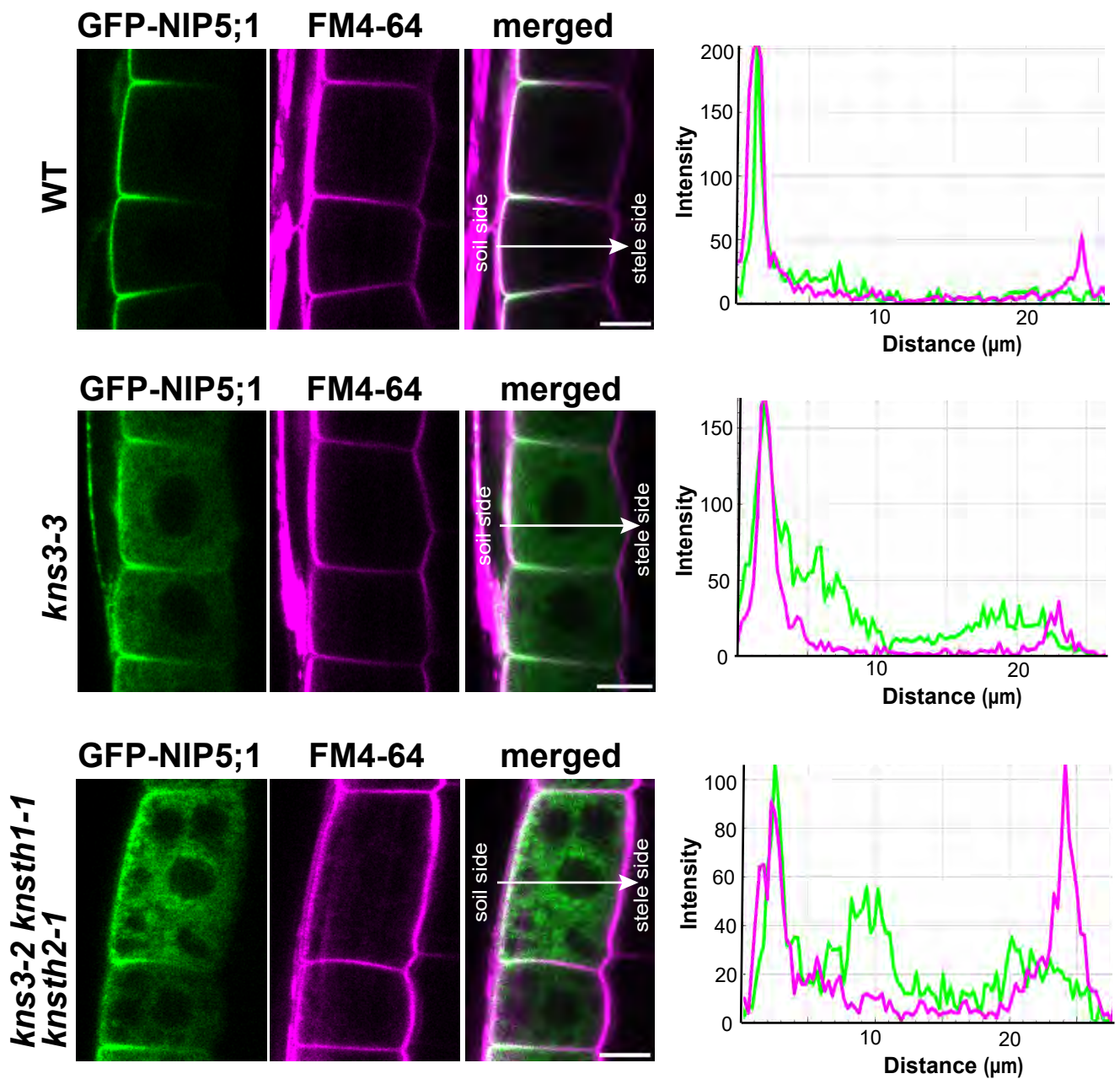


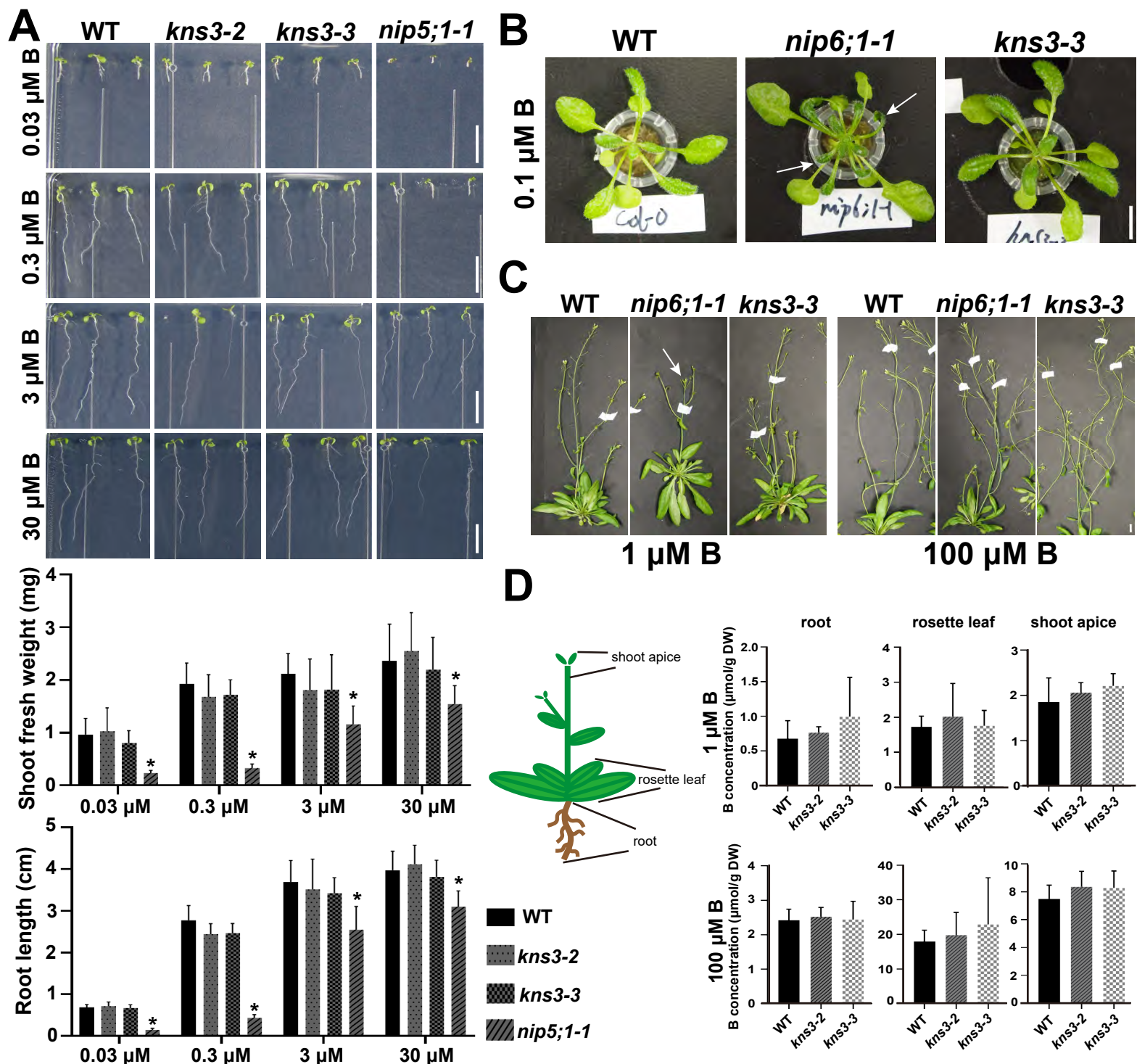
**Fig. S1. *At5g58100* (*KNS3*) is the causative gene for the ER retention of NIP5;1.**

(A) GFP-NIP5;1 in root epidermal cells of F1 plants between EMS mutants. Plants were grown on solid medium containing 30  $\mu$ M B for 7–10 days. Scale bar=10  $\mu$ m. (B) Summary of rough mapping using the F2 generation between ecotype *Ler* and line1–3, line10–6, line14–3, and line15–2. Recombination rates (%) at each marker position are indicated.



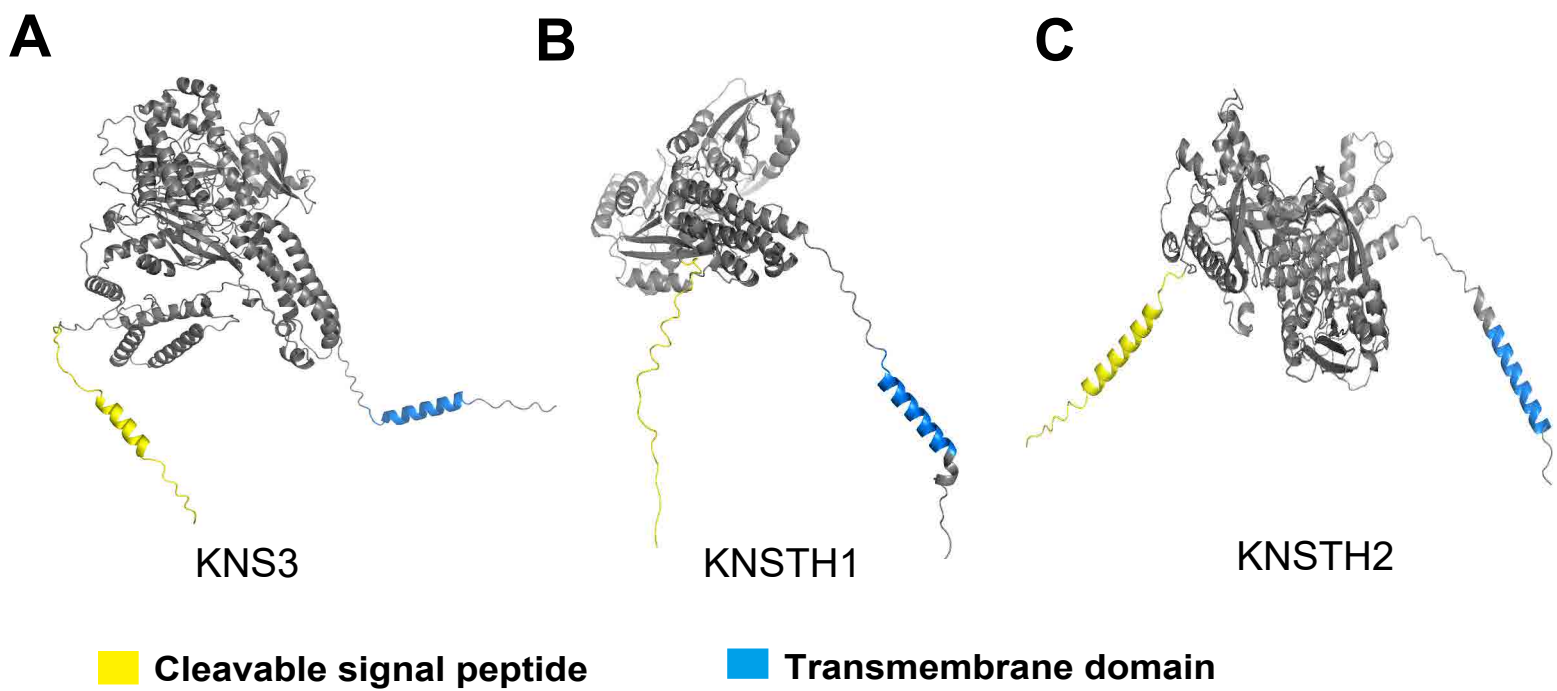
**Fig. S2. GFP-NIP5;1 shows polar localization in mutants of *KNS3* and its homologs.**

Polar localization of GFP-NIP5;1 in root epidermal cells of *nip5;1-1* (WT), a *KNS3* single mutant (*kns3-3*), and a triple mutant (*kns3-2 knsth1-1 knsth2-1*). Plant roots were stained with FM4-64 for 1 min and an optical longitudinal section of the root meristem zone was imaged by a confocal microscope. Plants were grown with 30  $\mu\text{M}$  B for 4–7 days. Scale bar=10  $\mu\text{m}$ .



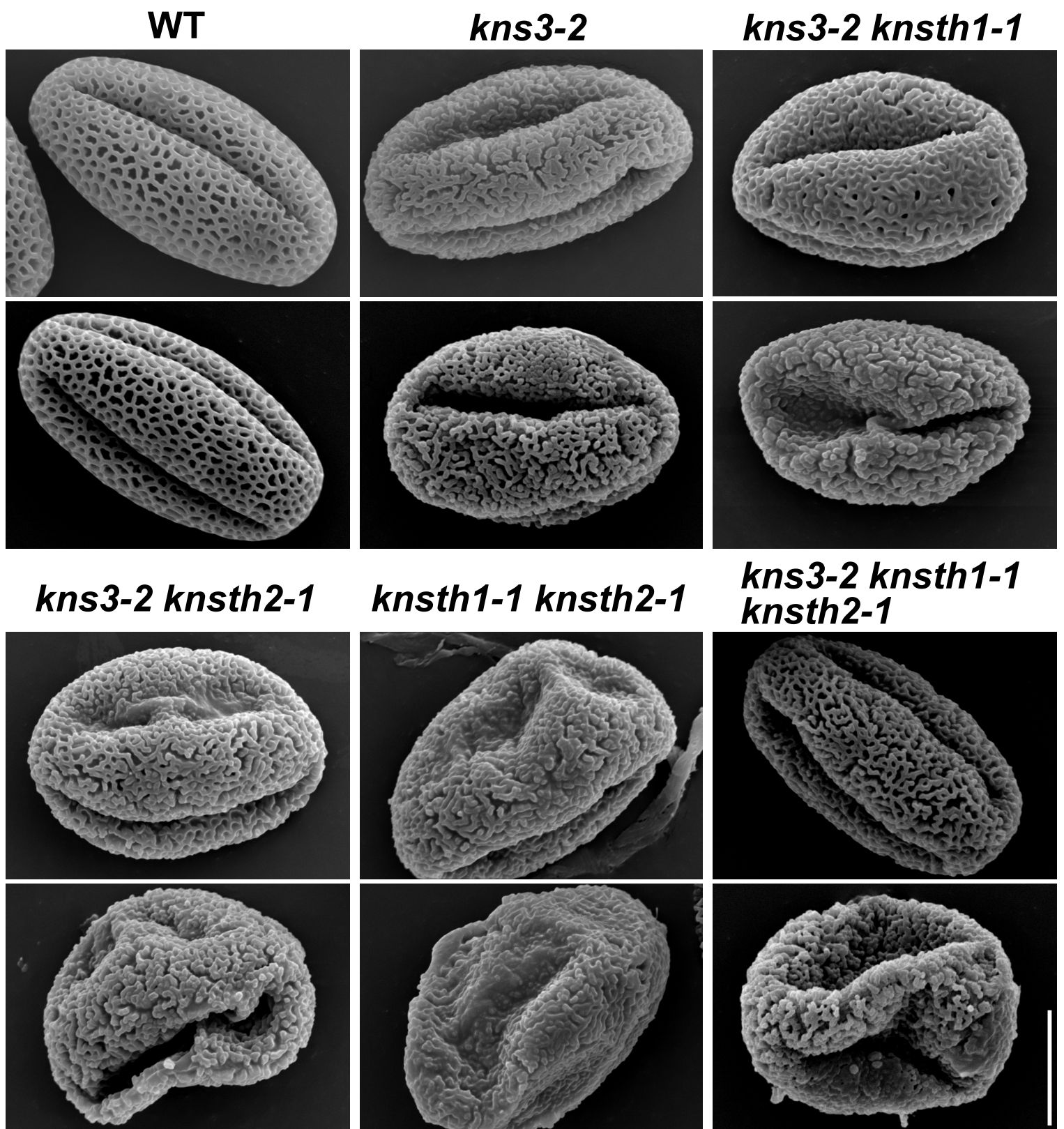
**Fig. S3. Growth of *kns3* mutants under different B conditions.**

(A) WT, *kns3-2*, *kns3-3*, and *nip5;1-1* were grown on solid medium contained 0.03, 0.3, 3, and 30  $\mu\text{M}$  B for seven days. Fresh weights of shoots and root lengths were measured from 8–13 plants. Data represent the mean  $\pm$  SD. The asterisks indicate mutants that showed significant differences to the WT (Dunnett' s test,  $*P < 0.01$ ). (B) WT, *kns3-3*, and *nip6;1-1* plants were grown hydroponically supplied with 0.1  $\mu\text{M}$  B under a short-day condition (8 h/16 h light/dark cycle) for 30 days. Arrows indicate young rosette leaves with reduced expansion. (C) WT, *kns3-3*, and *nip6;1-1* plants were grown hydroponically supplied with 1 and 100  $\mu\text{M}$  B under a long-day condition (16 h/8 h light/dark cycle) for 30 days. An arrow indicates the flowers of the main stem. (D) Boron concentrations in tissues of WT, *kns3-2*, and *kns3-3* plants grown hydroponically with 30  $\mu\text{M}$  B for 10–12 days and then with 1 or 100  $\mu\text{M}$  B for 15 days. Roots, rosette leaves, and shoot apices (1.5 cm from top) were harvested from three to four plants. Data represent the mean  $\pm$  SD. No significant differences were observed (Mann-Whitney U-test,  $P > 0.05$ ). Scale bar=1 cm.



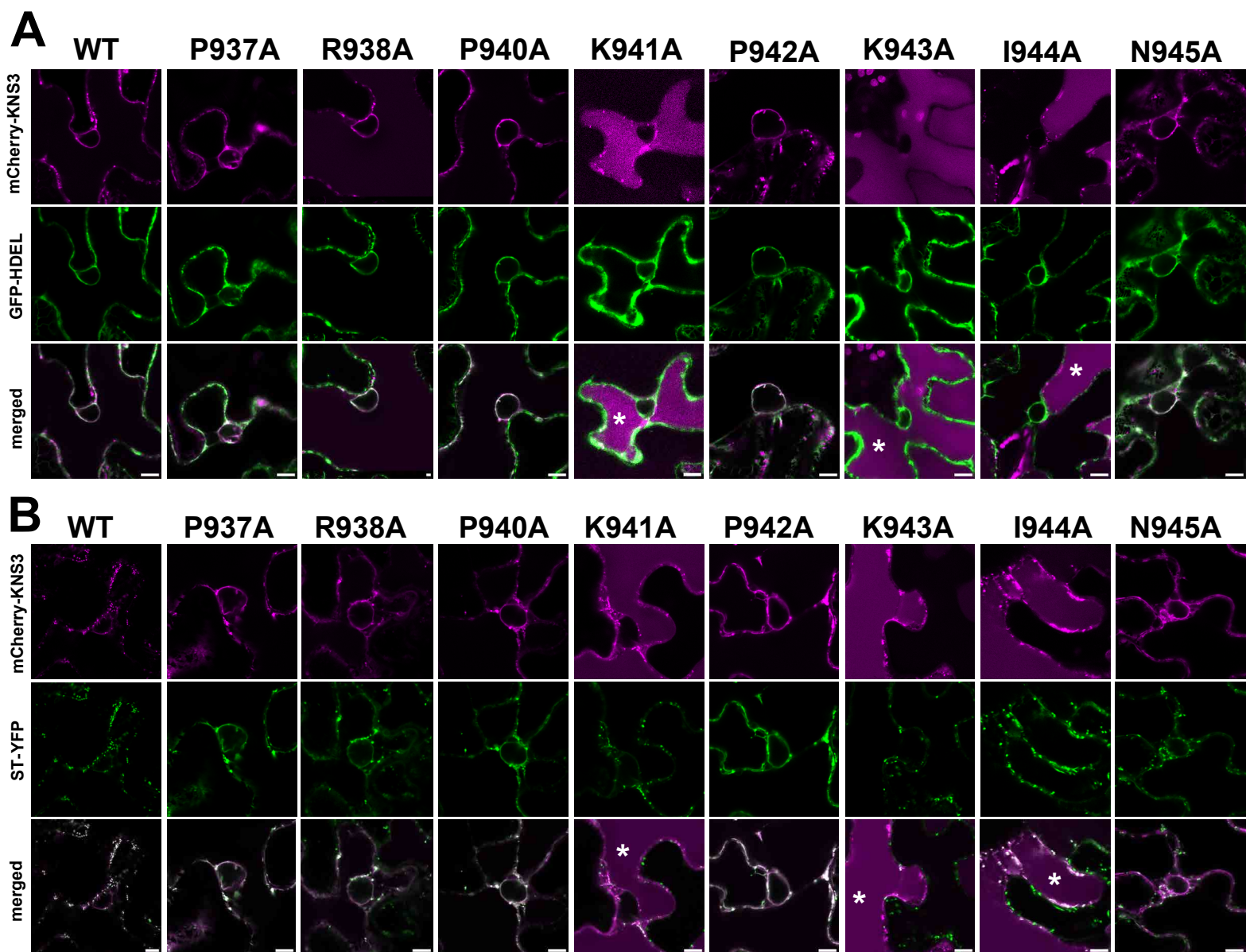
**Fig. S4. Topologies of KNS3, KNSTH1, and KNSTH2.**

Topologies of KNS3 (A), KNSTH1 (B), and KNSTH2 (C) as predicted by AlphaFold protein structure database.



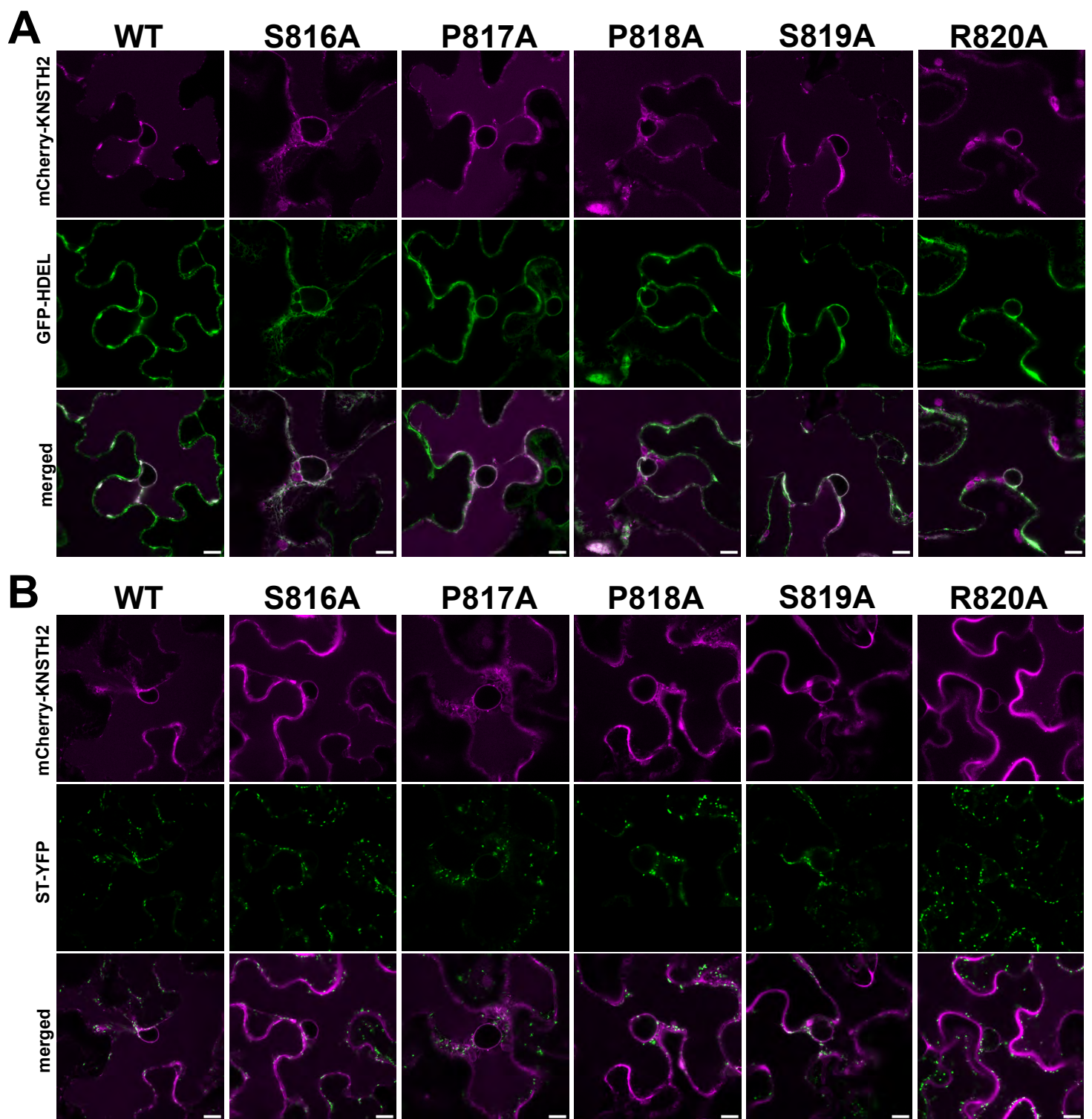
**Fig. S5. Pollen structure in *kns3*, *knsth1*, and *knsth2* multiple mutants.**

SEM images of pollens from WT, *kns3-2*, *kns3-2 knsth1-1*, *kns3-2 knsth2-1*, *knsth1-1 knsth2-1*, and *kns3-2 knsth1-1 knsth2-1* mutants. Plants were grown in pots with vermiculite supplied with 1/1000 diluted Hyponex solution (Hyponex Japan). Scale bar=10  $\mu$ m.



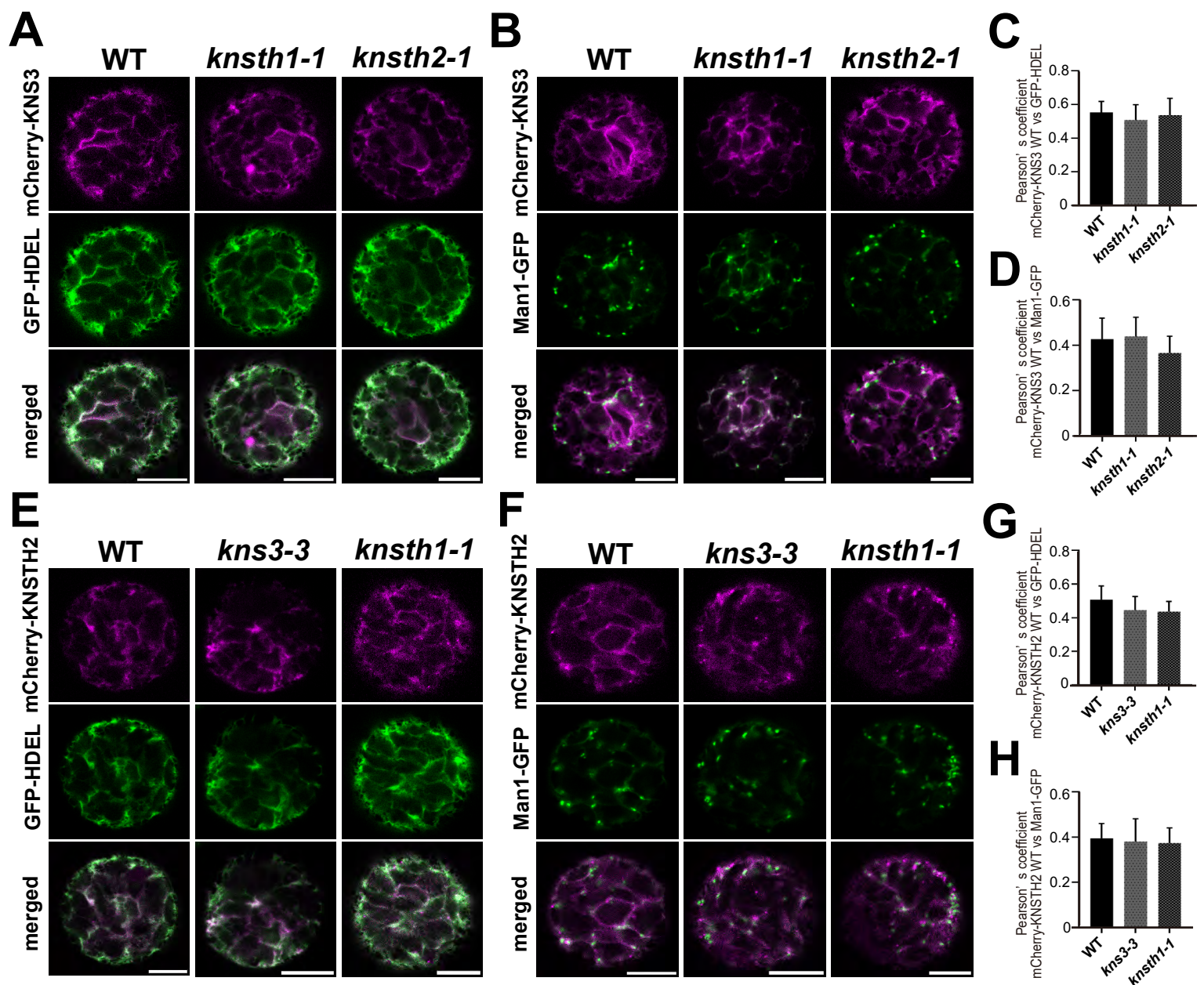
**Fig. S6. K941, K943, and I944 in the C-terminal tail of KNS3 are important for its trafficking from the Golgi to the ER.**

(A, B) mCherry-KNS3 WT and variants were introduced with GFP-HDEL (A) or ST-YFP (B) in *N.benthamiana* leaf epidermal cells by agroinfiltration. Asterisks indicate the vacuole. Scale bar=10  $\mu$ m.



**Fig. S7. Mutations in the C-terminal tail of KNSTH2 do not affect its ER localization.**

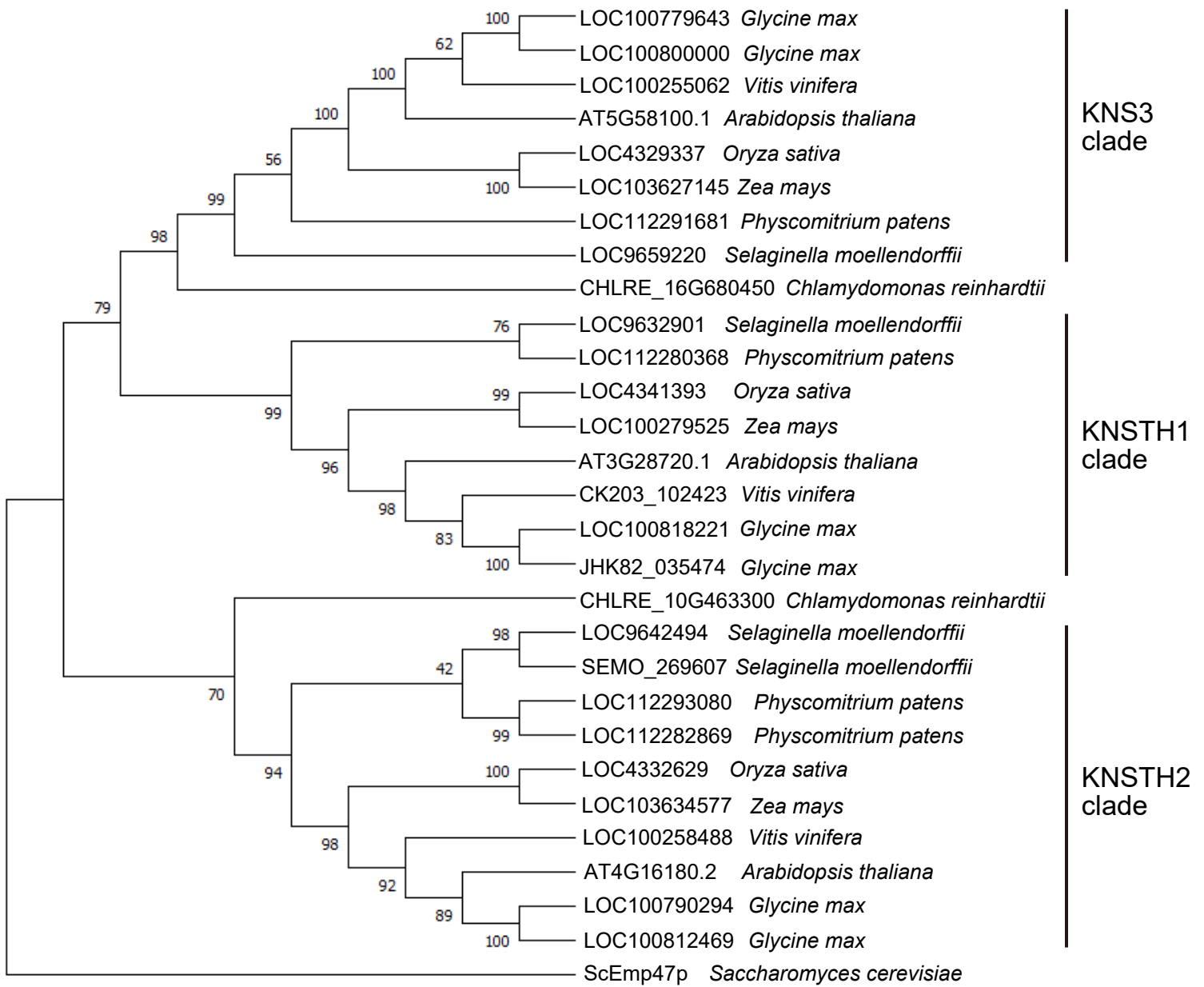
(A, B) mCherry-KNSTH2 WT and variants were introduced with GFP-HDEL (A) or ST-YFP (B) in *N.benthamiana* leaf epidermal cells by agroinfiltration. Scale bar=10  $\mu$ m.



**Fig. S8. Localization of mCherry-KNS3 and KNSTH2 is unchanged in single mutants of their homologs.**

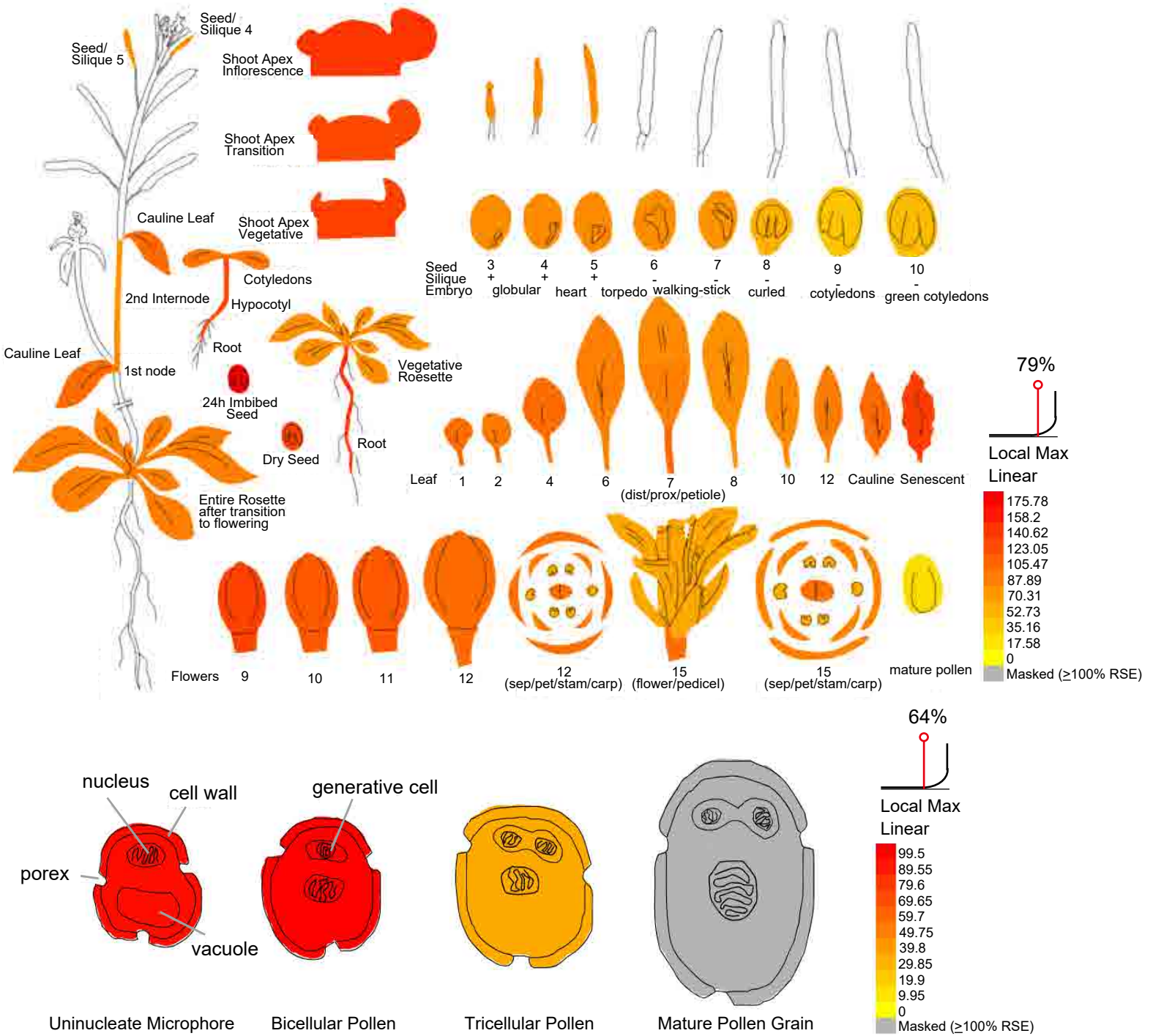
(A-D) mCherry-KNS3 and GFP-HDEL (A) or Man1-GFP (B) in protoplasts from WT (Col-0), *knsth1-1*, and *knsth2-1* Arabidopsis leaf mesophyll cells. Pearson' s coefficients of mCherry-KNS3 with GFP-HDEL (C) or Man1-GFP (D). Data represent the mean  $\pm$  SD of 10 to 16 protoplasts. No significant differences were observed (Dunnett' s test,  $P > 0.05$ ). (E-H) mCherry-KNSTH2 and GFP-HDEL (E) or Man1-GFP (F) in protoplasts from WT (Col-0), *kns3-3*, and *knsth1-1* Arabidopsis leaf mesophyll cells. Pearson' s coefficients of mCherry-KNSTH2 with GFP-HDEL (G) or Man1-GFP (H). Data represent the mean  $\pm$  SD of 10 to 11 protoplasts. No significant differences were observed (Dunnett' s test,  $P > 0.05$ ). Scale bar=10  $\mu$ m.





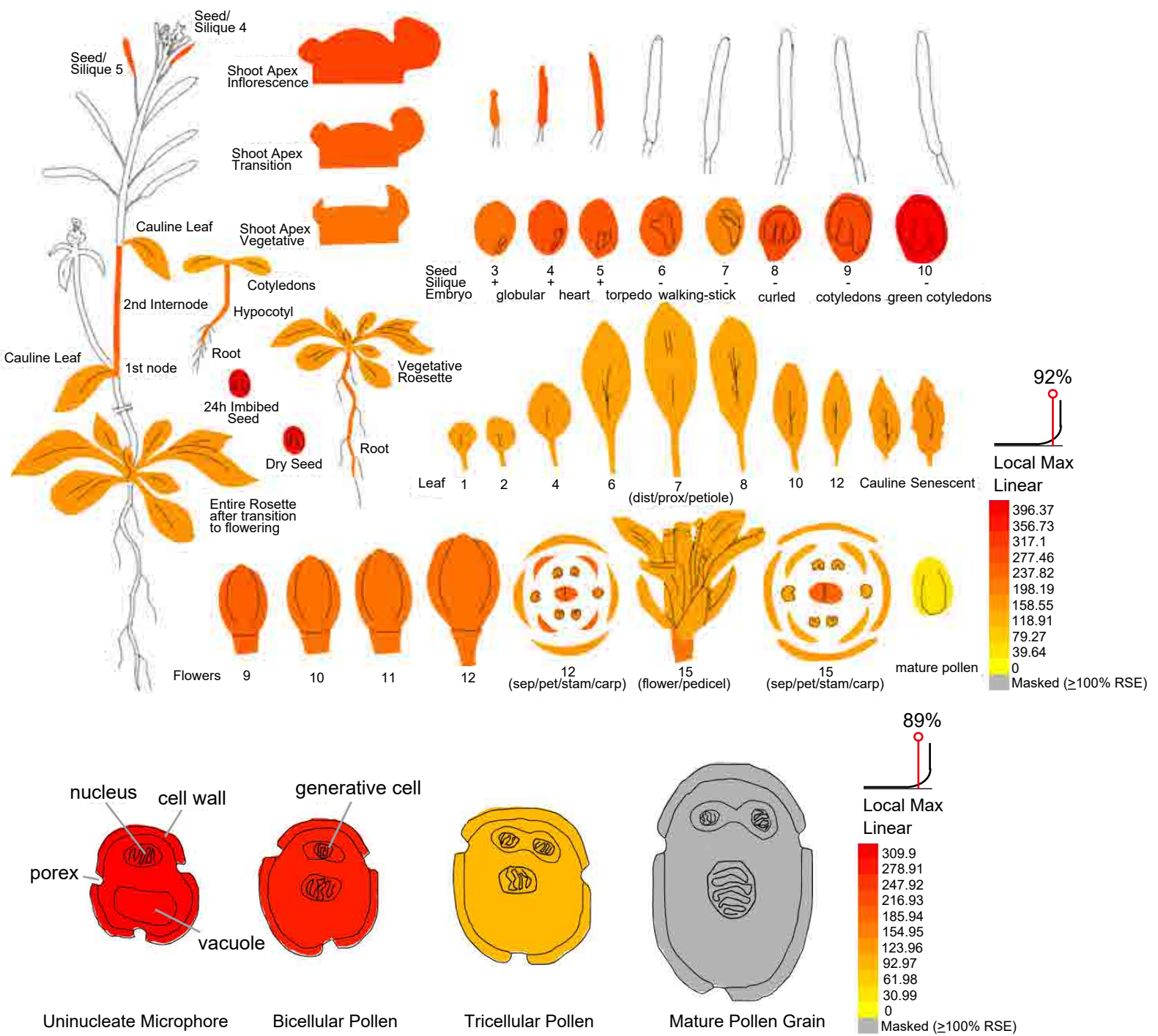
**Fig. S9. Phylogenetic tree of KNS3 and its homologs.**

Protein sequences of KNS3 homologs (from the National Center for Biotechnological Information Database) in different plant species were used for alignment, and a maximum likelihood-based tree was generated using the MEGA X program. Bootstrap testing was conducted with 1000 replicates. Values are indicated at branch nodes.



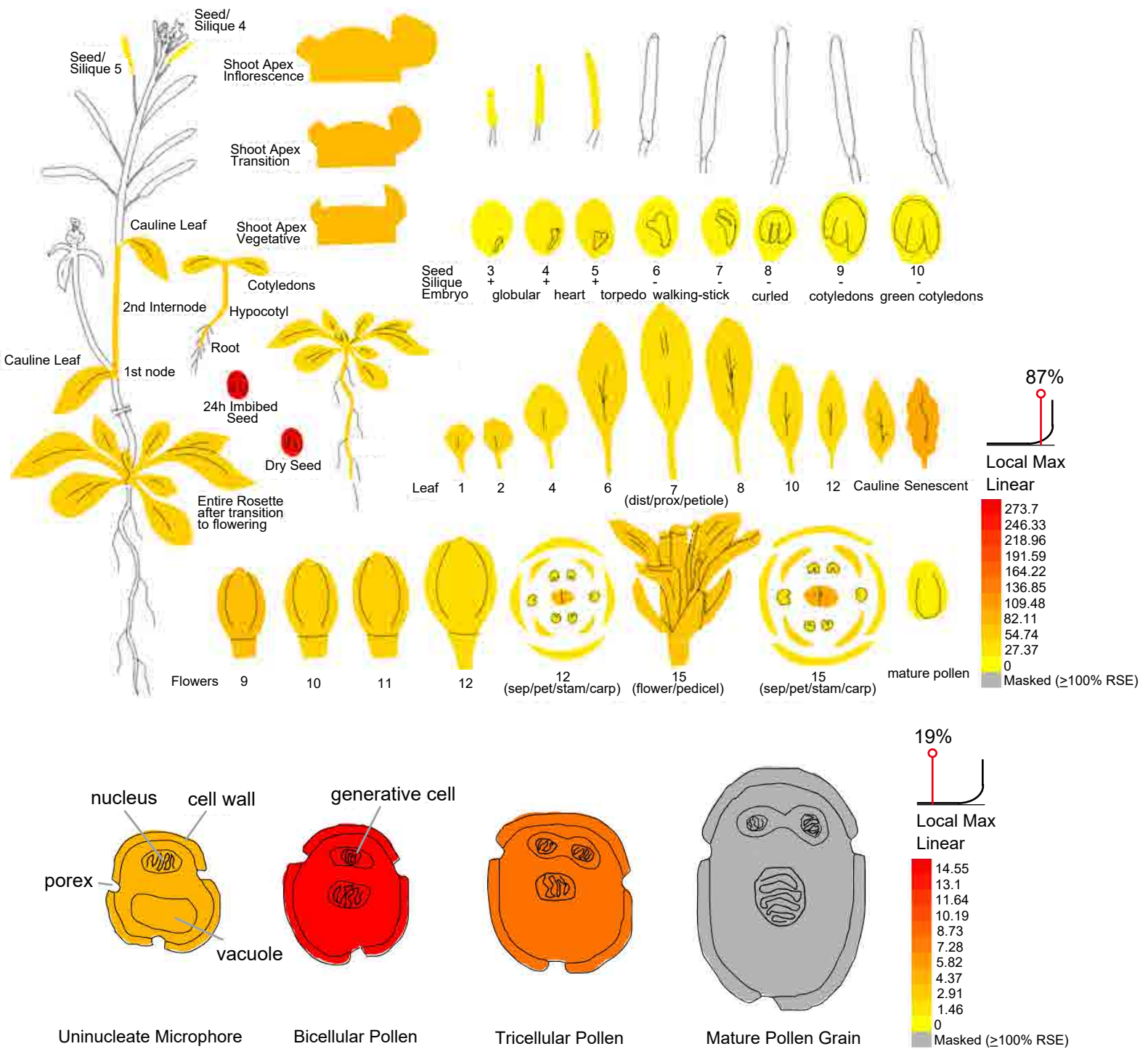
**Fig. S10. Expression pattern of *KNS3*.**

Expression patterns of *KNS3* in whole plants and pollen. Data were obtained from the ePlant database (<https://bar.utoronto.ca/eplant/>).



**Fig. S11. Expression pattern of *KNSTH1*.**

Expression patterns of *KNSTH1* in whole plants and pollen. Data were obtained from the ePlant database (<https://bar.utoronto.ca/eplant/>).



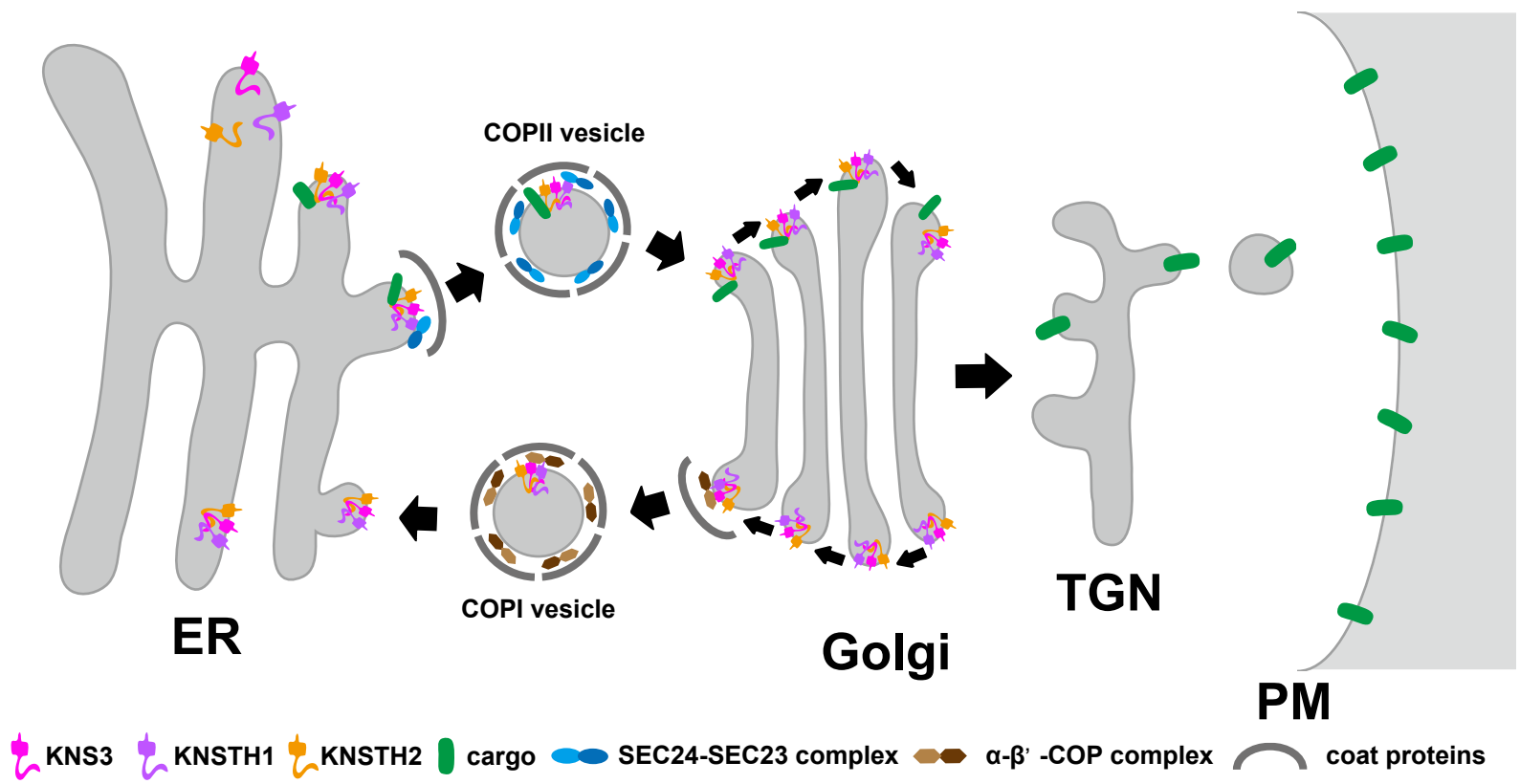
**Fig. S12. Expression pattern of *KNSTH2*.**

Expression patterns of *KNSTH2* in whole plants and pollen. Data were obtained from the ePlant database (<https://bar.utoronto.ca/eplant/>).

|                 |                             |                                   |   |   |   |   |   |   |   |   |   |   |   |   |     |     |     |
|-----------------|-----------------------------|-----------------------------------|---|---|---|---|---|---|---|---|---|---|---|---|-----|-----|-----|
| KNS3<br>clade   | AT5G58100.1                 | <i>Arabidopsis thaliana</i>       | - | - | - | - | R | P | R | A | P | K | P | K | I   | N   | 945 |
|                 | LOC100779643                | <i>Glycine max</i>                | - | - | - | - | R | P | R | R | P | K | P | K | I   | N   | 948 |
|                 | LOC100800000                | <i>Glycine max</i>                | - | - | - | - | R | P | R | R | P | K | P | K | I   | N   | 956 |
|                 | LOC100255062                | <i>Vitis vinifera</i>             | - | - | - | - | R | P | R | R | P | K | P | K | I   | N   | 938 |
|                 | LOC4329337                  | <i>Oryza sativa</i>               | - | - | - | - | R | P | R | R | P | K | P | K | I   | N   | 951 |
|                 | LOC103627145                | <i>Zea mays</i>                   | - | - | - | - | R | P | R | R | P | K | P | K | I   | N   | 953 |
|                 | LOC9659220                  | <i>Selaginella moellendorffii</i> | - | - | - | - | - | P | R | R | L | K | P | K | I   | N   | 949 |
|                 | LOC112291681                | <i>Physcomitrium patens</i>       | - | - | - | - | R | R | R | R | P | K | P | K | I   | N   | 953 |
| KNSTH1<br>clade | AT3G28720.1                 | <i>Arabidopsis thaliana</i>       | - | K | R | D | R | L | F | R | N | K | R | K | Q   | F   | 687 |
|                 | LOC100818221                | <i>Glycine max</i>                | - | R | R | D | K | L | F | R | N | K | R | K | Q   | F   | 685 |
|                 | JHK82_035474                | <i>Glycine max</i>                | - | R | R | D | K | L | F | R | N | K | R | K | Q   | F   | 686 |
|                 | CK203_102423                | <i>Vitis vinifera</i>             | - | K | R | D | K | L | F | R | N | K | R | K | Q   | F   | 673 |
|                 | LOC4341393                  | <i>Oryza sativa</i>               | - | K | R | D | K | L | F | R | S | K | R | K | Q   | F   | 672 |
|                 | LOC100279525                | <i>Zea mays</i>                   | - | K | R | D | K | L | F | R | S | K | R | K | Q   | F   | 671 |
|                 | LOC9632901                  | <i>Selaginella moellendorffii</i> | - | R | R | E | Q | L | F | A | S | K | R | K | R   | F   | 678 |
|                 | LOC112280368                | <i>Physcomitrium patens</i>       | N | K | R | D | K | F | L | V | N | K | K | K | R   | F   | 676 |
| KNSTH2<br>clade | AT4G16180.2                 | <i>Arabidopsis thaliana</i>       | - | - | - | - | - | - | - | - | - | S | P | P | S   | R   | 820 |
|                 | LOC100790294                | <i>Glycine max</i>                | - | - | - | - | - | - | - | - | - | S | P | V | R   | 803 |     |
|                 | LOC100812469                | <i>Glycine max</i>                | - | - | - | - | - | - | - | - | - | S | P | V | R   | 803 |     |
|                 | LOC100258488                | <i>Vitis vinifera</i>             | - | - | - | - | - | - | - | - | - | S | P | V | R   | 809 |     |
|                 | LOC4332629                  | <i>Oryza sativa</i>               | - | - | - | - | - | - | - | - | - | S | P | V | R   | 807 |     |
|                 | LOC103634577                | <i>Zea mays</i>                   | - | - | - | - | - | - | - | - | - | S | P | V | R   | 804 |     |
|                 | LOC9642494                  | <i>Selaginella moellendorffii</i> | - | - | - | - | - | - | - | - | - | S | G | D | K   | W   | 806 |
|                 | SEMO_269607                 | <i>Selaginella moellendorffii</i> | - | - | - | - | - | - | - | - | - | S | G | D | K   | W   | 803 |
| LOC112293080    | <i>Physcomitrium patens</i> | -                                 | - | - | - | - | - | - | - | - | S | S | E | R | 820 |     |     |
| LOC112282869    | <i>Physcomitrium patens</i> | -                                 | - | - | - | - | - | - | - | - | S | S | E | R | 817 |     |     |

**Fig. S13. Multiple alignments of the amino acid sequences of the C-terminal tail of KNS3 and its homologs.**

Multiple alignments of the C-terminal tails of KNS3 homologs were performed using Clustal Omega. The conserved amino acids are highlighted in gray.



**Fig. S14. A working hypothesis of the functions of KNS3, KNSTH1, and KNSTH2 in an ER-Golgi cargo-receptor complex.**

In our hypothetical model, KNS3, KNSTH1, and KNSTH2 form a cargo-receptor complex that interacts with boric acid channels and other cargoes in the ER, packaging them into COPII vesicles for transport to the Golgi. In the Golgi, the cargo-receptor complex separates from the cargo and returns to the ER via COPI vesicles. Boric acid channels and other PM cargoes are transported from the Golgi apparatus to the trans-Golgi network, and then to the PM via the secretion pathway.

|              | Name        | Location (Mbp) | Sequence                       |                            | Product size Col-0/Ler (bp) |
|--------------|-------------|----------------|--------------------------------|----------------------------|-----------------------------|
|              |             |                | forward                        | reverse                    |                             |
| Chromosome 1 | map 1-3M    | 3              | CGTGAACCCACTCGTTAC<br>ATT      | TGCATTTCAACTTTAC<br>CAACCA | 248/204                     |
|              | map 1-13.8M | 13.8           | ATGTTGGATTCAAGCACT<br>TCC      | AAGGTCCGTCAGAC<br>GTG      | 200/156                     |
|              | map 1-24.4M | 24.4           | TACTCATGCGGATGCGGT<br>TA       | TCTCCCTCCCTTTTCT<br>TGCT   | 187/132                     |
| Chromosome 2 | map 2-3.5M  | 3.5            | ATCAACATCCGCAAAGTT<br>CC       | ACCTCCTTAGTCGCG<br>TGAAA   | 383/327                     |
|              | nga 168     | 16.3           | GAGGACATGTATAGGAGC<br>CTCG     | TCGTCTACTGCACTG<br>CCG     | 150/130                     |
| Chromosome 3 | nga 162     | 4.6            | CTCTGTCACTCTTTTCCTC<br>TGG     | CATGCAATTTGCATCT<br>GAGG   | 110/85                      |
|              | map 3-18M   | 18.2           | TCGAGGACTTTTATTGAT<br>AGATTGAA | TGGATGAAAAGAAGG<br>CAAGG   | 265/182                     |
| Chromosome 4 | NG A8       | 5.6            | TGGCTTTCGTTTATAAAC<br>ATCC     | GAGGGCAAATCTTTA<br>TTTCGG  | 154/198                     |
| Chromosome 5 | 2.5M        | 2.5            | CCAAGACCAAACCAAA<br>ACC        | CATGCAATAGGCTTC<br>GGAGT   | 247/173                     |
|              | map 5-19.9M | 19.9           | TGACAACCTTTGGGCAATT<br>AAGA    | CGCATGATGCATAGC<br>AAAGT   | 246/209                     |

**Table S1. SLP markers for rough mapping.**



| Primer name         | Sequence (5'>3')                            | Purpose                                     |
|---------------------|---|---|
| KNS3 (1-34aa) F     | CTGATTAACACTCGAATGCGGAGATTCGGGGCT           | KNS3 (1-34aa) for In-Fusion cloning         |
| KNS3 (1-34aa) R     | TCCTCCTCGCCCTTGCTCAATTGTGAAGCTCCATACGATA GA |   |
| mCherry F           | TTGAGCAAGGGCGAGGAG                          | mCherry for In-Fusion cloning               |
| mCherry R           | CTTGACAGCTCGTCCATGCC                        |   |
| KNS3 (35-945aa) F   | GCATGGACGAGCTGTACAAGGGGAACCGGAAGACGGCG AA   | KNS3 (35-945aa) for In-Fusion cloning       |
| KNS3 (35-945aa) R   | AGTTGGATATCTCGATCAGTTGATCTTTGGCTTAG         |   |
| KNSTH2 (1-36aa) F   | CTGATTAACACTCGAGTCATGGAGTTGAGATCGG          | KNSTH2 (1-36aa) for In-Fusion cloning       |
| KNSTH2 (1-36aa) R   | TCCTCCTCGCCCTTGCTCAATTGCTGAGCCGAGTCGGTA     |   |
| KNSTH2 (37-820aa) F | GCATGGACGAGCTGTACAAGCCTTCCGTCGCGAGCCA       | KNSTH2 (37-820aa) for In-Fusion cloning     |
| KNSTH2 (37-820aa) R | AGTTGGATATCTCGACTAGCGAGAAGGAGGAGA           |   |
| P937A F             | TTAAGGGCTAGAGCTCCTAAGCCAAAG                 | Introduction of mCherry-KNS3 P937A mutation |
| P937A R             | AGCTCTAGCCCTTAAGACAGCGTAAAG                 |   |
| R938A F             | AGGCCAGCTGCTCCTAAGCCAAAGATC                 | Introduction of mCherry-KNS3 R938A mutation |
| R938A R             | AGGAGCAGCTGGCCTTAAGACAGCGTA                 |   |
| P940A F             | AGAGCTGCTAAGCCAAAGATCAACTGA                 | Introduction                                |

|         |                             |   |
|---------|-----------------------------|---|
| P940A R | TGGCTTAGCAGCTCTTGGCCTTAAGAC | n of mCherry-KNS3 P940A mutation            |
| K941A F | GCTCCTGCTCCAAAGATCAACTGATCG | Introduction of mCherry-KNS3 K941A mutation |
| K941A R | CTTTGGAGCAGGAGCTCTTGGCCTTAA |   |
| P942A F | CCTAAGGCTAAGATCAACTGATCGAGA | Introduction of mCherry-KNS3 P942A mutation |
| P942A R | GATCTTAGCCTTAGGAGCTCTTGGCCT |   |
| K943A F | AAGCCAGCTATCAACTGATCGAGATAT | Introduction of mCherry-KNS3 K943A mutation |
| K943A R | GTTGATAGCTGGCTTAGGAGCTCTTGG |   |
| I944A F | CCAAAGGCTAACTGATCGAGATATCCA | Introduction of mCherry-KNS3 I944A mutation |
| I944A R | TCAGTTAGCCTTTGGCTTAGGAGCTCT |   |
| N945A F | AAGATCGCTTGATCGAGATATCCA    | Introduction of mCherry-KNS3 N945A mutation |
| N945A R | CGATCAAGCGATCTTTGGCTTAGGAGC |   |
| S816A F | TTCTCTGCTCCTCCTTCTCGCTAGTCG | Introduction                                |

|                |                              |   |
|----------------|------------------------------|---|
| S816A R        | AGGAGGAGCAGAGAAGAAAATGACAAG  | n of mCherry-KNSTH2 S816A mutation            |
| P817A F        | TCTTCTGCTCCTTCTCGCTAGTCGAGA  | Introduction of mCherry-KNSTH2 P817A mutation |
| P817A R        | AGAAGGAGCAGAAGAGAAGAAAATGAC  |   |
| P818A F        | TCTCCTGCTTCTCGCTAGTCGAGATAT  | Introduction of mCherry-KNSTH2 P818A mutation |
| P818A R        | GCGAGAAGCAGGAGAAGAGAAGAAAAT  |   |
| S819A F        | CCTCCTGCTCGCTAGTCGAGATATCCA  | Introduction of mCherry-KNSTH2 S819A mutation |
| S819A R        | CTAGCGAGCAGGAGGAGAAGAGAAGAA  |   |
| R820A F        | CCTTCTGCTTAGTCGAGATATCCA ACT | Introduction of mCherry-KNSTH2 R820A mutation |
| R820A R        | CGACTAAGCAGAAGGAGGAGAAGAGAA  |   |
| LBb1.3         | ATTTTGCCGATTTTCGGAAC         | Genotyping for SALK T-DNA mutant              |
| SALK_041228 LP | TCAGTGCATACATATGCTGGC        | Genotyping for <i>kns3-2</i>                  |
| SALK_041228    | ACCATCAGGCTGTTGACATTC        |   |

|                  |                                   |                                  |
|------------------|-----------------------------------|----------------------------------|
| RP               |                                   |                                  |
| SALK_061320 LP   | AAAGGAGCCAACCTTGAGAAG             | Genotyping for <i>kns3-3</i>     |
| SALK_061320 RP   | AAAGAAGCCTTTCCTTGATGC             |                                  |
| SALK_027378 LP   | GTTCAAGAAAACGTCAGACGC             | Genotyping for <i>knsth1-1</i>   |
| SALK_027378 RP   | CGTCAAGGTGGAGAGAGTGAG             |                                  |
| SALK_106609 LP   | CATCGGAGACTCTTTCCTTC              | Genotyping for <i>knsth1-2</i>   |
| SALK_106609 RP   | GCCCGTTGCAAGTATAATCAC             |                                  |
| LB3              | TAGCATCTGAATTCATAACCAATCTCGATACAC | Genotyping for SAIL T-DNA mutant |
| SAIL_731_H0 3 LP | AGGTGTAGGCTAGCGAGAAGG             | Genotyping for <i>knsth2-1</i>   |
| SAIL_731_H0 3 RP | ATGCTGTCCCATCACAGGTAC             |                                  |
| SAIL_670_H0 1 LP | TAGCCGATGTAGATCCAATGC             | Genotyping for <i>knsth2-3</i>   |
| SAIL_670_H0 1 RP | ACCAGCCACAAGTATTCCTCC             |                                  |

**Table S2. Primers used in this research.**

|               |                                   | localization               |                          |                       |                   |
|---------------|-----------------------------------|----------------------------|--------------------------|-----------------------|-------------------|
|               |                                   | in Arabidopsis protoplasts |                          | in tobacco leaf cells |                   |
| KNS3          | WT                                | ER, Golgi                  | (Figs 6, 8)              | ER, Golgi             | (Fig. 6, Fig. S6) |
|               | P937A                             | ER, Golgi                  | (Fig. 8)                 | ER, Golgi             | (Fig. S6)         |
|               | R938A                             | ER, Golgi                  |                          | ER, Golgi             |                   |
|               | P940A                             | ER, Golgi                  |                          | ER, Golgi             |                   |
|               | K941A                             | ER, Golgi, vacuole         |                          | Golgi, vacuole        |                   |
|               | P942A                             | ER, Golgi                  |                          | ER, Golgi             |                   |
|               | K943A                             | ER, Golgi, vacuole         |                          | Golgi, vacuole        |                   |
|               | I944A                             | Golgi                      |                          | Golgi, vacuole        |                   |
|               | N945A                             | ER, Golgi                  |                          | ER, Golgi             |                   |
| KNSTH2        | WT                                | ER                         | (Figs 7, 9)              | ER                    | (Fig. 7, Fig. S7) |
|               | S816A                             | ER                         | (Fig. 9)                 | ER                    | (Fig. S7)         |
|               | P817A                             | ER                         |                          | ER                    |                   |
|               | P818A                             | ER                         |                          | ER                    |                   |
|               | S819A                             | ER                         |                          | ER                    |                   |
|               | R820A                             | ER                         |                          | ER                    |                   |
|               | in Arabidopsis protoplasts        |                            |                          |                       |                   |
|               | WT                                | <i>knsth1-1</i>            | <i>knsth2-1</i>          |                       |                   |
| KNS3 WT       | ER, Golgi<br>(Figs 6, 8, Fig. S8) | ER, Golgi<br>(Fig. S8)     | ER, Golgi<br>(Fig. S8)   |                       |                   |
| KNSTH2<br>WT  | WT                                | <i>kns3-3</i>              | <i>knsth1-1</i>          |                       |                   |
|               | ER<br>(Figs 7, 9, Fig. S8)        | ER<br>(Fig. S8)            | ER<br>(Fig. S8)          |                       |                   |
| KNS3<br>I944A | WT                                | <i>knsth1-1/knsth1-2</i>   | <i>knsth2-1/knsth2-3</i> |                       |                   |
|               | Golgi<br>(Figs 8, 10)             | ER, Golgi<br>(Fig. 10)     | ER, Golgi<br>(Fig. 10)   |                       |                   |

**Table S3. Summary of the localization of mCherry-KNS3 and mCherry-KNSTH2 in Arabidopsis protoplasts and tobacco leaf cells.**

| Organism                   | Name            | Protein length (aa) | NCBI protein number |
|----------------------------|-----------------|---------------------|---------------------|
| Arabidopsis thaliana       | AT5G58100.1     | 945                 | NP_001318823.1      |
|                            | AT4G16180.2     | 820                 | NP_001154242.2      |
|                            | AT3G28720.1     | 687                 | NP_189514.1         |
| Glycine max                | LOC100779643    | 948                 | XP_003516388.1      |
|                            | LOC100800000    | 956                 | XP_003532318.1      |
|                            | LOC100818221    | 685                 | XP_003554877.2      |
|                            | JHK82_035474    | 686                 | KAG5112205.1        |
|                            | LOC100790294    | 803                 | XP_003528615.1      |
|                            | LOC100812469    | 803                 | XP_003550564.1      |
| Vitis vinifera             | LOC100255062    | 938                 | XP_010655027.1      |
|                            | CK203_102423    | 673                 | RVW26491.1          |
|                            | LOC100258488    | 809                 | XP_002273166.2      |
| Oryza sativa               | LOC4329337      | 951                 | XP_015624632.1      |
|                            | LOC4341393      | 672                 | XP_015644546.1      |
|                            | LOC4332629      | 807                 | XP_015632688.1      |
| Zea mays                   | LOC103627145    | 953                 | XP_008645675.1      |
|                            | LOC100279525    | 671                 | XP_001145995.2      |
|                            | LOC103634577    | 804                 | XP_008655047.1      |
| Selaginella moellendorffii | LOC9659220      | 949                 | XP_024530236.1      |
|                            | LOC9632901      | 678                 | XP_002991685.1      |
|                            | LOC9642494      | 806                 | XP_024516482.1      |
|                            | SEMO_269607     | 803                 | EFJ08873.1          |
| Physcomitrium patens       | LOC112291681    | 953                 | XP_024395234.1      |
|                            | LOC112280368    | 676                 | XP_024371568.1      |
|                            | LOC112293080    | 820                 | XP_024397913.1      |
|                            | LOC112282869    | 817                 | XP_024376759.1      |
| Chlamydomonas reinhardtii  | CHLRE_16G680450 | 1079                | XP_042916023.1      |
|                            | CHLRE_10G463300 | 1012                | XP_042920595.1      |

**Table S4. List of proteins collected using BLAST in the NCBI database.**