Supplements to:

A Nucleostemin-like GTPase Required for Apical and Floral Meristem Development in Arabidopsis

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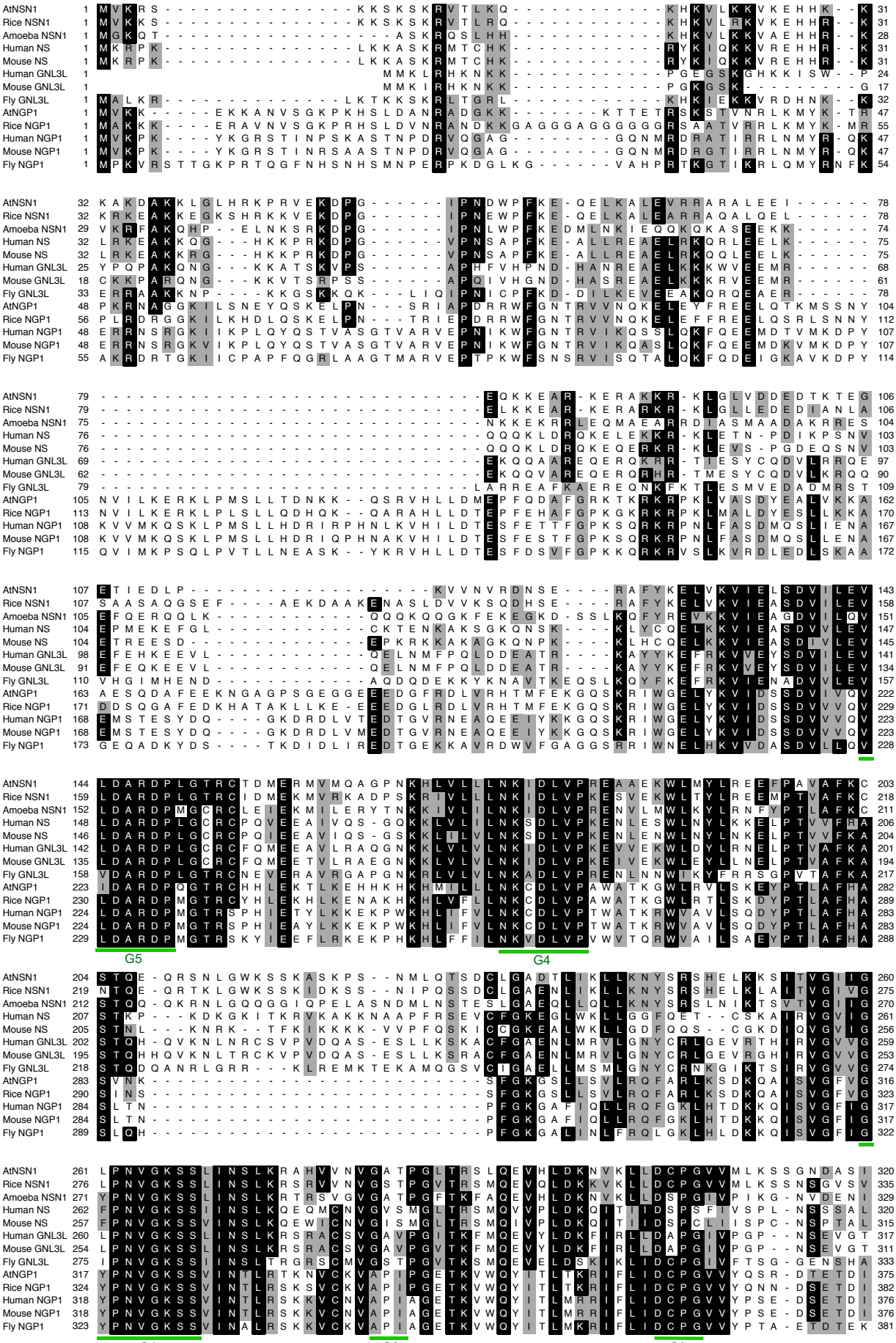
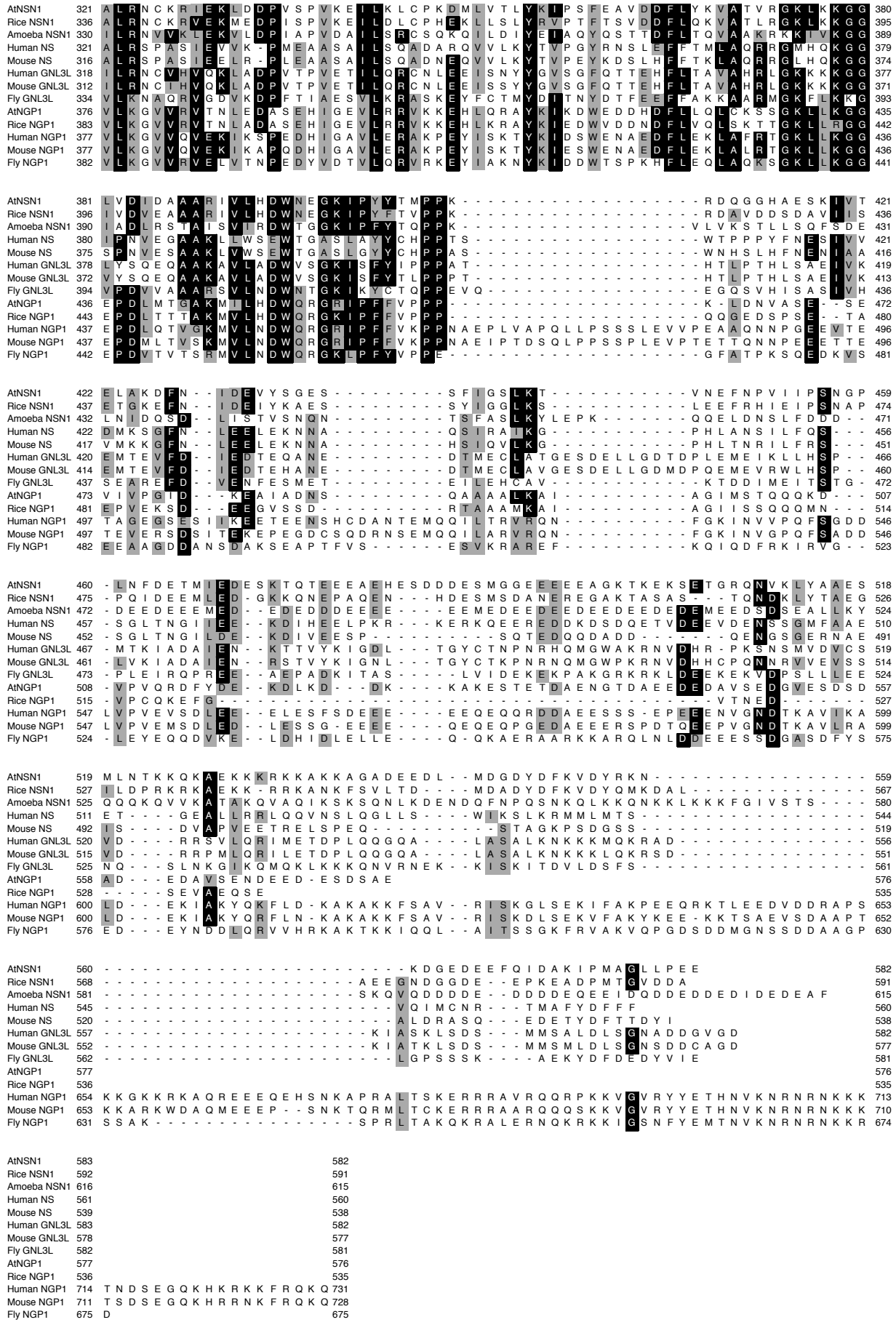
Table S1. Reduced floral organ numbers in *nsn1 ap2* double mutants

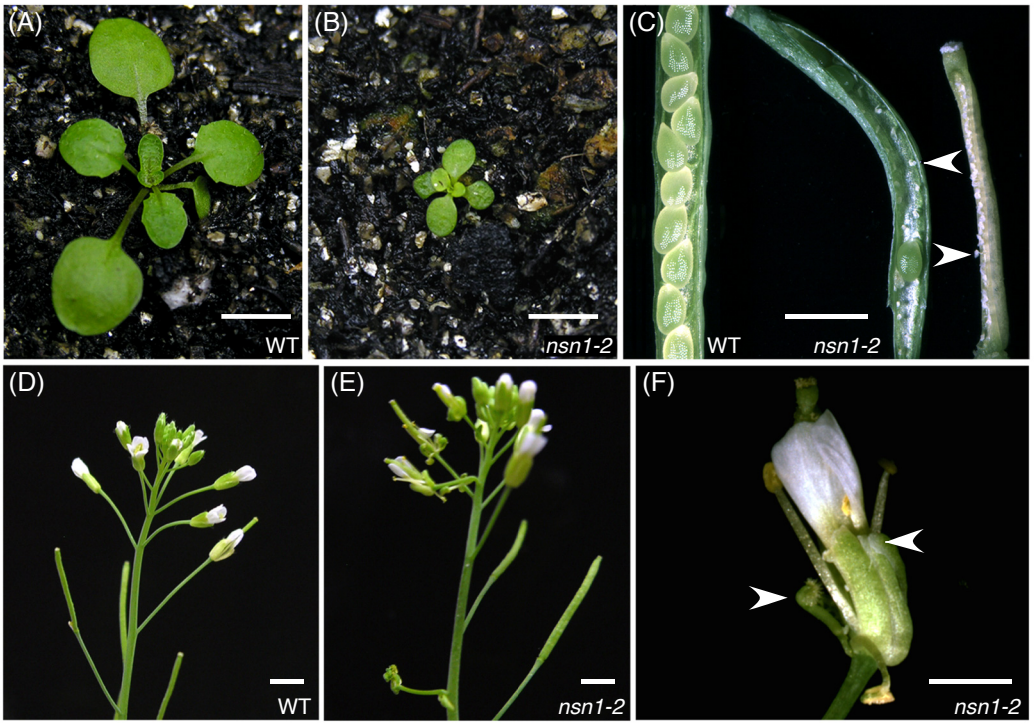
Genotype	No. of flowers analyzed	No. of organ in whorl 1	No. of organ in whorl 2	No. of organ in whorl 3	No. of organ in whorl 4
WT	42	4 ± 0	4 ± 0	6 ± 0	2 ± 0
nsn1	42	2.2 ± 0.9	0.7 ± 1.2	2.4 ± 1.9	1.6 ± 0.7
ap2-1	42	4 ± 0	4 ± 0	5.9 ± 0	2 ± 0
nsn1 ap2-1	42	3.4 ± 0.9	1.6 ± 1.2	4.4 ± 1.7	2.0 ± 1.0
ap2-2	42	2.3 ± 0.7	0 ± 0	1.7 ± 1.2	1.9 ± 0.4
nsn1 ap2-2	42	1.5 ± 0.9	0 ± 0	0.1 ± 0.3	1.4 ± 0.8


AtNSN1
Rice NSN1
Amoeba NSN1
Human NS
Mouse NS
Human GNL3L
Mouse GNL3L
Fly GNL3L
AtNGP1
Rice NGP1
Human NGP1
Mouse NGP1
Fly NGP1
G5
G4
G1
G2
G3

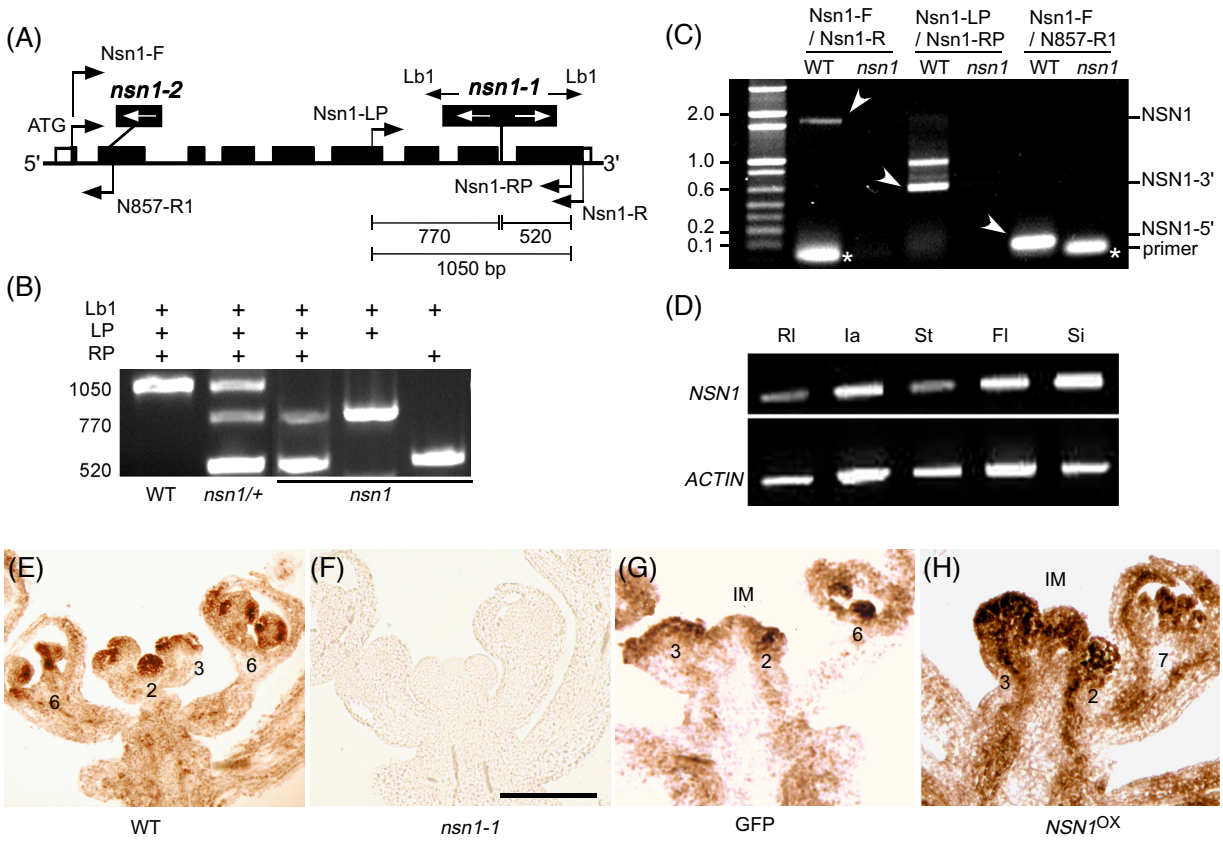


Suppl Figure S1. Amino acid sequence alignment of NSN1 homologs.

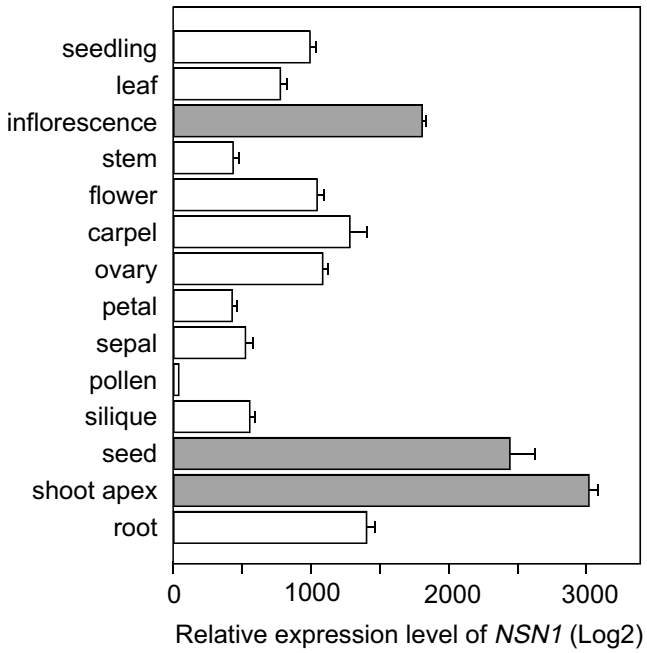
Dark shades indicate identical residues appearing in at least 7 peptide sequences, and light shades indicate similar residues appearing in at least 7 peptides. GTP binding sundomains (G1 -G5) are marked with green lines.



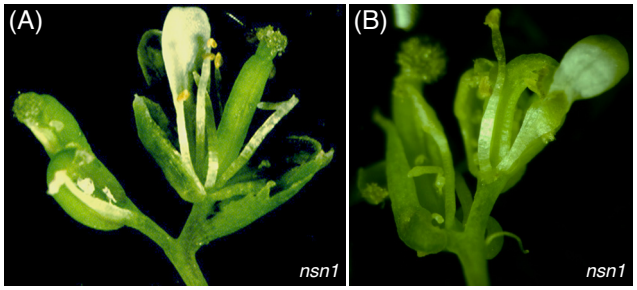
Suppl. Figure S2. Growth and reproduction phenotypes of *nsn1-2* mutant plants. (A-B) 20-day-old plants of the WT control (A) and *nsn1-2* (B). (C) Siliques of *nsn1-2* contained aborted ovaries and produced few seeds, as compared to the wild type (WT). Arrow-heads indicate the aborted ovaries in *nsn1-2* homozygote siliques. (D) Indeterminate inflorescence of a 35-day-old wild type plant. (E) Terminating inflorescence with carpelloid flowers of a 45-day-old *nsn1-2* mutant plant. (F) An enlarged defective flower from (E). Scale bars, 5 mm in (A-B), 2 mm in (C-F).



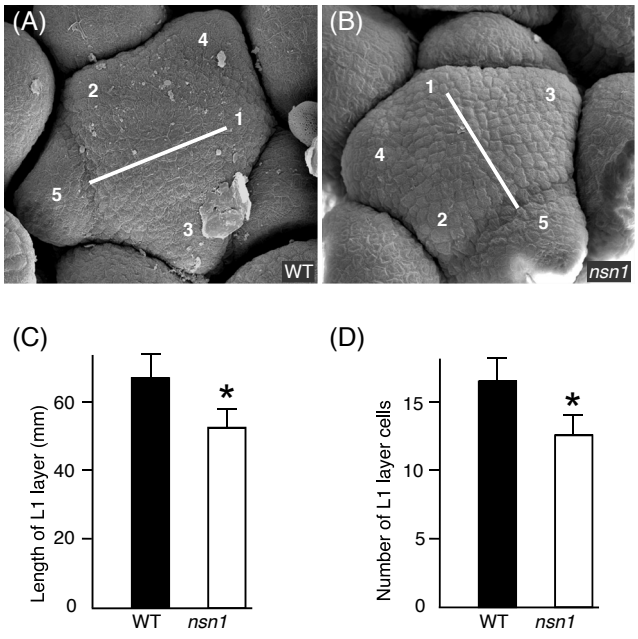
Suppl. Figure S3. Expression of *NSN1* mRNA in wild type *Arabidopsis*, *nsn1-1* mutant and *NSN1*^{OX} plants. (A) Positions of three pairs of primers used to detect *NSN1* mRNA transcript in *nsn1-1* mutant plants. Primers Nsn1-F and Nsn1-R correspond to the cDNA sequences in the start codon and stop codon regions, and produce a PCR product of 1,750 bp using genomic DNA of WT plants. Primers Nsn1-LP and Nsn1-RP flank the T-DNA insertion site and produced a 1050-bp PCR product in WT. Nsn1-F and N857-R1 amplify a 256-bp genomic DNA product or a 133-bp cDNA band in WT plants. Filled boxes are coding exons of *NSN1* gene and open boxes are non-coding exons. Lines represent introns of *NSN1*. (B) Genomic DNA isolated from individual plants was used for PCR amplification using primers as indicated in (A). (C) RT-PCR results using three pairs of primers. Note that the 5'-mRNA coding sequence, the mRNA region flanking the T-DNA insertion site, and the full-length *NSN1* mRNA were undetectable in *nsn1-1* mutant, suggesting that it is a null-mutation. Primer dimers are indicated by asterisks. (D) Tissue-specific expression of *NSN1* using RT-PCR. RT-PCR was done using total RNAs from different tissues, including rosette leaf (Rl), inflorescence apex (Ia), stem (St), flower (Fl), and silique (Si). The expression of *Actin* gene served as an internal template control. (E-H) Expression levels of *NSN1* mRNA in the inflorescence meristem of wildtype (E), *nsn1-1* (F), and transgenic plants expressing *35S$_{pro}$:GFP* (a control, G) and *35S$_{pro}$:NSN1-GFP* (*NSN1*^{OX}, H). In the controls of wild type and GFP-expressing plants, the *NSN1* mRNA signals could be detected in the IM and floral primordia at stages 2-6. In *NSN1*^{OX} transgenic plants, the *NSN1* mRNA signal was enhanced, and could be detected in the IM and floral primordia of various stages. The *NSN1* mRNA could also be detected in the pedicles of developing flowers. Scale bars, 100 μm in (E-H).



Suppl. Figure S4. Expression profile of *NSN1* mRNA in different tissues of wild type *Arabidopsis* plants. The expression level of At3g07050 (*NSN1*) is presented in relative values in log2. Data were retrieved from the public microarray data set (https://www.genevestigator.ethz.ch).



Suppl. Figure S5. Non-terminal carpelloid flowers of *nsn1-1*. Carpelloid flowers were produced at non-terminal positions of inflorescences of *nsn1-1* plants. Shown were a carpelloid flower at position 38 (A) and position 35 (B) of a 40 day-old *nsn1-1* plant, which developed a terminal carpelloid flower at the position of flower number 41.



Suppl. Figure S6. Reduced size of spical domes in *nsn1*. A-B, Scan electron microscope (SEM) images of the wild type (A) and *nsn1-1* (B) shoot apical meristems (SAM). Floral primordia are successively numbered from 1 to 5. The lines indicate the distance along which meristem sizes and meristem cell numbers were measured. C-D, Quantification of the apical domes. The length of L1 layer epidermal cells (C) and the number of epidermal cells along the line (D) of eight plants for each genotype were analyzed. A star (*) indicates a statistically significant difference between nsn1 and the wide type (T-test proceeded by Origin 6.0, P<0.01).