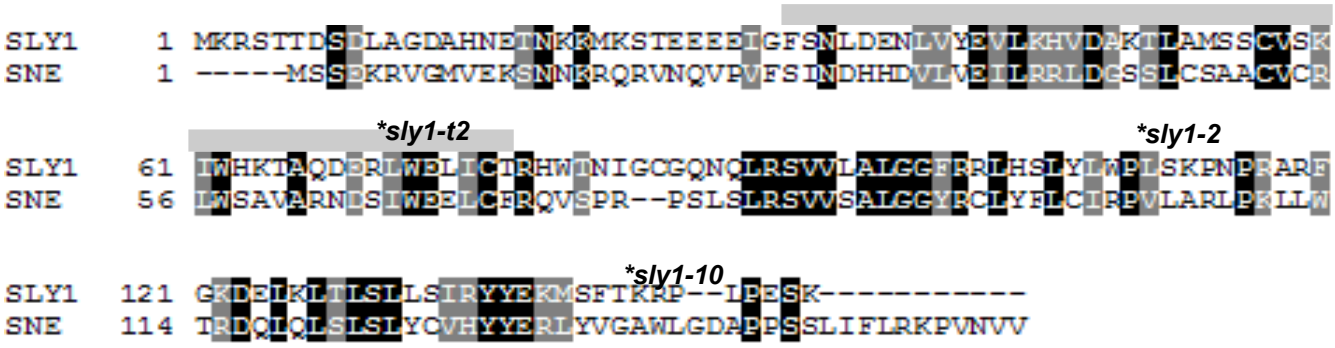
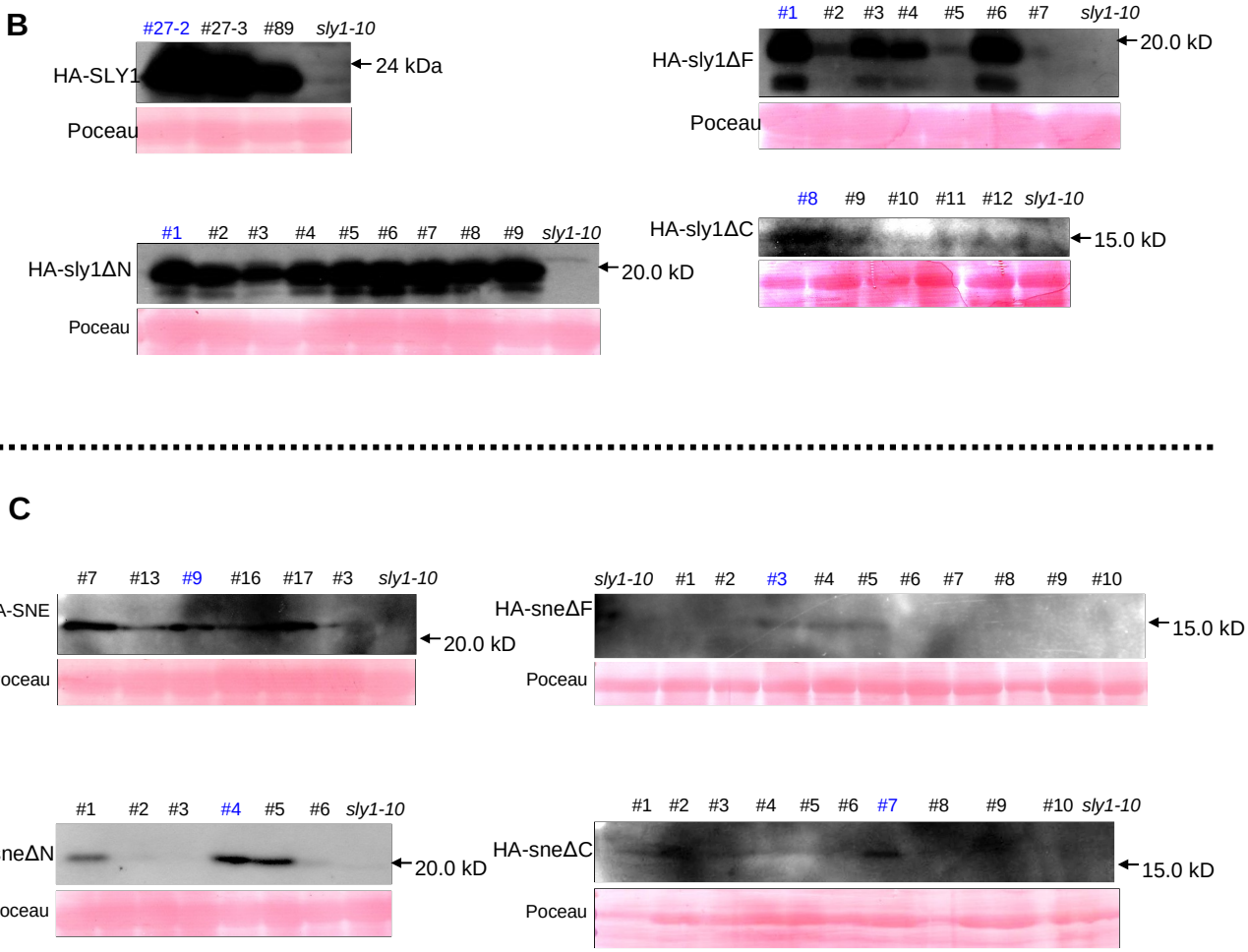


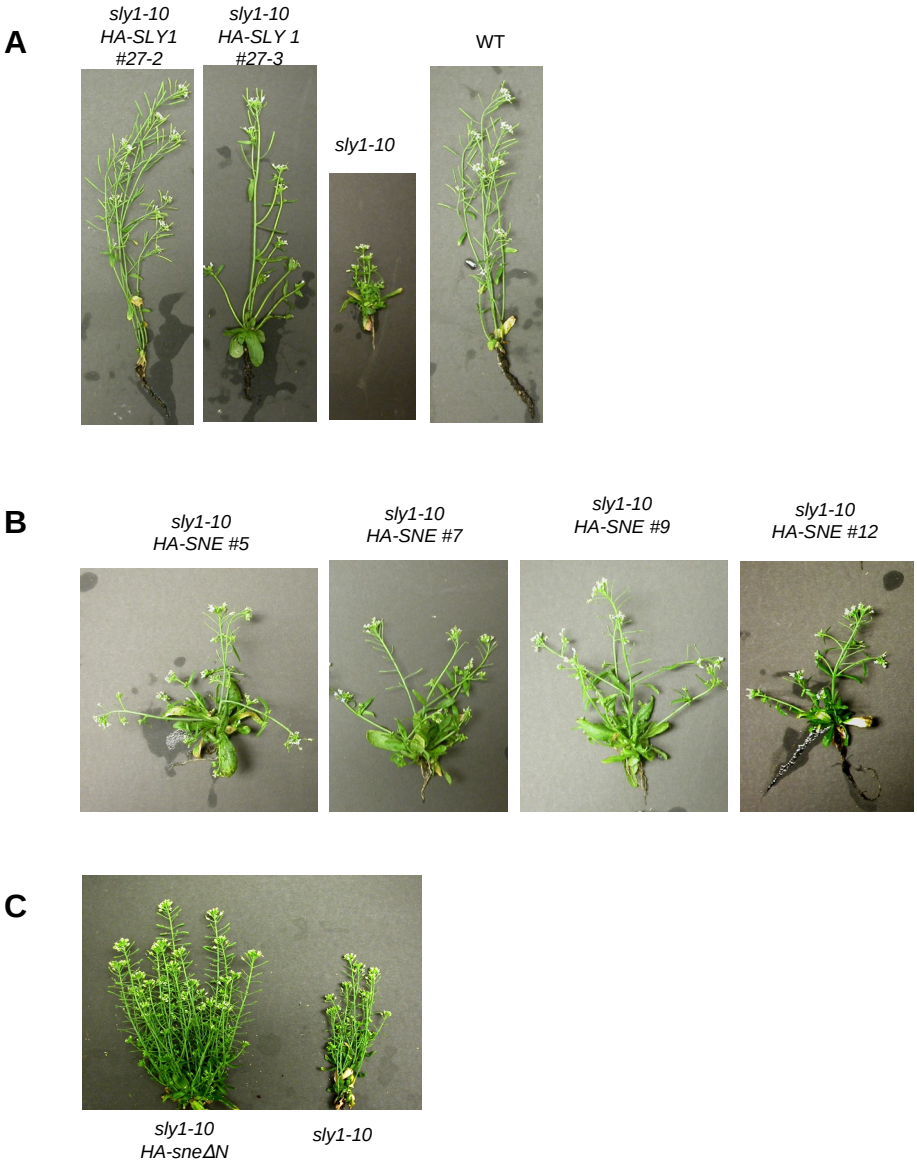
Supplemental Fig. S1. Amino acid sequence alignment of two F-box proteins, SLY1 and SNE. Shaded areas indicate areas of sequence homology as determined by a ClustalW alignment with Boxshade (BCM search launcher). The position of each *sly1* allele is indicated by an asterisk above the changed amino acid.

A

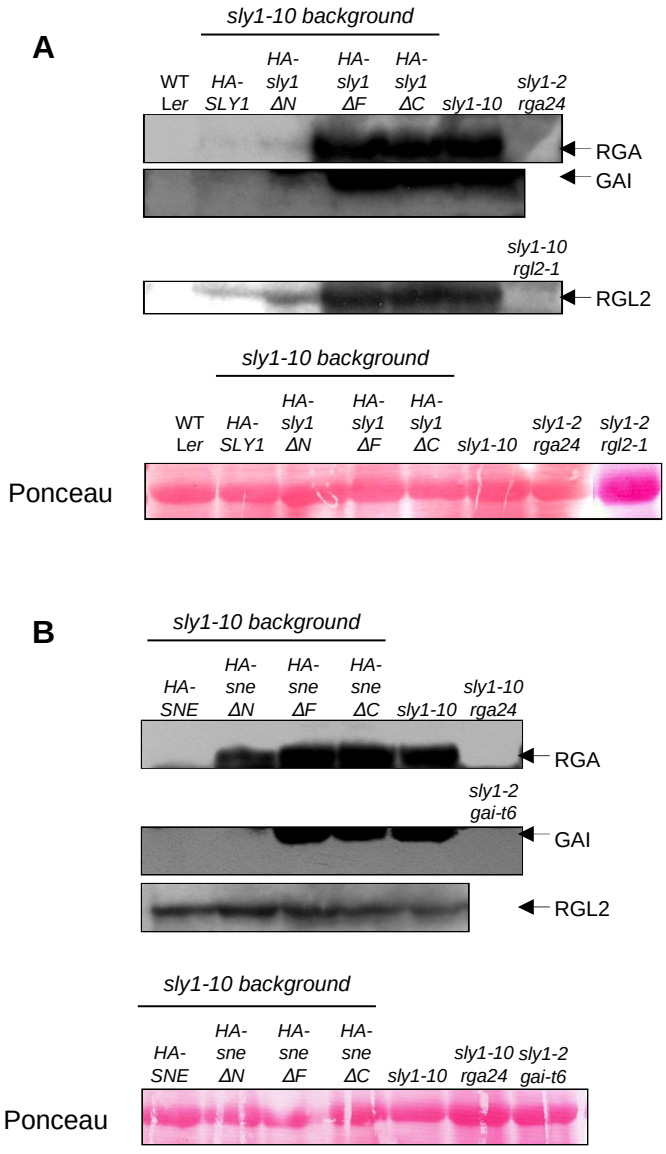
Construct name	Predicted Molecular Weight
HA-SLY1	23.3 kD
HA-sly1ΔN	20.0 kD
HA-sly1ΔF	18.0 kD
HA-sly1ΔC	14.0 kD
HA-SNE	23.9 kD
HA-sneΔN	21.5 kD
HA-sneΔC	18.4 kD
HA-sneΔF	14.0 kD



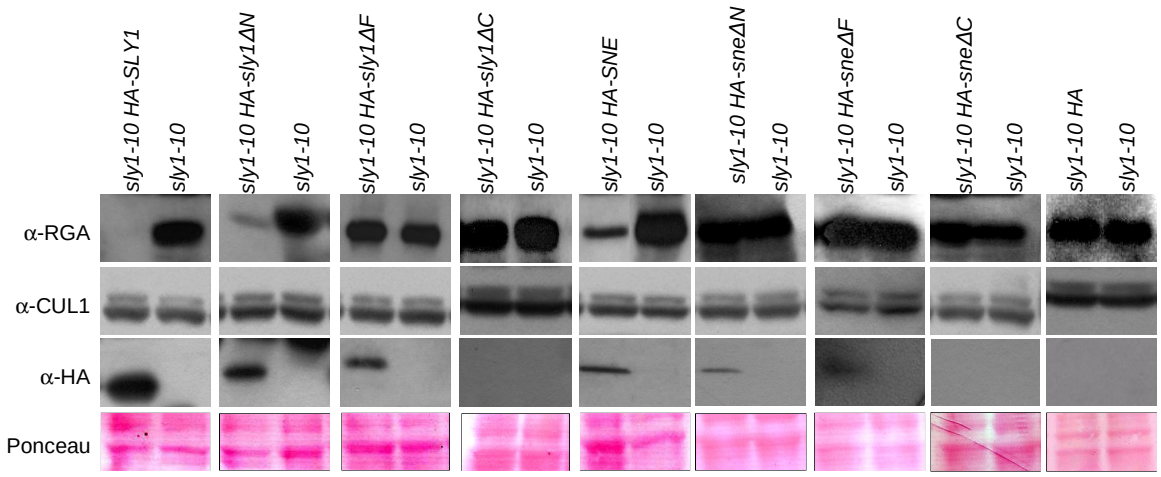
Supplemental Fig. S2. Protein blot analysis detected truncated SLY1 and SNE protein fusions. **(A)** Predicted molecular weight of HA fusion proteins containing C-terminal truncations was shown as determined with the Compute pI/Mw tool (http://au.expasy.org/tools/pi_tool.html). **(B)** Total protein was extracted from 14-d-old seedlings of the *sky1-10* and *sly1-10* transformants with *HA-SLY1*, *HA-sly1ΔN*, *HA-sly1ΔF*, *HA-sly1ΔC*, and **(C)** *HA-SNE*, *HA-sneΔN*, *HA-sneΔF*, *HA-sneΔC*. 40 µg total protein was loaded on an 18% polyacrylamide gel for SDS-PAGE analysis. HA fusions proteins were detected with monoclonal HA antibody. The lines indicated in blue were used for co-IP analysis.



Supplemental Fig. S3. *SNE* overexpression partly rescued the *sly-10* dwarfism while altering growth habit. Shown are 30-d-old WT L*er*, *sly1-10*, and *sly1-10* transformed with **(A)** *HA-SLY1,* **(B)** *HA-SNE,* and **(C)** *HA-sne*Δ*N*. All of the independent *HA-SNE* overexpression lines in the *sly1-10* background partially rescued the *sly1-10* dwarfism, but also caused loss of apical dominance and a prone growth habit.



Supplemental Fig. S4. *SNE* overexpression rescue of *sly1-10* fertility is associated with decreased DELLA RGA and GAI, not of RGL2 protein. Protein blot analysis of RGA, GAI and RGL2 protein accumulation was performed using 40 µg total protein extracted from flower buds from WT L*er*, *sly1-10*, and *sly1-10* transformed with **(A)** *HA-SLY1*, *HA-sly1*Δ*N*, *HA-sly1*Δ*F* and *HA-sly1*Δ*C*, or with **(B)** *HA-SNE*, *HA-sne*Δ*N*, *HA-sne*Δ*F*, and *HA-sne*Δ*C*. Ponceau staining confirmed equal loading.



Supplemental Fig. S5. Input control for the co-immunoprecipitation experiment in Figure 5. 40µg protein extract was loaded and used for protein blot analysis with antibodies to RGA, HA, and CUL1. The untransformed *sly1-10* line was loaded next to each transformed line for comparison. HA-SLY1, HA-SLY1ΔN, and HA-SNE caused a decrease in DELLA RGA accumulation. Note that co-immunoprecipitation assays were performed using the same extract shown above to which either no GA (mock solution) or GA was added. 40 µg total protein were loaded, and equal loading was confirmed by Ponceau staining.

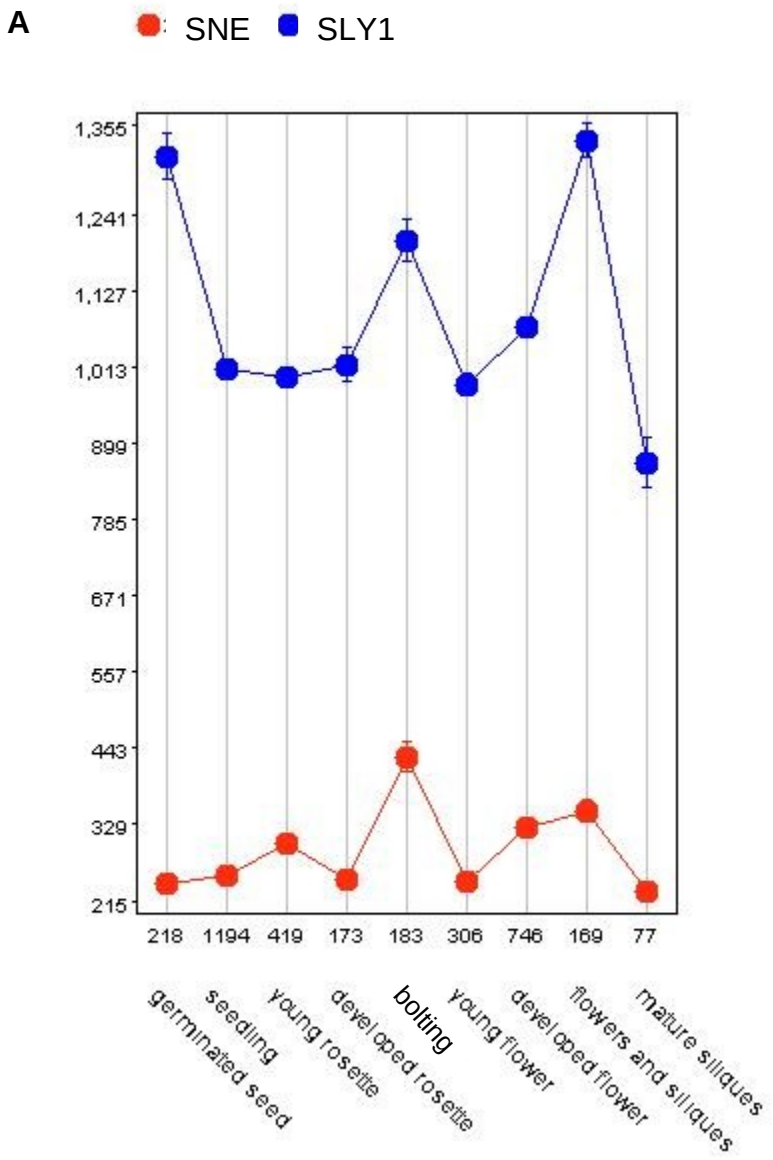
A

Genotype	Number of transformants	Aberrant phenotype
Ler (WT)	**4**	4
ga1-3	**8**	8

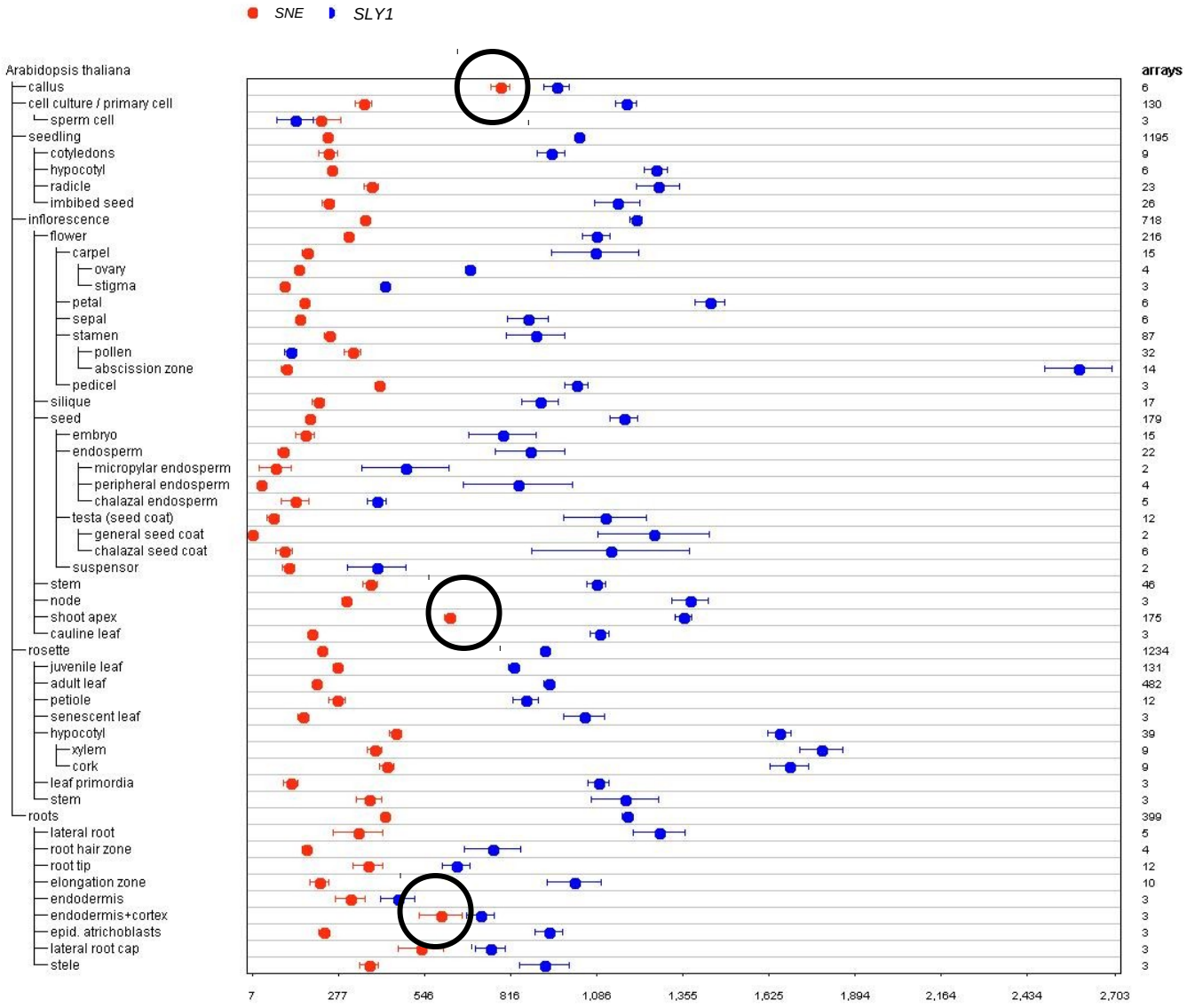
B

C

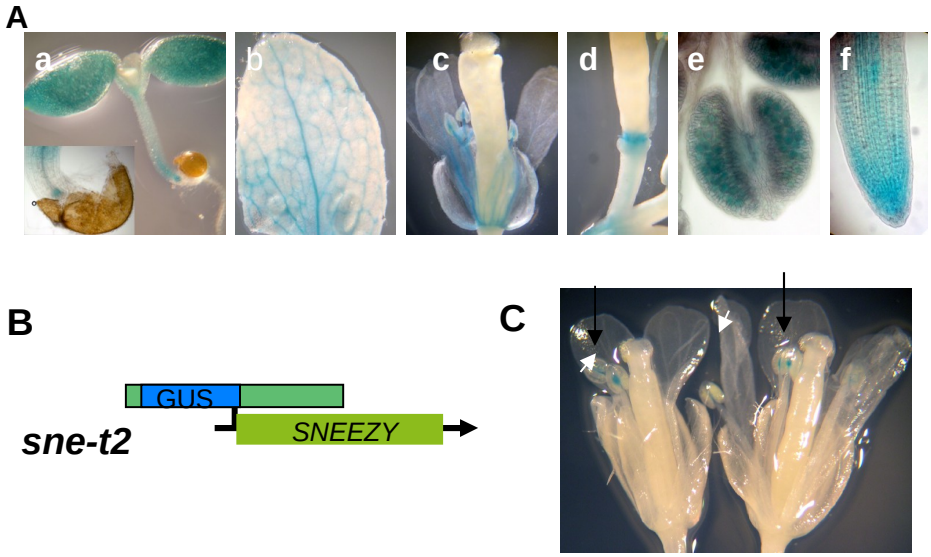
Supplemental Fig. S6. The effect of *HA-SNE* overexpression on WT Ler and *ga1-3* plant growth habit. L*er* and *ga1-3* plants were transformed with *HA-SNE*. (A) The number of transformants showing the prone growth habit and loss of apical dominance phenotypes. (B) Shown are the 35-d-old WT L*er* and representative L*er* lines transformed with *HA-SNE*, (C) Shown are the 35-d-old *ga1-3* and a representative *ga1-3* line transformed with *HA-SNE* grown with and without GA application. GA was applied by spraying with an aqueous solution of 10 µM GA_3 every 3 days.



Supplemental Fig. S7. Expression analysis of *SLY1* and *SNE* genes. Digital northern analysis to examine the pattern of *SLY1* (blue) and *SNE* (red) mRNA expression during Arabidopsis development.



Supplemental Fig. S8. Digital northern analysis to examine mRNA expression of *SLY1* (blue) and *SNE* (red) at key stages in Arabidopsis development. Circles indicate key tissues showing higher levels of *SNE* mRNA accumulation. Performed using Genevestigator.



Supplemental Fig. S9. Developmental analysis *SLY1* and *SNE* expression using promoter-GUS fusions. GUS histochemical staining was performed according to Ariizumi et al., (2002). **A)** Expression analysis using the GUS reporter gene under control of the 2.0 kb *SLY1* promoter. Every transgenic plant sample was soaked in GUS solution for 12 h except for (b)**: (a)** 6 day-old seedling; **(b)** Leaf sample stained in GUS solution for 6 h showed expression in the vascular tissue; **(c)** Mature flower tissue showed GUS staining in the filament and anthers; **(d)** Staining at the silique receptacle; **(e)** Magnified view of an anther from a young flower, **(f)** GUS expression was observed in primary root tip. **B)** The *sne-t2* line has an enhancer trap T-DNA containing the GUS reporter gene inserted at 1 bp before the translational start. **C)** SNE expression was detectable only in anthers of the *sne-t2* line (arrows) after GUS histochemical staining for 12 h.