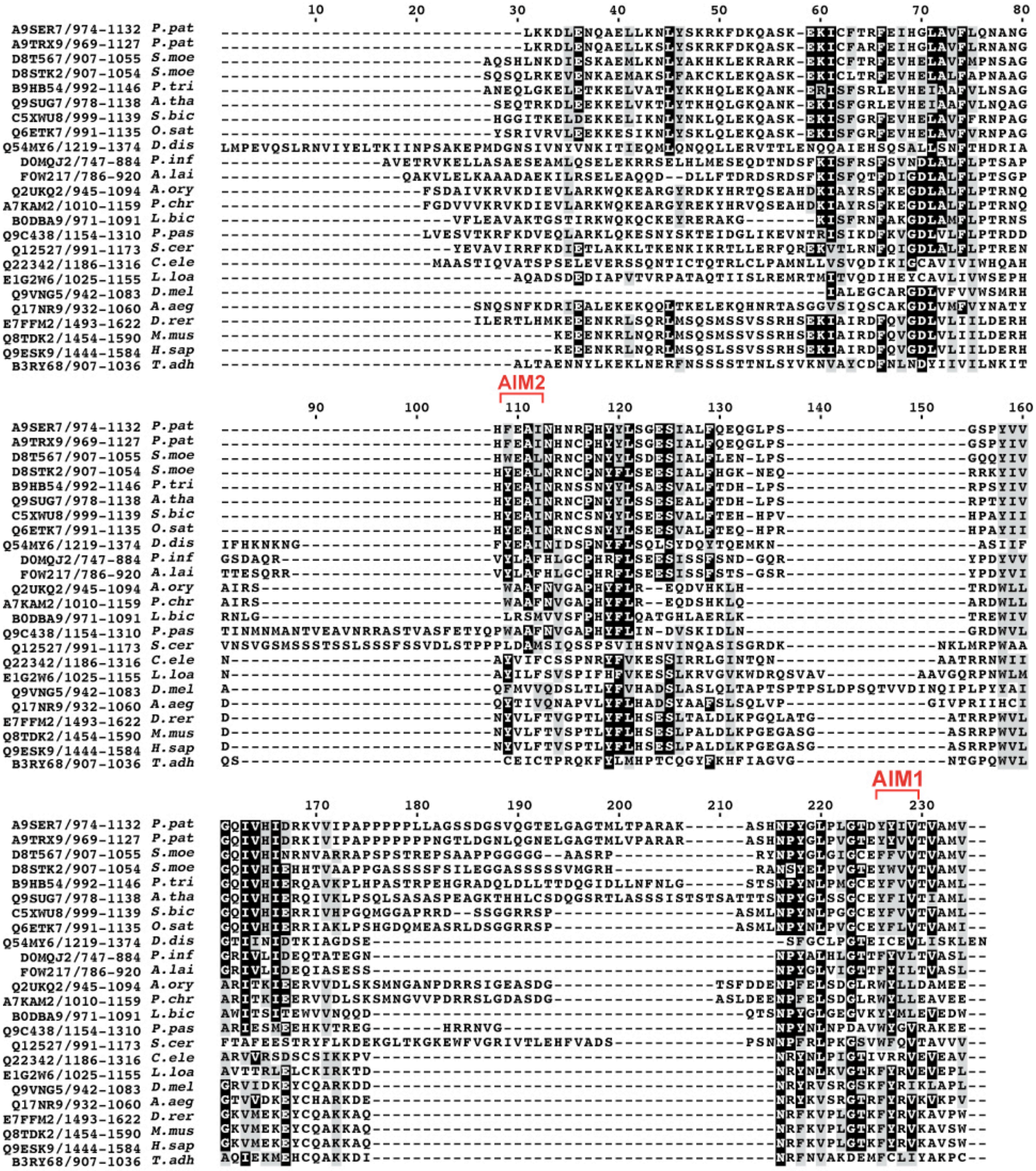

Supplemental Figure 1. Amino Acid Sequence Alignment of the ATG11 Domains within ATG11/FIP200-Related Proteins.

Representative proteins found in plants, *Amoebozoa*, *Metazoa*, fungi, and *Stramenopiles* were selected from Pfam (pfam.sanger.ac.uk/) and the predicted ATG11 domains were aligned by ClustalX. The residues were colored using Boxshade version 3.21; black and grey boxes identify identical and similar amino acids. Sequence designations refer to the UniProt accession number and the residue number of the putative ATG11 domains, separated by a slash.

Possible AIM sequences are indicated by the red brackets; whereas AIM1 is relatively conserved among ATG11 proteins, the AIM? sequence is more degenerate. A9SER7 and A9TRX9 are proteins from *P. patens*, D8STK2 and D8T567 from *S. moellendorffii*, B9HB54 from *P. trichocarpa*, Q9SUG7 from *A. thaliana*, C5XWU8 from *S. bicolor*, Q6ETK7 from *O. sativa*, Q54MY6 from *D. discoideum*, D0MQJ2 from *P. infestans*, F0W217 from *A. laibachii*, Q2UKQ2 from *A. oryzae*, B6H4J6 from *P. chrysogenum*, B0DBA9 from *L. bicolor*, Q9C438 from *P. pastoris*, Q12527 from *S. cerevisiae*, Q22342 from *C. elegans*, E1G2W6 from *L. loa*, Q17NR9 from *A. aegypti*, E7FFM2 from *D. rerio*, Q8TDK2 from *M. musculus*, Q9VNG5 from *D. melanogaster*, Q9ESK9 form *H. sapiens*, B3RY68 from *T. adhaerens*.

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A9TRX9/335-481 P.pat  ------------------------------------------------------------------------------------------
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B9HB54/304-497 P.tri  ------------------------------------------------------------------------------------------
Q9SUG7/348-494 A.tha  ------------------------------------------------------------------------------------------
D7MBM1/347-495 A.lyr  ------------------------------------------------------------------------------------------
C5XWU8/358-503 S.bic  ------------------------------------------------------------------------------------------
Q6ETK7/352-509 O.sat  ------------------------------------------------------------------------------------------
D0MQJ2/356-519 P.inf  ------------------------------------------------------------------------------------------
F0W217/374-533 A.lai  ------------------------------------------------------------------------------------------
E1G2W6/325-506 L.loa  ------------------------------------------------------------------------------------------
Q22342/282-474 C.ele  ------------------------------------------------------------------------------------------
B3RY68/287-473 T.adh  ------------------------------------------------------------------------------------------
Q17NR9/352-539 A.aeg  ------------------------------------------------------------------------------------------
E7FFM2/372-559 D.rer  ------------------------------------------------------------------------------------------
Q8TDK2/373-560 H.sap  ------------------------------------------------------------------------------------------
Q9VNG5/369-560 D.mel  ------------------------------------------------------------------------------------------
Q9ESK9/372-558 M.mus  ------------------------------------------------------------------------------------------
 Q2UFN7/33-480 A.ory  -ISHLVAAKRSLSSINHVWRANEIVTAARSALEESVVVSARTGFLRRGLNNQLRLLYSVRTEVQEVSLRGRSEFATVLKSLDVADARLRK
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  A7TM40/4-402 V.pol  ERFVNASRKTLVEAQVLCQDANSRISNARSSFSHWERSISKIRFLLNCLKNQGSFIKNCILKVGIEENLIEKEWTQSILVDLAKELKYWN
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B6H4J6/211-403 P.chr  ------------------------------------------------------------------------------------------
Q2UKQ2/165-336 A.ory  ------------------------------------------------------------------------------------------
Q9C438/336-521 P.pas  ------------------------------------------------------------------------------------------
A7TL57/302-474 V.pol  ------------------------------------------------------------------------------------------
Q12527/339-512 S.cer  ------------------------------------------------------------------------------------------

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Q9SUG7/348-494 A.tha  ------------------------------------------------------------------------------------------
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Q17NR9/352-539 A.aeg  ------------------------------------------------------------------------------------------
E7FFM2/372-559 D.rer  ------------------------------------------------------------------------------------------
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Q9VNG5/369-560 D.mel  ------------------------------------------------------------------------------------------
Q9ESK9/372-558 M.mus  ------------------------------------------------------------------------------------------
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  C4R1E4/5-415 P.pas  VLDTLHKIELEPSFRSTQGNKALSLYHFVSDDKIDELFNGVDDILRESTDLYGRDEIDNNLADISREIEGYGKELEVRYAEFILNEVPDT
 Q6CS99/14-410 C.sph  NEITTKMKILQGTKYDLTDDHS------SLSDFICMDHVDILQQKIDEIPIIKQQVTNIRQHYKSIKDRIENQLVAVKLKKLRTYFDSHF
  A7TM40/4-402 V.pol  SKINEQVRVLDSIENILDEDTKSESK--NLGYFVSRDNLDILEKRLKEIPNVKYHIDNIRGQYNTMFKKVSNYLINKRLKSVQEYFLTNF
  Q06410/7-406 S.cer  YEITSKVQRLDGIVNELSISEKDDTDPSKLGDYISRDNVNLLNDKLKEVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVTQKFQSKF
B6H4J6/211-403 P.chr  ------------------------------------------------------------------------------------------
Q2UKQ2/165-336 A.ory  ------------------------------------------------------------------------------------------
Q9C438/336-521 P.pas  ------------------------------------------------------------------------------------------
A7TL57/302-474 V.pol  ------------------------------------------------------------------------------------------
Q12527/339-512 S.cer  ------------------------------------------------------------------------------------------

                             190       200       210       220       230       240       250       260       270
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A9SER7/335-481 P.pat  ------------------------------------------------------------------------------------------
A9TRX9/335-481 P.pat  ------------------------------------------------------------------------------------------
D8STK2/340-486 S.moe  ------------------------------------------------------------------------------------------
D8T567/340-486 S.moe  ------------------------------------------------------------------------------------------
B9HB54/304-497 P.tri  ------------INEMKSIMQSLRDDVSTVKELVHDCLS---------------------------------------------------
Q9SUG7/348-494 A.tha  ------------------------------------------------------------------------------------------
D7MBM1/347-495 A.lyr  ------------------------------------------------------------------------------------------
C5XWU8/358-503 S.bic  ------------------------------------------------------------------------------------------
Q6ETK7/352-509 O.sat  ------------------------------------------------------------------------------------------
D0MQJ2/356-519 P.inf  ------------------------------------------------------------------------------------------
F0W217/374-533 A.lai  ------------------------------------------------------------------------------------------
E1G2W6/325-506 L.loa  --------------------DAMFHSKEQETKLLKDLC----------------------------------------------------
Q22342/282-474 C.ele  -----------GINKRFSQLEFSLKSCEERKNLVHKLV----------------------------------------------------
B3RY68/287-473 T.adh  ----------------SQLVSSGQEIAQNQTEMAQGFA----------------------------------------------------
Q17NR9/352-539 A.aeg  ----------------ERKMVDVRKLVQEQNELAQSIQ----------------------------------------------------
E7FFM2/372-559 D.rer  ----------------DQMIASCKKLVNEQKELAQGFL----------------------------------------------------
Q8TDK2/373-560 H.sap  ----------------DQMIASCGRLVNEQKELAQGFL----------------------------------------------------
Q9VNG5/369-560 D.mel  ------------LYALDQMIASCSRLVNEQKELAQGFL----------------------------------------------------
Q9ESK9/372-558 M.mus  ----------------DQMIASCSRLVNEQKELAQGFL----------------------------------------------------
 Q2UFN7/33-480 A.ory  SSPSTSNDSLPSLSSIPSMLHSLEMHAQEMANLLESLVRHFDLCVTAVKHTEGGGAAARSITGDVPATVHVNGRVGPNIEEGINANLNAP
 A7KAM6/32-479 P.chr  SSSSASDSGLLTLSSMPGQIQSLEAHAQEMATLLEALVRHFDLCVTAVKHTDGGGAVARSITGDMPAGVDGSNDGMPNIGAEINANLNAP
  C4R1E4/5-415 P.pas  PSKGNKKNSANHDNIITKLITSNNELETDMASLLESLTNHFDQCK---------------------------------------KGQDLL
 Q6CS99/14-410 C.sph  SRDSKNNLFKLLESDYVTELNEFENELADFLRSITDHFD---------------------------------------------KCTILK
  A7TM40/4-402 V.pol  END--SDDIKKLTTTLPSKLVSLEHDLADYLSSITNHYD---------------------------------------------QSKLLQ
  Q06410/7-406 S.cer  GID--NLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFD---------------------------------------------KTLLLQ
B6H4J6/211-403 P.chr  -----GDIASDTQRLVDEALASDSDGVDGLLEEVETIAK---------------------------------------------------
Q2UKQ2/165-336 A.ory  -------------------------GVEGLLQEVETISR---------------------------------------------------
Q9C438/336-521 P.pas  --------------RLTELVNQVVKDSKELPILDELLTTS--------------------------------------------------
A7TL57/302-474 V.pol  ---------------------KFTELVKNLRNDSKVILE---------------------------------------------------
Q12527/339-512 S.cer  ---------------------SFEVLVSEMRTRSRNVLD---------------------------------------------------
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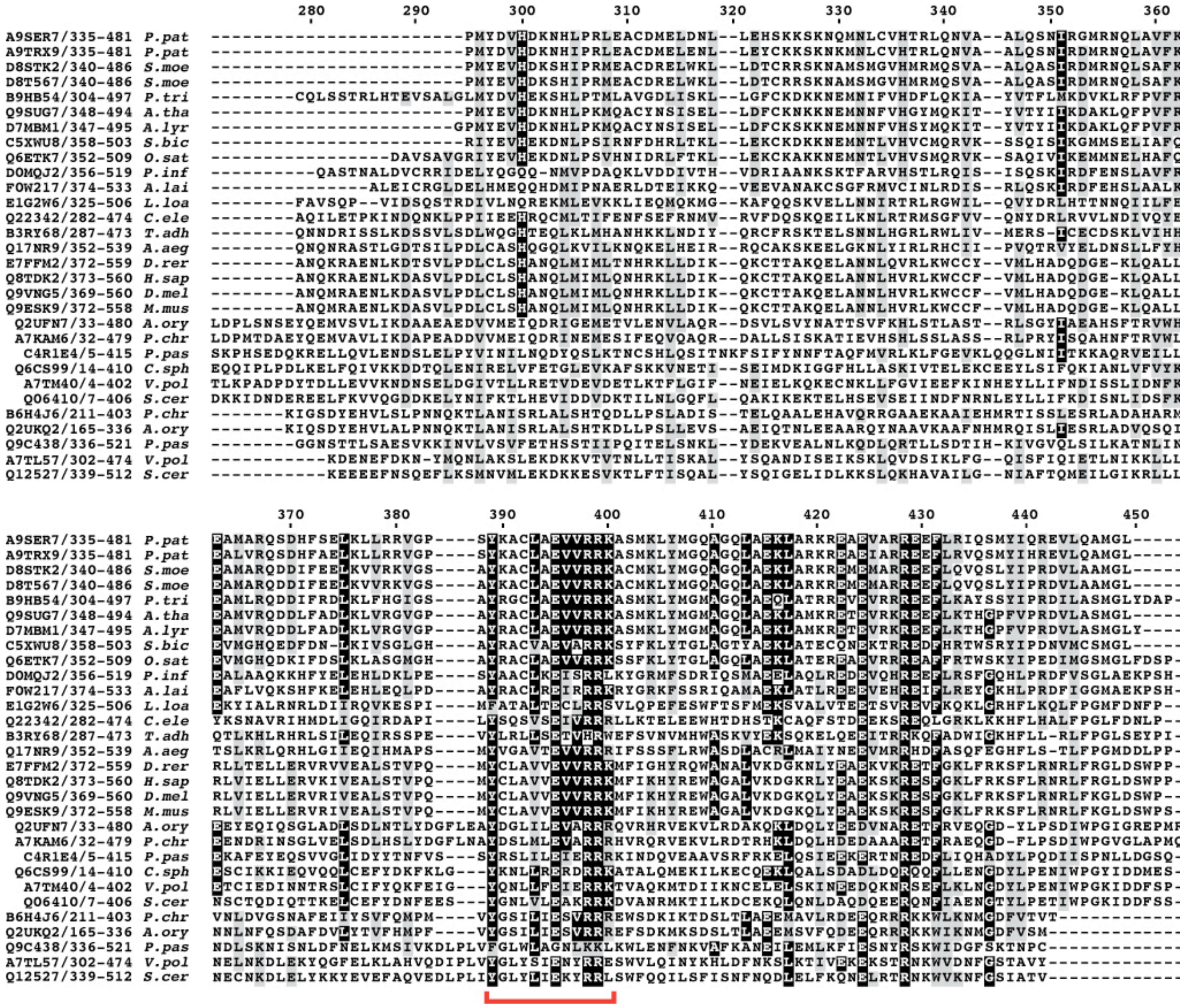
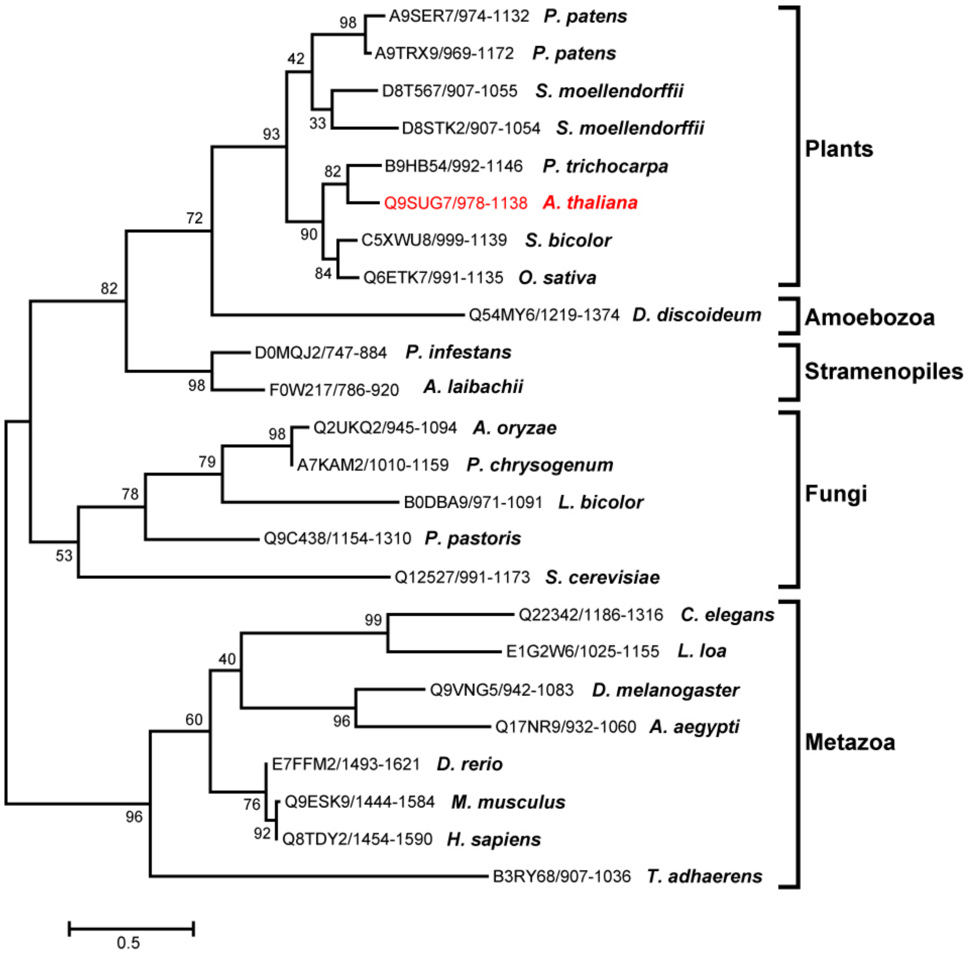


Supplemental Figure 2. Amino Acid Sequence Alignment of the ATG17 and ATG17-like Domains within ATG11/ATG17-Related Proteins.

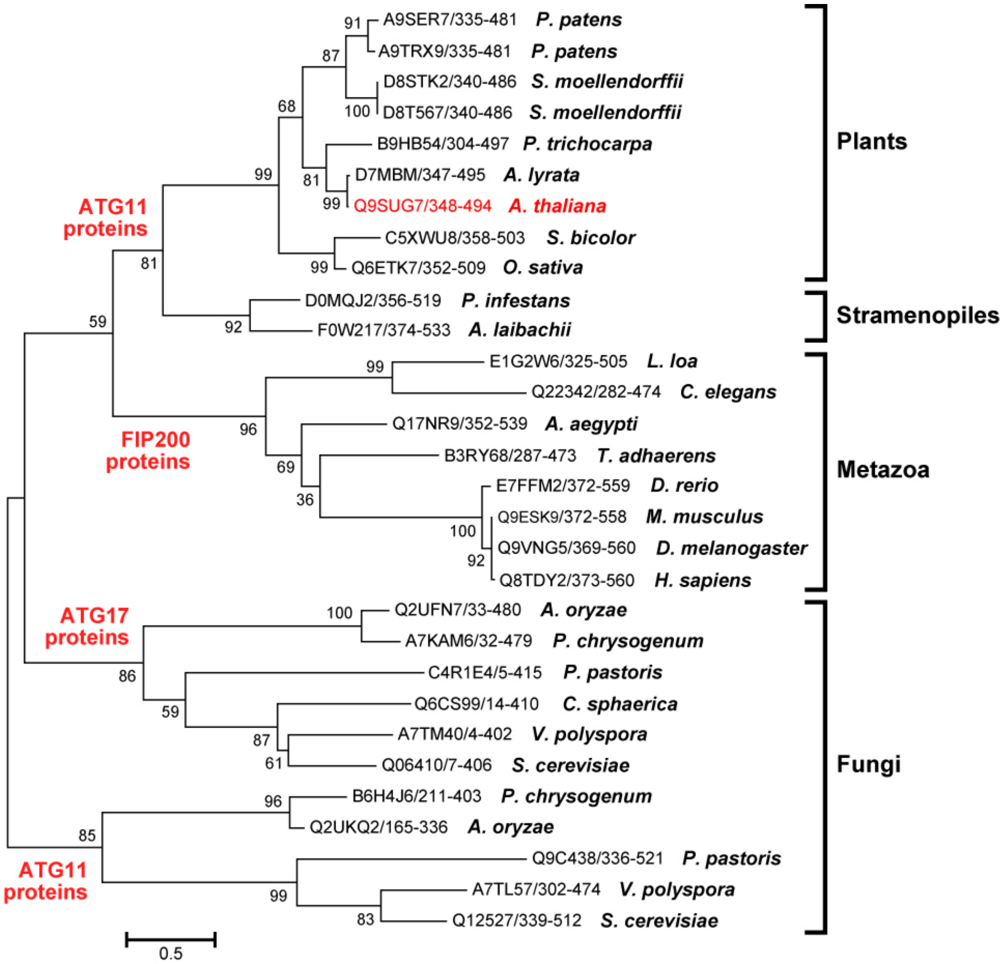
Representative proteins found in plants, *Amoebozoa*, *Metazoa*, fungi, and *Stramenopiles* were selected from PFAM (pfam.sanger.ac.uk/) and the predicted ATG17 domains were aligned by ClustalX. The residues were colored using Boxshade version 3.21; black and grey boxes identify identical and similar amino acids. Sequence designations refer to the UniProt accession number and the residue number of putative ATG17 domains, separated by a slash. The consensus Y-X-X-X-L/V/I-X-E-V/I-X-R-R-R/K sequence common among ATG17 and ATG17-like domains is indicated by the red bracket. A9SER7 and A9TRX9 are proteins from *P. patens*, D8STK2 and D8T567 from *S. moellendorffii*, B9HB54 from *P. trichocarpa*, D7MBM1 from *A. lyrata*, Q9SUG7 from *A. thaliana*, C5XWU8 from *S. bicolor*, Q6ETK7 from *O. sativa*, D0MQJ2 from *P. infestans*, F0W217 from *A. laibachii*, E1G2W6 from *L. loa*, Q22342 from *C. elegans*, Q17NR9 from *A. aegypti*, B3RY68 from *T. adhaerens*, E7FFM2 from *D. rerio*, Q9ESK9 from *M.*

musculus, Q9VNG5 from *D. melanogaster*, Q8TDK2 form *H. sapiens*, Q2UFN7 and Q2UKQ2 from *A. oryzae*, A7KAM6 and B6H4J6 from *P. chrysogenum*, C4R1E4 and Q9C438 from *P. pastoris*, Q6CS99 from *C. sphaerica*, A7TM40 and A7TL57 from *V. polyspora*, Q06410 and Q12527 from *S . cerevisiae*.



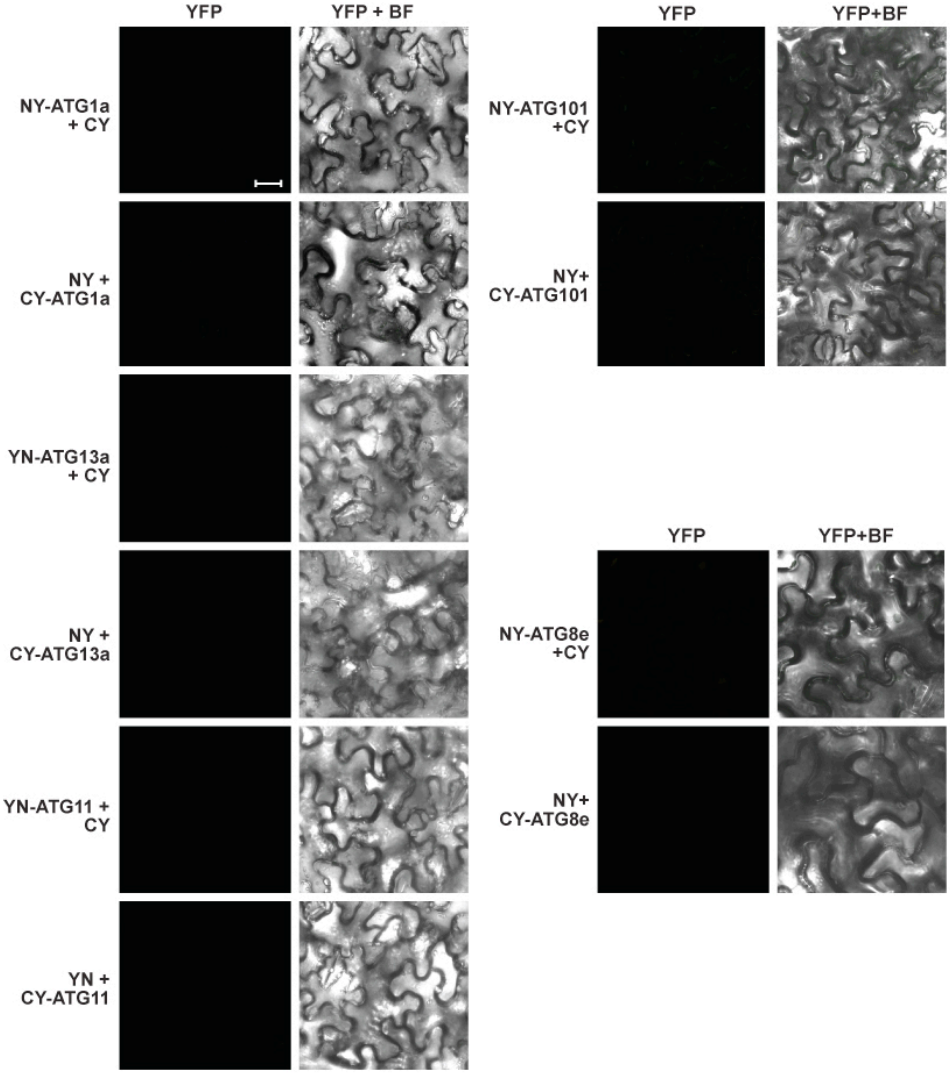
Supplemental Figure 3. Phylogenetic Analysis of ATG11 Domain-Containing Proteins.

The amino acid sequences of predicted ATG11 domains were aligned by ClustalX (see Supplemental Figure 1 online) and used to construct a maximum likelihood tree based on the Jones/Taylor/Thornton method in MEGA 5.1. Sequence designations refer to the UniProt accession number and amino acid residue number of putative ATG11 domains, separated by a slash. The *Arabidopsis* member is highlighted in red.

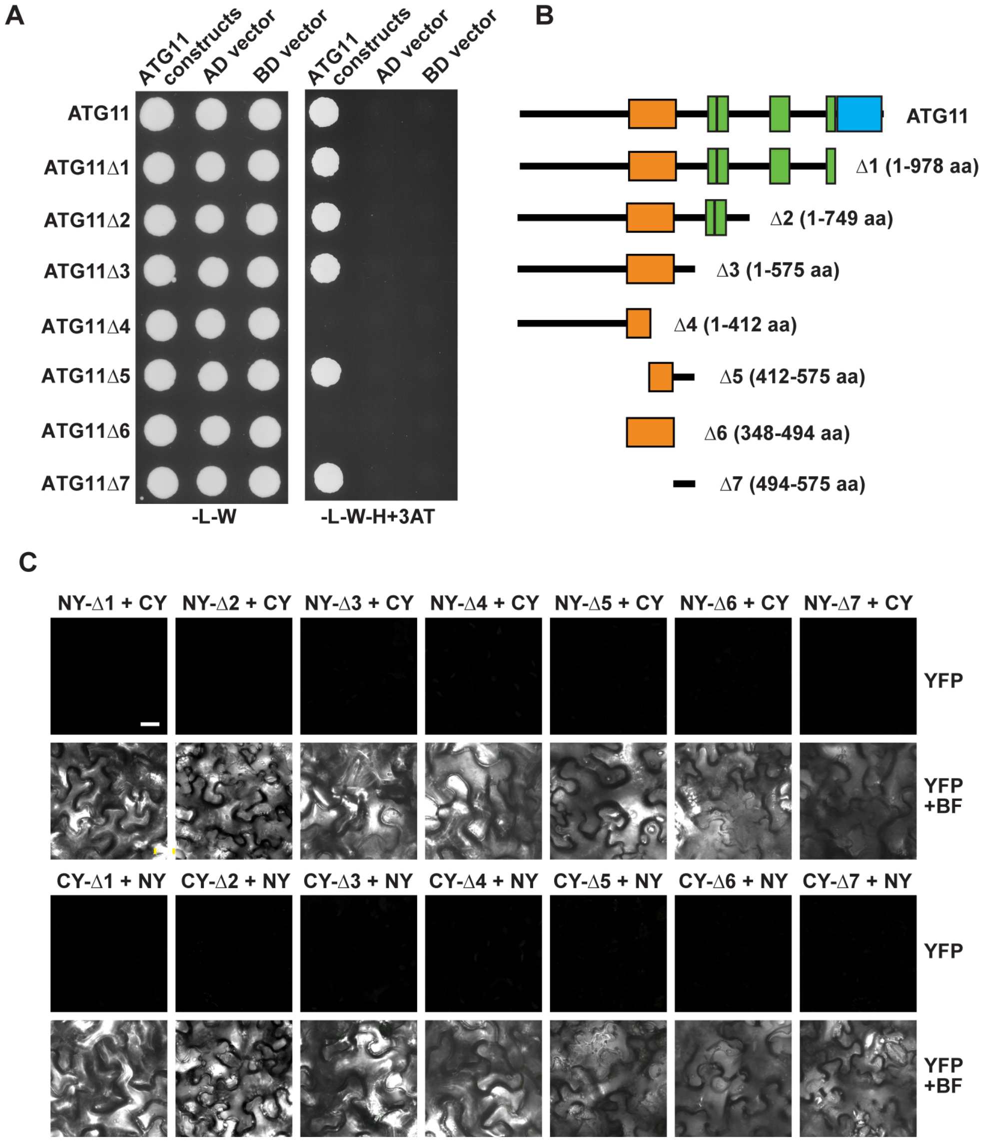


Supplemental Figure 4. Phylogenetic Analysis of ATG17 Domain-Containing Proteins.

The amino acid sequences of predicted ATG17 domains in ATG11, ATG17, and FIP200-related proteins were aligned by ClustalX (see Supplemental Figure 2 online) and used to construct a maximum likelihood tree based on Jones/Taylor/Thornton method method in MEGA 5.1. Sequence designations refer to the UniProt accession number and amino acid residue number of putative ATG17 domains, separated by a slash. The *Arabidopsis* member is highlighted in red.



Supplemental Figure 5. BiFC Controls Used to Examine the *in Planta* Interactions of ATG11, ATG101, or ATG8e with Other Components of the ATG1/13 Kinase Complex.
The indicated combinations fused to the N- or C-terminal fragments of YFP (NY and CY, respectively) were co-expressed in *N. benthamiana* leaf epidermal cells. Confocal fluorescence microscopy images were captured 36-48 hr after transfection. The comparative bright field (BF) image is included next to each picture. Scale bar = 10 μm.

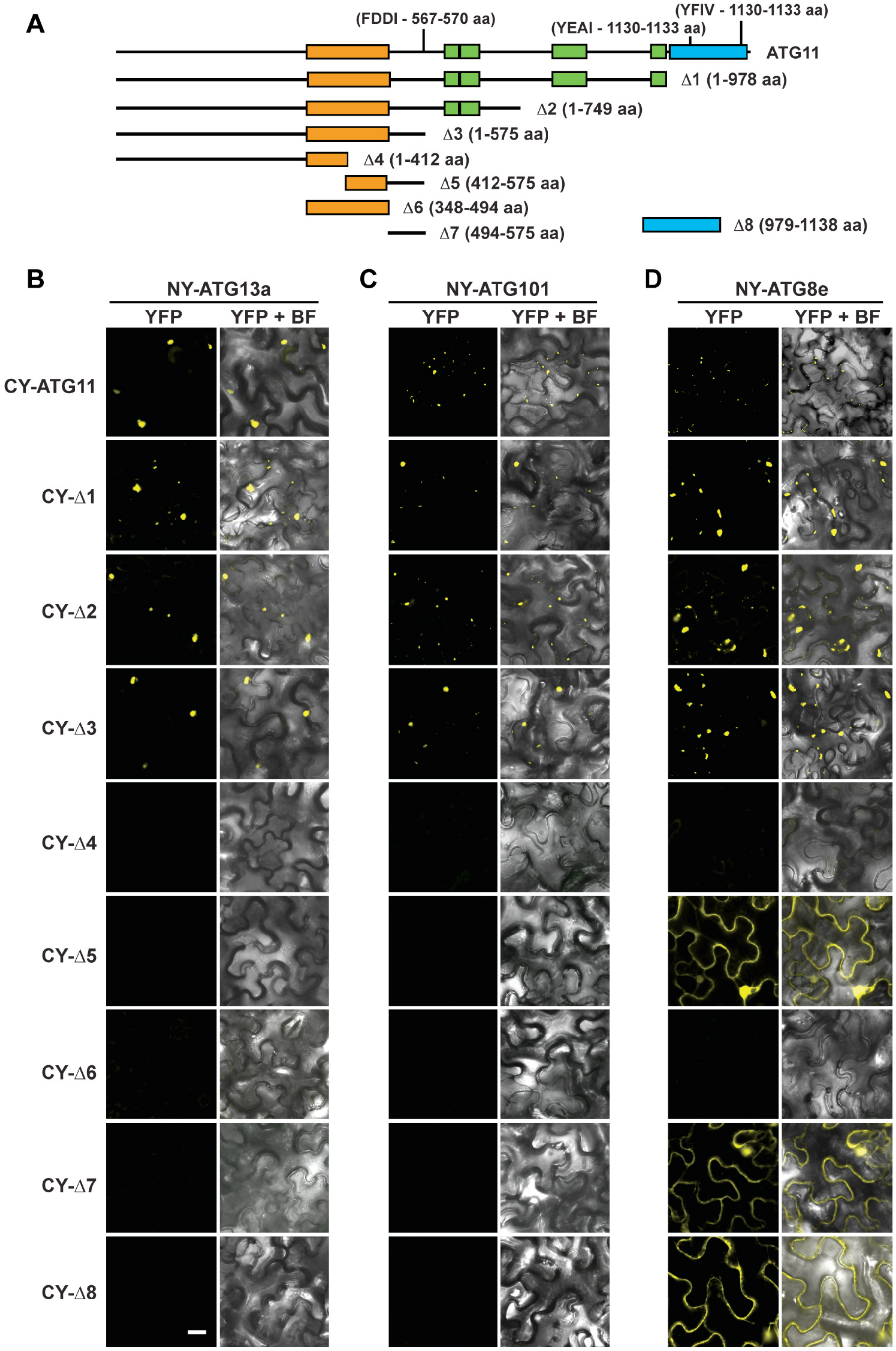


Supplemental Figure 6. Y2H and BiFC Controls Used to Map the ATG11 Dimerization Region.

(A) Full-length ATG11 and various truncated constructs were designed as N-terminal fusions to either the GAL4 activating (AD) or binding (BD) domains and co-transformed in yeast on selection medium lacking Trp and Leu or lacking Trp, Leu, and His and containing 3-amino-1,2,4-trizole (3AT).

(B) Diagram of the ATG11 truncations used in panels (A) and (C).

(C) BiFC of the ATG11 truncations. The indicated combinations were fused to the N- or C-terminal fragments of YFP (NY and CY, respectively) and co-expressed in *N. benthamiana* leaf epidermal cells. Confocal fluorescence microscopy images were captured 36-48 hr after transfection. The comparative bright field (BF) image is included below each picture. Scale bar = 10 μm.



Supplemental Figure 7. BiFC Mapping of the Interaction Site(s) Between ATG11 and ATG13a, ATG101, or ATG8e.

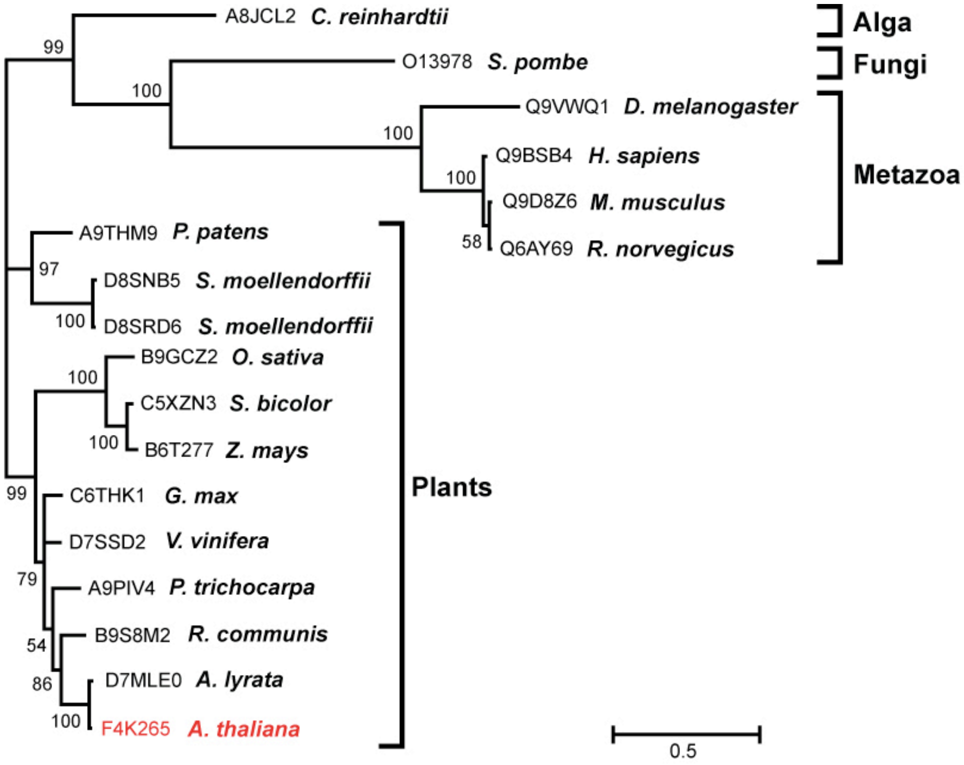
(A) Diagram of the ATG11 truncations used for BiFC in panels (B-D). Possible AIM sequences are identified. Whereas the FDDI and YFIV AIM sequences are relatively conserved within ATG11 family, the YEAI possible AIM sequence is more degenerate.

(B) BiFC of the ATG11 truncations with full-length ATG13a.

(C) BiFC of the ATG11 truncations with full-length ATG101.

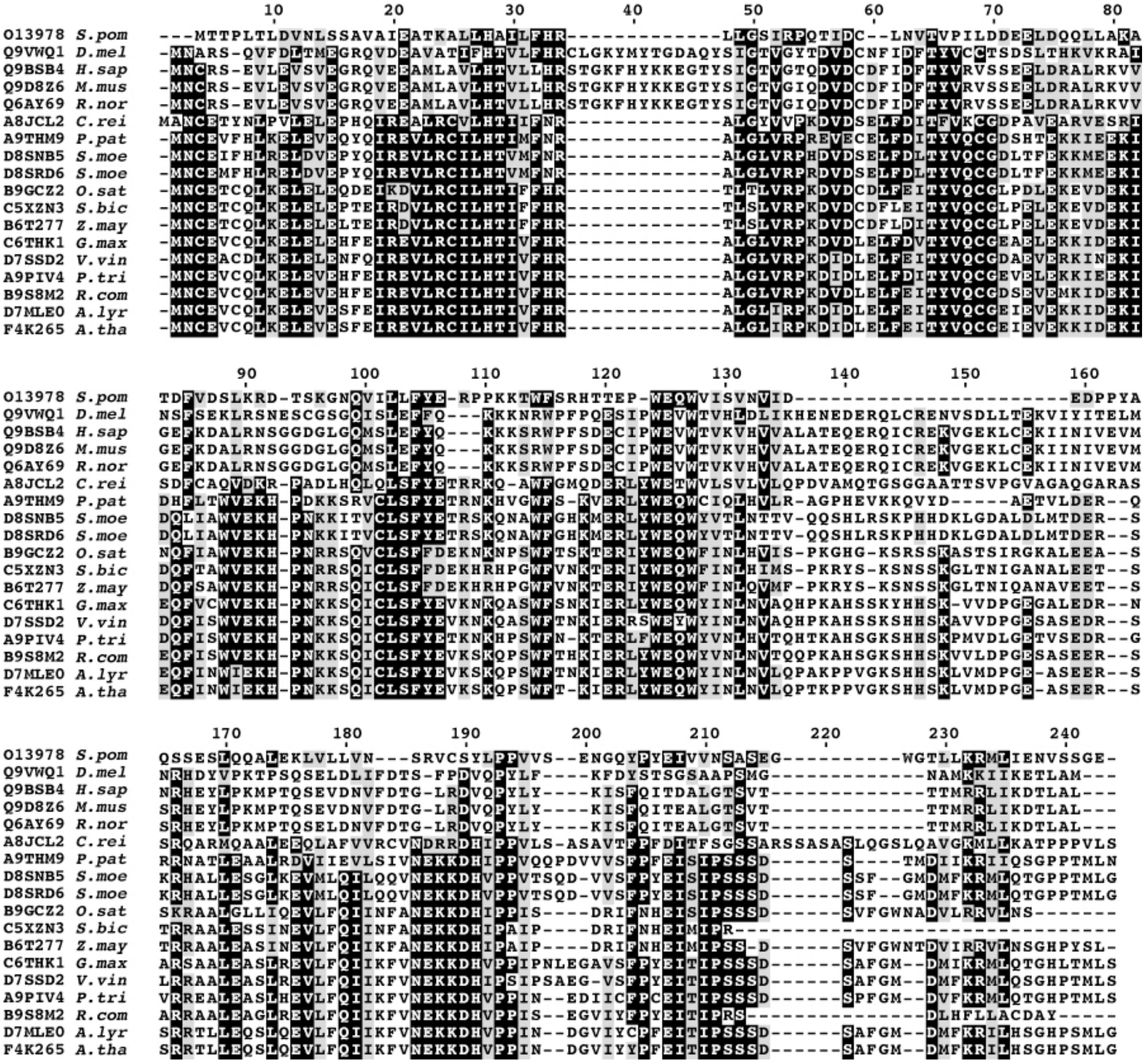
(D) BiFC of the ATG11 truncations with full-length ATG8e.

The indicated combinations were fused to the N- or C-terminal fragments of YFP (NY and CY, respectively) and co-expressed in the *N. benthamiana* leaf epidermal cells. Confocal microscopic images were captured 36-48 hr after transfection. The comparative bright field (BF) image is included next to each picture. Scale bar = 10 µm.



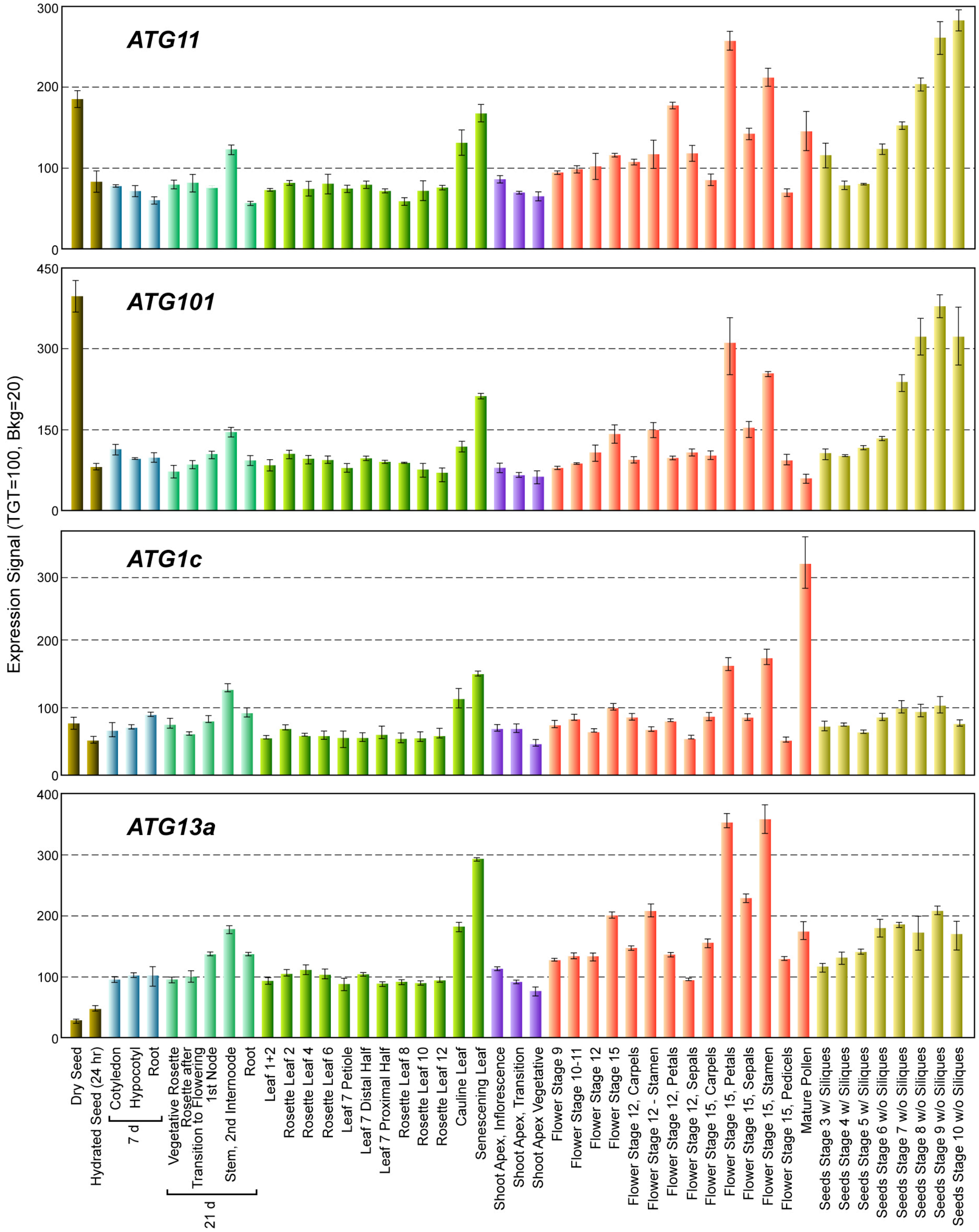
Supplemental Figure 8. Phylogenetic Analysis of ATG101 Proteins.

The amino acid sequences of predicted ATG101 proteins were aligned by ClustalX (see Supplemental Figure 9 online) and used to construct a maximum likelihood tree based on Jones/Taylor/Thornton method in MEGA 5.1. Sequence designations refer to the UniProt accession number (see Supplemental Table S5 online). The *Arabidopsis* member is highlighted in red.



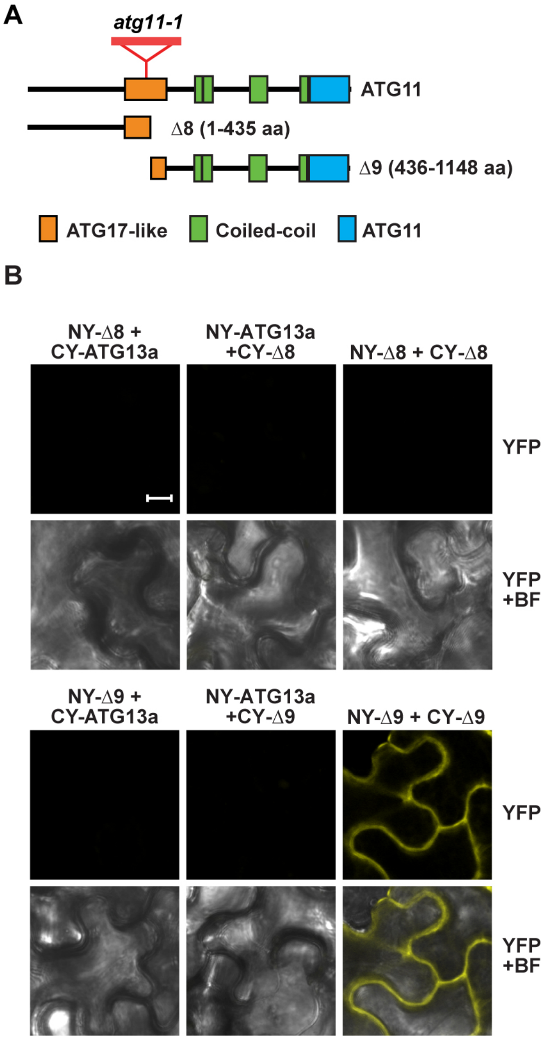
Supplemental Figure 9. Amino Acid Sequence Alignment of ATG101 Orthologs.

Representative proteins found in plants, *Metazoa* and fungi were selected from Uniprot Pfam (www.uniprot.org) using human ATG101 (Uniprot ID: Q9BSB4) as the query. The residues were colored using Boxshade version 3.21; black and grey boxes identify identical and similar amino acids. Sequence designations refer to the UniProt accession number. O13978 is the protein from *S. pombe*, Q9VWQ1 from *D. melanogaster*, Q9BSB4 from *H. sapiens*, Q9D8Z6 from *M. musculus*, Q6AY69 from *R. norvegicus*, A8JCL2 from *C. reinhardtii*, A9THM9 from *P. patens*, D8SRD6 and D8SNB5 from *S. moellendorffii*, B9GCZ2 from *O. sativa*, C5XZN3 from *S. bicolor*, B6T277 from *Z. mays*, C6THK1 from *G. max*, D7SSD2 from *V. vinifera*, A9PIV4 from *P. trichocarpa*, B9S8M2 from *R. communis*, D7MLE0 from *A. lyrata* and F4K265 from *A. thaliana*.



Supplemental Figure 10. Expression of *ATG11*, *ATG101*, *ATG1c*, and *ATG13a* in *Arabidopsis* Tissues at Various Stages of Development.

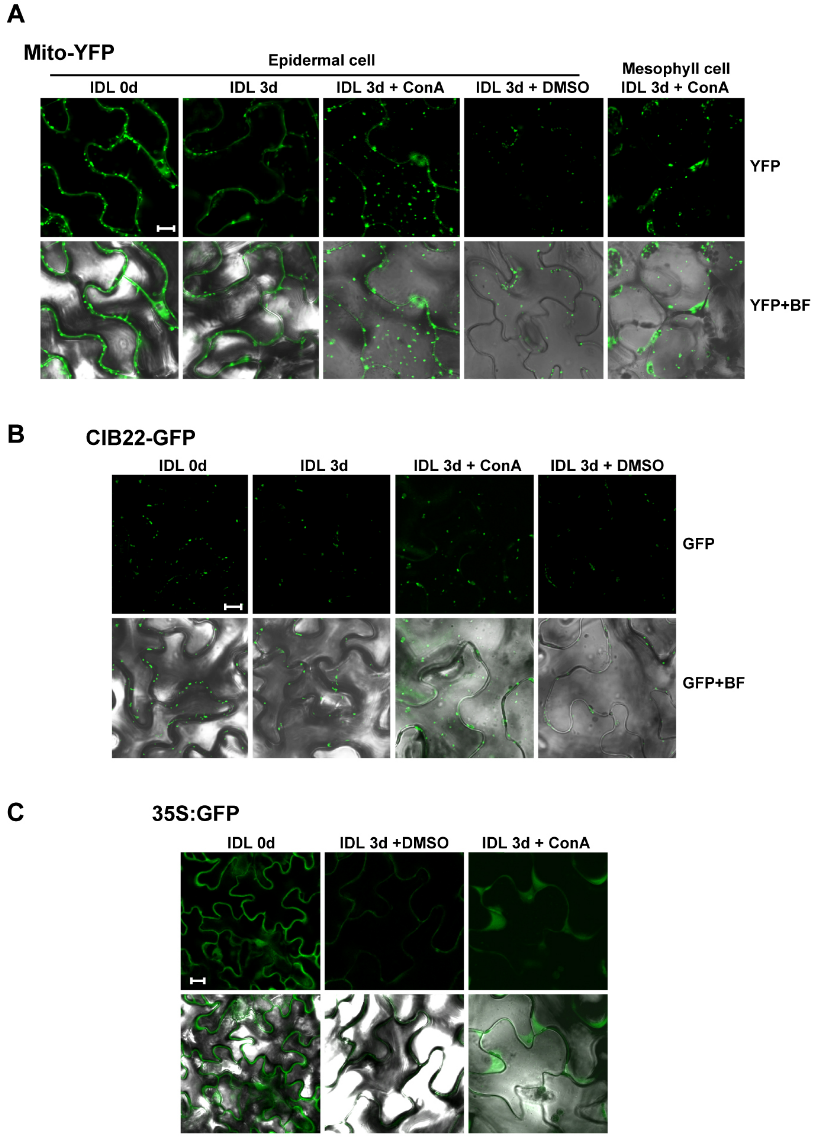
Normalized expression levels for *ATG11*, *ATG101*, *ATG1c*, and *ATG13a* were obtained from the eFP Browser (http://bar.utoronto.ca/efp_arabidopsis/cgi-bin/efpWeb.cgi) using the Gene Chip Operating Software and the Affimetrics 24K *Arabidopsis* DNA microarray. TGT, target. Bkg, background. Similar tissues and/or developmental stages are clustered by the various colors.



Supplemental Figure 11. Truncated Transcripts Posssibly Generated 5' and 3' to the T-DNA Insertion Site in *atg11-1* do not Generate Interaction-Competent ATG11 Proteins Even if Expressed.

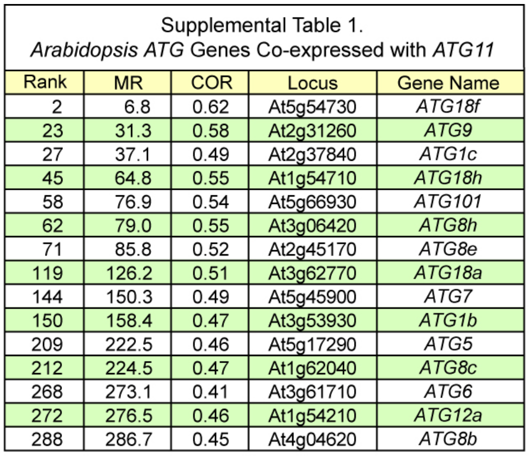
(A) Diagram of the *ATG11* gene showing the position of the *atg11-1* T-DNA insertion within codon 436. Positions of the signature ATG17-like, coiled coil, and ATG11 domains are indicated.

(B) BiFC of the possible N-terminal and C-terminal fragments of ATG11 (residues 1-435 and 436-1148) in *atg11-1* plants with themselves or with full-length ATG13a. The Δ8 and Δ9 coding regions upstream and downstream of the T-DNA insertion site were fused to the N- (NY) and C-terminal (CY) fragments of YFP, expressed in *N. benthaniana* leaf cells, and then assayed by fluorescence confocal microscopy. Scale bar = 10 um.



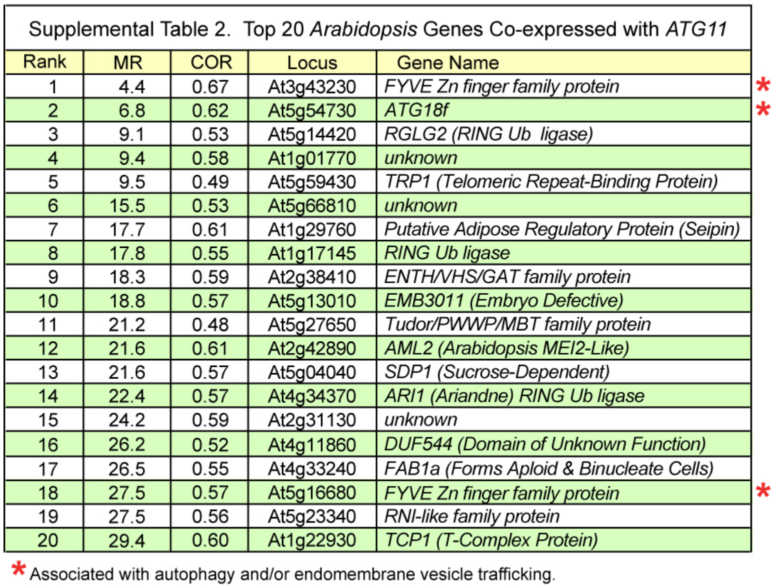
Supplemental Figure 12. Association of the Mitochondrial Markers Mito-YFP and CIB22-GFP with Autophagic Bodies during IDL-Induced Senescence.

Four-week-old wild-type plants expressing Mito-YFP **(A)**, CIB22-GFP **(B)** and free GFP **(C)** were subjected to IDL senescence for 3 d without or with a 20 hr pretreatment with 1 μM ConA or an equivalent volume of DMSO. Leaf epidermal and mesophyll cells from the 3rd and 4th rosette leaves were imaged by confocal fluorescence microscopy. The comparative bright field (BF) image is included below each picture. Scale bar = 10 μm.



Supplemental Table 1.
Arabidopsis ATG Genes Co-expressed with *ATG11*

Rank	MR	COR	Locus	Gene Name
2	6.8	0.62	At5g54730	*ATG18f*
23	31.3	0.58	At2g31260	*ATG9*
27	37.1	0.49	At2g37840	*ATG1c*
45	64.8	0.55	At1g54710	*ATG18h*
58	76.9	0.54	At5g66930	*ATG101*
62	79.0	0.55	At3g06420	*ATG8h*
71	85.8	0.52	At2g45170	*ATG8e*
119	126.2	0.51	At3g62770	*ATG18a*
144	150.3	0.49	At5g45900	*ATG7*
150	158.4	0.47	At3g53930	*ATG1b*
209	222.5	0.46	At5g17290	*ATG5*
212	224.5	0.47	At1g62040	*ATG8c*
268	273.1	0.41	At3g61710	*ATG6*
272	276.5	0.46	At1g54210	*ATG12a*
288	286.7	0.45	At4g04620	*ATG8b*



Supplemental Table 2. Top 20 *Arabidopsis* Genes Co-expressed with *ATG11*

Rank	MR	COR	Locus	Gene Name	
1	4.4	0.67	At3g43230	*FYVE Zn finger family protein*	*
2	6.8	0.62	At5g54730	*ATG18f*	*
3	9.1	0.53	At5g14420	*RGLG2 (RING Ub ligase)*	
4	9.4	0.58	At1g01770	*unknown*	
5	9.5	0.49	At5g59430	*TRP1 (Telomeric Repeat-Binding Protein)*	
6	15.5	0.53	At5g66810	*unknown*	
7	17.7	0.61	At1g29760	*Putative Adipose Regulatory Protein (Seipin)*	
8	17.8	0.55	At1g17145	*RING Ub ligase*	
9	18.3	0.59	At2g38410	*ENTH/VHS/GAT family protein*	
10	18.8	0.57	At5g13010	*EMB3011 (Embryo Defective)*	
11	21.2	0.48	At5g27650	*Tudor/PWWP/MBT family protein*	
12	21.6	0.61	At2g42890	*AML2 (Arabidopsis MEI2-Like)*	
13	21.6	0.57	At5g04040	*SDP1 (Sucrose-Dependent)*	
14	22.4	0.57	At4g34370	*ARI1 (Ariandne) RING Ub ligase*	
15	24.2	0.59	At2g31130	*unknown*	
16	26.2	0.52	At4g11860	*DUF544 (Domain of Unknown Function)*	
17	26.5	0.55	At4g33240	*FAB1a (Forms Aploid & Binucleate Cells)*	
18	27.5	0.57	At5g16680	*FYVE Zn finger family protein*	*
19	27.5	0.56	At5g23340	*RNI-like family protein*	
20	29.4	0.60	At1g22930	*TCP1 (T-Complex Protein)*	

* Associated with autophagy and/or endomembrane vesicle trafficking.

Supplemental Tables 1 and 2. Co-expression of *ATG11* with Genes Encoding Other Components of the ATG8-Mediated Autophagic Pathway (Table 1) and with Other *Arabidopsis* Genes (Table 2).

Potentially co-expressed genes were identified from the ATTED-II database using the CoexSearch function. The rank, mutual rank (MR), correlation coefficient (COR), *A. thaliana* Col-0 locus identifier, and gene name/prediction are indicated. Red asterisks in Supplemental Table 2 identify proteins that are known or are predicted to participate in autophagy and/or endomembrane vesicle trafficking.

Supplemental Table 3. Oligonucleotide Primers Used in This Study

ATG11 RT-PCR Primers

Primer 1: ATGAGCGGAAGCTTCACTGAGAGTTT
Primer 2: GTCGAGGTCAAGCGCAAGGTA
Primer 3: TCATGCACTTCGTACATAGGACCCAG
Primer 4: GCAACATTGACATCACACTGAGTAGG
Primer 5: CTCATATTCAAATTGTGGGCCTAA
Primer 6: TTAGGCCCACAATTTGAATATGAG
Primer 7: AATAATTCCTCCCGGTGTTTG

ATG11 Genotyping Primers

atg11-1 RP: AAGTGTCCTCATCTCTGCGTC
atg11-1 LP: TGCATTTGTTTTTCCTTGAGC
atg11-2 RP: AATAATTCCTCCCGGTGTTTG
atg11-2 LP: AAGCTTCTCGAAGAATCCCAG

Primers used to generate full-length and truncated form *ATG11*

ATG11 full-length cDNA Forward: ATGAGCGGAAGCTTCACTGAGAGTTT
ATG11 full-length cDNA Reverse: CGTGGCCATATAACTGAAAGCTGA
ATG11 (1-978aa) Reverse: TCAAGCAATCCCACTACCAGCACA
ATG11 (1-794aa) Reverse: TCAAGAGGAATCCACCATATTCTC
ATG11 (1-575aa) Reverse: TCATTCAGAGGCTGCTAGGATATCAT
ATG11 (1-412aa) Reverse: TCAGCCTCTCTAAAAACGGGA
ATG11 (412-575aa) Forward: CACCTTTCCCGTTTTTAGAGAGGCAAT
ATG11 (494-575aa) Forward: CACCACTCCTACTCAGTGTGATGTCAAT
ATG11 (348-494aa) Forward: CACCGATGCTGTTTCAGCCCTGGGTCCT
ATG11 (348-494aa) Reverse: TCAAGGAGTATCGTATAAACCCATTGA
ATG11 (1-435aa) Reverse: TCACTATAAGCGGGGCCAACACCACG
ATG11 (436-1148aa) Forward: CACCGGCCTGTCTTGCAGAGGTG

Primers used to generate full-length *ATG101* cDNA:

Forward: ATGAATTGCGAAGTTTGTCAGCTAA
Reverse: GGAATTTAGCCGAGCATTGATGGA

ATG1a AIM mutant QuickChange primers:

Forward: CTCATAGAGAGAGAGGCTGTTCTTGC
Reverse: GCAGAAGGACGGTTTGCAAGAACAG

UBC9

AtUBC9_F3: CCGTTGCGGAAGACATGTTTCATT
AtUBC9_R2: TAGGGCTCTTCCTTAAGGACAGTA

Primers used for qRT-PCR analysis of *ATG11* transcript in *atg11-1* mutant

P8: CTGCAAGTGACAGGGAAGTG
P9: GATGCATCATCCAAGGGATG
P10: GGGACAGAGACATAATAATAAG
P11: GAAACACAAGAGACCTCATC

T-DNA Left Border Primers

SAIL-LB1: GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCCTTGCTT
GK-TDNA: ATAATAACGCTGCGGACATCTACATTTT

Supplemental Table 4. Species Names, Data Sources, and Domain Positions for Various ATG11, ATG17, and FIP200 Proteins Used for the Phylogenetic Analysis

Protein	Organism	Uniprot ID	ATG11 Domain Position (AA)	ATG17 domain position (AA)
ATG11	*Physcomitrella patens*	A9SER7	974-1132	335-481
ATG11	*Physcomitrella patens*	A9TRX9	969-1127	335-481
ATG11	*Selaginella moellendorffii*	D8STK2	907-1054	340-486
ATG11	*Selaginella moellendorffii*	D8T567	907-1055	340-486
ATG11	*Populus trichocarpa*	B9HB54	992-1146	304-497
ATG11	*Arabidopsis thaliana*	Q9SUG7	978-1138	348-494
ATG11	*Arabidopsis. lyrata*	D7MBM1	978-1138	348-494
ATG11	*Sorghum bicolor*	C5XWU8	999-1139	358-503
ATG11	*Oryza sativa*	Q6ETK7	991-1135	352-509
ATG11	*Dictyostelium discoideum*	Q54MY6	1219-1374	308-497
ATG11	*Phytophtora infestans*	D0MQJ2	747-884	356-519
ATG11	*Albugo laibachii*	F0W217	786-920	374-533
ATG11	*Aspergillus oryzae*	Q2UKQ2	945-1094	165-336
ATG17		Q2UFN7	NA	33-480
ATG11	*Penicillium chrysogenum*	B6H4J6	1010-1159	211-403
ATG17		A7KAM6	NA	32-479
ATG11	*Laccaria bicolor*	B0DBA9	971-1091	332-501
ATG11	*Pichia pastoris*	Q9C438	1154-1310	336-521
ATG17		C4R1E4	NA	5-415
ATG11	*Saccharomyces cerevisiae*	Q12527	991-1173	339-512
ATG17		Q06410	NA	7-406
ATG17	*Candida sphaerica*	Q6CS99	NA	14-410
ATG11	*Vanderwaltozyma polyspora*	A7TL57	1045-1216	302-474
ATG17		A7TM40	NA	4-402
FIP200	*Caenorhabditis elegans*	Q22342	1186-1316	282-474
FIP200	*Loa loa*	E1G2W6	1025-1155	325-506
FIP200	*Aedes aegypti*	Q17NR9	932-1060	352-539
FIP200	*Trichoplax adhaerens*	B3RY68	907-1036	287-473
FIP200	*Danio rerio*	E7FFM2	1493-1622	372-559
FIP200	*Mus musculus*	Q9ESK9	1444-1584	372-558
FIP200	*Drosophila melanogaster*	Q9VNG5	942-1083	369-560
FIP200	*Homo sapiens*	Q8TDY2	1454-1590	373-560

Supplemental Table 5. Species Names and Data Sources for ATG101 Proteins Used for the Phylogenetic Analysis. The amino acid length of each protein is listed on the right.

Protein	**Organism**	**Uniprot ID**	**Protein length**
ATG101	*Chlamydomonas reinhardtii*	A8JCL2	259 aa
Mug66	*Schizosaccharomyces pombe*	O13978	184 aa
ATG101	*Drosophila melanogaster*	Q9VWQ1	218 aa
ATG101	*Homo sapiens*	Q9BSB4	218 aa
ATG101	*Mus musculus*	Q9D8Z6	218 aa
ATG101	*Rattus norvegicus*	Q6AY69	218 aa
ATG101	*Physcomitrella patens*	A9THM9	210 aa
ATG101	*Selaginella moellendorffii*	D8SNB5	217 aa
ATG101	*Selaginella moellendorffii*	D8SRD6	217 aa
ATG101	*Oryza sativa*	B9GCZ2	208 aa
ATG101	*Sorghum bicolor*	C5XZN3	189 aa
ATG101	*Zea mays*	B6T277	213 aa
ATG101	*Glycine max*	C6THK1	218 aa
ATG101	*Vitis vinifera*	D7SSD2	218 aa
ATG101	*Populus trichocarpa*	A9PIV4	216 aa
ATG101	*Ricinus communis*	B9S8M2	205 aa
ATG101	*Arabidopsis lyrata*	D7MLE0	216 aa
ATG101	*Arabidopsis thaliana*	F4K265	215 aa