**Table S1.** Primers used for genotyping and mRNA level analysis of *sec15b-1* and *sec15b-2* mutant lines.

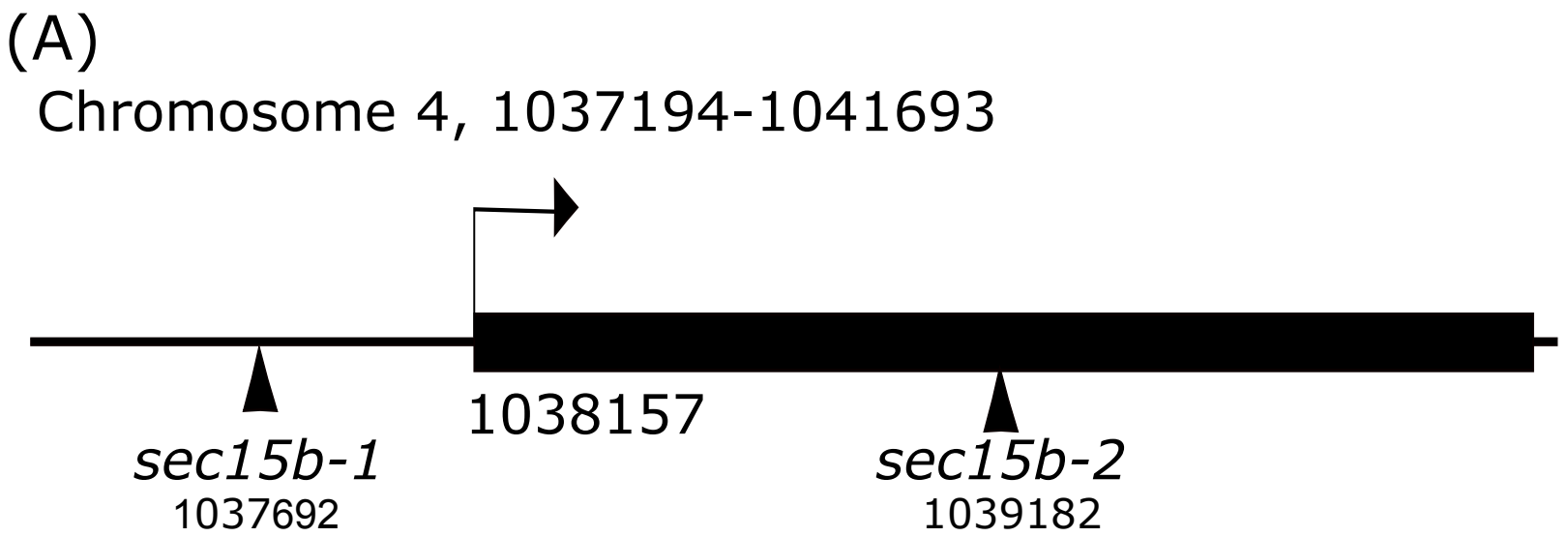
| Primer | Sequence (5' – 3') | Purpose |
|---|---|---|
| SEC15BPROM-RP | GTTGAATTCCTATGGTTTCTAGAAAAC | genotyping of SALK_130663 line |
| SEC15BPROM-LP | AAGCATCCGTTTCAGCGTTGAC | genotyping of SALK_130663 line |
| LBNEW | GAACAACACTCAACCCTATCTCGGGC | genotyping of SALK_130663 line |
| SEC15BRIK-RPBF | TTGGATCCATATGCAATCGTCGAAAGGA | genotyping of RATM15-1183-1_H line |
| SEC15BRIK-LPBIR | CAGTAAGAGATGATTAGCCGTC | genotyping of RATM15-1183-1_H line |
| DS52A | TCCGTTCCGTTTTCGTTTTTTAC | genotyping of RATM15-1183-1_H line |
| NPT_LP | TCCGAGTACGTGCTCGCTCGATGC | primers specific to kanamycin resistance gene |
| NPT_RP | GCTTGGGTGGAGAGGCTATTCGGC | primers specific to kanamycin resistance gene |
| SEC15BRIK-RPBF | TTGGATCCATATGCAATCGTCGAAAGGA | mRNA level analysis |
| SEC15BRIK-LPBIR | CAGTAAGAGATGATTAGCCGTC | mRNA level analysis |
| ACT7-FWD | GCCGATGGTGAGGATATTCAGC | mRNA level analysis |
| ACT7-REV | GAAACTCACCACCACGAACCAG | mRNA level analysis |

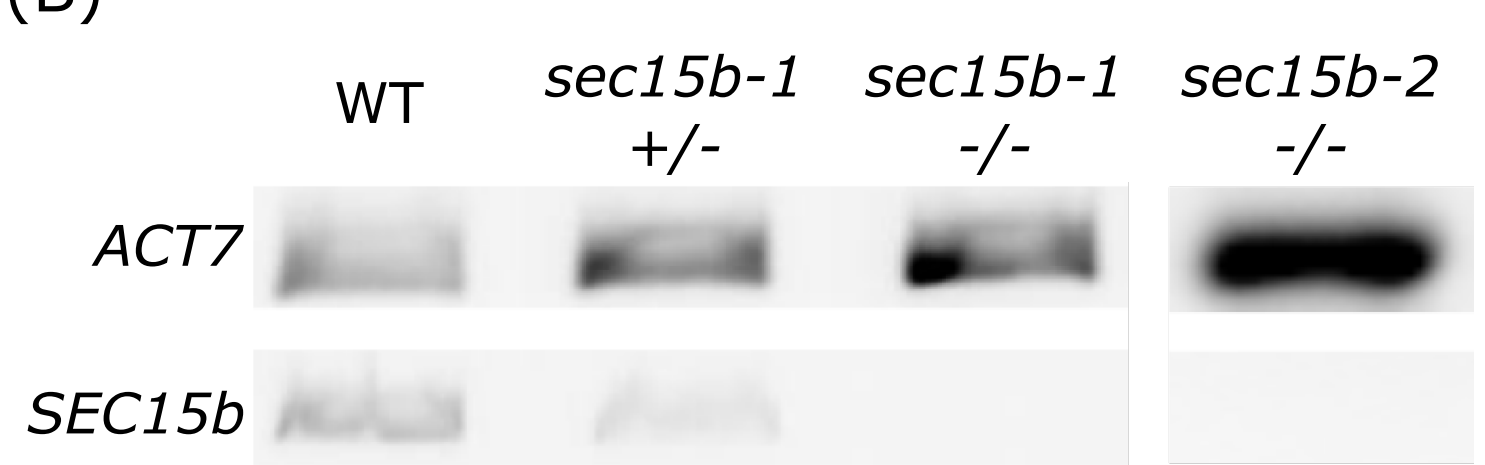
**Table S2. Formation of adventitious roots in etiolated seedlings upon transfer to light**

| Genotype | Plants No | Roots from hypocotyl | Roots from collet | Roots from collet (%) |
|---|---|---|---|---|
| WT *SEC15b* | 42 | 51 | 11 | 18 |
| *sec15b* | 56 | 6 | 40 | 87 |
| WT *EXO70A1* | 21 | 14 | 1 | 7 |
| *exo70A1* | 39 | 1 | 28 | 97 |

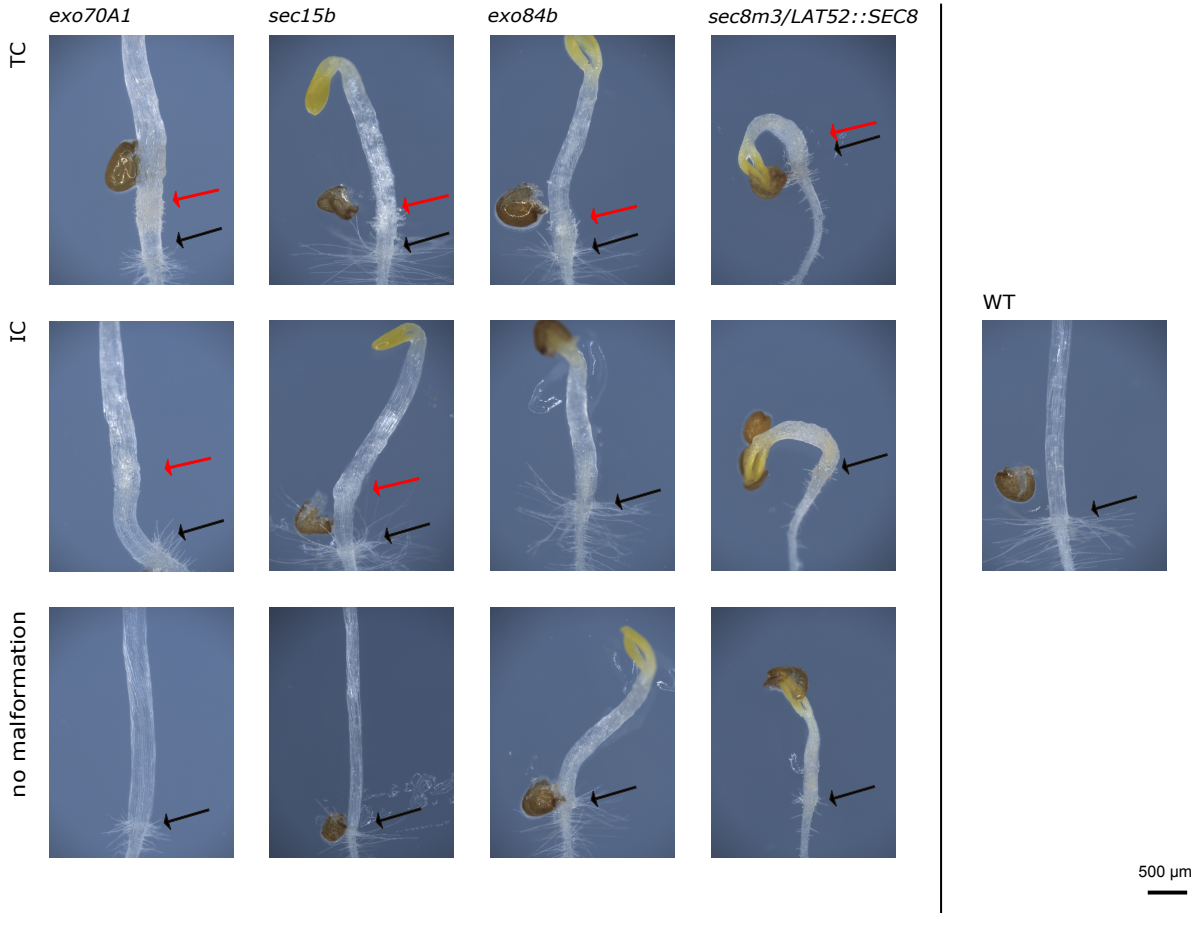
5-day-old etiolated seedlings were transferred to long day conditions and the presence of emerged adventitious roots was scored after 7 days. Sister WT segregants from the last backcross were evaluated for each genotype. For each gene, the mutation significantly affects adventive root location ($\chi^2$ test with Benjamini-Hochberg correction for multiple testing $p<<0.001$). The effect on overall adventitious root number is marginally significant for *sec15b* ($\chi^2$ test with Benjamini-Hochberg correction $p = 0.049$) and non-significant for *exo70A1*. GLMM analysis further confirmed that the distribution of adventitious roots is significantly affected by the genotype ($p = 0.027$ for WT vs. *sec15b*, $p = 0.007$ for WT vs. *exo70A1*), as well as by the location (collet vs. hypocotyl; $p<0.001$ for either genotype), and indicated significant interaction between genotype and location ($p<0.001$ for either genotype).

**Figure S1.**
(A) Graphical visualization of *sec15b-1* and *sec15b-2* insertions in *SEC15B* gene and promoter region.
(B) RT-PCR confirmation of the absence of *SEC15B* mRNA in *sec15b-1* and *sec15b-2* mutant lines.



(A)


exo70A1
sec15b
exo84b
sec8m3/LAT52::SEC8
WT
TC
IC
no malformation
500 µm

(B)

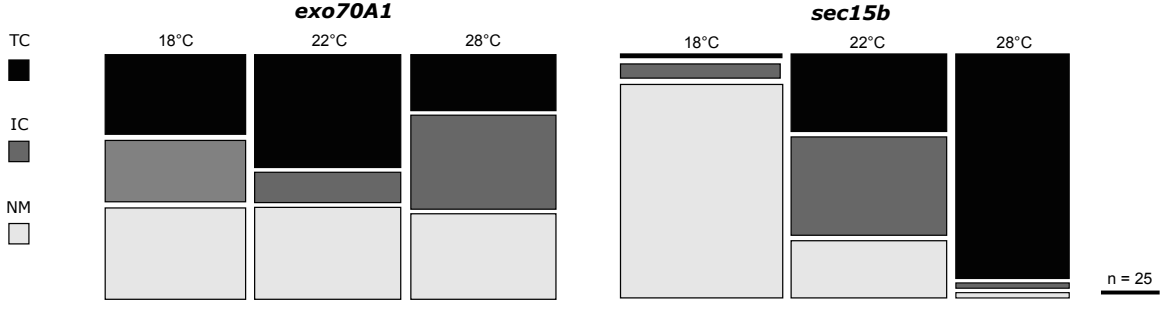

exo70A1
sec15b
18°C
22°C
28°C
TC
IC
NM
n = 25

**Fig. S2. Phenotypic defects of etiolated hypocotyls in exocyst mutants.**

(A) Typical phenotypic deviations - ectopic collet-like structures with or without developed hairs (phenotypes TC and IC) and shortened hypocotyls without malformations in 5 days old *exo70A1*, *sec15b*, *exo84b* and *sec8m3/LAT52::SEC8* seedlings. Black arrows - collet hairs, red arrows - ectopic collet-like structures. A WT seedling is shown alongside for comparison. (B) Effect of cultivation temperature on the proportion of the phenotypic deviations in *exo70A1* and *sec15b* seedlings. Mosaic diagrams display fraction of individuals in the phenotypic categories among seedlings developed at the indicated temperature (NM – no malformation). In total 233 *exo70A1* and 452 *sec15b* mutant plants were evaluated; temperature effects were reproducibly highly significant only for the *sec15b* mutant (pairwise $\chi^2$ test with Benjamini-Hochberg correction for multiple testing $p<<0.001$ for each temperature combination). Column width reflects the number of seedlings counted. Data from one experiment are shown; similar results were obtained in 3 experiments. All seedlings were 5 days old. No hypocotyl defects were ever observed in WT seedlings under these culture conditions.