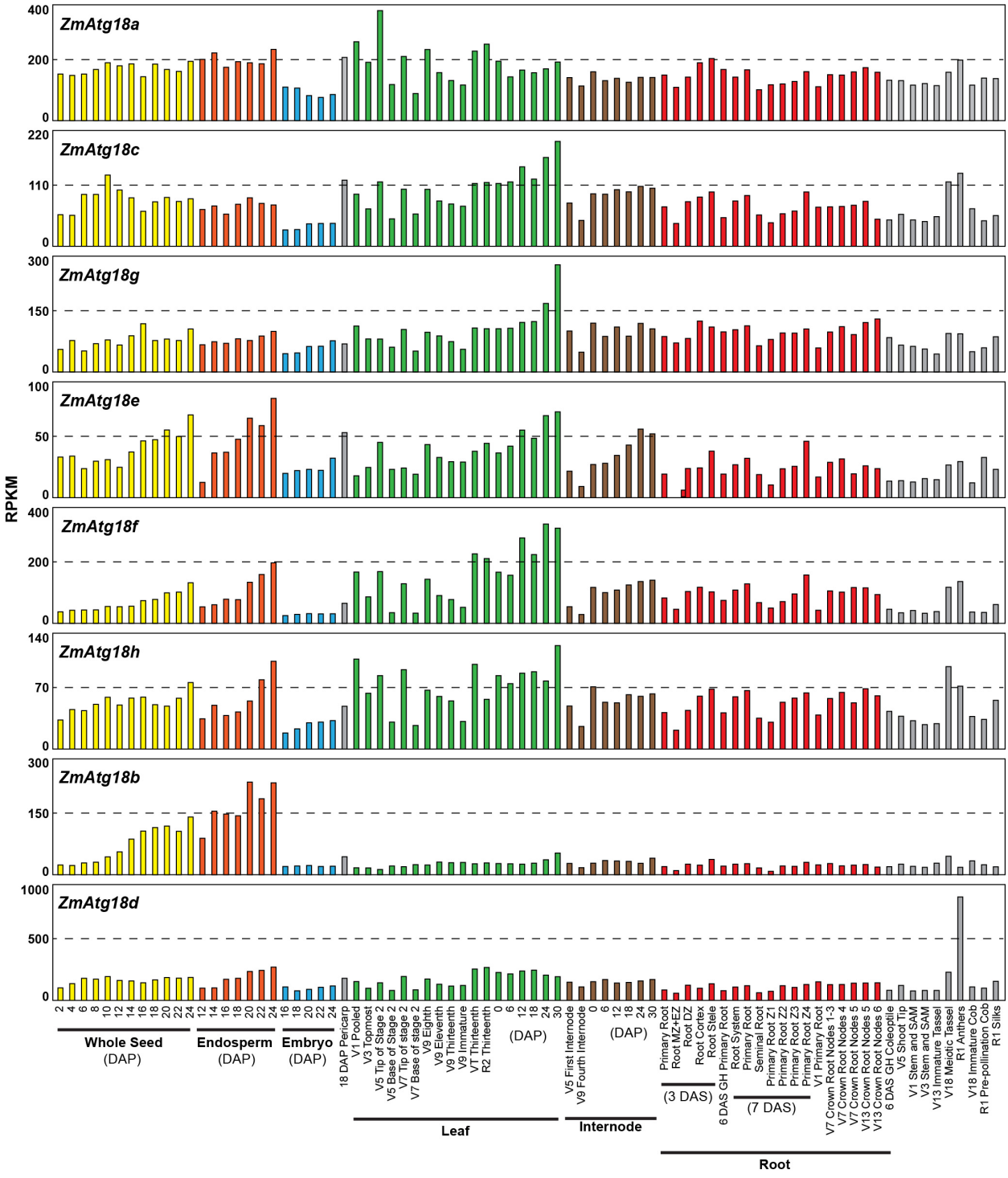

**Supplemental Figure 1.** Transcript Abundance from Selected Maize *Atg* Genes Increases as Leaves Mature or Senesce.

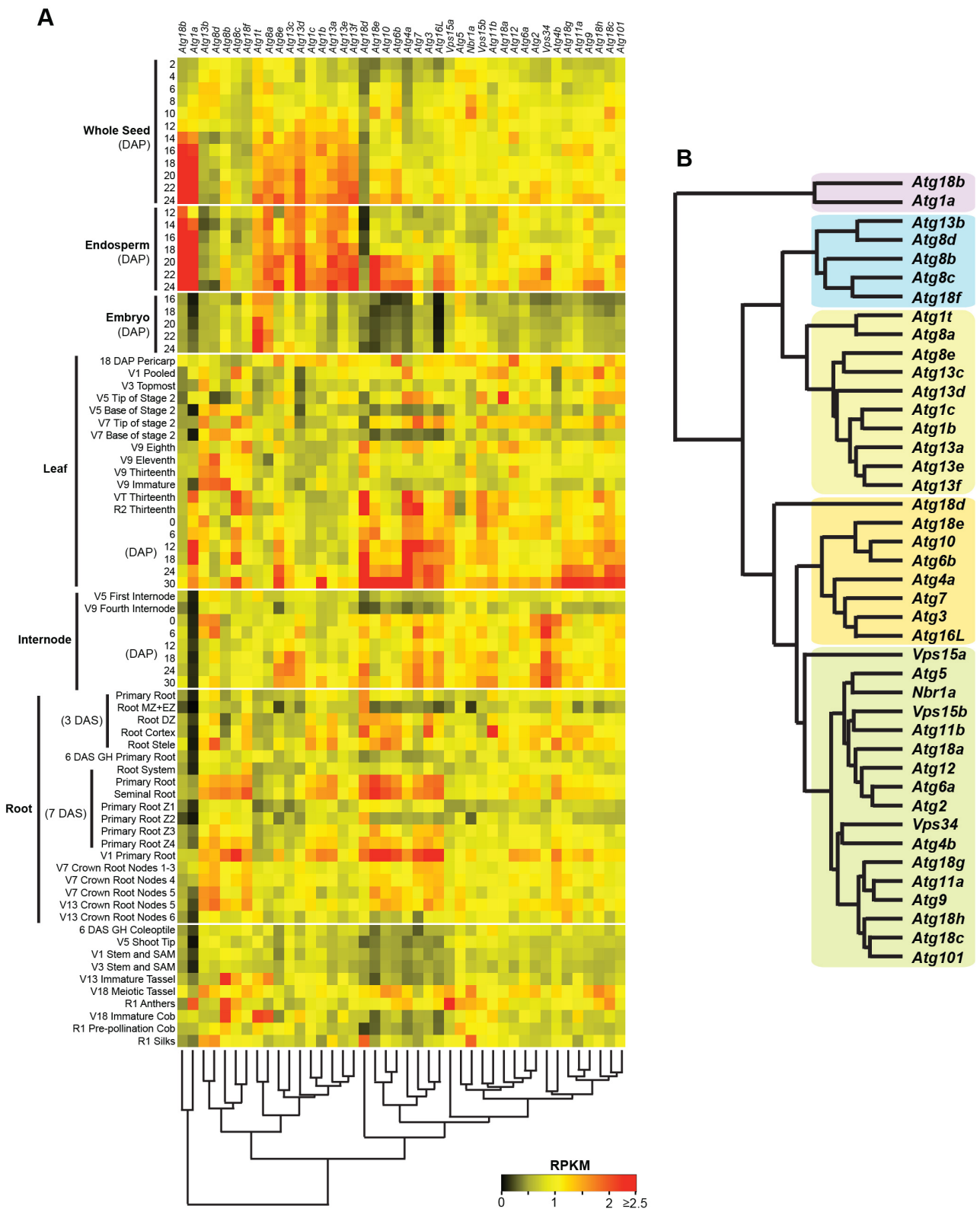
Total RNA was isolated from the leaves at the various positions in a mature plant (leaf 1 younger to leaf 12 older at pollination, green color), or from the base (B), middle (M), and tip (T) sections of the seventh leaf (orange color), and subjected to quantitative real time PCR using the comparative cycle threshold method. Values represent the means (±SD) of three biological replicates, each with three technical replicates, which were normalized to that determined for *UBC9*.




**Supplemental Figure 2.** Developmental and Tissue-Specific Expression Profiles of Maize *Atg18* Genes.

RNA-seq experiments representing 80 developmentally or anatomically distinct maize samples were analyzed for members of the *Atg18* gene family based on reads per kilobase per one million reads (RPKM). Vegetative (V1-18) and reproductive (R1-2)

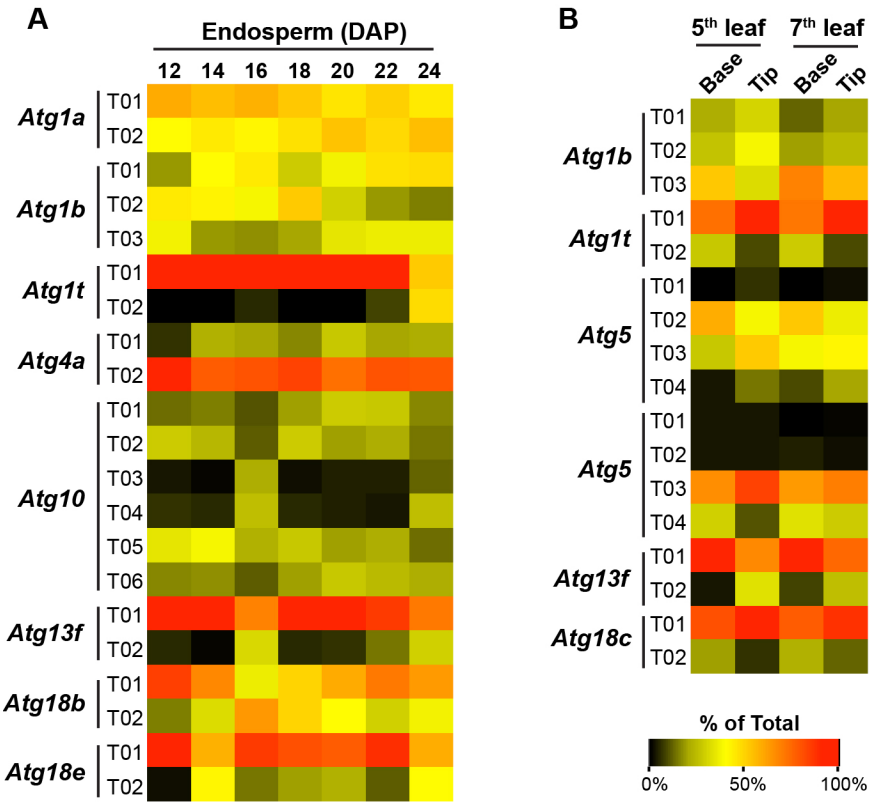
growth stages were defined based on the Corn Field Guide published by Iowa State University Extension (Abendroth et al., 2011). Dissected primary root- Z1 = Zone 1 (1st cm of root tip); Z2 = Zone 2 (from end of Z1 to the point of root hair/lateral root initiation); Z3 = Zone 3 (lower half of differentiation zone); Z4 = Zone 4 (upper half of differentiation zone). DAP, days after pollination. DAS, days after sowing. DZ, differentiation zone. EZ, elongation zone. MZ, meristematic zone. SAM, shoot apical meristem. More complete descriptions of the tissues are available in Supplemental Table 2 online.


A
Atg18b
Atg1a
Atg13b
Atg8d
Atg8b
Atg8c
Atg18f
Atg1t
Atg8a
Atg8e
Atg13c
Atg13d
Atg1c
Atg1b
Atg13a
Atg13e
Atg13f
Atg18d
Atg18e
Atg10
Atg6b
Atg4a
Atg7
Atg3
Atg16L
Vps15a
Atg5
Nbr1a
Vps15b
Atg11b
Atg18a
Atg12
Atg6a
Atg2
Vps34
Atg4b
Atg18g
Atg11a
Atg9
Atg18h
Atg18c
Atg101
Whole Seed (DAP)
2 4 6 8 10 12 14 16 18 20 22 24
Endosperm (DAP)
12 14 16 18 20 22 24
Embryo (DAP)
16 18 20 22 24
Leaf
18 DAP Pericarp
V1 Pooled
V3 Topmost
V5 Tip of Stage 2
V5 Base of Stage 2
V7 Tip of stage 2
V7 Base of stage 2
V9 Eighth
V9 Eleventh
V9 Thirteenth
V9 Immature
VT Thirteenth
R2 Thirteenth
(DAP) 0 6 12 18 24 30
Internode
V5 First Internode
V9 Fourth Internode
(DAP) 0 6 12 18 24 30
Root
(3 DAS)
Primary Root
Root MZ+EZ
Root DZ
Root Cortex
Root Stele
6 DAS GH Primary Root
(7 DAS)
Root System
Primary Root
Seminal Root
Primary Root Z1
Primary Root Z2
Primary Root Z3
Primary Root Z4
V1 Primary Root
V7 Crown Root Nodes 1-3
V7 Crown Root Nodes 4
V7 Crown Root Nodes 5
V13 Crown Root Nodes 5
V13 Crown Root Nodes 6
6 DAS GH Coleoptile
V5 Shoot Tip
V1 Stem and SAM
V3 Stem and SAM
V13 Immature Tassel
V18 Meiotic Tassel
R1 Anthers
V18 Immature Cob
R1 Pre-pollination Cob
R1 Silks
RPKM
0 1 2 ≥2.5
B
Atg18b
Atg1a
Atg13b
Atg8d
Atg8b
Atg8c
Atg18f
Atg1t
Atg8a
Atg8e
Atg13c
Atg13d
Atg1c
Atg1b
Atg13a
Atg13e
Atg13f
Atg18d
Atg18e
Atg10
Atg6b
Atg4a
Atg7
Atg3
Atg16L
Vps15a
Atg5
Nbr1a
Vps15b
Atg11b
Atg18a
Atg12
Atg6a
Atg2
Vps34
Atg4b
Atg18g
Atg11a
Atg9
Atg18h
Atg18c
Atg101

**Supplemental Figure 3.** Developmental and Tissue-Specific RNA-seq Expression Profiles of Maize Autophagy Genes Clustered by Co-expression.

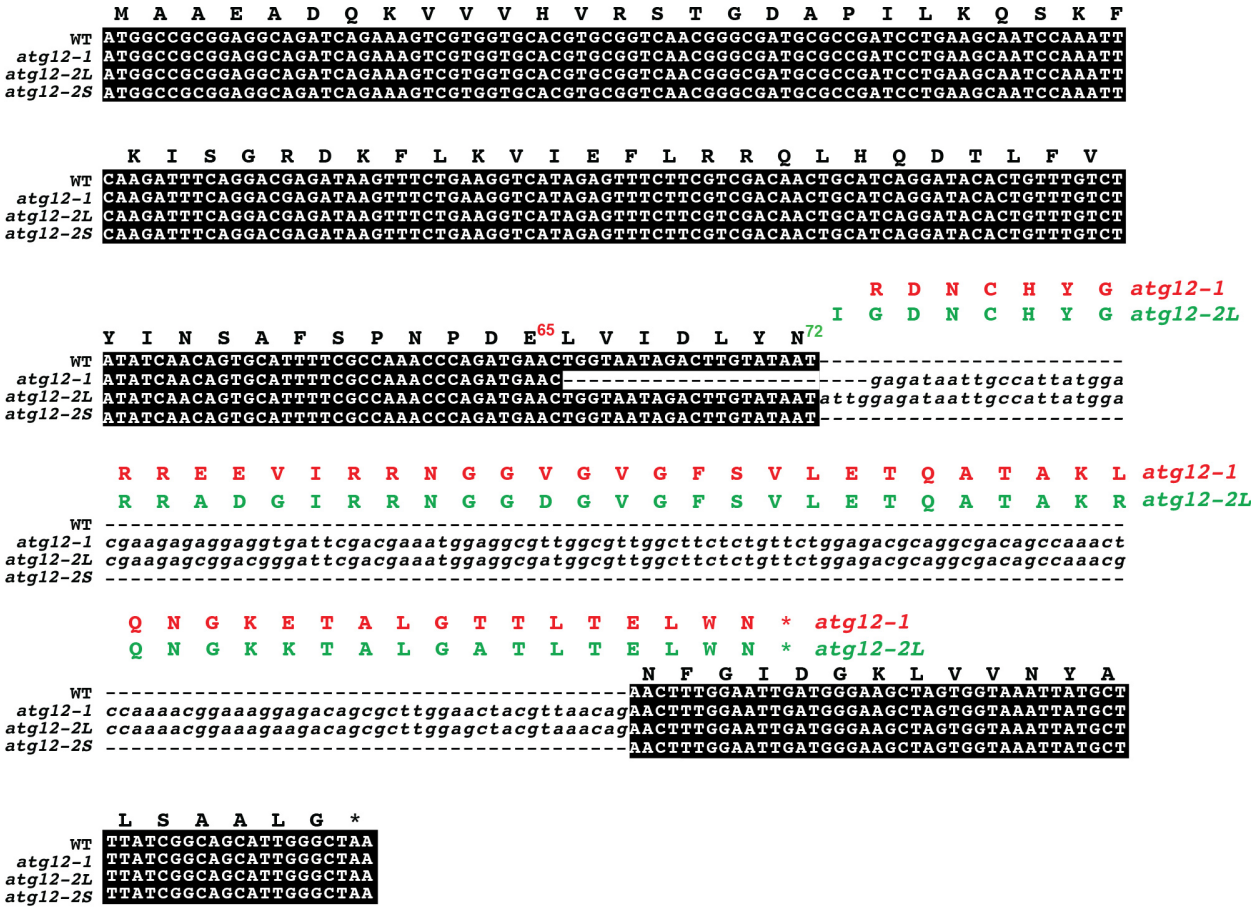
**(A)** Heat map of *Atg* genes showing the spatio-temporal expression pattern after hierarchical clustering. RNA-seq experiments representing 80 developmentally or anatomically distinct maize samples were analyzed for autophagy-related genes based on reads per kilobase per one million reads (RPKM) and clustered in R based on co-expression. The color indicates the degree of fold change: red, high; black, low. Vegetative (V1-18) and reproductive (R1-2) growth stages were defined based on the Corn Field Guide published by Iowa State University Extension (Abendroth et al., 2011). Dissected primary root- Z1 = Zone 1 (1st cm of root tip); Z2 = Zone 2 (from end of Z1 to the point of root hair/lateral root initiation); Z3 = Zone 3 (lower half of differentiation zone); Z4 = Zone 4 (upper half of differentiation zone). DAP, days after pollination. DAS, days after sowing. DZ, differentiation zone. EZ, elongation zone. MZ, meristematic zone. SAM, shoot apical meristem. See Supplemental Table 2 online for full descriptions of the tissues analyzed.

**(B)** Hierarchical cluster display of maize *Atg* genes analyzed in (A).



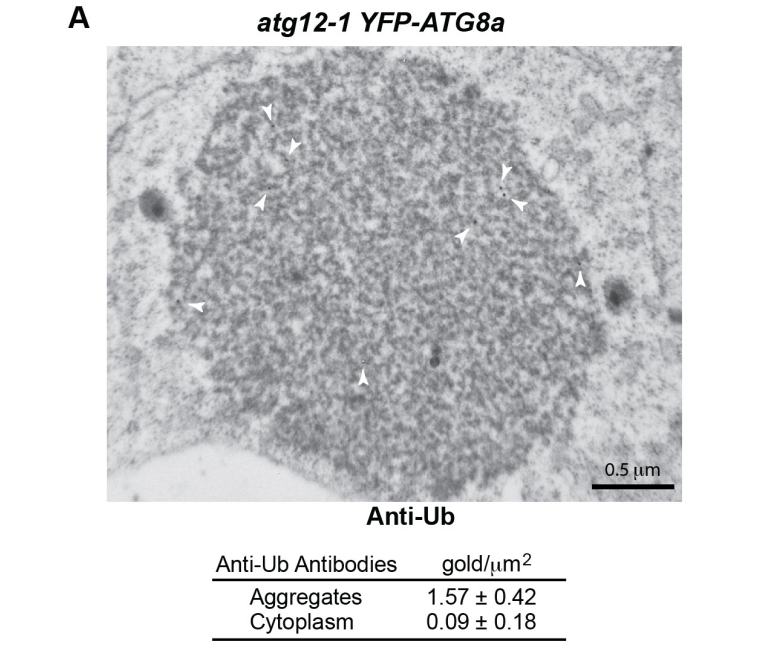

**Supplemental Figure 4.** Developmental and Tissue-Specific Alternative Splicing of Maize *Atg* Gene Isoforms in Endosperm and Leaf Tissues.

RNA-seq experiments spanning **(A)** endosperm development (DAP 12 to 24) and **(B)** dissected fifth and seventh leaves (Base and Tip) were analyzed for splice-specific isoforms from various *Atg* loci. Gene families encoding particular ATG factors are highlighted on the left along with the number for each transcript isoform. The color indicates the degree of fold change based on reads per kilobase per one million reads (RPKM): red, high; black, low. DAP, days after pollination.




**Supplemental Figure 5.** Nucleotide and Amino Acid Sequence Alignment of Wild-Type *ATG12* and the *atg12-1* and *atg12-2* Mutants.

The amino acid sequence of wild-type B73 ATG12 and the regions changed by the *atg12-1* and *atg12-2* mutations are shown in black, red, and green letters above the nucleotide sequences. Nucleotides not shaded in black represent those introduced by the *UniformMu* insertion. The *atg12-1* transcript contains a 156-bp insertion derived from *UniformMu* that introduced a random 51-amino acid sequence (red color) followed by a stop codon after Glu-65. A 159-bp insertion was appended by *UniformMu* to the *atg12-2* long transcript (*atg12-2L*) that also introduced a 52-amino acid sequence (green color) followed by a stop codon after Asn-72. Asterisk indicates stop codon.

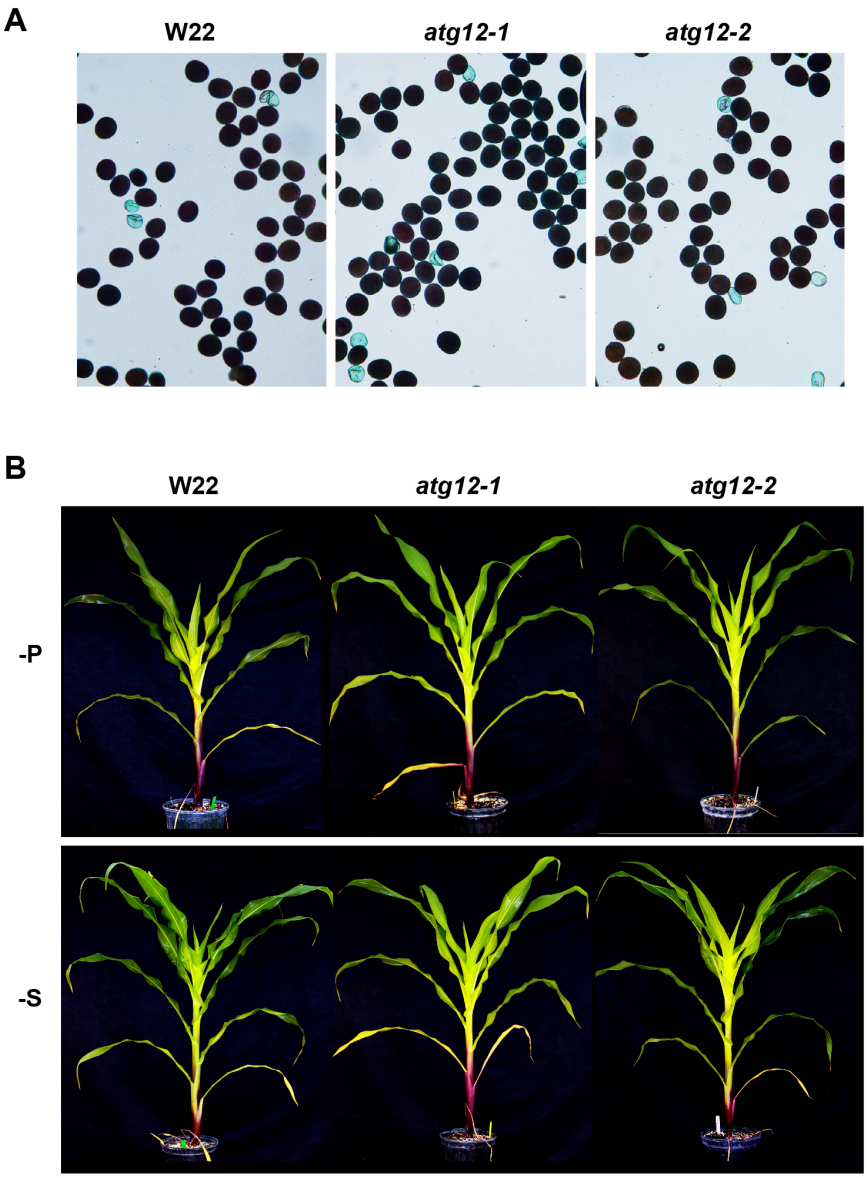



| Anti-Ub Antibodies | gold/$\mu m^2$ |
|---|---|
| Aggregates | 1.57 ± 0.42 |
| Cytoplasm | 0.09 ± 0.18 |

**Supplemental Figure 6.** Electron Microscopy Images of Cells from *atg12* Mutants.

**(A)** Images of N-starved *atg12-1* root cells pretreated with ConA showing that the YFP-ATG8a-containing aggregates also contain ubiquitin (arrowheads) as determined by immunogold-labeling with anti-ubiquitin antibodies. Table shows quantification of gold particles in six independent aggregates and 15 random areas of surrounding cytoplasm. The data indicate a strong enrichment (17 fold) of ubiquitin in the YFP-ATG8a aggregates.

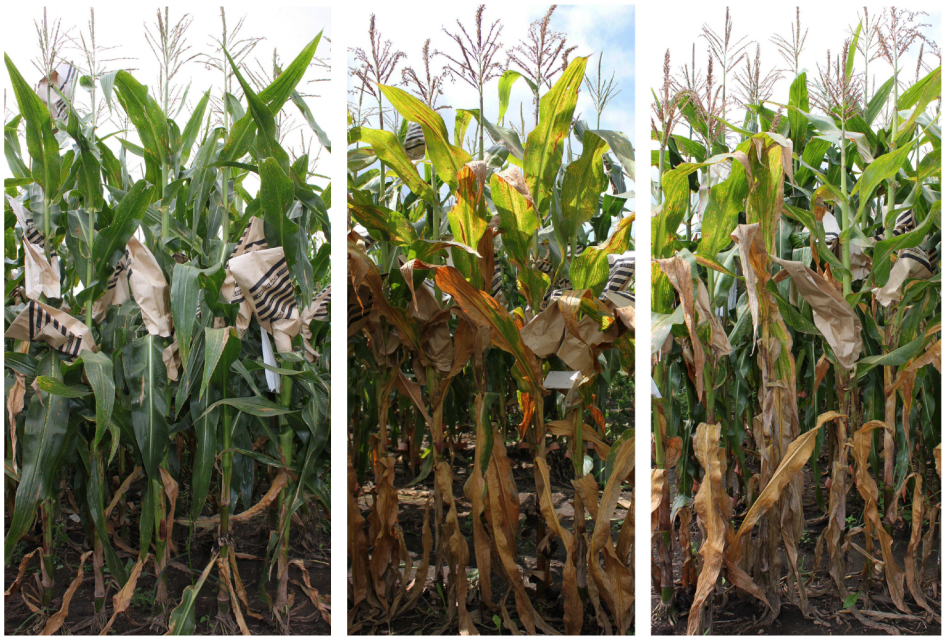
**(B)** The *atg12-1* mutant accumulates seed storage proteins normally. Shown are transmission EM pictures after cryofixation of aleurone and starchy endosperm cells from wild-type (WT) W22 and mutant seeds at 24 DAP. PSV, protein storage vacuole. PB, ER-associated protein body. Asterisks, storage protein-rich aggregates.



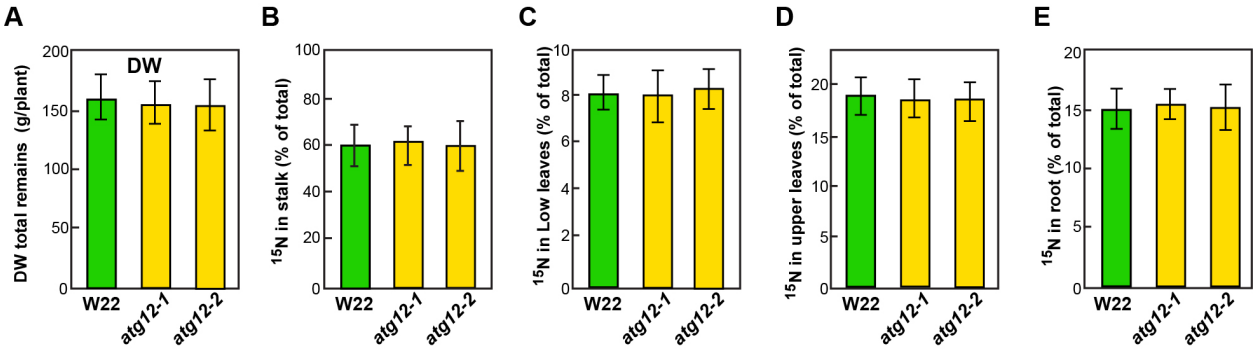

**Supplemental Figure 7.** *atg12* Mutants Produce Viable Pollen and are not Hypersensitive to Phosphorus or Sulfur Limitation.

**(A)** *atg12* mutants produce healthy pollen. Pollen was obtained from anthers of wild-type W22, *atg12-1* and *atg12-2* plants, and tested for viability with Alexander stain (Alexander, 1969). Non-viable pollen remains translucent in the stain. Bar = 50 µm.

**(B)** *atg12* plants grown normally without added phosphate or sulfur. Plants were grown on pre-washed Metro-Mix 360 soil and watered with phosphorus-deficient (-P) (5 mM $KNO_3$, 2 mM $MgSO_4$, 5 mM $Ca(NO_3)_2$, 0.05 mM Fe-EDTA, 1x Micronutrients, and 1 mM KCl), or sulfur-deficient (-S) Hoagland solutions (5 mM $KNO_3$, 2 mM $MgCl_2$, 1 mM $KH_2PO_4$, 5 mM $Ca(NO_3)_2$, 0.05 mM Fe-EDTA, 1x Micronutrients) for 7 weeks before the photographs were taken.




**Supplemental Figure 8.** Field-Grown *atg12* Mutants Display Early Leaf Senescence. Wild type W22, and the homozygous *atg12-1* and *atg12-2* mutants were grown on N-fertilized soil at the West Madison Agricultural Research Station during the summer of 2014. Photographs were taken 3 months after sowing and 20 DAP.




**Supplemental Figure 9.** $^{15}N$ Labeling Efficiency of Wild-Type, *atg12-1,* and *atg12-2* Maize Plants.

Plants at 40 DAG were labeled for 2 days with $^{15}NO_3^-$, harvested 7 days later, and then measured for dry weight (DW) and $^{15}N$ incorporation in various plant parts. Two biological replicates each containing six plants were used for data analysis (n=12). Values are adjusted means (±SD).

**(A)** Biomass as measured by dry weight of remains (stalk + upper leaves + lower leaves).

(**B-E**) $^{15}N$ accumulation in stalk (B), lower leaves (C), upper leaves (D), and roots (E).

## Supplemental Table 1. Collection of Arabidopsis and Maize *Atg* Genes

| Gene | *Arabidopsis* ID | Gene | Maize ID | Splicing variant[a] | No. of Amino Acid Residues | Identity/Similarity to Arabidopsis |
|---|---|---|---|---|---|---|
| **ATG1/13 kinase complex** | | | | | | |
| At *ATG1a* | AT3G61960 | Zm *Atg1a* | GRMZM2G105415 | 2 | 538 | 34/47% |
| At *ATG1b* | AT3G53930 | Zm *Atg1b* | GRMZM2G160428 | 3 | 703 | 47/61% |
| At *ATG1c* | AT2G37840 | Zm *Atg1c* | GRMZM2G164160 | 2 | 704 | 48/62% |
| At *ATG1t* | AT1G49180 | Zm *Atg1t* | GRMZM2G104658 | 2 (T01) | 283 | 47/62% |
| At *ATG13a* | AT3G49590 | Zm *Atg13a* | GRMZM2G129675 | 1 | 536 | 33/43% |
| At *ATG13b* | AT3G18770 | Zm *Atg13b* | GRMZM2G109348 | 1 | 533 | 33/45% |
| | | Zm *Atg13c* | GRMZM5G825909 | 1 | 511 | 32/44% |
| | | Zm *Atg13d* | GRMZM2G000973 | 1 | 512 | 32/43% |
| | | Zm *Atg13e* | GRMZM2G044733 | 1 | 606 | 35/50% |
| | | Zm *Atg13f* | GRMZM2G125352 | 2 (T01) | 606 | 34/50% |
| At *ATG11* | AT4G30790 | Zm *Atg11a* | GRMZM2G143445 | 1 | 1,139 | 45/64% |
| | | Zm *Atg11b* | GRMZM2G119571 | 1 | 1,143 | 45/64% |
| At *ATG101* | AT5G66930 | Zm *Atg101* | GRMZM2G160174 | 4 (T03) | 213 | 40/54% |
| **PI3 kinase complex** | | | | | | |
| At *PI3K* | AT1G60490 | Zm *PI3K* | GRMZM2G103721 | 2 (T01) | 803 | 73/85% |
| At *ATG6* | AT3G61710 | Zm *Atg6a* | GRMZM2G092112 | 1 | 499 | 55/70% |
| | | Zm *Atg6b* | GRMZM2G027857 | 1 | 579 | 52/63% |
| At *VPS15* | AT4G29380 | Zm *Vps15a* | GRMZM2G179662 | 2 (T01) | 1,480 | 52/68% |
| | | Zm *Vps15b* | GRMZM2G111491 | 1 | 1,561 | 49/64% |
| **ATG9/2/18 complex** | | | | | | |
| At *ATG2* | AT3G19190 | Zm *Atg2* | GRMZM2G042889 | 1 | 1,438 | 23/38% |
| At *ATG9* | AT2G31260 | Zm *Atg9* | GRMZM2G035461 | 1 | 888 | 50/63% |
| At *ATG18a* | At3g62770 | Zm *Atg18a* | GRMZM2G122607 | 1 | 442 | 63/73% |
| At *ATG18b* | AT4G30510 | Zm *Atg18b* | GRMZM2G146280 | 2 (T01) | 449 | 61/71% |
| At *ATG18c* | AT2G40810 | Zm *Atg18c* | GRMZM2G069177 | 2 (T01) | 417 | 47/61% |
| At *ATG18d* | AT3G56440 | Zm *Atg18d* | GRMZM2G143211 | 2 (T01) | 417 | 65/77% |
| At *ATG18e* | AT5G05150 | Zm *Atg18e* | GRMZM2G018573 | 2 (T01) | 371 | 48/63% |
| At *ATG18f* | AT5G54730 | Zm *Atg18f* | GRMZM2G116700 | 2 (T01) | 865 | 33/48% |
| At *ATG18g* | AT1G03380 | Zm *Atg18g* | GRMZM2G546452 | 2 (T02) | 381 | 16/22% |
| At *ATG18h* | AT1G54710 | Zm *Atg18h* | GRMZM2G078468 | 2 (T02) | 1,557 | 31/40% |
| | | Zm *Atg18i* | GRMZM2G301031 | n.d | | |
| | | Zm *Atg18j* | GRMZM2G103793 | n.d | | |
| **ATG8/12 conjugation pathway** | | | | | | |
| At *ATG3* | AT5G61500 | Zm *Atg3* | GRMZM5G818887 | 2 (T01) | 311 | 71/84% |
| At *ATG4a* | AT2G44140 | Zm *Atg4a* | GRMZM2G064212 | 2 (T02) | 492 | 50/67% |
| At *ATG4b* | AT3G59950 | Zm *Atg4b* | GRMZM2G173682 | 2 | 492 | 50/66% |
| At *ATG5* | AT5G17290 | Zm *Atg5* | GRMZM2G098420 | 4 | 374 | 50/68% |
| At *ATG7* | AT5G45900 | Zm *Atg7* | GRMZM2G005304 | 1 | 1,021 | 48/63% |
| At *ATG8a* | AT4G21980 | Zm *Atg8a* | GRMZM2G336871 | 2 (T02) | 119 | 85/94% |
| At *ATG8b* | AT4G04620 | Zm *Atg8b* | GRMZM2G419694 | 5 (T04) | 120 | 86/94% |
| At *ATG8c* | AT1G62040 | Zm *Atg8c* | GRMZM2G076826 | 5 (T01) | 120 | 86/94% |
| At *ATG8d* | AT2G05630 | Zm *Atg8d* | GRMZM2G134613 | 2 (T02) | 119 | 86/94% |
| At *ATG8e* | AT2G45170 | Zm *Atg8e* | GRMZM2G014975 | 8 (T02) | 119 | 85/94% |
| At *ATG8f* | AT4G16520 | | | | | |
| At *ATG8g* | AT3G60640 | | | | | |
| At *ATG8h* | AT3G06420 | | | | | |
| At *ATG8i* | AT3G15580 | | | | | |
| At *ATG10* | AT3G07525 | Zm *Atg10* | GRMZM2G066059 | 8 | 215 | 44/60% |
| At *ATG12a* | AT1G54210 | Zm *Atg12* | GRMZM5G842517 | 3 (T02) | 91 | 82/89% |
| At *ATG12b* | AT3G13970 | | | | | |
| At *ATG16L* | AT5G50230 | Zm *Atg16L* | GRMZM2G078252 | 2 (T02) | 505 | 54/74% |
| **Cargo receptor** | | | | | | |
| At *NBR1* | AT4G24690 | Zm *Nbr1a* | GRMZM2G092447 | 1 | 842 | 34/46% |
| | | Zm *Nbr1b* | GRMZM2G139846 | n.d. | | |

[a] Number of splicing variants were detected by analyzing RNA-seq data; Names of the dominant splice isoforms are shown in parentheses. n.d. = not detected.

## Supplemental Table 2. List of Tissues Analyzed by RNA-seq in this Study

| | Tissue name | | Tissue name |
|---|---|---|---|
| 1. | Whole Seed, 2 DAP | 41. | Leaf, 18 DAP |
| 2. | Whole Seed, 4 DAP | 42. | Leaf, 24 DAP |
| 3. | Whole Seed, 6 DAP | 43. | Leaf, 30 DAP |
| 4. | Whole Seed, 8 DAP | 44. | First Internode, V5 |
| 5. | Whole Seed, 10 DAP | 45. | Fourth, Internode, V9 |
| 6. | Whole Seed, 12 DAP | 46. | Internode, 0 DAP |
| 7. | Whole Seed, 14 DAP | 47. | Internode, 6 DAP |
| 8. | Whole Seed, 16 DAP | 48. | Internode, 12 DAP |
| 9. | Whole Seed, 18 DAP | 49. | Internode, 18 DAP |
| 10. | Whole Seed, 20 DAP | 50. | Internode, 24 DAP |
| 11. | Whole Seed, 22 DAP | 51. | Internode, 30 DAP |
| 12. | Whole Seed, 24 DAP | 52. | Primary Root, 3 DAS |
| 13. | Endosperm, 12 DAP | 53. | Root Meristematic Zone (MZ) and Elongation Zone (EZ), 3 DAS |
| 14. | Endosperm, 14 DAP | 54. | Root differentiation zone (DZ), 3 DAS |
| 15. | Endosperm, 16 DAP | 55. | Root Cortex, 3 DAS |
| 16. | Endosperm, 18 DAP | 56. | Root Stele, 3 DAS |
| 17. | Endosperm, 20 DAP | 57. | Primary Root, 6 DAS |
| 18. | Endosperm, 22 DAP | 58. | Root System, 7 DAS |
| 19. | Endosperm, 24 DAP | 59. | Primary Root, 7 DAS |
| 20. | Embryo, 16 DAP | 60. | Seminal Roots 7 DAS |
| 21. | Embryo, 18 DAP | 61. | Primary Root Zone 1 (1st cm of root tip); 7 DAS |
| 22. | Embryo, 20 DAP | 62. | Primary Root Zone 2 (from end of Z1 to the point of root hair/lateral root initiation), 7 DAS |
| 23. | Embryo, 22 DAP | 63. | Primary Root Zone 3 (lower half of differentiation zone), 7 DAS |
| 24. | Embryo, 24 DAP | 64. | Primary Root Zone 4 Zone 4 (upper half of differentiation zone), 7 DAS |
| 25. | Pericarp, 18 DAP | 65. | Primary Root, V1, 4 day after emergence |
| 26. | Pooled Leaves, V1, 4 day after emergence | 66. | Crown Roots, Nodes1-3, V7 |
| 27. | Topmost Leaf, V3 | 67. | Crown Roots, Node4, V7 |
| 28. | Leaf Bottom, V5 | 68. | Crown Roots, Node5, V7 |
| 29. | Leaf Tip, Stage2, V5 | 69. | Crown Roots, Node5, V13 |
| 30. | Leaf Bottom, V7 | 70. | Brace Roots, Node6, V13 |
| 31. | Leaf Tip, V7 | 71. | Coleoptile, 6 DAS |
| 32. | Eighth Leaf, V9 | 72. | Shoot Tip, V5 |
| 33. | Eleventh Leaf, V9 | 73. | Stem and SAM, V1, 4 day after emergence |
| 34. | Thirteenth Leaf, V9 | 74. | Stem and SAM, V3 |
| 35. | Immature Leaves, V9 | 75. | Immature Tassel, V13 |
| 36. | Thirteenth Leaf, VT | 76. | Meiotic Tassel, V18 |
| 37. | Thirteenth Leaf, R2 | 77. | Anthers, R1 |
| 38. | Leaf, 0 DAP | 78. | Immature Cob, V18 |
| 39. | Leaf, 6 DAP | 79. | Pre-pollination Cob, R1 |
| 40. | Leaf, 12 DAP | 80. | Silks, R1 |

**Supplemental Table 3. Oligonucleotide Primers Used in This Study**

Zm *Atg12* RT-PCR primers

| | |
|---|---|
| Primer 1: | ATGGCCGCGGAGGCAGATCAGAAAG |
| Primer 2: | TTAGCCCCATGCTGCCGATAAAGCA |
| Primer 3: | CTGAAGGTCATAGAGTTTCTTCGTCG |
| Primer 4: | CGACGAAGAAACTCTATGACCTTCAG |

Primers used for qRT-PCR analysis of wild type-like transcripts in maize *atg12-2* mutant

| | |
|---|---|
| Primer 5: | CCGCGGAGGCAGATCAGAAA |
| Primer 6: | TCAATTCCAAAGTTATTATACA |

Zm *Atg12* mutant genotyping primers

| | |
|---|---|
| *ZmAtg12-1* RP: | GCCCCGATTTTTTTATCCCCAGAT |
| *ZmAtg12-1* LP: | CTGAAGGTCATAGAGTTTCTTCGTCG |
| *ZmAtg12-2* RP: | TTAGCCCCATGCTGCCGATAAAGCA |
| *ZmAtg12-2* LP: | TGTACTTCCAAGCTCTTTACCTGAGG |
| TIR6: | AGAGAAGCCAACGCCAWCGCCTCYATTTCGTC |

Primers used for qRT-PCR analysis of maize *Atg* genes

| | |
|---|---|
| ZMATG1a-RT-F1: | GTGACTTTGGGTTTGCCAGGTC |
| ZMATG1a-RT-R1: | TGGCGACCCACATATTGTAGCAG |
| ZMATG2-RT-F1: | CACTTCTTGGGCTAAGGAACAGC |
| ZMATG2-RT-R1: | CGCCAAAGAATGAACCGACCAC |
| ZMATG3-RT-F1: | GTACTACCAAACTCCACGTGTCTG |
| ZMATG3-RT-R1: | GGCATTAATGGCATTCTTGACTCG |
| ZMATG4a-RT-F1: | CCATGTTTCGTGCTACTGCTAGAC |
| ZMATG4a-RT-R1: | GCAAGCTCGTCATCACCTAACG |
| ZMATG4b-RT-F1: | TGGGACGTCAACATACATTGCTG |
| ZMATG4b-RT-R1: | GCCAAATCTCGGACAACACTGC |
| ZMATG5-RT-F1: | AGACTCGCAAGGCTGAAGGTAG |
| ZMATG5-RT-R1: | GCTGAAGAACTCCGGAAGCAATG |
| ZMATG6-RT-F1: | GCTGTTGCATACCATGGCTCAG |
| ZMATG6-RT-R1: | GGGTGAATCTTGATCCGGTATTGG |
| ZMATG7-RT-F1: | ACGTCATTGCTCCTGTCGACTC |
| ZMATG7-RT-R1: | AGCGCGTCCTGATGCAATAGAG |
| ZMATG8a-RT-F1: | AGAACACCTTGCCACCAACTGC |
| ZMATG8a-RT-R1: | ATTGCTCTAGGCAGAGCCGAAG |
| ZMATG8b-RT-F1: | TCTTCGTTCGATCCGTTCGC |
| ZMATG8b-RT-R1: | ATCACGCTCCTTCCTGCCTTAC |
| ZMATG8c-RT-F1: | TTCGATCCAACTGGCAGGAAGG |
| ZMATG8c-RT-R1: | AGCCTCAGACTGCCTCTTCTCAAG |
| ZMATG8d-RT-F1: | TCTGTTCCAGGTCGCTTCTCTCTG |
| ZMATG8d-RT-R1: | TTAGCCTCAGCTTGCCTCCTTTCG |
| ZMATG8e-RT-F1: | ACTGTCAGCTCTGGGTTGCTTC |
| ZMATG8e-RT-R1: | TTTGCCACATCGACAAGCTCACG |
| ZMATG9-RT-F1: | GTGGGAGATGTATGCAGTCTAAGC |
| ZMATG9-RT-R1: | AGAGCATTGAATGGTGACCCATAG |
| ZMATG10-RT-F1: | AAGCCGTGCAGCAAATTGGG |

ZMATG10-RT-R1: ACAGCTGCGGTACACTCTTTCC
ZMFIP200a-RT-F1: AGAAGAGGGTGGAAGGCTTATTCC
ZMFIP200a-RT-R1: TGAGGTGTCCACATCTTTGCTTAG
ZMFIP200b-RT-F1: AGGAATCTGTCGCCTTGTTCACC
ZMFIP200b-RT-R1: ACGATCTGCCCGATTATGTACGC
ZMATG12-RT-F1: GGCTCGTGGTAACTTGTTGTCG
ZMATG12-RT-R1:: TGCACCACGACTTTCTGATCTGC
ZMATG16-RT-F1: AGGCTGAACTTGAGAAGACAAGCG
ZMATG16-RT-R1: AGCTCGGATTTCACTGTCTGATGC
ZMATG101-RT-F1: AAGGGCTGACAAACATCCAAGC
ZMATG101-RT-R1: TCGTTAATCGACGCCTCCAATGC
ZMATG18a_RT-F1: ACTGCTAGCACCAAGGGAACAC
ZMATG18a_RT-R1: TCAGCACCTCTCCTTACTTCCTG
ZMATG18e_RT-F1: TCCAAATTTCCCTCGCTGAAGAC
ZMATG18e_RT-R1: TTCACGCTCCAACAACCATGAAG
ZmATG18f-RT-F1: ACCAGTCTTCGACTCCCTCCATAC
ZmATG18f-RT-R1: TCAGGAGCGTTCAACCTTGTCTG
ZmUBC-F1: AAGATGCAGGCATCTAGGGCAAGG
ZmUBC-R1: AGGCTCTTGGCTTGGCACATGTTC

Primers used for generating Gly117Ala mutant of maize ATG8a

ZmATG8a_F1: CACCATGGCCAGGACCTCTTTCAAAATG
ZmATG8a_R2: TGCTCTAGGCAGAGGCGAAGGTGT