTAAAAGCTGTGCAGTTGTGTAAG	
$ERL2_{CD}$*-BF*	AAAAAGCAGGCTTCAAGTCAAAGCAGCAGAAACCAG	
$ERL2_{CD}$*-BR*	AGAAAGCTGGGTCTTATAAGCTACTTTTGGAGATATC	
$PEPR1_{CD}$*-BF*	AAAAAGCAGGCTTCAAAGGAAGACCAGAGAAAGATGCT	
$PEPR1_{CD}$*-BR*	AGAAAGCTGGGTCTTACCGAACTGAATCAGAGGAGC	
$RPK2_{KD}$*-BF*	AAAAAGCAGGCTTCTGGCGGTATTCCTCATGATTTCG	
$RPK2_{KD}$*- BR*	AGAAAGCTGGGTCCTATTGGTCGTGGAGGTAAGCGA	
$BAK1_{(K364E)}$*-F*	CTTTAGTGGCCGTTGAAAGGCTAAAAGAGGAG	Site-directed mutagenesis to make inactive kinases.
$BAK1_{(K364E)}$*-R*	CTCCTCTTTTAGCCTTTCAACGGCCACTAAAG	
$CIK1_{(K329E)}$*-F*	ACTTTGGTGGCTGTCGAACGTCTCAAGGACTGT	
$CIK1_{(K329E)}$*-R*	ACAGTCCTTGAGACGTTCGACAGCCACCAAAGT	
$CIK3_{(K331E)}$*-F*	ACAATGGTGGCAGTGGAACGGTTGAAGGATATT	
$CIK3_{(K331E)}$*-R*	AATATCCTTCAACCGTTCCACTGCCACCATTGT	
$CLV1_{(K720E)}$*-F*	GTAGACGTCGCGATTGAACGACTCGTTGGCCGT	
$CLV1_{(K720E)}$*-R*	ACGGCCAACGAGTCGTTCAATCGCGACGTCTAC	
pUBQ10Hind	CCCAAGCTTAGTCTAGCTCAACAGAGCTTTTAACC	To clone the promoter of *UBQ10*.
pUBQ10Kpn	CGGGGTACCCTGTTAATCAGAAAAACTCAGA	
UBQ10 RT-F	AACAATTGGAGGATGGTCGT	*UBQ10* RT-PCR.
UBQ10 RT-R	TTCCAGGGAAGATGAGACG	
CIK1probe-F	ACTCAATTCAATCCATCTCATCG	To make probes of *CIKs* for in situ hybridization. Partial T3 promoter sequences are underlined.
CIK1probe-R	CCTCACTAAAGGGAGAATAATCCGAGTAATACCTCACACG	
CIK2probe-F	AGGAGATGGATTAGCTGAGAGATG	
CIK2probe-R	CCTCACTAAAGGGAGATTCCATGGCGAATGAATCTAACG	
CIK3probe-F	CTTGAAGGCGATGGATTAGC	
CIK3probe-R	CCTCACTAAAGGGAGATCATCGTCATCATCGAAAGCC	
CIK4probe-F	AGAGTTTGATGATTTGGTGTTGG	
CIK4probe-R	CCTCACTAAAGGGAGAGACTGCTCTTCATGACCATTACTGT	