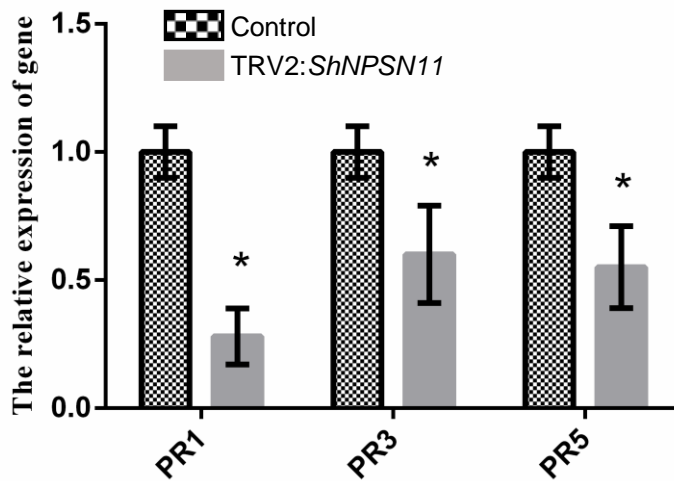


Cellular Compartment	LocDB	PotLocDB	Neural Nets	Pentamers	Integral
Nuclear	0.0	0.0	0.0	0.00	0.00
Plasma membrane	0.0	5.0	9.5	0.00	9.20
Extracellular	0.0	0.0	9.5	0.50	0.00
Cytoplasmic	0.0	0.0	0.0	1.70	0.00
Mitochondria	0.0	0.0	0.0	2.29	0.38
Endoplasmic reticulum	0.0	0.0	0.0	0.66	0.00
Peroxisomal	0.0	0.0	9.5	0.00	0.07
Golgi	0.0	0.0	1.5	0.21	0.00
Chloroplast	0.0	0.0	0.0	0.23	0.32
Vacuolar	0.0	0.0	0.0	0.00	0.02

Supplementary Figure S1. *In silico* predictions of cellular localization(s) of ShNPSN11

. Cellular compartments are denoted on the left. LocDB are scores based on the query protein's homology(ies) with proteins of known localization. PotLocDB are scores based on the query protein's homology(ies) with non-experimentally determined localizations, yet theoretical evidence exists. Neural Net scores are assigned by neural networks. Pentamers are based on comparisons of distributions calculated for the query sequence and existing database (DB) sequences. Integral scores are representative of the aforementioned (4) scores. A plasma membrane localization prediction score of 9.2 was calculated for SNARE13. A transmembrane spanning region from amino acids 212 to 236 was identified. A potential GPI anchoring site was identified at amino acid 253. LocDB, <https://www.rostlab.org/services/locDB/>; PotLocDB, <http://www.softberry.com/berry.phtml?topic=protcomp&group=help&subgroup=proloc>



Supplementary Figure S2. The expression of *PR1*, *PR3*, and *PR5* in *ShNPSN11*-silenced plants. mRNA transcript levels of *PR1*, *PR3*, and *PR5* in control (CK) and TRV2:*ShNPSN11*-silenced tomato leaves at 24 hpi as determined by quantitative real-time PCR. Error bars represent the standard variation of the mean among three independent replicates.

Primer name	Sequence (5'- 3')
<i>SIGPDPH-F</i>	CCATCACAGCCACTCAGAAGAC
<i>SIGAPDH-R</i>	TCAACCACGGACACATCAACAG
<i>ShNPSN11-F</i>	GGATCGGCATTGGTTGTG
<i>ShNPSN11-R</i>	GCTCTTGCTGCTCGGTCA
<i>SINPSN13-F</i>	AAAAGTGAGCATTGGCAGC
<i>SINPSN13-R</i>	GCACAACAGAGCAAATACGG
<i>SISNAP33-F</i>	TAATCTACCAGGTCCATCCC
<i>SISNAP33-R</i>	CTGCCTTCCAAATACCATAC
<i>SISYP132-F</i>	CTCTTCCTTTCTGCCTCC
<i>SISYP132-R</i>	CCGATCCAATAGTGTTCTC
<i>SISYP71-F</i>	CTCCAGTCTGTATTATGAAGTG
<i>SISYP71-R</i>	CTAGGCTTAACCACCGATAA
<i>SIMember1-1-F</i>	ATAGGACTACTGGACAGATGGATGG
<i>SIMember1-1-R</i>	GGAGGCGACTGCTGATATTGC
<i>SIMember1-2-F</i>	ACACAAGGAGGTTATGTAGAAGC
<i>SIMember1-2-R</i>	TGAGTAACAGAAGTGGTAGATGC
<i>SISyp61-F</i>	AGTTGGACACGGAGATGGACAGT
<i>SISyp61-R</i>	TTGACGCTCGCCTTCTTCATTACC

Supplementary Table S1. DNA primers for quantitative RT-PCR analysis.

Primer Name	Sequence 5'-3'	Product length
<i>ShNPSN11-F1</i>	acgggggactcttgaccatggATGGCGTCGTTGT CTGGCC	786 bp
<i>ShNPSN11-R1</i>	tactagtcatctaccatggTCAGTAAGGATAAG CAAGTAACCGTC	

Supplementary Table S2. DNA primers for gene cloning for subcellular localization. Letters denoted in red font indicate recombination sequence, while those in blue indicate the *NcoI* digestion sites

Primer name	Sequence 5' - 3'	Product length
<i>SISIPDS-VIGS-F</i>	CCGGAATTCAGTTAGTCGGAGTACCTGTG	
<i>SISIPDS-VIGS-R</i>	CGCGGATCCCAAGTATTTCTGTTTCGTGT	425 bp
<i>ShNPSN11-VIGS-F</i>	CCGGAATTCGAATAGGCAGAGCAGGCAGT	
<i>ShNPSN11-VIGS-R</i>	CGCGGATCCGTCTCGGTTCCAACATTTACAG T	393 bp

Supplementary Table S3. PCR primers sequence for virus-induced gene silencing. The red part is *BamHI* digestion sites and the blue parts is protection nucleosides.

Primer name	Sequence (5' - 3')
<i>ShNPSN11-RT-F1</i>	ATGGCGTCGTTGTCTGGC
<i>ShNPSN11-RT-R1</i>	CATTCTCGCATCTTTCCTGTTA
<i>SIGAPDH-RT-F1</i>	CCATCACAGCCACTCAGAAGAC
<i>SIGAPDH-RT-R1</i>	TCAACCACGGACACATCAACAG
<i>PR1-F</i>	CATCCCGAGCACAAAAC
<i>PR1-R</i>	TGAAGTCACCACCACCCT
<i>PR3-F</i>	CTTTTACTTGTTGGGCTTCT
<i>PR3-R</i>	ACTTCCTTTGAGGGCATT
<i>PR5-F</i>	ACGCCATCCCCTAAAGA
<i>PR5-R</i>	TGGACCCATCCCACATT

Supplementary Table S4. DNA primer sequences for evaluating VIGS efficiency and *PR* gene expression.

Primer name	Sequence (5'-3')	Product length
<i>ShNPSN11-F1</i>	agcatcgattcccgggtcgacATGGCGT CGTTGTCTGGCC	786 bp
<i>ShNPSN11-R1</i>	aaccgttcatcggcggtcgacTCAGTAAG GATAAGCAAGTAACCGTC	

Supplementary Table S5. DNA primers for tobacco transient expression. Residues labeled in red denote the recombination sequence. Underscored nucleotides denote the Sall restriction enzyme digestion site.