Table S1. Primers used for cloning of *PhENDO1*, gene expression analysis by qPCR, and making constructs for VIGS experiments.

Primer Function	Direction	Sequence
RT-PCR clone	Forward	5'- TGGAGCAAAGARGGNCA -3'
	Reverse	5'- TTTCNCCRGCTTCRACACCTT -3'
RACE	Forward	5'- TGGCGACTTATCGGCCCTCTGCGTGTGG -3'
	Reverse	5'- ACTTGGTCCGGCCACACGCAGAGGGC -3'
Full length sequence	Forward	5'- TCATTGTGCTTCTTTGAGCATGTGGG -3'
	Reverse	5'- GACTTGTCATCTCGTGTTACATGGAGAGC -3'
PhENDO1 qPCR	Forward	5'- CCACTTGCAGCAACTTGATCAACCA -3'
	Reverse	5'- TCGACGACGACGAACGATACTTGT -3'
PhCP10 qPCR	Forward	5'- ACTTTGTGGACTTGCAACGGAAGC -3'
	Reverse	5'- CCAAGCCTATCTCAATCCCATACA -3'
PhACTIN qPCR	Forward	5'- AGCCAACAGAGAGAAGATGACCCA -3'
	Reverse	5'- ACACCATCACCAGAGTCCAACACA -3'
PhRPS13 qPCR	Forward	5'- CAGGCAGGTTAAGGCAAAGC -3'
	Reverse	5'- CTAGCAAGGTACAGAAACGGC -3'
VIGS, Exp 1	Forward	5'- catctccatggTCAAGCCCTCTCCACTTCAT -3'
	Reverse	5'- catgtggtaccGTGCAAGTTTGACTTGTGCC -3'
VIGS, Exp 2	Forward	5'- tagtttggatccTGTCTTGCTTTCATTACCCAAC -3'
	Reverse	5'- cataattctagaTGCAAGCTTCATCTGGTGTAT -3'

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  1 ATGTTGGGGTTAACTTCATTAAGCATTAGTTTCTTTCTCTGTCTT
    M  L  G  L  T  S  L  S  I  S  F  F  L  C  L

 46 GCTTTCATTACCCAACATGATGTTGAAGCATGGAGTAAAGAGGGT
    A  F  I  T  Q  H  D  V  E  A  W  S  K  E  G

 91 CATATGATGACTTGTCGAATCGCCCAGGAGCTCTTGAATGATGAG
    H  M  M  M  T  C  R  I  A  Q  E  L  L  N  D  E

136 GCAGCTCATGCGGTTAAGATGTTGTTACCGGATTATGTTAATGGC
    A  A  H  A  V  K  M  L  L  P  D  Y  V  N  G

181 GACTTATCGGCCCTCTGCGTGTGGCCGGACCAAGTCCGGCATTGG
    D  L  S  A  L  C  V  W  P  D  Q  V  R  H  W

226 TACAAGTATAGGTGGTCAAGCCCTCTCCACTTCATTGATACACCA
    Y  K  Y  R  W  S  S  P  L  H  F  I  D  T  P

271 GATGAAGCTTGCAACTTTGATTATGATAGGGATTGTCATGATGAA
    D  E  A  C  N  F  D  Y  D  R  D  C  H  D  E

316 CATGGAGTGAAGGATATGTGTGTTGCTGGTGCCATCCAAAACTTT
    H  G  V  K  D  M  C  V  A  G  A  I  Q  N  F

361 ACCACTCAGCTTTCCCATTACCCAGAGGGAACTTCCGATCGCCGA
    T  T  Q  L  S  H  Y  P  E  G  T  S  D  R  R

406 TATAATATGACAGAGGCCTTGTTATTCTTGTCACATTTCATGGGA
    Y  N  M  T  E  A  L  L  F  L  S  H  F  M  G

451 GATATCCATCAACCGTTGCATGTTGGATTTACAAGTGATGAAGGA
    D  I  H  Q  P  L  H  V  G  F  T  S  D  E  G

496 GGAAATACAATTAATCTGCGCTGGTTTAGGCACAAGTCAAACTTG
    G  N  T  I  N  L  R  W  F  R  H  K  S  N  L

541 CACCATGTATGGGATAGAGAGATGATTCTACAAGCTGCAAAAGAC
    H  H  V  W  D  R  E  M  I  L  Q  A  A  K  D

586 TATTATGCAAAGGATGTAAACCTCCTTGAAGCAGACATTGAAGGA
    Y  Y  A  K  D  V  N  L  L  E  A  D  I  E  G

631 AACTTCACTGATGGAATCTGGACTGATGATCTTTCTTCTTGGAGG
    N  F  T  D  G  I  W  T  D  D  L  S  S  W  R

676 GAATGTGGAAATCTCTTCTCCTGTGTGAATAAGTTTGCTGCGGAA
    E  C  G  N  L  F  S  C  V  N  K  F  A  A  E

721 AGTATAAGTATAGCTTGCAAATGGGGATACAAAGGTGTTGAGGCT
    S  I  S  I  A  C  K  W  G  Y  K  G  V  E  A

766 GGCGAAACATTATCAGATGATTACTTCAATTCAAGACTCCCAATT
    G  E  T  L  S  D  D  Y  F  N  S  R  L  P  I

811 GTGATGAAAAGAATAGCTCAAGGTGGAGTACGATTAGCTATGCTT
    V  M  K  R  I  A  Q  G  G  V  R  L  A  M  L

856 CTAAATCGGGTTTTTGGAGATTCTCAAGAAGATCCACTTGCAGCA
    L  N  R  V  F  G  D  S  Q  E  D  P  L  A  A

901 ACTTGA
    T  *
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Figure S1. The sequences of the *PhENDO1* coding region and the predicted protein. The *PhENDO* cDNA encodes a protein of 301 amino acids. The first 25 amino acids encode a signal peptide, and the arrow indicates the cleavage site of the signal peptide. The solid lines are the 14-12 endonuclease peptides that were sequenced from 2-DE [31]. Three predicted glycosylation sites are located at 119, 137, and 211 (gray boxes).

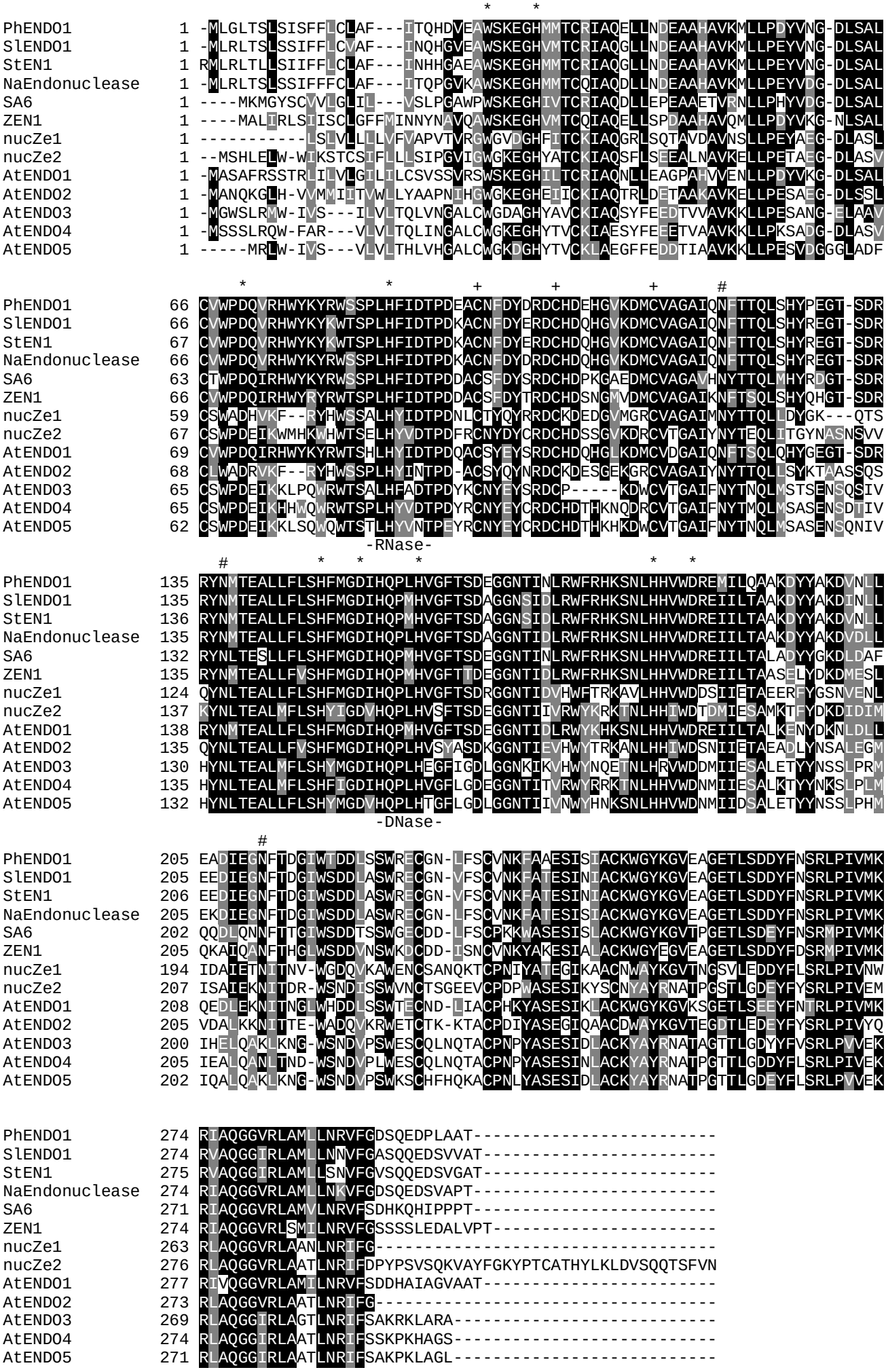
PhENDO1
SlENDO1
StEN1
NaEndonuclease
SA6
ZEN1
nucZe1
nucZe2
AtENDO1
AtENDO2
AtENDO3
AtENDO4
AtENDO5
-RNase-
-DNase-

Figure S2. Alignment of the deduced amino acid sequences of endonuclease enzymes. Endonuclease *PhENDO1* from petunia is compared with the amino acid sequences from *Nicotiana attenuata* NaEndonuclease1(XP_019234897), *Solanum tuberosum* StEN1 (AAT79582), *Solanum lycopersicum* SlENDO1 (BAL03523), *Arabidopsis thaliana* ENDO1/ BFN1, ENDO2, ENDO3, ENDO4 and ENDO5 (NP_172585, NP_176996, NP_001078420, NP_001328107 and NP_567631), *Zinnia elegans ZEN1*, *ZEN2*, and *ZEN3* (BAA28948, AAD00694 and AAD00695), and *Hemerocallis* hybrid *SA6* (AAC34856). Dark gray shading are residues that are identical in all sequences and light gray shading are residues that are functionally identical. Dashes indicate gaps introduced to produce the alignment, asterisks (*) are residues involved in the binding of zinc atoms, plus signs (+) identify residues involved in forming disulfide bonds; and number symbols (#) are structurally important glycosylation sites. Active sites for RNase and DNase activities in nucleases (His residues at positions 85 and 157, respectively, in PhENDO1) are also indicated under the alignment [17].

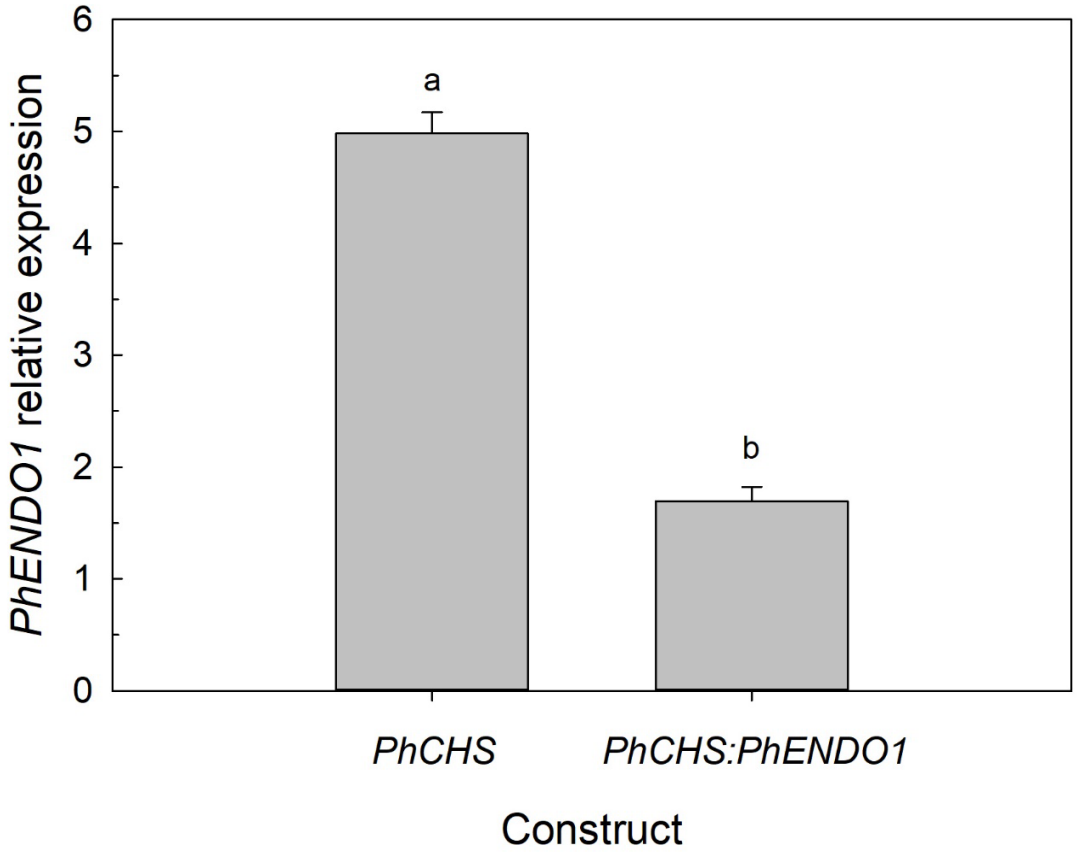

Figure S3. *PhENDO1* transcript abundance was reduced in senescing flowers from pTRV2:*PhCHS*:*PhENDO1* plants. Relative abundance of *PhENDO1* in senescing corollas (48 h after pollination) was determined by qPCR in pTRV:*PhCHS* and pTRV2:*PhCHS*:*PhENDO1* petunias. Bars represent mean ± SE (n=3) and least squared means were evaluated at $P<0.05$. Different letters indicate significant difference between the means.