| | | 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 |
|------------------|----------------|-------------------|----------|-------------|--------------------|--------------|---------------------------|--------------|----------------|
| A9SER7/974-1132 | P.pat | | | LKKDL | NOAFLLKN | SKRKFDKOAS | K-ROCETI | REETHGUAVEL | ONANG |
| A9TRX9/969-1127 | P.pat | | | LKRDL | NOAELLKS | SKRKFDKOAS | K-DRUCFAI | REEIHGLAVEL | RNANG |
| D8T567/907-1055 | S.moe | | | AOSHLNKDI | SKAEMLKN | AKHKLEKRAF | K-PKUCFT | REVHELAVEM | PNSAG |
| D8STK2/907-1054 | S.moe | | | SQSQLRKEV | NKAEMAKS | FAKCKLEKQAS | K-BKICLTI | RFEVHELALFA | PNAAG |
| B9HB54/992-1146 | P.tri | | | ANEQLGKEL | TKKELVAT | KKHQLEKQAN | K-BRISFSI | RLEVHEIAAFV | LNSAG |
| Q9SUG7/978-1138 | A.tha | | | SEQTRKDL | DEKKELVKT | TKHQLGKQAN | K-BKISFGI | RLEVHEIAAFV | LNQAG |
| C5XWU8/999-1139 | S.bic | | | HGGITKEL | DEKKELIKN | NKLQLEKQAS | SK – DKI SFGI | RFEVHELAVFF | RNPAG |
| Q6ETK7/991-1135 | 0.sat | | | YSRIVRVL | BEKKESIKNI | SKLQLEKQAS | SK-BKISFGI | RFEVHELAVFV | RNPAG |
| Q54MY6/1219-1374 | D.dis | LMPEVQSLRNVIYELT | KIINPSAR | EPMDGNSIVNY | VNKITIEQM | QNQQLLERVTT | LENQQAIE | HSQSALLSNFT | HDRIA |
| D0MQJ2/747-884 | P.inf | ; | AVETRVKE | LLASAESEAML | QSELEKRRSE: | LHLMESEQDIN | IDSF <mark>KI</mark> SFR: | SFSVNDLALFL | PTSAP |
| F0W217/786-920 | A.Iai | | QAKVLE | LKAAADAEKIL | RSELEAQQD- | -DLLFTDRDSF | RDSFRISFQ | IFDIGDLALFL | PTSGP |
| Q2UKQ2/945-1094 | A. ory | | FSDA | IVKRVKDIEVL | ARKWOKEARG | YRDKYHRTQSE | AHDRAYR | SFREGDLALFL | PTRNQ |
| A7KAM2/1010-1159 | P.CHP | | FGDV | VVKRVKDIEVL | ARKWQKEARG | YREKYHRVQSE | AHDROAYR | SFKEGDLALFL | PTRNQ |
| BODBA9/9/1-1091 | P pag | | | FLEAVARTGST | IRKWQKQCKE | IRERAKG | KISFRI | NFAKGDLAMFL | PTRNS |
| 090438/1154-1310 | S cer | | LVES | FULLTEREVEL | MARKLOKESNI | SKTEIDGLIKE | ODD WETRI | | PTRDD |
| 01252//991-11/3 | C.ele | | MAZ | STIOVATSPSE | LEVERSSONT | ICTOTPLCI.P. | MNLLVSVOI | DIKICCAVIVI | WHOAH |
| Q22342/1100-1310 | L.loa | | | AOADSD | DTAPVTVRP | ATAOTIISLEE | MRTMUTVOI | DTHEYCAVLTV | WSEPH |
| 09VNC5/942-1083 | D.mel | | | | | | ALE | CARODVEVV | WSMRH |
| 017NP9/932-1060 | A.aeg | | | -SNOSNFKDRI | ALEKEKOO | TKELEKOHNRT | ASGEVSIO | SCAKODIVMEV | YNATY |
| E7FFM2/1493-1622 | D.rer | | | -ILERTLHMKE | ENKRLSOR | SOSMSSVSSF | RHSERAIRI | DEOVEDIVLII | LDERH |
| 08TDK2/1454-1590 | M.mus | | | KE | BENKRLNÖR | SQSMSSVSSF | RHSERTAIRI | DFOVGDLVLII | LDERH |
| 09ESK9/1444-1584 | H.sap | | | KE | BENKRLNOR | SQSLSSVSSF | RHSEKIAIRI | DFQVGDLVLII | LDERH |
| B3RY68/907-1036 | T.adh | | | ALTAEN | NYLKEKLNER | FNSSSSSTTNLS | SYVKNVAYCI | DENLNDYIIVI | LNKIT |
| | | | | ΔIM2 | | | | | |
| | | | | | | | | | |
| | | 90 | 100 | 110 | 120 | 130 | 140 | 150 | 160 |
| A9SER7/974-1132 | P.pat | | | HFENINHN | REHVYDSGES | TALEOEOGLPS | · | G | SPYVV |
| A9TRX9/969-1127 | P.pat | | | HFEAINHN | CPHYYLSGES | IALSOEOGLPS | | G | SPYIV |
| D8T567/907-1055 | S.moe | | | HWEALNRN | CPNYYLSDES | IAL LEN-LPS | 3 | G | VIYOO |
| D8STK2/907-1054 | S.moe | | | HYEALNRN | CPNYFLSEES | IALFHGK-NEC | 2 | R | RKYIV |
| B9HB54/992-1146 | P.tri | | | HYEAINRN | SSNYYLSAES | VALETDH-LPS | | R | PSYIV |
| Q9SUG7/978-1138 | A.tha | | | | CPNYYLSSES | EALFTDH-LPS | 8 | R | ΡΤΥΙν |
| C5XWU8/999-1139 | S.bic | | | HYEAINRN | CSNYYLSEES | VALETEH-HPV | / | H | PAYII |
| Q6ETK7/991-1135 | 0.sat | | | HYEAINRN | CSNYYLSEES | VAL TEQ-HPF | | н | PAYII |
| Q54MY6/1219-1374 | D.dis | IFHKNKNG | | FVEAINID | SPNYFLSQLS | YDQYTQEMKN- | | | ASIIF |
| D0MQJ2/747-884 | P.inf | GSDAQR | | VYLAFHLG | CPHRFLSEES | ISSISND-GQF | 8 | ¥ | PDYVV |
| F0W217/786-920 | A.Iai | TTESQRR | | VYLAFHLG | CPHRELSEES | ISSESTS-GSF | 8 | Y | PDYVI |
| Q2UKQ2/945-1094 | A. OFY | AIRS | | WAAFRVG | APHYFLRE | DVHKLH | | T | RDWLL |
| A7KAM2/1010-1159 | P.Chr | AIRS | | TRANUUS | | UDSHKLQ | | A | RDWLL |
| BODBA9/9/1-1091 | P nas | TINMNMANTURAUNDE | ASTUASEE | TVOPWAREDVC | A DHVET TN - D | USKIDIN | | | REWIV RDWUL |
| 012527/001 1172 | S.cer | VNSVGSMSSSTSSLSS | SESSUDI | TPPPLDEMSTO | SSPSVTHSNV | INOASISGRO | | NKT.M | RPWAA |
| 01252//991-11/5 | C.ele | N | | AVVIECSS | PNRWWKESS | IRRLGINTON- | | AATR | RNWII |
| Q22342/1100-1310 | L.loa | N | | AVILFSVS | PIFHEVKESS | LKRVGVKWDRC | SVAV | AAVGOR | PNWLM |
| 09VNG5/942-1083 | D.mel | A | | OFMVVODS | LTLYFVHADS | LASLOLTAPTS | PTPSLDPS | DTVVDINOIPL | PYYAI |
| 017NP9/932-1060 | A.aeq | D | | QUTIVONA | PVLYFL HADS | YAASLSQLVE | · | GIVPR | IIHCI |
| E7FFM2/1493-1622 | D.rer | D | | NVVLFTVG | PTLYFLHSES | LTALDLKPGQI | ATG | ATR | RPWVL |
| OSTDK2/1454-1590 | M.mus | D | | NVVLFTVS | PTLYFLHSES | LPALDLKPGEG | GASG | ASR | RPWVL |
| 09ESK9/1444-1584 | H.sap | D | | NVLFTVS | PTLYFLHSES | LPALDLKPGEG | GASG | ASR | RPWVL |
| B3RY68/907-1036 | T.adh | QS | | CEICTPR | QKFYLMHPTC | QGYEKHFIAGV | /G | NTG | PQWVL |
| | | | | | | | | AIM1 | |
| | | | | 2.22 | | | | | |
| | | 170 | 180 | 190 | 200 | 210 | 220 | 230 | |
| A9SER7/974-1132 | P.pat | GQIVHIDRKVVIPAPP | PPPLLAGS | SDGSVQGTELG | AGTMLTPARA | KASH | PYGLPLGT | DYYIVTVAMV- | - |
| A9TRX9/969-1127 | P.pat | GQIVHIDRKIVIPAPP | PPPPPNG1 | LDGNLQGNELG | AGTMLVPARA | RASH | IPYGLPVGT | EYYVVTVAMV- | - |
| D8T567/907-1055 | S.moe | GQIVHINRNVARRAPS | PSTREPSA | APPGGGGGA | ASRP | R¥ | IPYGLGIGCI | EFFVVTVAMV- | - |
| D8STK2/907-1054 | S.moe | GQIVHIEHHTVAAPPG: | ASSSSFSI | LEGGASSSSSV | MGRH | RA | SYELPVGT | EYWVVTVAMV- | - |
| B9HB54/992-1146 | P.tri | GQIVHIERQAVKPLHP | ASTRPEHO | RADQLDLLTTD | QGIDLLNFNL | GSTS | PYNLPMGCI | EYFVVTVAML - | 7 |
| Q9SUG7/978-1138 | A.tha | GQIVHIDRQIVKLPSQ | LSASASPE | AGKTHHLCSDQ | GSRTLASSSI | STSTSATTTS | PYGE SCC | EYFINTIAML- | - |
| C5XW08/999-1139 | S.DIC | GOLVHISRRIVHPGOM | GGAPRRD- | -SSGGRRSP | | ASML | PYNLPGGC | EYFVVTVAML- | - |
| Q6ETK7/991-1135 | D. Sat | GOLVHISRRIAKLPSH | GDQMEASE | CLDSGGRRSP | | ASML | OT COL DOCT | EYFLVTVAMI - | - |
| Q54MY6/1219-1374 | D.uis D.inf | GTTINIDTRIAGDSE- | | | | | SFGCLPGN | EICEVLISKLE | N |
| DOMQJ2/747-884 | P.Ini | GRIVLIDEQTATEGN- | | | | | ID YOT WIGHT | PPUTT TWASL- | - |
| FUW217/786-920 | A. orv | ARTKIDERVUDISKS | MNGANPDE | PSTGEASDG | | TSEDDE | IPERTSPCI. | PWULLDAMEE - | _ |
| 220K02/945-1094 | P.chr | ARITKIDERVVDLSKS | MNGVVPDE | RSLGDASDG | | ASLDEE | FEISDOL | RWYLLEAVEE - | |
| BODBA9/071 1001 | L.bic | AW TS TEWVVNOOD- | | | | OTS | PYGIGEGVI | KYMLEWEDW- | - |
| 090438/1154-1210 | P.pas | ARIESMOEHKVTREG- | HF | RNVG | | | PYNLNPDA | WYGURAKEE- | - |
| 012527/991_1173 | S.cer | FTAFEESTRYFLKDEK | GLTKGKEW | FVGRIVTLEHF | VADS | PSN | PFRLPKGS | WFQVTAVVV- | _ |
| 022342/1186-1316 | C.ele | ARVWRSDSCSIKKPV- | | | | R | RYNLPIGT | IVRRVEVEAV- | - |
| E1G2W6/1025-1155 | L.loa | AVTTRLELCKIRKTD- | | | | N | RYNLKVGTI | KFYRVEVEPL- | - |
| Q9VNG5/942-1083 | D.mel | GRVIDKEYCQARKDD- | | | | B | RYRVSRGSI | KFYRIKLAPL- | - |
| Q17NR9/932-1060 | A.aeg | GTVVDKBYCHARKDE- | | | | | RYKVSRGTI | RFYRVKVKPV- | - |
| E7FFM2/1493-1622 | D.rer | GKVMEKBYCQAKKAQ- | | | | N | RFKVPLGT | KFYRVKAVPW- | - |
| Q8TDK2/1454-1590 | M.mus | GKVMEKBYCQAKKAQ- | | | | | RFKVPLGT | KFVRVKAVSW- | 7 |
| Q9ESK9/1444-1584 | H.sap | CKVMEKBYCQAKKAQ- | | | | R | RFKVPLGT | KFMRWKAVSW- | - |
| B3RY68/907-1036 | T.adh | AQUE KMOHCQAKKDI- | | | | | KFNVAKDEI | AFCLIYAKPC- | - |

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.

Supplemental Data. Li et al. (2014). Plant Cell 10.1105/tpc.113.120014

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*.

| | | 10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 | 90 |
|---|--|--|---|--|--|----------------------------------|------------------------------|---------------------------|--------------------------------------|--|
| A9SER7/335-481 | P.pat | | | | | | | | | |
| A9TRX9/335-481 | P.pat | | | | | | | | | |
| D8T567/340-486 | S.moe | | | | | | | | | |
| B9HB54/304-497 | P.tri | | | | | | | | | |
| Q9SUG7/348-494 | A.tha | | | | | | | | | |
| D7MBM1/347-495 | A.lyr | | | | | | | | | |
| C5XWU8/358-503 | S.bic | | | | | | | | | |
| DOMO 12/356-519 | D.sat P inf | | | | | | | | | |
| FOW217/374-533 | A.lai | | | | | | | | | |
| E1G2W6/325-506 | L.loa | | | | | | | | | |
| Q22342/282-474 | C.ele | | | | | | | | | |
| B3RY68/287-473 | T.adh | | | | | | | | | |
| Q1/NR9/352-539 | A.aeg | | | | | | | | | |
| O8TDK2/373-560 | H.sap | | | | | | | | | |
| Q9VNG5/369-560 | D.mel | | | | | | | | | |
| Q9ESK9/372-558 | M.mus | | | | | | | | | |
| Q2UFN7/33-480 | A.ory | -ISHLVAAKRSLSSI | NHVWRANEI | VTAARSALEE | SVVVSARTG | FLRRGLNNQL | LLYSVRTEVQ | EVSLRGRSEF | ATVLKSLDVAD | ARLRK |
| A/KAM6/32-4/9 | P.Chr P.nae | -ISYLLGAKRSLSSI | THVWRANEI | VTASHSALEK | BONILLERIT | FLERGLNGQL | LLIDVRSEVE | QISIRGRDEF | SIALKNLDAAD | PLIPS |
| 06CS99/14-410 | C.sph | DKLWNKARNOLVEAO | VECEESLKI | LSKVRTEMDS | SOKSRFKLK | FILNCLVNOVE | FFKNIMLEKC | ISTELIDNEW | SKLVLVEIVND | VSYWO |
| A7TM40/4-402 | V.pol | ERFVNASRKTLVEAQ | VLCQDANSR | ISNARSSFSH | WERSISKIR | FLLNCLKNQGS | FIKNCILKVG | IEENLIEKEW | TQSILVDLAKE | LKYWN |
| Q06410/7-406 | S.cer | TKFVNNARKTLTDAQ | LLCSSANLR | IVDIKKKLSS | WQLSISKLN | FLIVGLRQQGH | FLY-TILKEG | IGTKLIQKQW | NQAVLVVLVDE | MKYWQ |
| B6H4J6/211-403 | P.chr | | | | | | | | | |
| Q2UKQ2/165-336 | A.ory | | | | | | | | | |
| A7TT.57/302_474 | V. pol | | | | | | | | | |
| 012527/339-512 | S.cer | | | | | | | | | |
| 2 - 19 - 19 - 19 - 19 - 19 - 19 - 19 - 1 | | | | | | | | | | |
| | | 100 | 110 | 120 | 130 | 140 | 150 | 160 | 170 | 180 |
| 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 | | | | | | | | | |
| D7MBM1/347-495 | A.lvr | | | | | | | | | |
| C5XWU8/358-503 | S.bic | | | | | | | | | |
| Q6ETK7/352-509 | 0.sat | | | | | | | | | |
| DOMQJ2/356-519 | P.inf | | | | | | | | | |
| FUW217/374-533 F1G2W6/325-506 | L loa | | | | | | | | | |
| 022342/282-474 | C.ele | | | | | | | | | |
| B3RY68/287-473 | T.adh | | | | | | | | | |
| Q17NR9/352-539 | A.aeg | | | | | | | | | |
| E7FFM2/372-559 | D.rer | | | | | | | | | |
| Q01DK2/3/3-560 | n.sap D.mel | | | | | | | | | |
| Q9ESK9/372-558 | M.mus | | | | | | | | | |
| Q2UFN7/33-480 | A.ory | TLDLLRDTIVHASFR | PEGEESKTL | HDFVDERGVG | ELHTTLKRS | IDRTNAAQADI | ESSNRAFDDE | LQSIKEALGN | YRAATQLASSE | TSASS |
| A7KAM6/32-479 | P.chr | TLDLLRGTIVHASFR | PGDEEQKSL | HDFVDERGVE | ELHASLKAS | IDRTNTARAEI | DTSNHEFDDE | LQAIKKSLRH | YHTATKLASSE | LSITS |
| C4R1E4/5-415 | P.pas | VLDTLHKIELEPSFR | STQGNKALS | LYHFVSDDKI | DELFNGVDD | ILRESTDLYG | DEIDNNLADI | SREIEGYGKE | LEVRYAEFILN | EVPDT |
| A7TM40/4-402 | V.pol | SKINEOVRVLDSIEN | ILDEDTKSE | SKNLGYFV | SRDNLDILE | KRLKEIPNVK | HIDNIRGOYN | TMFKKVSNYL | INKRLKSVOEY | FLINF |
| Q06410/7-406 | S.cer | YEITSKVQRLDGIVN | ELSISEKDD | TDPSKLGDYI | SRDNVNLLN | DKLKEVPVIER | QIENIKLQYE | NMVRKVNKEL | IDTKLTDVTQK | FQSKF |
| B6H4J6/211-403 | P.chr | | | | | | | | | |
| Q2UKQ2/165-336 | A.ory | | | | | | | | | |
| Q9C438/336-521 | P.pas V pol | | | | | | | | | |
| 012527/339-512 | S.cer | | | | | | | | | |
| 2 | | | | | | | | | | |
| | | 190 | 200 | 210 | 220 | 230 | 240 | 250 | 260 | 270 |
| AGEED7/335-481 | P nat | | | | · · · · · · · · · · · · · · · · · · · | | | | | |
| A9TRX9/335-481 | P.pat | | | | | | | | | |
| D8STK2/340-486 | S.moe | | | | | | | | | |
| D8T567/340-486 | S.moe | | | | | | | | | |
| B9HB54/304-497 | P.tri | INEN | IKSIMQSLR | DDVSTVKELVI | HDCLS | | | | | |
| D7MBM1/347-494 | A.tha | | | | | | | | | |
| C5XWU8/358-503 | S.bic | | | | | | | | | |
| Q6ETK7/352-509 | 0.sat | | | | | | | | | |
| DOMQJ2/356-519 | P.inf | | | | | | | | | |
| FOW217/374-533 | A.lai | | DAME | UCVPOPTVIII | | | | | | |
| 022342/282-474 | C.ele | GINKE | FSOLEFSL | KSCEERKNLVI | HKLV | | | | | |
| B3RY68/287-473 | T.adh | | SOLVSSGO | EIAONOTEMAG | OGFA | | | | | |
| Q17NR9/352-539 | A.aeg | | ERKMVDVR | KLVQEQNELA | 2510 | | | | | |
| E7FFM2/372-559 | D.rer | | DOMIASCK | KLVNEQKELAG | 2GFL | | | | | |
| Q8TDK2/373-560 | H.sap | | DOMIASCO | RLVNEQKELAG | QGFL | | | | | |
| Q9VNG5/369-560 | D.mel | LYAI | DOMIASCS | RLVNEQKELA(| OGFL | | | | | |
| 220007/3/2-558 | 21 - HIUS | | | | | | | | | |
| 02UFN7/33-480 | A.orv | SSPSTSNDSLPSLSSI | PSMLHSLE | MHAOEMANLL | ESLVRHFDLO | CVTAVKHTEGG | GAAARSITGD | VPATVHVNGR | VGPNIEEGINA | NLNAP |
| Q2UFN7/33-480 A7KAM6/32-479 | A.ory P.chr | SSPSTSNDSLPSLSSI | PSMLHSLE PGQIQSLE | MHAQEMANLLI AHAQEMATLLI | ESLVRHFDLO | CVTAVKHTEGG CVTAVKHTDGG | GAAARSITGD GAVARSITGD | VPATVHVNGR MPAGVDGSND | VGPNIEEGINA GMPNIGAEINA | NLNAP NLNAP |
| Q2UFN7/33-480 A7KAM6/32-479 C4R1E4/5-415 | A.ory P.chr P.pas | SSPSTSNDSLPSLSSI SSSSASDSGLLTLSSN PSKGNKKNSANHDNII | PSMLHSLE PGQIQSLE TKLITSNN | MHAQEMANLLI AHAQEMATLLI ELETDMASLLI | ESLVRHFDLO EALVRHFDLO ESLTNHFDQO | CVTAVKHTEGG CVTAVKHTDGG CK | GAAARSITGD GAVARSITGD | VPATVHVNGR MPAGVDGSND | VGPNIEEGINA GMPNIGAEINA K | NLNAP NLNAP GQDLL |
| Q2UFN7/33-480 A7KAM6/32-479 C4R1E4/5-415 Q6CS99/14-410 | A.ory P.chr P.pas C.sph | SSPSTSNDSLPSLSSI SSSSASDSGLLTLSSN PSKGNKKNSANHDNII SRDSKNNLFKLLESD | PSMLHSLE PGQIQSLE TKLITSNN VTELNEFE | MHAQEMANLLI AHAQEMATLLI ELETDMASLLI NELADFLRSI HDI ADVISSI | ESLVRHFDLO EALVRHFDLO ESLTNHFDQO TDHFD | CVTAVKHTEGG CVTAVKHTDGG CK | GAAARSITGD GAVARSITGD | VPATVHVNGR MPAGVDGSND | VGPNIEEGINA GMPNIGAEINA K | NLNAP NLNAP GQDLL CTILK |
| Q2UFN7/33-480 A7KAM6/32-479 C4R1E4/5-415 Q6CS99/14-410 A7TM40/4-402 Q06410/7-405 | A.ory P.chr P.pas C.sph V.pol | SSPSTSNDSLPSLSSI SSSSASDSGLLTLSSN PSKGNKKNSANHDNI SRDSKNNLFKLLESD ENDSDDIKKLTTTI GIDNLMETNUFFO | PSMLHSLE IPGQIQSLE ITKLITSNN VTELNEFE PSKLVSLE | MHAQEMANLLI AHAQEMATLLI ELETDMASLLI NELADFLRSI HDLADYLSSI KDLAETMNSI | SLVRHFDLC EALVRHFDLC ESLTNHFDQC FDHFD FNHYD | CVTAVKHTEGG CVTAVKHTDGG CK | GAAARSITGD GAVARSITGD | VPATVHVNGR MPAGVDGSND | VGPNIEEGINA GMPNIGAEINA K Q | NLNAP GQDLL CTILK SKLLQ TLLLQ |
| Q2UFN7/33-480 A7KAM6/32-479 C4R1E4/5-415 Q6CS99/14-410 A7TM40/4-402 Q06410/7-406 B6H4J6/211-403 | A.ory P.chr P.pas C.sph V.pol S.cer P.chr | SSPSTSNDSLPSLSSI SSSSASDSGLLTLSSN PSKGNKKNSANHDNI SRDSKNLFKLLESD ENDSDDIKKLTTI GIDNLMETNVAGO GDIASDTORL | PSMLHSLE IPSQIQSLE ITKLITSNN IVTELNEFE PSKLVSLE SRELTDLE VDEALASDS | MHAQEMANLLI AHAQEMATLLI ELETDMASLLI NELADFLRSI HDLADYLSSI KDLAEIMNSL DGVDGLLEEVI | ESLVRHFDLG EALVRHFDLG ESLTNHFDQG TDHFD TNHYD TQHFD ETIAK | CVTAVKHTEGG CVTAVKHTDGG CK | GAAARSITGD GAVARSITGD | VPATVHVNGR MPAGVDGSND(| VGPNIEEGINA GMPNIGAEINA | NLNAP NLNAP GQDLL CTILK SKLLQ TLLLQ |
| Q2UFN7/33-480 A7KAM6/32-479 C4R1E4/5-415 Q6CS99/14-410 A7TM40/4-402 Q06410/7-406 B6H4J6/211-403 Q2UKQ2/165-336 | A.ory P.chr P.pas C.sph V.pol S.cer P.chr A.ory | SSPSTSNDSLPSLSSJ SSSSASDSGLLTLSSN PSKGNKKNSANHDNIJ SRDSKNNFKLLESDJ ENDSDDIKKLTTTI GIDNLMETNVAEQP GDIASDTQRLV | IPSMLHSLE IPSQIQSLE ITKLITSNN VTELNEFE PSKLVSLE SRELTDLE VDEALASDS | MHAQEMANLLI AHAQEMATLLI ELETDMASLLI NELADFLRSIT HDLADYLSSIT KDLAEIMNSLT DGVDGLLEEVI -GVEGLLQEVI | ESLVRHFDLG ESLVRHFDLG ESLTNHFDQG TDHFD FNHYD EQHFD STIAK STISR | CVTAVKHTEGG CVTAVKHTDGG CK | GAAARSITGD GAVARSITGD | VPATVHVNGR MPAGVDGSND | VGPNIEEGINA GMPNIGAEINA | NLNAP NLNAP GQDLL CTILK SKLLQ TLLLQ |
| Q2UFN7/33-480 A7KAMG/32-479 C4R1E4/5-415 Q6CS99/14-410 A7TM40/4-402 Q06410/7-406 B6H4J6/211-403 Q2UKQ2/165-336 Q9C438/336-521 | A.ory P.chr P.pas C.sph V.pol S.cer P.chr A.ory P.pas | SSPSTSNDSLPSLSSJ SSSSASDGGLLTLSSS PSKGNKKNSANHDNIJ SRDSKNNLFKLLESDJ ENDSDDIKKLTTI GIDNLMETNVAEQQ GDIASDTQRL | PSMLHSLE PSMLHSLE TKLITSNN VTELNEFE PSKLVSLE SRELTDLE VDEALASDS | MHAQEMANLLI AHAQEMANLLI ELETDMASLLI NELADFLRSIT HDLADYLSSIT KDLAEIMNSL DGVDGLLEEVI -GVEGLLQEVI KDSKELPILDI | ESLVRHFDL EALVRHFDL ESLTNHFDQ TDHFD TINHYD STIAK ETISR ELLTSS | CVTAVKHTEGG CVTAVKHTDGG CK | GAAARSITGD GAVARSITGD | VPATVHVNGR MPAGVDGSND | VGPNIEEGINA GMPNIGAEINA | NLNAP NLNAP GQDLL CTILK SKLLQ TLLLQ |
| Q2UFN7/33-480 A7KAM6/32-479 C4R1E4/5-415 Q6CS99/14-410 A7TM40/4-402 Q06410/7-406 B6H4J5/211-403 Q2UKQ2/165-336 Q2UKQ2/165-336 Q9C438/336-521 A7TL57/302-474 012577/324 513 | A.ory P.chr P.pas C.sph V.pol S.cer P.chr A.ory P.pas V.pol | SSPSTSNDSLPSLSSJ SSSSASDSGLLTLSSS PSKGNKNSANHDNIJ SRDSKNNLFKLESDJ END-SDDIKKLTTI GIDNLMETNVAEQE GDIASDTQRL | PSMLHSLE PSMLHSLE TKLITSNN VTELNEFE PSKLVSLE SRELTDLE VDEALASDS TELVNQVV | MHAQEMANLLE AHAQEMATLLE ELETDMASLLE NELADFLRSIT HDLADYLSSIT KDLAEIMNSLT GVEGLLQEVU KDSKELPILDE ELVKNLRNDSE | ESLVRHFDL(ESLTNHFDL(ESLTNHFDQ(TDHFD TQHFD TQHFD STIAK ETIAK ELLTTS KVILE | CVTAVKHTEGG CVTAVKHTDGG CK | GAAARSITGD GAVARSITGD | VPATVHVNGR MPAGVDGSND | VGPNIEEGINA GMPNIGAEINA | NLNAP NLNAP GQDLL CTILK SKLLQ TLLLQ |

| 280 290 300 310 320 330 340 | 350 360 |
|--|--|
| A9SER7/335-481 P. Dat | VAALOSN RGMRNOLAVFR |
| A97RX9/335-481 P. patPMYDVIDKNHIPRLEACDMELENL-LEYCKKSKNKMNLCVHTRLOF | VAALOSNIRDMRNOLAVFK |
| D8STK2/340-486 S.moePMYEVHDKSHIPRMEACDRELWKLLDTCRRSKNAMSMGVHMRMQS | SVAALQAS RDMRNQLSAFK |
| D8T567/340-486 S.moePMYEVHDKSHIPRMEACDRELWKLLDTCRRSKNAMSMGVHMRMQS | SVAALQASIRDMRNQLSAFK |
| B9HB54/304-497 P.triCQLSSTRLHTEVSALGLMYDVHEKSHLPTMLAVGDLISKLLGFCKDKKNEMNIFVHDFLQF | XIAYVTFLMKDVKLRFPVF |
| Q9SUG7/348-494 A.thaDMYEVHDKNHLPKMQACYNSISEL-LDFCKNKKNEMNNFVHGYMQF | KITYVTYI I KDAKLQFPVFF |
| D7MBM1/347-495 A.lyrGPMYEVIDKNHLPKMQACYNSISEL-LDFCKSKKNEMNNFVHSYMQF | (ITYVTYIIKDAKLQFPVFF |
| C5XWU8/358-503 S.bicRIYEVHEKDNLPSIRNFDHRLTKLLEKCKDKKNEMNTLVHVCMQF | RVKSSQISEKGMMSELIAFC |
| QDETK//325-509 0.sat | VKSAQIVEREMANELHAFQ |
| DONGU2/300-519 P.101 | TSRLOSK PDFFHSLATE |
| | IIIOVYDRIHTTNNOTILEE |
| 022342/282-474 C.eleAOILETPKINDONKLPPIIEEIROCMLTIFENFSEFRMWVRVFDOSKOEILKNLRTRMSGF | VVONYDRLRVVLNDIVOYE |
| B3RY68/287-473 T.adhQNNDRISSLKDSSVLSDLWQGHTEQLKLMHANHKKLNDIYQRCFRSKTELSNNLHGRLRWI | IVMERS-MCECDSKLVIHH |
| Q17NR9/352-539 A.aegQNQNRASTLGDTSILPDLCASHQGQLKVILKNQKELHEIRRQCAKSKEELGKNLYIRLRHC | CIIPVQTRVYELDNSLLFYH |
| E7FFM2/372-559 D.rerANQKRAENLKDTSVLPDLCLSHANQLMIMLTNHRKLLDIKQKCTTAKQELANNLQVRLKWC | CCYVMLHADQDGE-KLQALI |
| Q8TDK2/373-560 H.sapANQKRAENLKDASVLPDLCLSHANQLMIMLQNHRKLLDIKQKCTTAKQELANNLHVRLKWC | CCFVMLHADQDGE-KLQALI |
| Q9VNG5/369-560 D.melANQMRAENLKDASVLPDLCLSHANQLMIMLQNHRKLLDIK-QKCTTAKQELANNLHVRLKWC | CCFVMLHADQDGE-KLQALI |
| Q9ESK9/372-558 M.musANQMRAENLKDASVLPDLCLSHANQLMIMLQNHRKLLDIKQKCTTAKQELANNLHVRLKWC | CFVMLHADQDGE-KLQALI |
| Q20FN/33-480 A.OFY LDPLSNSEIQENVSVLIKDAREAEDVVMEIQDRIGEMETVLENVLAQKDSVLSVINATTSVFKHLSTLA | ASTRLSGI AEAHSFTRVWH |
| ARAMO/32-4/9 F.CHI EDIMIDABIYEMVAVILABREADDIVMETYDAINESITEYYAAA-DALESISAAIIEVASHISSIA | UKLOOGI NI TKKAORVETLI |
| 06C399/14_10 C sph EOOTPLEDIKELFOTVKKDDTOLENTRELVFETGLEVKESKKVNETT_STIMKTGGFHLLSKTVTET | EKCEEVI.STFORTANI.VEVYB |
| A7TM40/4-402 V. pol TLKPADPDYTDLLEVVKNDNSELDGIVTLLRETVDEVDETLKTFLGIFNEIELKOKECNKLLFGVIEEF | KINHEYLLIFNDISSLIDNFR |
| 006410/7-406 S.cer DKKIDNDEREELFKVV0GDDKELYNIFKTLHEVIDDVDKTILNLGOFLQAKIKEKTELHSEVSEIINDF | NRNLEYLLIFKDISNLIDSFR |
| B6H4J6/211-403 P.chrKIGSDYEHVLSLPNNQKTLANISRLALSHTQDLLPSLADISTELQAALEHAVQRRGAAEKAA | AIEHMRTISSLESRLADAHARM |
| Q2UKQ2/165-336 A.oryKIQSDYEHVLALPNNQKTLANISRLALSHTKDLLPSLLEVSAEIQTNLEEAARQYNAAVKAA | AFNHMRQISL ESRLADVQSQI |
| Q9C438/336-521 P.pasGGNSTTLSAESVKKINVLVSVFETHSSTIIPQITELSNKLYDEKVEALNLKQDLQRTLLSE | DTIH-KIVGVQLSILKATNLIN |
| A7TL57/302-474 V.polKDENEFDKN-YMQNLAKSLEKDKKVTVTNLLTISKALYSQANDISEIKSKLQVDSIKI | LFGQISFIQIETLNIKKLLI |
| 012527/339-512 S.cerKEEEEFNSOEFLKSMNVMLEKDKKESVKTLFTISOALYSOIGELIDLKKSLOKHAVAI | |
| F | LGNIAFTQMEILGIKRLLI |
| | LLGNIAFTQMEILGIKRLLI |
| 370 380 390 400 410 420 430 | 440 450 |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat CANAROSDHFSECKLLERVGPSEKACHARVERTASMKLIMGORGOMART | 440 450 RIQSMYIQREVLQAMGL |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat EAMARQSDHFSETKLLRRVGPSWKACLAEVVRRKASMKLYMGQAGOTAEKHARKEAEVAREEELI A9TRX9/335-481 P.pat EALVRQSDHFAEKLLRRVGPSWKACLAEVVRRKASMKLYMGQAGOTAEKHARKEAEIARREELI | 440 450 RIQSMYIQREVLQAMGL RVQSMYIHREVLQAMGL |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat BAMARQSDHFSETKLLRRVGPSWAACHAEVVRRKASMKLYMGOAGODAEKUARKRBAEVARREETL BALVRQSDHFSETKLLRRVGPSWAACHAEVVRRKASMKLYMGOAGODAEKUARKRBAEJARREETL D8STK2/340-486 S.moe BAMARQDDIFEEKVVRKVGSAWKACHAEVVRRKACMKLYMGOAGODAEKUARKRBAEJARREETL | 440 450 RIQSMYIQREVLQAMGL RVQSMYIQREVLQAMGL 2VQSMYIRREVLQAMGL |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat EANARQSDHFSETKLLRRVGPSUKACTAEVVRRASMKLIMGQAGQTAEKLARKREAEVARREETL A9TRX9/335-481 P.pat EALVRQSDHFAETKLLRRVGPSUKACTAEVVRRASMKLIMGQAGQTAEKLARKREAETARREETL D8STR2/340-486 S.moe EANARQDDIFEETKVVRRVGSAUKACLAEVVRRACMKLIMGQAGQTAEKLARKREMEMARREETL D857/340-486 S.moe EANARQDDIFEETKVVRRVGSAUKACLAEVVRRACMKLIMGQAGQTAEKLARKREMEMARREETL | 440 450 RIQSMYIQREVLQAMGL QVQSLYIPRDVLAMGL QVQSLYIPRDVLAMGL |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat EAMARQSDHFSEEKLLRVGPSHKACHAEVVRHASMKLIMGQAGQHAEKHARKEAEVAREEFLI A9TK9/335-481 P.pat EALVRQSDHFAEKKLLRVGPSHKACHAEVVRHASMKLIMGQAGQHAEKHARKEAEIAREEFLI D8STK2/340-486 S.moe EAMARQDDIFEEKVVRKVGSAWKACHAEVVRHASMKLIMGQAGQHAEKHARKEAEIAREEFLI D8T567/340-486 S.moe EAMARQDDIFEEKVVRKVGSAWKACHAEVVRHACMKLIMGQAGQHAEKHARKEMEMARREEFLI D8T567/340-486 S.moe EAMARQDDIFEEKVVRKVGSAWKACHAEVVRHACMKLIMGQAGQHAEKHARKREMEMARREEFLI 08T567/340-486 S.moe EAMARQDDIFEEKVVRKVGSAWKACHAEVVRHACMKLIMGQAGQHAEKHARKREMEMARREEFLI 09T567/340-486 S.moe EAMARQDDIFEEKVVRVUGSAWKACHAEVVRHACMKLIMGQAGQHAEKHARKREMEMARREEFLI 09T567/340-486 S.moe EAMARQDDIFEEKVVRVUGSAWKACHAEVVRHACMKLIMGGAGQHAEKHARKREMEMARREEFLI 09T567/340-486 S.moe EAMARQDDIFEEKVVRVUGSAWKACHAEVVRHACMKLIMGGAGQHAEKHARKREMEMARREEFLI 09T577/340-486 S.moe EAMARQDDIFEEKVVVRVUGSAWKACHAEVVRHACMKLIMGGAGQHAEHAAHAARKEEFLI 09T577/340-497 P.tri EAMLRQDDIFEUWUFWUGSAWKACHAEVVRNAGMAGUAEUWUFWUFWUFWUGFWUFWUFWUFWUFWUFWUFWUFWUFWUFWUFWUFWUFWUF | 440 450 RIQSMYIQREVLQAMGL RVQSMYIHREVLQAMGL QVQSLYIPRDVLAAMGL QVQSLYIPRDVLAAMGL RAYSSYIPRDVLASMGLYDAP- KAYSSYIPRDVLASMGLYDAP- |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat DAMAROSDHFSETKLLRRVGPSWACLAEVVRRTASMKLYMGORGOTAEKHARKRDAEVARDEEFL DATASJA5-481 P.pat DATASTATION CONTRACTATION CONT | 440 450 RIQSMYIQREVLQAMGL RVQSMYIQREVLQAMGL QVQSLYIPRDVLAAMGL XQSLYIPRDVLAAMGL XAYSSYIPRDVLASMGLYDAP- KYHCPFVPRDVLASMGLY |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat EAMARQSDHFSETKLLRRVGPSUKACTAEVVRRKASMKLYMGORGOTAEKLARKEAEVAREEELI A9TRX9/335-481 P.pat EALVRQSDHFAETKLLRRVGPSUKACTAEVVRRKASMKLYMGORGOTAEKLARKEAEVAREEELI DSSTX2/340-486 S.moe EAMARQDDIFEETKVVRVGSAUKACLAEVVRRKASMKLYMGORGOTAEKLARKEEMARREEELI DSSTX2/340-486 S.moe EAMARQDDIFEETKVVRVGSAUKACLAEVVRRKACMKLYMGORGOTAEKLARKEEMARREEELI D9H554/340-497 P.tri EAMARQDDIFEETKVVRKVGSAUKACLAEVVRRKASMKLYMGORGOTAEKLARKREMEMARREEELI D9H554/340-497 P.tri EAMARQDDIFEDTKVVRKVGSAUKACLAEVVRRKASMKLYMGORGOTAECTAEKTARKEE D9H554/340-497 P.tri EAMURQDDIFADTKLVRGVGPAUKACLAEVVRRKASMKLYMGAGOTAECTAEVVRRKEEELI D9SUG7/348-494 A.tha EAMURQDDIFADTKLVRGVGPAUKACLAEVVRRKASMKLYMGMAGOTAECTAEKTAMKRETEVRKEEELI D7MBM1/347-495 A.lyr EAMURQDDLFADTKLVRGVGPAUKACLAEVVRRKASMKLYMGMAGOTAEKTAMKRETEVRKEEEFI C5XWUB/358-503 S.hic DVMGHOEDFDN-KKUSGLGHAUKACLAEVVRRKASMKLYMGMAGOTAEKTAMKRETEVRKEEFI | 440 450 RIQSMYIQREVLQAMGL RVQSMYIREVLQAMGL QVQSLYIPRDVLAAMGL QVQSLYIPRDVLAAMGL RAYSYIPRDVLASMGLYDAP- KTHCPFVPRDVLASMGL RTHCPFVPRDVLASMGL RTHCPFVPRDVLASMGL |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat EAMARQSDHFSETKLLRRVGPSWAACLAEVVRRWASMKLYMGOAGOLAEKLARKREAEVAREEELI A9TRX9/335-481 P.pat EALVRQSDHFAEKLLRRVGPSWAACLAEVVRRWASMKLYMGOAGOLAEKLARKREAEVAREEELI D8STK2/340-486 S.moe EAMARQDDIFEEKVVRKVGSAWAACLAEVVRRWASMKLYMGOAGOLAEKLARKREAEVARREEELI D8TS67/340-486 S.moe EAMARQDDIFEEKVVRKVGSAWAACLAEVVRRWACMKLYMGOAGOLAEKLARKREAEVARREEELI D8TS67/340-486 S.moe EAMARQDDIFEEKVVRKVGSAWAACLAEVVRRWACMKLYMGMAGOLAEKLARKREAENARREEELI D9TS67/340-486 S.moe EAMARQDDIFEEKVVRKVGSAWAACLAEVVRRWASMKLYMGMAGOLAEKLARKREAENARREEELI 09TS67/340-486 S.moe EAMARQDDIFEEKVVRKVGSAWAACLAEVVRRWASMKLYMGMAGOLAECHARKREAENARREEELI 09SUG7/348-494 A.tha BAMURQDDIFADIKLFRGIGSAWAACLAEVVRRWASMKLYMGMAGOLAECHARKREAENARREEELI 09SUG7/348-494 A.tha BAMURQDLFADIKLVRGVGPAWAACLAEVVRRWASMKLYMGMAGOLAEKLAMKRETEVRKREEELI 07MBM1/347-495 A.lyr EAMVRQDLFADIKLVRGVGGPAWAACUAEVVRRWASHLYMGMAGOLAEKLAMKRETEVRKREEELI 05KWU8/358-503 S.bic EVMGHQDKIFDSEKLASGMGHAWAACVAEVARWRSFKLITGLAGTYAEKLAMKRETEVRREEEFEFFF 06ETKK7/352-509 O.sat EVMGHQDKIFDSEKLASGMGHAWAACVAEVVRRWSFKLITGLAGTYAEKLATEREEFEFF <td>440 450 RIQSMYIQREVLQAMGL RVQSMYIRREVLQAMGL QVQSLYIPRDVLAAMGL XAYSSYIPRDVLAAMGL KAYSSYIPRDVLASMGLY KTHOPFVPRDVLASMGLY RTWSKYIPDNVCSMGL RTWSKYIPDDIMGSMGLFDSP-</td> | 440 450 RIQSMYIQREVLQAMGL RVQSMYIRREVLQAMGL QVQSLYIPRDVLAAMGL XAYSSYIPRDVLAAMGL KAYSSYIPRDVLASMGLY KTHOPFVPRDVLASMGLY RTWSKYIPDNVCSMGL RTWSKYIPDDIMGSMGLFDSP- |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat BAMARQSDHFSEJKLLRRVGPSWACLAEVVRRVASMKLYMGQAGQTAEKTARKRDAEVAREEETL BALVRQSDHFSEJKLLRRVGPSWACLAEVVRRVASMKLYMGQAGQTAEKTARKRDAEVAREEETL BSTK2/340-486 S.moe BAMARQDDIFEEJKVVRKVGSAWACLAEVVRRVACMKLYMGQAGQTAEKTARKRDAEMARREETL B9H554/340-486 S.moe BAMARQDDIFEEJKVVRKVGSAWACLAEVVRRVACMKLYMGQAGQTAEKTARKRDAEMARREETL B9H554/340-486 S.moe BAMARQDDIFEEJKVVRKVGSAWACLAEVVRRVACMKLYMGQAGQTAEKTARKRDAEMARREETL B9H554/340-497 P.tri BAMLRQDDIFFDIKLVRGVGPAWACLAEVVRRVACMKLYMGQAGQTAEKTARKRDAEMARREETL OSUG7/348-494 A.tha BAMVRQDDLFADIKLVRGVGPAWACLAEVVRRVASMKLYMGMAGQTAEKTAMKRD EVRKREETL D7MBM1/347-495 A.Jyr BAMVRQDDLFADIKLVRGVGPAWACLAEVVRRVASMKLYMGMAGQTAEKTAMKRD EVRKREETL OSXNU8/358-503 S.bic EVMGHQDLFADIKLVRGVGPAWACLAEVVRRVASHKLYMGMAGABKTAMKRD EVRKREETL GETKT/352-509 O.sat EVMGHQDKIPDSIKLASGMGHAWACLAEVVRRVSFKLYTGLAGTYAEKTATECONSKTREEDH D0M02/2/356-519 P.inf BALAQKKHPTELEHDKLPESWAACLAEVVRRWSFKLITGLAGTAEKTARKRDEVRREETH | 440 450 RIQSMYIQREVLQAMGL RVQSMYIREVLQAMGL 2VQSLYIPRDVLAAMGL 2VQSLYIPRDVLAAMGL KTHGPFVPRDVLASMGL |
| 370 380 390 400 410 420 430 A9SER7/335-481 P.pat EAMARQSDHFSETKLLRRVGPSTAACLAEVVRRAASMKLYMGORGOTAEKLARKEBAEVARREETL BOSTK2/340-486 S.moe EAMARQDDIFEETKVVRVGSATKACLAEVVRRAASMKLYMGORGOTAEKTARKEBAETARREETL BOSTK2/340-486 S.moe EAMARQDDIFEETKVVRVGSATKACLAEVVRRAASMKLYMGORGOTAEKTARKEBAETARREETL BYH554/340-486 S.moe EAMARQDDIFEETKVVRVGSATKACLAEVVRRAASMKLYMGORGOTAEKTARKEBAMARREETL BYH554/340-486 S.moe EAMARQDDIFEETKVVRVGSATKACLAEVVRRAASMKLYMGORGOTAEKTARKEBAMARREETL BYH554/340-487 P.tri EAMIRQDDIFADTKLYNRVGSATKACLAEVVRRAASMKLYMGORGOTAEKTARKEBAMARREETL DYMBH/347-495 A.lyr EAMVRQDDIFADTKLYNRVGSATRACLAEVVRRAASMKLYMGMAGOTAEKTARKEBAMARREETL CSXWU8/358-503 S.bic EVMGHQDDIFADTKLVNRVGGATRACLAEVVRRAASMKLYMGMAGOTAEKTAMKETEVRKEETL OGETK7/352-509 O.sat EVMGHQDDFADTKLVNRVGGHATRACLAEVVRRASMKLYMGMAGOTAEKTAMKETEVRKEETL DOMGJ2/356-519 P.inf EALAQKKHYTETEHLDKIPEATRACLAEVVRRASSFLITGLAGOTAEKTATECON EALAQKKHTPETEHLDKIPEATRACLAEVVRRKSSFLITGLAGOTAEKTATECON FOW21/374-533 A.LAI EALAQKKHTPETEHLDKIPEATRACLAETVRRESSTLITGLAGOTAEKTATECON EALAQKKHTPETEHLDKIPEATRACLAETVRRKSSFLITGLAGOTAEKTATEREDEVRREETLI DOMGJ2/356-519 P.inf EALAQKKHTPETEHLDKIPEATRACLAETVRRKSSFLITGLAGOTAEKTATECON EALAQKKHTPETEHLDKIPEATRACLKTKTRATKSSTLITGLAGOTAEKTATECON EALAQKKHTPETEHLDKIPEATRACLKTKTGRKTSSTLITGLAGOTAEKTATEREDEVRREETLI DOMGJ2/356-519 A.LAI | 440 450 RIQSMIIQREVLQAMGL RVQSMIIREVLQAMGL QVQSLIIPRDVLAAMGL DVQSLIIPRDVLAAMGL RXNSSIPRDILASMGLYDAP- KTHCPFVPRDVLASMGL RTWSRIPPDNVMCSMGL RTWSRIPPDNVMCSMGL RTWSRIPPDNVMCSMGL RTWSRIPPDNVMCSMGL RTWSRIPPDNVMCSMGL RTWSRIPPDNVMCSMGL |
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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-K/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 = $10 \mu m$.







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 μ m.



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 = $10 \mu m$.



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.

| | | 10 | 2 | 0 | 30 | 40 | 50 | 60 | 70 | 80 |
|---------------|--------|--------------|--------------------|-----------|-------------|---------------|--------------|--------------------|------------|---------------|
| 013978 | S.pom | MTTPLTL | DVNLSSAVAT | BATKAL | SAULETS. | | LITES TRE | | PTLODER | DOOLLANA |
| 09VW01 | D.mel | -MINARS-OVEL | TMOGROVI | AVATOR | TVLEHR | CLGKYMYTGDA | OVSICTUCS | TDVDCNFIDE | VCHTSDSL | THEVERA |
| 09BSB4 | H.sap | -MNGRS-EVL | VSVGROVE | AMLAV | TVLLER | STGKFHYKKEG | TYSICTUGI | ODVDCDFIDFTY | WRVSSEDL | DRALRKVV |
| 09D8Z6 | M.mus | -MNCRS-EVL | VSVIGROVE | AMLAV | TVLLHR | STGKFHYKKEG | TYSICTUGI | ODVDCDF IDFTY | VRVSSEDL | DRALRKVV |
| 06AY69 | R.nor | -MNCRS-EVL | VSVIGROVE | AMLAV | TVLLER | STGKFHYKKEG | TYSIGTUGI | ODVDCDF IDFTY | VRVSSEDL | DRALRKVV |
| A8JCL2 | C.rei | MANCETYNEP | VIBLIPHOUT | REALROVL | HTTIFNR | | ALGYVVR | KDVDSELFDIT | VKCCDPAV | ARVESR |
| A9THM9 | P.pat | -MNCEVFHLK | STORA DI SOLO YOUR | REVLRCIL | TIMENR | | ALGLVRF | REVECELFDITY | VOCGDSHT | EKKIEEKI |
| D8SNB5 | S.moe | -MNCEIFHLR | DVOPYOI | REVLRCIL | TVMENR | | ALGLVRF | HDVDSELFDLTY | VOCGDLTF | EKKMEEKI |
| D8SRD6 | S.moe | -MNCEMFHIR | DVOPYOU | REVLRCIL | UVMENR. | | ALGLVRF | RDVDSELFDLTY | VOCGDLTF | KKMEDKI |
| B9GCZ2 | 0.sat | -MNCETCQLK | ELEQDEIF | DVLRCIL | HTIFFHR | | | KDVDCDLFEITY | VQCGLPDL | EKEVDEKI |
| C5XZN3 | S.bic | - MNCETCQLK | SLELEPTEIR | DVLRCIL | HTIFFHR | | | KDVDCDFLEITY | VQCGLPEL | EKEVDEKI |
| B6T277 | z.may | -MNCETCQLK | SLELELTE I R | DVLRCIL | HTIFFHR | | | KDVDCDFLDIT | VQCGLPEL | EKEVDEKI |
| C6THK1 | G.max | -MNCEVCQIK | JUSLISHFEID; | REVLRCIL | HTIVFHR | | ALGLVRF | KDVDLELFDVTY | VQCGEAEL | EKKIDEKI |
| D7SSD2 | V.vin | -MNCEACDLK | BUBLENFQUE | REVLRCIL | HTIVFHR | | ALGLVRF | KDIDLELFEITY | VQCGDAEV | DRKINEKI |
| A9PIV4 | P.tri | -MINCEVCQU K | STISVISH FEILE | REVLRCIL | HITTVEHR | | ALGLVRE | RDIDLELFDITY | VOCGEVEL | DKKIEDKI |
| B9S8M2 | R.com | | SLOVEHFEIR | EVLRCIL | HTIVFHR- | | | KDVDLELFEITS | | BMKIDERI |
| D/MLEO | A.lyr | | STOVE SPET | EVLRCIL. | ITT VEHR. | | ALGLIRE | KDIDLELFEIT | WOCCETEV | |
| F4K265 | A.tha | | STO VISTER | CEVERCIE. | | | Andria | KUTULENSE IN | VQCGLIEV | JAKID |
| | | | | | | | | | | |
| | | 90 | 100 | 11 | 10 | 120 | 130 | 140 | 150 | 160 |
| 013978 | S.pom | TDEVDSLKRD | -TSKGNOVI | LFYD-RPI | PKKTWFSI | RHTTEP-WEQW | VISVNVID- | | | EDPPYA |
| Q9VWQ1 | D.mel | NSESEKLRSNI | ESCGSGOIS | EFFQ | KKNRWPI | FPQBSIPWBVØ | TVHEDLIKH | IENEDERQLCREN | VSDLLTOK | VIYITELM |
| Q9BSB4 | H.sap | GESKDALRNSO | GGDGLGOMS | EEVQ | KKSRWPI | FSDOCIPNOV | TVKVHVVAL | ATEQERQICRE | VGEKLCDK | IINIVEVM |
| Q9D826 | M.mus | GEEKDALRNSC | GGDGLGOMS | E 3 Y Q | KKSRWPI | FSDICIPNIOV | TVKVHVVAL | ATEQERQICRE | VGEKLCOK | IINIVEVM |
| DOATON 2 | R. nor | GERKDALKNSC | GDGLGOMS | SEVEMBE | KKSRWP | | UT SUT UT OF | ATEVERVICE | VGEKLCIK | CROCARAS |
| AGUCLZ | C.rei | DHOT THUNKR | DERSPUS | SEVETRN | UVC NOS | WUERLYWEOW | CTOURNER | ACDUEVEVENOUVI | | VIDER-0 |
| D8SNB5 | F.pat | DOLTAWVEKH. | PNKKTTVCI | SEVETRS | CNAMEGI | HKMERITYWEOW | VVTINTTV- | OOSHLRSKPHHI | KI.GDALDI. | WTDERS |
| D8SRD6 | S.moe | DOLTAWVEKH | PNKKITVC | SEVETRS | ONAMEGI | HKMERITYWEOW | VVTINTTV- | OOSHLRSKPHHI | KLGDALDL | MTDER S |
| B9GCZ2 | 0.sat | NOFLAWVERH | PNRRSOVCI | SFFDEKN | NPSWET | SKTERTYWEOW | FIN HVIS- | PKGHG-KSRSS | ASTSIRGK | ALEEAS |
| C5XZN3 | S.bic | DOFTAWVEKH | PNRRSOICI | SFFDEKH | RHPGMEVI | NKTERIYWEOW | FIN HIMS- | PKRYS-KSNSS | GLTNIGAN | ALEETS |
| B6T277 | Z.may | DOFSAWVEKH- | PNRRSOICI | SFFDEKHI | RHPGWFVI | NKTERIYWEQW | FINLOVMF- | PKRYS-KSNSS | GLTNIQAN | AVEETS |
| C6THK1 | G.max | EQFVCWVEKH | - PNKKSQICI | SFYEVKN | QASWESI | NKIERLYWEQW | YINLNVAQH | PKAHSSKYHHS | -VVDPGDG | ALEDRN |
| D7SSD2 | V.vin | DQFISWVEKH | - PNKKSQICI | SFYEVKN | KQASWFTI | NKIERRSWEYN | YINLNVAQH | IPKAHSSKSHHS | AVVDPGDS | ASEDRS |
| A9PIV4 | P.tri | DQFISWVEKH | - PNKKSQICI | SFYETKN | KHP SWFN · | -KTERLFWEQW | YVNLHVTQH | ITKAHSGKSHHS | PMVDLGDT | VSEDRG |
| B9S8M2 | R.com | EQFISWVERH | - PNKKSQICI | SFYEVKS | XQ P SWF TI | HKIERLYWEQW | YVNLNVTQQ | PKAHSGKSHHS | VVLDPGDS. | ASEERS |
| D7MLEO | A.lyr | EQFINWIEKH | PNKKSQICI | SFYEVKS | QPSWFT | NKIERIYWEQW | YINDNVLQP | PAKPPVGKSHHS | LVMDPGD- | ASEERS |
| F4K265 | A.tha | EQFINMIERH | PNKKSQICI | SEYEVKS | QPSMET. | -KIERDYWEQW | XIN NVLQP | TKPPVGKSHHS | LVMDPGD- | ASEER S |
| | | | | | | | | | | |
| | | 170 | 180 | 190 | | 200 2 | 210 | 220 23 | 30 | 240 |
| 013978 | S.pom | QSSESIQQALI | EKLVLLVN | SRVCSY | LPPVVS | - ENGQYPYBIV | VNSASEG | WGTI | LKRMLIEN | VSSGE- |
| 09VWQ1 | D.mel | NRHDYVPKTP | SQSELDLIFI | DTS-FPDV | QPYLF | KFDYSTSGS | AAPSMG | N7 | MKIIKET | LAM |
| 098584 | H.sap | NUHEYDPKMP | IQSEVDNVFI | DTG-LRDV | 013 Y L Y | KISEQITDA | LGTSVT | T | TMRELIKDT | LAL |
| 063869 | R nor | SCHEYOPKMP | FQSEVDNVFI | DTG-LRDVQ | | KISEQITEA | LGTSVT | T1 | TMRELIKDT | LAL |
| 18.TCT.2 | C rei | SCHEYNPKMP | FOSELDNVFI | TG-LRDVO | | | EGTSVT | A SA STOCSTON | CHRELIKDT. | LAL |
| AGTHMO | P. nat | DUNATU DANI | | VNEKKDH | | ASAVINET DI I | TDSSSARDS | SASASLQGSLQA | THAT | PPPVLS |
| D8SNB5 | S.moe | KOHALIDSCU | | VNEKKDH | VPPVTSO | D-VVSEDVETS | TPSSSD | SFGMDA | THE MUOTO | PPTMLG |
| D8SRD6 | S.moe | KEHALTESGI | KEVMI.OTI.OC | VNEKKDH | VPPVTSOI | D-VVSEPVETS | TPSSSD | SFGMDA | TERMIOTO | PPTMLG |
| B9GCZ2 | 0.sat | SKRAAUGLLI | DEVLFOIINE | ANEKKDH | IPPIS | -DRISNHEIS | IPSSSD | SVFGWNAD | LR.VINS- | |
| C5XZN3 | S.bic | TRAATSSI | NEVLFOIINF | ANEKKDH | IPAIP | DRIENHETM | IPR | | | |
| B6T277 | z.may | TRRAALSASI | NEVLFQIIKE | ANEKKDH | IPAIP | DRIENHEIM | IPSS-D | SVFGWNTD | IRRVENSG | HPYSL- |
| C6THK1 | G.max | ARSAALFASLI | REVLFQIIKF | VNEKKDH | VPPIPNLI | EGAVSFPYEIT | IPSSSD | SAFGMDA | IKRMLQTG | HLTMLS |
| D7SSD2 | V.vin | LRRAADBASL | REVLFQIIKF | VNEKKDH | IPSIPSA | EG-VSFPYEIT | IPSSSD | SAFGMDA | 4FKRMLQSG | HPTMLS |
| A9PIV4 | P.tri | VRREALBASLI | HEVLFQIIKF | VNEKKDH | VPPIN1 | EDIICFPCEIT | IPSSSD | SPFGMD | FKRMLQTG | HPTMLS |
| B9S8M2 | R.com | ARRAADAGU | REVLFQIIKF | VNEKKDH | VPPISI | EGVIYFPYBIT | IPRS | DI | HFLLACDA | ¥ |
| D7MLE0 | A.lyr | SERTLIPQSL | QEVLFQIIKF | VNEKKDH | VPPINI | DGVIYCEFEIT | IPSSSD | SAFGMDM | IFKRILHSG | HPSMLG |
| F4K265 | A.tha | SKRTLLEQSL | DEVLFQIIKF | VNEKKDH | VEPINI | DGVIYYPFEIT | IPSSSD | SAFGMDA | FKRILHSG | HPSMLG |

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*.





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 Δ 8 and Δ 9 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 μ M 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 μ m.

| Arabio | 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 |
| 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: TCAAGAGGAATCCCACCATATTCTC 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

<u>ATG1a AIM mutant QuickChange primers:</u> Forward: CTCATAGAGAGAGAGGCTGTTCTTGC Reverse: GCAGAAGGACGGTTTGCAAGAACAG

<u>UBC9</u>

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 | Asporaillus onzao | Q2UKQ2 | 945-1094 | 165-336 |
| ATG17 | Aspergilius oryzae | Q2UFN7 | NA | 33-480 |
| ATG11 | Poniaillium obruggenum | B6H4J6 | 1010-1159 | 211-403 |
| ATG17 | rencinium cinysogenum | A7KAM6 | NA | 32-479 |
| ATG11 | Laccaria bicolor | B0DBA9 | 971-1091 | 332-501 |
| ATG11 | Dichia pastoris | Q9C438 | 1154-1310 | 336-521 |
| ATG17 | r icilia pasions | C4R1E4 | NA | 5-415 |
| ATG11 | Saccharomycos corovisiao | Q12527 | 991-1173 | 339-512 |
| ATG17 | Saccharonnyces cerevisiae | Q06410 | NA | 7-406 |
| ATG17 | Candida sphaerica | Q6CS99 | NA | 14-410 |
| ATG11 | Vanderwaltozyma | A7TL57 | 1045-1216 | 302-474 |
| ATG17 | polyspora | 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 |