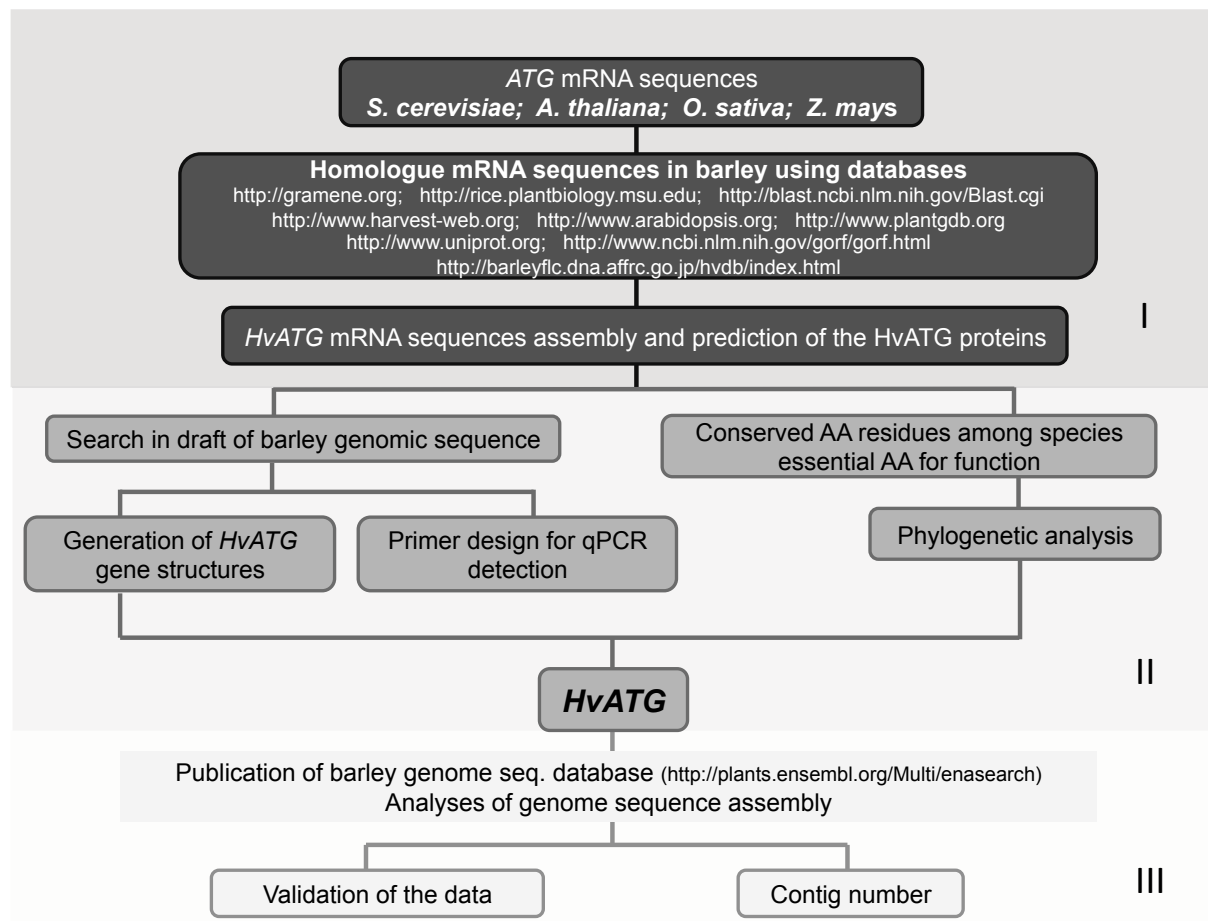


Identification of barley (*Hordeum vulgare* L.) autophagy genes and their expression levels during leaf senescence, chronic nitrogen limitation and in response to dark exposure.

Liliana Avila-Ospina¹, Anne Marmagne¹, Fabienne Soulay¹ and Céline Masclaux-Daubresse¹

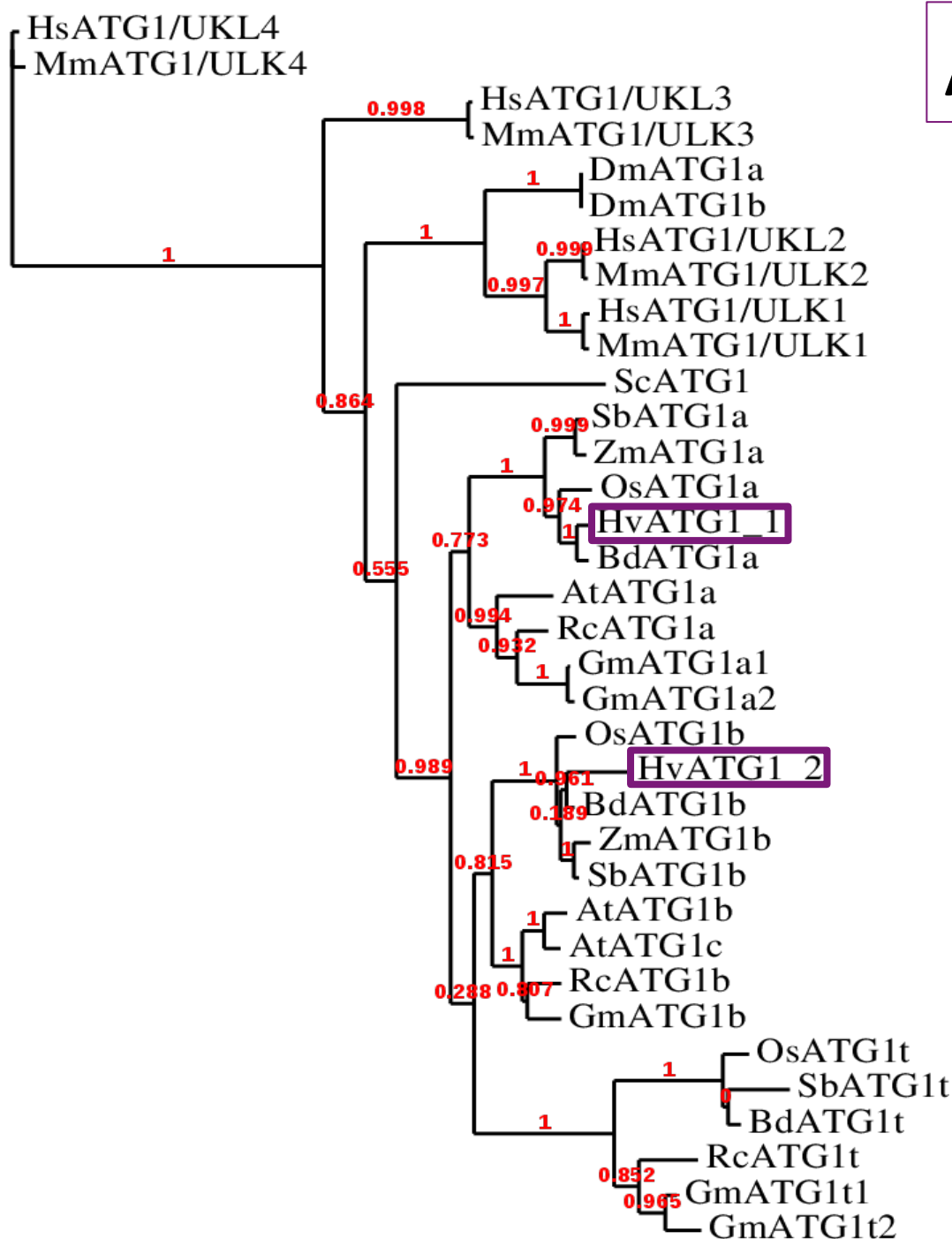
(1) INRA-AgroParisTech, Institut Jean-Pierre Bourgin, UMR1318, ERL CNRS 3559, Saclay Plant Sciences, Versailles, France

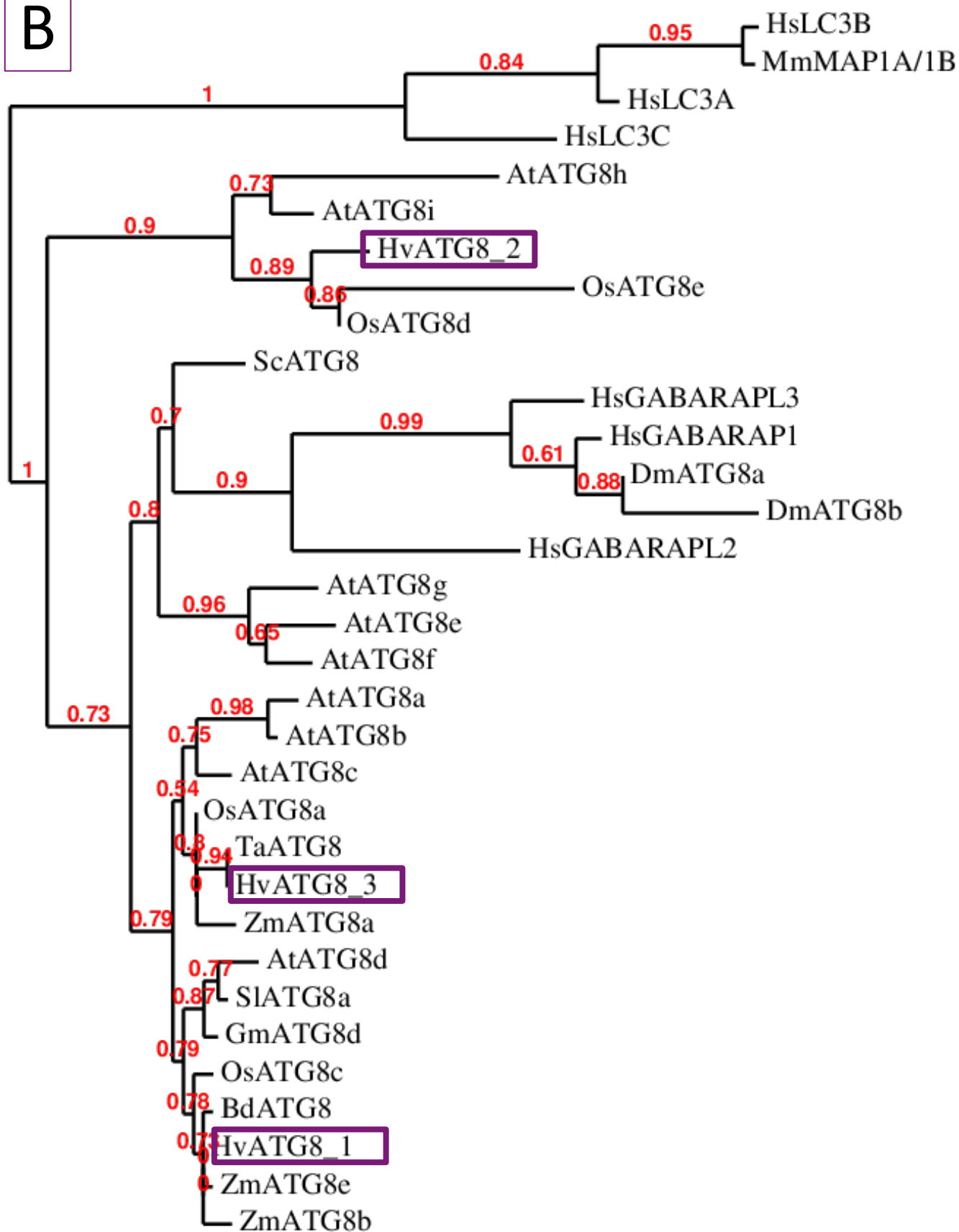
Supplementary Figures and Tables



Supplementary Figure 1. Searching of barley autophagy genes. ATG mRNA sequences of *S. cerevisiae*, *A. thaliana*, *O. sativa* and *Z. mays* were used as queries to find barley homologues in several databases. Subsequently, a mRNA assembly of several mRNA sequences found that codified for the same gene was performed and based on that, a protein prediction was made for each gene found (I). Afterwards, mRNA sequences were aligned to a draft of the barley genome sequence and protein sequences were analyzed for conserved and essential amino acids characteristic of ATG proteins. From these analyses, *HvATG* gene sequences were obtained allowing us to generate the *HvATG* gene structures and to design primers for qPCR detection. On the other hand, protein sequences were used to perform phylogenetic analysis (II). After the publication of the barley genome sequence, *HvATG* mRNA and genomic sequences obtained in our previous studies were validated and the contig numbers for each one of our genes were obtained (III).

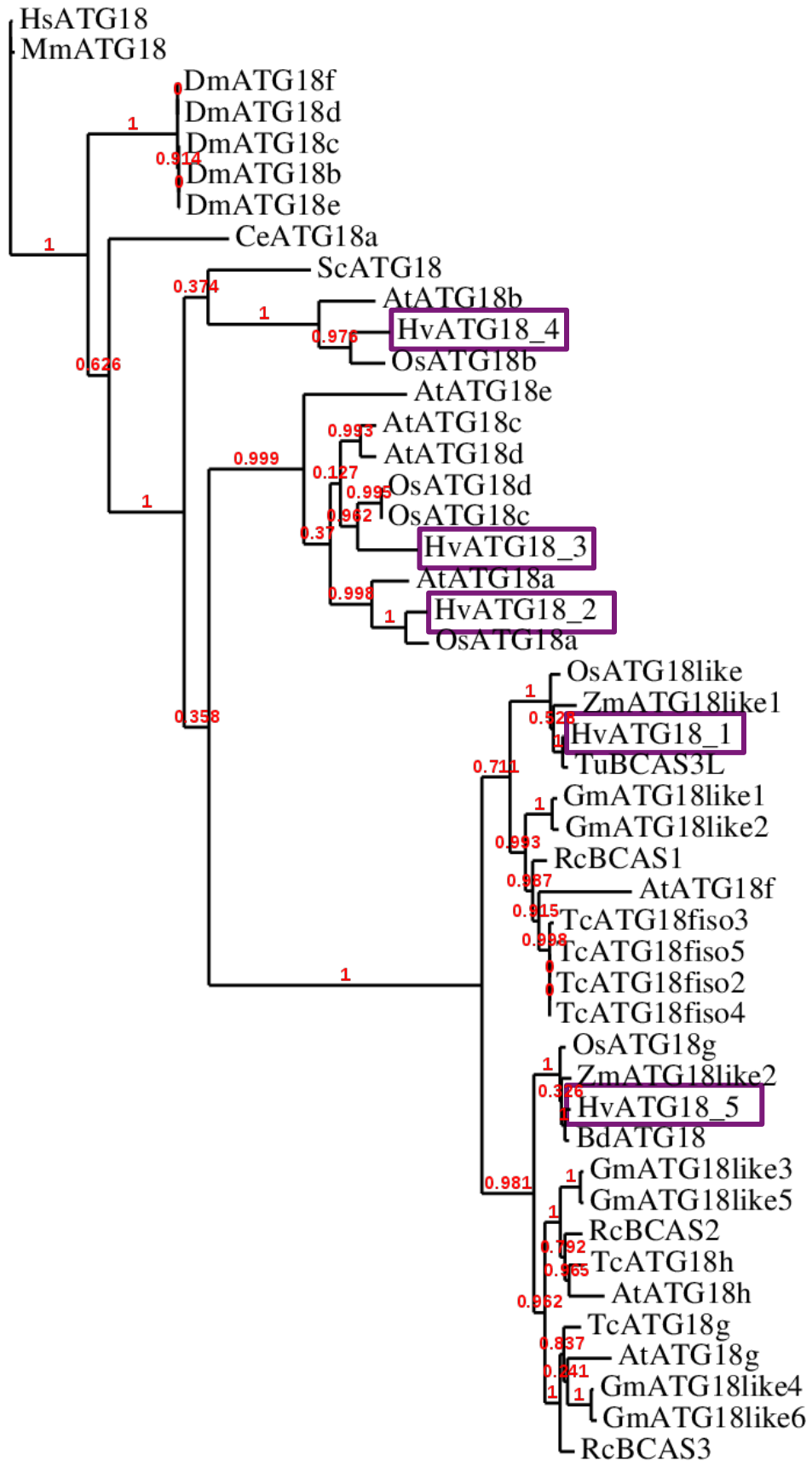
Supplementary Figure 2. Phylogenetic trees of HvATG1 (A) and HvATG8 (B) and HvATG18 (C) gene families. DNA coding sequences (CDS) were translated to protein and then aligned using MABL phylogeny program (http://www.phylogeny.fr/simple_phylogeny.cgi). Species abbreviation are as follows: At (*Arabidopsis thaliana*), Tc (*Theobroma cacao*), Rc (*Ricinus communis*), Gm (*Glycinemax*), Os (*Oryza sativa*), Hv (*Hordeum vulgare*), Sc (*Saccharomyces cerevisiae*), Dm (*Drosophila melanogaster*), Hs (*Homo sapiens*), Mm (*Mus musculus*), Ce (*Caenorhabditis elegans*), Tu (*Triticum urartu*) Zm (*Zea mays*), Bd (*Brachypodium distachium*), Cv (*Chlorella variabilis*), Gm (*Glycine max*), Lb (*Laccaria bicolor*), Vv (*Vitis vinifera*).



B

0.3

C



Supplementary Figure 3. Alignment of HvATG proteins. HvATG1 (A), HvATG2 (B), HvATG3 (C), HvATG4 (D), HvATG5 (E), HvATG6 (F), HvATG7 (G), HvATG9 (H), HvATG10 (I), HvATG11 (J), HvATG12 (K), HvATG13 (L), HvATG16 (M), HvATG101 (N), HvATI1 (O) and HvNBR1 (P) proteins were aligned with homologues ATG proteins of different species using ClustalW. Conserved amino acids (aa) are showed by shades of blue colors going from less conserved aa (light blue) to more conserved aa (dark blue). Species abbreviation are as follows : Hv (*Hordeum vulgare*), Os (*Oryza sativa*), Ta (*Triticum aestivum*), Sc (*Saccharomyces cerevisiae*), At (*Arabidopsis thaliana*), Cr (*Caenorhabditis remanei*), Hs (*Homo sapiens*), Mm (*Mus musculus*), Dm (*Drosophila melanogaster*), Xl (*Xenopus laevis*), Dr (*Danio rerio*), Bd (*Brachypodium distachium*), So (*Saccharum officinarum*), Zm (*Zea mays*), Sb (*Sorghum bicolor*), Rc (*Ricinus communis*).

A	HvATG1_1	1	--MGGG-----PASPRPPRVVGEYELGEMVGKG-TFAEVFRAVHATT-GARVAVKEIDRRRV-DDHVRRG	61
	HvATG1_2			
	OsATG1a	1	MTMAAAPARSAGAAAEKRMVDPPRVVGEYKLEELIGVG-SFAKVYLATHLRT-GDVVAVKEIDPRRI-DEVRVGG	72
	OsATG1b	1	--MGDRA---AGSGGGGGGGSGVRRVGDYLVLRQIGSG-AYARVWLKHRTR-GTEVALKEIAVERL-SSKLRES	67
	OsATG1t	1	-----MASTPEPETTVGGYELRERLGGRPSTVWRAVERSS-GSPVVVKQVRLTGL-PSTLRDS	58
	AtATG1a	1	-----MESARLVGDYALGPRIGSG-SFAVVWLAKHRSS-GLEVAVKEIDKKLL-SPKVRDN	53
	AtATG1b	1	-----M---AQSSLVAAAGRSGRVIGDYAVGRQIGSG-SFSVWVEGRHLVH-GTVVAIKEIAMARL-NKKLQES	63
	AtATG1c	1	-----MAQFTGRVVG DYLVGRQIGSG-SFSVWVEARHRVD-GTEVAIKEIAMDRL-NKKLQES	55
	ScATG1	1	--MGDIKNKDHT--TSVNHNLMASAGNYTAEKEIGKG-SFATVYRGHLTSDKSQHVAIKEVSRAKLKNKKLLEN	69
	HvATG1_1	62	ILQEMSILGSLSHPNILRLIDTJETGEKLFVLVEYCDGGDLEAYRLTHGGP-----RNRL	116
	HvATG1_2			
	OsATG1a	73	ILEEKAILSTLSHPNILRLIDTIE-ENLYLILEYCNNGDLEGYRT-KGGE-----DARL	125
	OsATG1b	68	LLSEVDILRRIRHPNVIALHESIRDGGKIYLVLEYCRGGDLHSYLQQHK-----RV	118
	OsATG1t	59	LDCEVRFLAAVTHPNIIRLLDLITQTSNLYLVLELCEGGDLAAYIQRNG-----RV	109
	AtATG1a	54	LLKEISILSTIDHPNIIRFYEAJETGDIRFLVLEYCSGGDLAGYINRHG-----KV	104
	AtATG1b	64	LMSEIIILRKINHPNIIRFIDMIEAPGKINLVLEYCKGGDLSMYIHKHG-----SV	114
	AtATG1c	56	LMSEIFILRRINHPNIIRLIDMKSPGKVHLVLEYCKGGDLVYVQRHG-----IV	106
	ScATG1	70	LEIEIAILKKIKHPIVGLIDCERTSTDFYLIMEYCALGDLTFLLRKRELMEHNPRLRTVFEKYPPPSSENHNGL	144
	HvATG1_1	117	PEATARDFAQLAEGLKVLRGKRIVHRDLKPQNLLLSTDG-----DAITLKIGDFGFARSLM	173
	HvATG1_2			
	OsATG1a	126	PDATARDFMRLAEGLKMLRGRSIVHRDLKPQNLLLSTNG-----DAITLKIGDFGFARSLV	182
	OsATG1b	119	SETVAKHFIQQLASGLQMLRENNVVHRDLKPQNILLVANN-----ENSLKLIADFGFAKFL	175
	OsATG1t	110	EERVASNFMRIAGAGLQVLRHHIVHRDLKPENILLSPD-----SNAIKLISDFGLSRVLR	166
	AtATG1a	105	PEAVAKHFMRLALGLQVLRQEKHFIRHDLKPQNLLSSKE-----VTPLLKIGDFGFARSLT	161
	AtATG1b	115	PEATAKHFMLQLAAGLQVLRDNNIIRHDLKPQNLLLSTDD-----NDAALKIADFGFARSLQ	171
	AtATG1c	107	PEATAKHFMQLAAGLQVLRDNNIIRHDLKPQNLLLSTNE-----NDADLKIADFGFARSLQ	163
	ScATG1	145	HRAFLVLSYQLLASALKFLRSKNLVHRDIKPQNLLLSTPLIGYHDSKSFHELGFVGIYNLPILKLIADFGFARFLP	219
	HvATG1_1	174	HENLAATFCGSPYMAPEIWRGDKYDAKADLWSVGVIILFQLVTGELPFLGENRVELREKVLTSNG-LSFPDIEA	247
	HvATG1_2	1		
	OsATG1a	183	QENLAATMCGSPSYMAPEIMRCEDYDAKADLWSVGVIILFQLVTGKLPFYGANLFLKLRQNIHESNG-VKFPKEIKD	256
	OsATG1b	176	PSSLAETLCGSPLYMAPEVMQAQKYDAKADLWSVGIIILYQLVTGSPPTGDSQIQLLRNLIQREIRFSPDCD-	248
	OsATG1t	167	PGEYTDNCGTCLYMAPEVMLFQKYDGGVDLWSIAAILFELNLGYPPFRGRSNVQLLQCINRTVS-LPFSEVVIS	240
	AtATG1a	162	PESMAETFCGSPLYMAPEIIRNQKYDAKADLWSAGAILFQLVTGKPPFDGNNHILFHNIVRDE-LKFPEDTRN	235
	AtATG1b	172	PRGLAETLCGSPLYMAPEIMQLQKYDAKADLWSVGAIFLQLVTGRTPTGTNSQIQLLQNIIRSTE-LHFPADCR-	244
	AtATG1c	164	PRGLAETLCGSPLYMAPEIMQLQKYDAKADLWSVGAIFLQLVTGRTPTGTNSQIQLLQNIIRSTE-LHFPADCR-	236
	ScATG1	220	NTSLAETLCGSPLYMAPEILNYQKYNAKADLWSVGTVVFMCCGTPPFRASNHLELFKKIKRANDVITFPSYCN-	293
	HvATG1_1	248	DLHPEFIDLCLRRILCLDPAMRMPFEFFFNHKKFLATARDS-----EIVAES-HH	294
	HvATG1_2	8	SINGTIL---ICVIDAVERLTVEEFVNHPPFLFEHAPETILSR--TPSDTRDGLPLTKSSPMRLSSQSSQEDCM	75
	OsATG1a	257	DLHPDFIDLCRGLLRLLDPKKRISFEFFFNHKKFLSTTGSTL-----YSGGSIQRKREIRFSPDNHP	315
	OsATG1b	249	-LSHGCIDLCKLLRINSVERLTVEEFVNHPPFLAEHALERTLSR--TPSDIRDGFPFINSSPTRPSSQSSQEDCM	320
	OsATG1t	241	KLRPDSIDICTRLLCSPNVKRLSFQEFFSHSLRP-----	275
	AtATG1a	236	EIHPCDVLCLRRNPIERLTREFFFNHPPFLREPRQIPDVEHSGFSTCTGKSLPLS-----	293
	AtATG1b	245	DLSTCDKDLQKLLRRNPVERLTFFEFFHPPFLSDKQSYD-FTRSRLDSRTMNDHFSSGSSPSRNIIEISQEDGL	318
	AtATG1c	237	DLSLDCIDLQKLLRRNPVERLTFFEFFHPPFLSDRQSYD-FRSRLGLRTMDGFLSSGSSPSRNMEESSQEDCL	310
	ScATG1	294	-IEPELKEILICSLTDFDPAQRIGFEFFFNKVVNEDLSSYELED-----DLPELESKS-KGIVE-----SN	352
	HvATG1_1	295	ALD-----LKDTCQTISS-----AVV-	310
	HvATG1_2	76	PFPLDL-STGQEESPAESN--APLKSYGATSKKLDKT-SGQSPSKHTGLFSRYIMGNYYA-----PSSQRLD	140
	OsATG1a	316	ADL-----LRDTCQIISSE-----DVL-	331
	OsATG1b	321	PFPLDDESTGQDEGPVSDSK--SAIKSYGFATSKRLDKT-SGQSPTKHSSLVSKYIRGNYYA-----SSSQRLD	386
	OsATG1t			
	AtATG1a	294	-----AQPSTSTNRFKSSAEN-----VHKHSGSSSSASNSQIS-----MPHTSFKEKTRK-	336
	AtATG1b	319	PFLLDDSSGPEGSPSSFKHTSPMKSSYGFSV--ERREASPLKNMDSLRYSRVSHRAETNRFKFEGRHS	389
	AtATG1c	311	PFLLDDSSGPEGSPSYLKKTSSMKSSSGIKVDTRI ERKEVESSPLKHTELTSGYSSFNQKVENDRFRFETQINS	385
	ScATG1	353	MFVSEYLSKQP-KSPNS-----NLAGHQSMADNPAELSDALKNSNILT	394
	HvATG1_1	311	---K-----VKSESADS--KVFDSWEWIEREYLVYANTTSMELLSSLEKPMKEVTGARSRCDDMSA--	367
	HvATG1_2	141	HPGQRTKESKIGEGHGAKGVYPEDSPIIDSLFVDQEYFVSGHAEGSSSSTSASL--Q--RNLPAKYENPSVS	210
	OsATG1a	332	---K-----DKSESVDNRNLQAFDSWEWIEREYLVQANSTSTEILSSLEKSMKDGTAKPASYDRST-	391
	OsATG1b	387	HPR-RIKENKGDEGHNPKGYPEDSPIIDSLFVDQEYFVH--PEGSSSSMNDSR--Q--RTMPSKLDSLSLS	453
	OsATG1t			
	AtATG1a	337	-----DTEGCSSNQSGVVDSLELIEREYLVNRPASLEGSDDC-----FDTSLQDSG	385
	AtATG1b	390	DR-SQFKPS--SLPDSRSFSTQGR-GDSPDSMDQDYVLISGPPVDIPSSSSGSP-----KPFNYPFKSHS	450
	AtATG1c	386	DRNRNREPT--GLTDSRSLIAPGRVDSQDSMDQDFVLVSGPPVDMPSSSSSSS-----KPYNFPFKSQS	448
	ScATG1	395	APAVKTDHTQA--VDKASNNKYHNSLVDSRSFEREYVVVEKKSVEVNSLADEVA--QAGFNPNPIKHPTSTQN	464
	HvATG1_1	368	-----INGPIQNNRDSL--C--R-VK-----T-H-----GCTPLSAS	394
	HvATG1_2	211	PPNL-----AAPSAMPINGTAINRQQ--SAGTGSLD--SHC-----SPISGTSQ	251
	OsATG1a	392	-----VKRSAWNQNRNSV--SRGVA-IK-----S-N-----GCTPLSTS	421
	OsATG1b	454	PPKLL-----TAVSAPRPIHGMAINRQQ--SGGTGSLD--SHC-----SPVSGTSQ	495
	OsATG1t			
	AtATG1a	386	FPNILPRNEKVSS-----SSLEAQKPLSDVS-----GPRPAS	417
	AtATG1b	451	PPVEFI-KRNV-----TNLTAPMPIASATGNL-----SRFGSLE-----SQN-----CIPGTS	494
	AtATG1c	449	PPVELF-NRSI-----S-STAMPPIGATSNSI-----GQFGSLD-----SQY-----SAPSTSH	491
	ScATG1	465	QNVLLN--EQFSPNNQYFQNGENPRLLRATSSSSGSDGSRPSLVDRRLSISSLNPSNALSRALGIASTRLF	537

Gene	Protein	Accession	Length
HvATG1_1	395	RESTTMEN-LRGRPLDYYTRLHLNQYIVILT ELAQEKLFGKGLDLEALSLE	450
HvATG1_2	252	GSAYLSDG-LDQPPSDYLTRLRLGGYASTIAELVKEEIKGGRHLEAFS IQ	307
OsATG1a	422	HESTAAN-LNPPY-CYTRLQLLNQYIVLVLT ELAEKELFGKGLDLEALSVE	476
OsATG1b	496	GSADLND A-MDQPPSDCLTRVRLLEQYASTIAELVKEKIKDAKHLEGFSIQ	551
OsATG1t			
AiATG1a	418	VSYLLTEV-QRLTIVHPPYTKLQLLHQYQAALT ELASEMGNTGQVKEFAVVT	473
AiATG1b	495	GSLDLVDA-FEQPSTNSLTRIRSLQKCAAAIAELVHERGENGKHLEAFS IQ	550
AiATG1c	492	GSLDLGDA-FEQPSTHSLTRIRSLRKYAATAELVYERIESDKHLEAFS IQ	547
ScATG1	538	GGANQQQQQQQITSSPPYSQTLTNSQLFHELT ENILRLDHLQHPEITLKDNTNIVSILESAAKAFVVYSYAEV	612
HvATG1_1	451	-WKEALNGCTLL-PDASDDGSFSTFAHENY-FPKSD-	483
HvATG1_2	308	-WKQAIHICNSY-AASAARESPSHDITMKGLD TDAP-	341
OsATG1a	477	-WNEALNACSLS-TDATHDGFFLTQAHVNF-LPKND-	509
OsATG1b	552	-WKQAIYICTSY-ASSATRENPSHDVTAKGFGSNAP-	585
OsATG1t			
AiATG1a	474	-WRKALEICDSW-MMSVGENEVNPDPTTAPETS-	504
AiATG1b	551	-WNQALHICHTQ-AVSGIEGSLQLDINRVG-	578
AiATG1c	548	-WKQALHICHTQ-AISGLEGPSQDINKLRSSSLKH-	581
ScATG1	613	KFSQIVPLSTTLKGMANFENRRSMDSNAIAEEQSDSDAAEEEDETLK KYKEDCLSTKTFGKGRTL SATSQLSATFN	687
HvATG1_1	484	QHQSPNVA-----QG L-----DFTRPASVRYWVWESGFIKAYDRAEKISHRLRE	526
HvATG1_2	342	HL-----LV-----NSQMADEECTQIERQFLTEVEHAEELASTVGQ	377
OsATG1a	510	HRPSRNVV-----QG L-----DFTRLVSVCSWAESGFIKAYDRAEKISHRLRD	552
OsATG1b	586	HL-----LA-----NSQLLYDTCMEIESQFLVQMEYAEELANTIGQ	621
OsATG1t			
AiATG1a	505	-----I-----PDL-----NS--PAPAKTWWTQEFVTALNQAE NLSTQLNE	538
AiATG1b	579	-----RN I-----SHGGSEKLLPQIQKEFVQVEVERAEELAKFV--	611
AiATG1c	582	DTHSSNKV-----TD L-----SHDGS EEISSQIQRFIQEI ELAEELAKSI--	622
ScATG1	688	KLP RSEMILLCNEAIVLYMKALSILSKSMQVTSNWWYESQEKSCSLRVNVLVQWLREKFNECLEKADFLRLKIND	762
HvATG1_1	527	-----NNDNTEMPDA-VEIIFQTALVYGKSGATKELLGQKNRS-MALYSKAIILLTFILQEAT-	582
HvATG1_2	378	-----IPDATAMPDA-MEIIFQYALEYGRHGGVVEMMGKVARS-MSRYTKAICLLRFLIEAT-	433
OsATG1a	553	-----NNDNTEMPDA-VEIIFQTALVYGTGAAKEVLGYQNRS-VALYSKAIILLTFVLQEAT-	608
OsATG1b	622	-----TVDATEMPDA-IEIIFQTALNLGRHGGVDEM MGKSASA-MVLYSKAVSMLRFLLT EAP-	677
OsATG1t			
AiATG1a	539	-----TSAATHMPDA-METIYERALAYGKSGGAEFYL SNKESA-ATLYKKA ILLLSFIIIEAV-	594
AiATG1b	612	-----ESDNAKMPDA-MEMILQAALALGISGGVDEVMGDAENA-GNLYSKAVRLLVFLAVEAQ-	667
AiATG1c	623	-----EPGNTKMPDA-METIFEAALDLGKLGKVEVMGDENA-GNQYSKAVRLLVFLV EAP-	678
ScATG1	763	LRFKHASEVAENQTL EEKGSSEEPVYLEKLLYDRALEISKMAAHMELKGENLYNCELAYATSLVMMLETSLDDDDDF	837
HvATG1_1	583	-----ALPL-----NPLFSLSPFNQQRIRHRYIANLRSHLCSAQLTGQHQRSIKN-----	626
HvATG1_2	434	-----SLAL-----NPPLSLTRSDRHLRLTYIEALNARLSQLQCPSH-----	470
OsATG1a	609	-----NLPL-----NPPFSLSSSDQQRIRHRYIANLRSHLCSAQLTGQQERYVQN-----	652
OsATG1b	678	-----SLAL-----NPALSLTRDDRRRLRTYIEAVNARLVPLQYQRH-----	714
OsATG1t			
AiATG1a	595	-----TLSL-----NPSFSLTPDDKKRILYIISNLQHRSSH L-----	626
AiATG1b	668	-----TLIL-----NPPLTLTNSVRYRLRTYIDSLITRLKHLQSHRRTSYPQKQ-----	711
AiATG1c	679	-----MLIL-----NPPLSLTNSVRYRLRTYIDFLSRRLKHLQSHRRSSAGMQGSSLAMMNRQS	733
ScATG1	838	TNAYGDYPFKTNILHLSKNDVEDKEKYSVLDENDRIIRKYIDISANRLKILRQKMNHQN-----	879

B	<i>HvATG2-1</i>	1	-----MGLLRGFSVGAVMKRMCKAVLKKGLG-DLFLGELDLQDLQDLQTRG-TLELTDLALNADYINSQLSGL	66
	<i>HvATG2-2</i>	1	-----SGS	3
	<i>AtATG2</i>	1	MVFPWNIAKSAEEAFSRWAVKRVVFKLLKKKLG-KLILGDLIDLQDLQDLQTRG-TIQLSDLAINVVDYLDNKFDA	72
	<i>OsATG2</i>	1	-----MNFSGVWVRTMMKRLCKSLLKKRLG-DLILGDLDLQDFDLQDLQTRG-TLHLSDIALNADFVNRRKLSGS	66
	<i>ZmATG2</i>		-----	
	<i>HvATG2-1</i>	67	SIMVKEGSIKSLLVKFLPLQLKSC---EIVVEDLELVLAPSVAIEIPPVVAECVSVSGNSSSTQAS-VN-TKRNE-S	135
	<i>HvATG2-2</i>	4	PITVKEGSIKSLLVKFLPLQLRSW-KIEIVVEGLEFVLAPSVAEAPPVDTGCSVSGGDSDEARSAE-TKRNEPD	76
	<i>AtATG2</i>	73	PLVKEGSIKSLLVKMPWKTNGC---QVEVDELELVLAPRLSENKSSSNEASTSASTREDLHNIRLEIGKHENEM	144
	<i>OsATG2</i>	67	AIMMKEGSIKSLLVRIPLLLNMRDCEIIVVEDLELVLAAVSSEDPSGDTECSVSGSNTDDTQKSVQ-AKRNESD	140
	<i>ZmATG2</i>		-----	
	<i>HvATG2-1</i>	136	DKHCSTASRDVDEGVKRIANAVKWFNTFKIKFKNTYVVFDPQTILDNKISEFNRSLVFRVKEIEFGTNLS---	207
	<i>HvATG2-2</i>	77	SNPCSTASRDVDDGVKRIANAIKQFLTRFNIKLRNTYVVFDPQSLDKRALEFNRSLVFRTKEIQCGTNFS---	148
	<i>AtATG2</i>	145	LMNAAKSASIDVHEGVKTVAIKVWFLTSFHVKIKNLIIAFDPDFGKKQSEAGPRPTLVLRMTIEEGISSEEQVS	219
	<i>OsATG2</i>	141	GNQCSTASRDVDKGVQRIANAVTCFLTNFNIKLKNSYVVFDPQNILDNKVPEFNRSLVFRIKETEFGTNLS---	212
	<i>ZmATG2</i>		-----	
	<i>HvATG2-1</i>	208	-----TDGLVKLNNFVTFHEAVIEFLKMDDVDV---LHQNGLDKATADISSGHSTTSVLTGPIGGFSGTLNLS	272
	<i>HvATG2-2</i>	149	-----TEGPVKLNNLVTFQEAVIEFLKMDDVDA---NLQNDLDRGTADISSNHSTTAVLTGPIGGFSGTLNLS	213
	<i>AtATG2</i>	220	ANESVPDNFLGILNRLANCVKFGQAVVELLMDDDDDDG-----KTCDDKTSNDVTLIMTGVGGSGLNLS	286
	<i>OsATG2</i>	213	-----TDGIIKLHNFVTFHEAVIEFLKMDDVDAHALLQDDLDRGPADISSGHSTTAVLTGPIGGFSGKLNLS	279
	<i>ZmATG2</i>		-----	
	<i>HvATG2-1</i>	273	IPWSNGCLNLKKI---DADVSDSLELLQISSIQWFMDVWDSLHRNQA-IEQIRPHNTADMSLSTSRSALEST--	341
	<i>HvATG2-2</i>	214	IPWNSGCLNFQKI---DADVSDSLELLQMQSSIQWFMDVYDSLCRNSA-DEHNCVHSTADMSMNASRASLCAS	284
	<i>AtATG2</i>	287	IPWNGSLDIRKV---DADISIDPVEVRFQPTIRWFLQLWKTFTSFGSDCFPSVSHSD--F--LTDSPITP--	352
	<i>OsATG2</i>	280	IPWNG--LNFKKL---DADISLNSLELRLQLSSIQWLMVWDSLQRRNLVHEQSYAHNTADISRSASS-----YV	344
	<i>ZmATG2</i>		-----	
	<i>HvATG2-1</i>	342	---LKSGLD SVMIRREDTDQIALSQNRQDKYQDSFLTK---AHV IQDWIPELVVHEDQGDPPSDCDESIDQFFECF	411
	<i>HvATG2-2</i>	285	SSSSKSGSASATASREGLSQRAFSSRSRQHNFQDGYLNKAQAHV IQDWIPDLVVNSDQGEFSDCDESISQFFECF	359
	<i>AtATG2</i>	353	-----NVMVTP---PATLSLGGQEL---EHDITPNLQFIPDWFPSSFSK-KEEDGEVDIGASVDQFFECF	411
	<i>OsATG2</i>	345	SSSSKSGSGSVIASREHLEDTFSQLRQEKTEPESLTM--PYLIPDWIPVL-IHEDHGDPDSVCDESIDQFFECF	416
	<i>ZmATG2</i>		-----	
	<i>HvATG2-1</i>	412	EELRNSQTNLGNSGIWDWTCVSVFNAITFASTLASGSDQVPKEAP-----IEKTLRASIAEISVILLFSDEM DTG	480
	<i>HvATG2-2</i>	360	DELRSSTNLGNSGIWDWTCVSVFNAITFASALASGSDQVPKETL-----IEKTLRASITQIGIILLFSDEMVTG	428
	<i>AtATG2</i>	412	DAMRSYQSASGSGGMWNWTSVFTAINAASSLASGSLLLPSEQQH-----VETSCKVSFAGVSVVLFFQDEVNWK	481
	<i>OsATG2</i>	417	EELMNSQTNLGNSGIWDWTCVSVFNAITFVSTLASGSDQIPKEPP-----IEKTLRASIAEISVLLFSDEM DAG	485
	<i>ZmATG2</i>		-----	
	<i>HvATG2-1</i>	481	DSSVPVSLVNDMRNSEMFSCLSSPQIEQSMMPATASSLNMHHLEAKCQNIHLELETYP--KKLGFKALI----	549
	<i>HvATG2-2</i>	429	SSSIPLNLVKDMRSSEMFSCLSPAHEEQSMISPASTSSLNMHHLEYKCQNIHLDLETYP--KNLRLKASI----	497
	<i>AtATG2</i>	482	GVS-----NVMVTP---PATLSLGGQEL---EHDITPNLQFIPDWFPSSFSK-KEEDGEVDIGASVDQFFECF	514
	<i>OsATG2</i>	486	NSSVPI SQFNDRNSEMFSCLSF AHEEQSMISPAPAAASLNMHHVEAKCQNIHLSLETYP--ENLSLKGSI----	554
	<i>ZmATG2</i>	1	-----MRHSEMFSCLSSSEHFEKSIISPATASSLNMHHLKAKCENIHLDLQTYP--KNVRLKASI----	58
	<i>HvATG2-1</i>	550	AHMKLDEYYSTN-HDSNH-----LHLGTAFLNNNFCREVQAALPEFPF-----AAQDYWVETAGSS	604
	<i>HvATG2-2</i>	498	GHMRLDEYYSTEKHDSH-----TPGSAPFLNSDYCHEVQAALPPFPF-----AAQDYWVESSGYS	553
	<i>AtATG2</i>	515	NSMEIADY CQGGNVVDTA-----NAESQTLIKDLQAKVQTS LPPFA-----SSDMHSDSERLS	568
	<i>OsATG2</i>	555	AAIKLDEYYGSKNNDSDH-----PNLGA AFLNNNFCREVQASLPQSVF-----AYQDYHEETSRRH	610
	<i>ZmATG2</i>	59	AQIKLDEYYHAGNNISDD-----SNLGNHFLNNNL RQG VQASLPQCLF-----AVGDHSVETYEFC	114
	<i>HvATG2-1</i>	605	-----SRRSEKFIKVELLKTFGESTFHYDVS-STDQDGNVSSTLSIYLAPLTSVWHFHTVYMLNLFVSKV	670
	<i>HvATG2-2</i>	554	-----SNSSKLAKVELLKTFGDSTFHYDVISSTDGNSVSSSTLSICLAPLVWVWHFHTVHMLNLFISKI	620
	<i>AtATG2</i>	569	EIVSDGFLFRNKGFAYKTLTVIAAGSGGFQFTVNFQS-SKASHRGSNSFSLSLPPTTFWNLNHSVEMLNDLVNDV	642
	<i>OsATG2</i>	611	-----TNNNDLTKVELLNTFGECV FHYDVS-SSGQDGNPVSSTLSVCLAPLVWVWHFHTIYMLNLFISKI	676
	<i>ZmATG2</i>	115	-----GNSSTELTRVELLKTFGECTFCYDVS-TKDQDGNLVSSSTSMIYLAPLALLVWHFHTIYMLLSFVSNV	180
	<i>HvATG2-1</i>	671	ESDVLHGEHRL--NRDGDERSKSLA---NTSSSDSLKVQIAPSHARIVFCFPSEPS-WDLGRPSILDKFLVIDHT	739
	<i>HvATG2-2</i>	621	ESDVVHGEHKL--HMRGDTERRSKLTTKTNI SPSSGLKVQMALSPSRITICFPTESP-WDLSRPSILDTFLVIDRT	692
	<i>AtATG2</i>	643	SESIPTISHER--NQV-----ASSSKSES LRGSVSI CNARVILWFPFESI-SERFCNSLGQQFIIVDLS	703
	<i>OsATG2</i>	677	ESDVLHGEDIK--HRKNDEKNVNL SMKSNVSLGGSQKVQIALSPARVIFCFPSE-S-WDLSCPMSLDKFLVIDHT	747
	<i>ZmATG2</i>	181	ESDLSHGEHKI--QKHGDEKGSRLTTSTTMSSSGSLKVQISLAQARIVLFCFPSEFS-WDLSHPSVLDKFLVIDHT	252
	<i>HvATG2-1</i>	740	TSHNSAEASSPLRNERFNDVHP-STQSTSLHLATGNFDIYLVKPSSALD--GICALSR-QTF SALKILSVTRS-D	809
	<i>HvATG2-2</i>	693	SSLDREASSPFRKERPNDAHS-SIPSTSLHLAAGNFDIYLLRPMSEYELGDRSRSLR-QTF FALKIISVTSY-S	764
	<i>AtATG2</i>	704	SSPPSDKE--RAKERSPGEMHF-PSATRSICFSVGDASIYLVTSDLKDS--ETNSYHRQVEFSAYNILHTNNKTR	773
	<i>OsATG2</i>	748	PSLKSGADSSPHQNEMPNDVNA-ITPSTLVHLATGNFDIYLVVRPVNDELNARTCSLSR-QTFSSLKIFSVTGS-N	819
	<i>ZmATG2</i>	253	SCLNMVETASHPQNEMQNEVHL-SKSCTSIHLAVGDI DVYLVKPVNNVLVGRICSSSR-QTF SAMKILSVTGS-S	324
	<i>HvATG2-1</i>	780	YEDSSI RMIRKNHPVTGPEMVSKVWSLP SLHDQKITQKENNKWGVASSTTSQDLVESSLIRQELIRSTEFLH	884
	<i>HvATG2-2</i>	615	CGDSSI MMIRWKYPVTGPEMVSKAWSLPNLHNQKITQRERNCAGVSSYTTSDLEEYSYIRQELLQSTECFLH	839
	<i>AtATG2</i>	774	HQLSTIGMFWDQDRPTVSPWLVERAKMLATQEESIQTOKSGGRGLEFAAVATPKDQDDIYSRKRKEIILASSFLY	848
	<i>OsATG2</i>	820	CHETGITMLWKYP LKDPPEMVSKTWSLPNLHEQKIAQNKNGKWGVSSSTTSEDLEESSSIIRRELLRSTEFLLH	894
	<i>ZmATG2</i>	325	YNDSGITLIRRKYPVTGPEMILNNAWSLPKMHEKIKTNQNSKWAGISPS--SNDLLETGSSMRQELLKSTELFLH	397
	<i>HvATG2-1</i>	885	VQLPCVSVHLNKKDCGLNLQLLDHVL DGLSDGAPHSSSENVKDK--NNEIAIQTSVTFECSMLDICTELDETEMEV	956
	<i>HvATG2-2</i>	840	IKLSSVSVHLNKKDCGLNLQLLDHIPSGLSDGATSSSESGSKSMHINDVAMQSAITFECSFLDICTELNETVVV	914
	<i>AtATG2</i>	849	VHLLPLA IHLDSWQYSKLCNLIEEAKNWL SRMAANTA EQ-----TEESVVCQTSLVVDQDSIDLVRPEPRMGI	917
	<i>OsATG2</i>	895	IKLSCVSVHL SKKDCGILNHL LKNIL DGLSDGATGNFENDSDNCMP IHD TASQTSVIFEC SILDICTELDETEVEV	969
	<i>ZmATG2</i>	398	VQLSCVSLRLSKKDCELLNKLLDHYIKGISNEQTSISGNSKQDSVLINDTFIQTSVIFEC SILDICTELNETVEV	472

HvATG2-1 957 GPSLQTELEGSWNRLKLSISKLSLCSFSNVGGVKNTSFLWVNHGEGELWGSVT-GTDDKT--CEESKDFLLVICK 1028
 HvATG2-2 915 GPLLQTELEGSWNCFKLSISKFSLSFSNVGGTKNASFLLWNHGESLWGSIT-GTNDKA--YAESKVFLLLVACK 986
 AtATG2 918 KKQLQTELPGSWIQFNLRVQKLNLMSPVNLGSGVSGADFFWLAHGEGLTSGSVT-GLPDQ-----ELLLSCN 983
 OsATG2 970 GPLLQTELEGSWNCCLKLSISKFSLLSSNVGGVNNANFLWVNHGEGELWGSIT-GTDDY----EESKDVLLLVCK 1039
 ZmATG2 473 GPLLQAELEKGSWNSVKLVNSKFLCFCFSNVGGLNNAFLWVNHGEGELWGSVS-AKNDKI--PGESKDFLLIVACK 544

HvATG2-1 1029 DS-----ASRRGDGEGNNVLSFGTAGCSVTHIRPNLQENYTSVNVRSGTIVAPGGRMDWVSGISSLFSSSGSS 1096
 HvATG2-2 987 DS-----ANMRGDGEGNNAISFGTSGCSVTHIRPNLQENYTSVSFRSGTIVAPGGRMDWISAMCLLFSSAGSC 1054
 AtATG2 984 NS-----AIKRGNGGGSNALSSRFAGLDLFLHQEPGICNDYLAVSARGCTISAVGGRLDWIEVATSFSSFEDE 1051
 OsATG2 1040 DS-----ASRRGDGEGSNILSFGTAGCSVTHIMNPFKQKNYTSINVRSATAVAPGGRMDWISAILCLLFSSASD 1107
 ZmATG2 545 DS-----ACRRGDGEGTNVLSIGAAGCSVTHIRPNLKENYTSVDVRSGTIVAPGGRMDWINAICLLFSSSGSD 612

HvATG2-1 1097 GTEQSKNSNSTNNSQAGEPFWSSFFLELADVALSYEPHLKNSSFNADAPDCKFFSCLLAASSFKLHNKSA----- 1166
 HvATG2-2 1055 GTEQSNNSRTEDNLC--PSDRSSFFLELVDVAASYESHVKNSTFSAEAHDRKLFSCILAASSFKLHSISA----- 1122
 AtATG2 1052 KKTQEIINSS-----SSSGSSFILNFVDVGLSYEPHENTDHLRQA-SDPWVACLVAASSFSLSKKSL----- 1112
 OsATG2 1108 GTEQPANSSSTMNDSSQGEPPSSLFLELVDVAVSYEPHFRSSALSAETPDCKYFSCLLAASLFLKHSKSA----- 1177
 ZmATG2 613 RTEKSDDSNTPNYSQSGEPYSSSLFIELADVAVSYPHFHKSTLSAGAADRKFSSCLLAASSFKLHNKSA----- 682

HvATG2-1 1167 -----SDS-----AATDFDIQLRDLGLLICESSGSKNVTCGYDVEYLRQMGYAKIGHNTFIEA 1219
 HvATG2-2 1123 -----SDS-----TATDFDIQLRDLGLLICESSGSKNATCGYGDYLRKMGYTKIARDTFIEA 1175
 AtATG2 1113 -----VDS-----IRNDYRIRIQDLGLLLSVDFDL SKLGGTY SSEHLHESGYVKVANDSLIEA 1165
 OsATG2 1178 -----SNS-----TATDFDIQLRDLGLVICGSSSFKNVSCGYGADYLRMGYAKIVQNTFIEA 1230
 ZmATG2 683 -----SAS-----AATDFDIQLRDLGLVLIQSSGSTNGTCSYGVDYLRQAGYKVVQNTFIEA 735

HvATG2-1 1220 ALRTDT--SFWKLEISESLFDIGTCRDTTHGLVRLVSQQLKLY-APDMRDALAHQSRWNI VQQANAAQNMPSDA 1290
 HvATG2-2 1176 TLRIDT--SFWKLEISDSQFDIGTCRDTTHGLIQLCSQLKLY-APDMRDALVHLQSRWNSVQQANNNHMTSDA 1246
 AtATG2 1166 ILRTNSENGLLWELECSKSHLV IETCSDTTSGLIRLATQLQQLL-APDLEESAVHLQTRWDSIQQANARNDLDIS 1239
 OsATG2 1231 VLRIDT--SFWKLEISDSQFDIGTCRDTTHGLIQLCSQLKLY-APDMRDALDHLQSRWNSVQQANKQNMGTDV 1301
 ZmATG2 736 SLRLDS--SFWKLEISDSQFDIGTCRDTTHGLIQLCSQLQQLY-GPDMQDALDHLQSRWNSVQQANKQNMAADA 806

HvATG2-1 1291 SDMSE-----STDNLADSGECKSDGLLDDIIEDAFYTDQAYTDYNFWDNRCHN-SSSEMNI-----AEYE 1349
 HvATG2-2 1247 SDKSE-----SSIDNLAYSGECLSDGLLDDIIENAFYTDQDYKAYNVSSRNCHN-SPCSNG-----TDVD 1305
 AtATG2 1240 DRLSSSDSSGEMKYLRLESENETGVIGLMDEINEDAFQFDVNP-TYQSDSVECCNNYMSPHGISHG-----QAYN 1308
 OsATG2 1302 SEKSE-----SSIDNLTDEECKSDGLLDDIIENAFCTDQDFASY-----SLSGSEMD-----EEFG 1353
 ZmATG2 807 SDKSE-----SSLEILVDSGDYQSDGLLDDIIENAFNTEDCMDNTN-FWENNYHHLFSSSETD-----DGEF 866

HvATG2-1 1350 MNMANPEAADVGVSQI-----VAPKANTAQIPI-----KQNSCPEQIIDSYYMP---DLLNSSLSSSPCNVN 1408
 HvATG2-2 1306 SKSPTPGATDVGVSHILFGSSLATPKVNTTEIPL-----KQDSCHEQIIDSYYMP---DLHTSS--STLCNVG 1368
 AtATG2 1309 WV--PATEKLPSNQSIGSS-----SRINSESSQVFLERE-SLPEIFENYCLS---EFRPSSEVP---QEG 1365
 OsATG2 1354 LSKA-----IPEANDACISLESLLVTPEASTSDDLIESYYMP---PSSSS---TLYN--- 1400
 ZmATG2 867 LNAATSHVF-----PISTPEGNVQTQISL-----EQNVCPDQIIDSYCVP---EFHQSL--STLCDEE 918

HvATG2-1 1409 HQ-SSGDDARKTMDCCDDGGWYNNPLTIVENHVYKRNPS-HGEHVYQQEGKPAVCSLNSDESCNLKQKILIHIDID 1481
 HvATG2-2 1369 HQCI SGDDAYKTMFEFEDGGWYNSIPLTIVESHVLETNPN-QGGHVARQEGKPTVCGLYEESCYLKQKVI IHDVN 1442
 AtATG2 1366 DSSGRELFPEPDLRRGNSGWYDDASLRIVEDHVSATEEDHEEHI LD--GECSSFGQTSYSAVAANGRI LLKNID 1438
 OsATG2 1401 --EDQGNCAPRTVECDGEWYNNFPTI-DENHVQR-NKP-REEQIFQKQKPAIFILNSDESCSLKQKVL IHDID 1470
 ZmATG2 919 HKCTSGDNSHRTLESEDAGWYNNVPLTIVENHV LK-K--KNEQVLQHKV-SSVCSLNPDEYCNLKQKVHIHDID 988

HvATG2-1 1482 VKWRMYAGDDWPLAHNDSTSHLCSNGRDRSSSLEFIVSGLGVQFDMYPDGA VSVSRLSISAQDLNLCDQNTHAPW 1556
 HvATG2-2 1443 VNWRMYAGDDWSLAQKDVNSFSCSSGRDMSSSLEFLISGLGVQFDMYPDGGVYVSKLSISARDINLCDQ RVDAPW 1517
 AtATG2 1439 LKWRIYSGSDWHD SRKKG ENFKHTKGRD TTSCELEL SG----- 1477
 OsATG2 1471 VKWRMYEGNDWKL AQKDTISRPCSNGRDKRSYLEFIMSALNIQFNMYPDGDI FVSKLSISAKDINI CDQSTHAPW 1545
 ZmATG2 989 VKWRMYAGDDWLPQKDLTSLTCTDGRNRS SLEFIVRGLNIQVDMYPNGDVSISRLSVA AEDITLCDQSIHAPW 1063

HvATG2-1 1557 KMLVLCYSSKDYPRESCSTAFKLELESVRPEPQAPLEDYRY----- 1597
 HvATG2-2 1518 KMLVLCYDP-DHPRESCSSAFTLELESVKPEPQTPLE----- 1553
 AtATG2 1478 --VLGYYSNKDHPRDSSSYAFKLELKA VRPDPETPLEENRFFGANS L-----EKPVV 1527
 OsATG2 1546 KMLVLCYNSKDYPRESCSSAFMLELESVRPEPQAPLEDYRLHLEILPLQLHL DQQLNFLISFFQNDLCNN-PNL 1619
 ZmATG2 1064 KLVLCYNSKDYPRESCSSAFRLELESVRPEPQAPLEDYRLHLEILPLQLHL DQEQLNFLINFFKNDSCNNDPHL 1138

HvATG2-1 -----
 HvATG2-2 -----
 AtATG2 1528 SMGDSGGSTMSVSVQGHNIIEEALPYFQKFDIWPVNVRVDYSPHHVDIAALTGKGYAELVNLVPWKGIELQLKH 1602
 OsATG2 1620 ACENENIDAQSTMYSRDTIADEALLPFFQKFDVKPLVLHINYIPRHFD PVALSKGNYAELLNIFPWKGIDLK LKQ 1694
 ZmATG2 1139 HCENDTV DVKSTSNGSNMVVDEALLPFFQKFDVKPLILHINYIPRQFDPIALSKGNYAELLNIFPWKGIDLK LKQ 1213

HvATG2-1 -----
 HvATG2-2 -----
 AtATG2 1603 VHAAGIYGWGNVCETILGEWLEDV SQNQIHQLLKG IPTVRSLSALYAAALKLVSSPVESYRKDRRLVKG VQRGTV 1677
 OsATG2 1695 VSAMGVYGFNNICEIVAAEWLEDISKQNVHKLKGLPPIKSLVAVSSGTTKLVSLPIKSYKKDRKLLKGMQRGAV 1769
 ZmATG2 1214 VSAMGIYGWNSIGD TVAAEWLEDISKQNVHKLKGLPPIRSLVAVSGSTRKLVSLPIKSYKKDRKLLKGMQRGAV 1288

HvATG2-1 -----
 HvATG2-2 -----
 AtATG2 1678 AFLRSISLEAVGLGVHLAAGAHDI LLRAEYIFASSPS--LPQ----- 1717
 OsATG2 1770 AFIRSVSIEAVGLGVHLAAGAHDMLLKTESALTAIPPLASR----- 1811
 ZmATG2 1289 AFIRSVTIEAVGLGVHLAAGAHDMVLKTECALTTVPPLASC----- 1330

HvATG2-1 -----
 HvATG2-2 -----
 AtATG2 1718 -----PQGRKTKNVRHNQPRNAKQGM LKACESIGDGIKTASALVRTPLKKYQRG-DG 1769
 OsATG2 1812 -----EAKRTKDNVRANQPESAQEGLKKAYESLTDGFGRTASALIGNPIKVYNRG-AG 1863
 ZmATG2 1331 -----EVKRTKHNI RANQPESAQQGMKQAYESLTDGFGRTSSAIGNPIKVYNRG-AG 1382

HvATG2-1	-----	
HvATG2-2	-----	
AtATG2	1770 AGSAFATVVQGVPTAAIAPASACARAVHSALVGIRNRSII SPFSLDPEHKKESMEKYLGPDKQRKQDQHR	1839
OsATG2	1864 AGSALATAICGAPGAAVAPLSASFRAAHYTLLGIRN-----SLDPERKKESMYKYHGPPQL-----	1919
ZmATG2	1383 VGSVLATAICGAPAAAVAPI SASARALHYALLGLRN-----SLDPEHKKESMYKYQGPSQA-----	1438

<i>HvATG3</i>	1	-MQV	KQKVYEL	YKGTVERV	TGPR	TVSAFL	EKGVL	SVPEF	ILAGD	NLVSK	PTWSWEK	-GDPS	KRKPYP	LP	SDKQFL	74																									
<i>OsATG3-1</i>	1	-MQV	KQKVYEL	YKGTVERV	TGPR	TVSAFL	EKGVL	SVPEF	ILAGD	NLVSK	PTWSWEA	-GDPS	KRKPYP	LP	PDKQFL	74																									
<i>OsATG3-2</i>	1	-MQV	KQKVYEL	YKGTVERV	TGPR	TVSAFL	EKGVL	SVPEF	ILAGD	NLVSK	PTWSWEA	-GDPS	KRKPYP	LP	PDKQFL	74																									
<i>TaATG3</i>	1	MGQV	KQKVYEL	YKGTVERV	TGPR	TVSAFL	EKGVL	SVPEF	ILAGD	NLVSK	PTWSWEA	-GDPS	KRKPYP	LP	SDKQFL	75																									
<i>ScATG3</i>	1	-----	MIRSTL	SSWREYL	TPIT	HKSTF	LTGQ	ITPEEF	VQAGD	YLCHMF	PTWKWNEESS	DSI	SYRDL	F	PKNKQFL	74																									
<i>AtATG3</i>	1	-MVL	SQKLHEAF	KGTVERI	TGPR	TSAFK	EKGVL	SVSEF	ILAGD	NLVSK	PTWSWES	-GASK	RKPYP	LP	SDKQFL	71																									
<i>CrATG3</i>	1	MSNLR	RHTLHTL	FKQTVETV	TPPL	TKSQF	EKKRVLT	PD	EFVAAGD	YL	VHACPTWSWEG	-GDPK	KRRTY	F	PPNKQFL	75																									
<i>HsATG3</i>	1	MQNV	INTVKGKALEVAEY	LPVL	KESK	FKETGV	ITPEEF	VAAAGD	HLVHH	CPTWQWAT	-GEEL	KVKAYL	PTG	KQFL	75																										
<i>MmATG3</i>	1	MQNV	INTVKGKALEVAEY	LPVL	KESK	FKETGV	ITPEEF	VAAAGD	HLVHH	CPTWQWAT	-GEEL	KVKAYL	PTD	KQFL	75																										
<i>DmATG3</i>	1	MQSV	LNTVKGKALNVAEY	LPVL	KESK	FKETGV	ITPEEF	VAAAGD	HLVHH	CPTWQWAA	-GDET	KTKPYL	PKDKQFL	I	75																										
<i>XIATG3</i>	1	MQNV	INTVKGKALEVAEY	LPVL	KESK	FKETGV	ITPEEF	VAAAGD	HLVHH	CPTWQWSA	-GEESK	I	KPYL	PNDKQFL	75																										
<i>DrATG3</i>	1	MQNV	INSVKGTALGVAEFL	TPVL	KESK	FKETGV	ITPEEF	VAAAGD	HLVHH	CPTWKWAS	-GEEAK	VKPYP	LP	NDKQFL	75																										
<i>HvATG3</i>	75	TRNV	PCLRR	AMSV	EE	YDAAA	E	VVLDD	DDGE	GW	LATHG	---	VQASEK	EEED	IP	SMDTL	DIGKVEE	I	KSIPSY	146																					
<i>OsATG3-1</i>	75	TRNV	PCLRR	AVSL	EE	YDAA	GA	E	VVLDD	DDGE	GW	LATHG	---	VQASK	EEED	IP	SMDTL	DIGKTEG	I	KSIPSY	146																				
<i>OsATG3-2</i>	75	TRNV	PCLRR	AVSL	EE	YDAA	GA	E	VVLDD	DDGE	GW	LATHG	---	VQASK	PEEED	IP	SMDTL	DIGKTEG	I	NSIPSY	146																				
<i>TaATG3</i>	76	TRNV	PCLRR	AAVE	EE	YDAA	GA	E	VVLDD	DDGE	GW	LATHG	---	LQASEK	EEED	IP	SMDTL	DIGKVEE	I	KSIPSY	147																				
<i>ScATG3</i>	71	IRKVP	CDKRA	EQCV	EE	VEGPD	VI	MKGFA	EDG	DD	VLEYIG	---	SETEH	VQST	PAGG	TK	DSS	-----	---	128																					
<i>AtATG3</i>	75	TRNV	PCLRR	AA	SV	AE	DY	EAA	GG	E	VLDD	-EDN	GW	LATHG	---	-KPKDK	KEED	NL	PSMAL	D	INEKNT	I	QSIP	TY	145																
<i>CrATG3</i>	76	TRNV	PCLRR	A	TELE	G	-Y	NP	N	-SEF	DVGGG	EGED	AW	VATHS	N	-PAA	ASG	SAGK	GEVPS	ID	GAGAG	SGG	GAGA	AAG	146																
<i>HsATG3</i>	76	TKNV	PCYKR	CKQME	Y	---	SDE	LE	A	I	EE	DG	DGG	WVD	TYHN	-	TG	IT	G	TEAV	KE	IT	LE	N	-K	D	N	I	R	L	Q	D	S	C	A	L	C	E	145		
<i>MmATG3</i>	76	TKNV	PCYKR	CKQME	Y	---	SDE	LE	A	I	EE	DG	DGG	WVD	TYHN	-	TG	IT	G	TEAV	KE	IT	LE	N	-K	D	S	I	K	L	Q	D	S	C	A	L	C	E	145		
<i>DmATG3</i>	76	TRNV	PCYKR	CKQME	Y	---	VGE	-	ETL	VE	E	S	DGG	WVETH	LQ	NDD	GT	TQ	LQ	E	I	C	E	L	T	M	E	E	T	K	E	E	M	T	P	D	S	K	A	P	147
<i>XIATG3</i>	76	TKNV	PCYKR	CKQME	Y	---	SDE	Q	E	A	I	EE	DG	DGG	WVD	TFHH	-	TGL	SG	V	TEAV	KE	IT	LE	T	-Q	D	C	G	K	T	T	D	N	I	A	V	C	D	145	
<i>DrATG3</i>	76	TRNV	PCYKR	CKQME	Y	---	SDE	LE	A	I</																															

D	HvATG4	1	MTSLPERGAAPSPDPSLEGAAA-----VASSSSSTSSAPDEQR-----KNGSPKQCKASILSSVLT	57
	AtATG4a	1	MKALCDRFVP-----QCCSSSSKSDTHD---KSPLVSDSGPSPDNKSKFTLWSNVFTSSSS	52
	AtATG4b	1	MKAICDRFVP-----SKCSSSSTSEKRDISSPTSLVSDSASSDNKSNLTLCSDVVASSSP	55
	OsATG4	1	MTSLPGRGVSPSSSDPLCEGNAA-----PSSSSSSG---QDLKQ-----LKN---SILSCVFSSPFS	51
	ZmATG4	1	MTSLPERGESVPVPLDSLRLQDSAVTVLAAAFAVSSAGSDRKEDSG-----SRQPKASILSGVFSPPFA	64
	HvATG4	58	I---FEPDQDHS-----SRSGGHASGSYAWSRVLRRFV-GGSSMWRF---LG---CGKALTAGDVWFLGKCYK	115
	AtATG4a	53	VSQPYRESSTSGHKQVCTTR-----NGWTAFFVKRVSMASGAIRRFQERVLPNRTGLPSTTSDVWLLGV	119
	AtATG4b	56	VSQLCREASTSGHNPVCTTH-----SSWTVILKTASMASGAIRRFQDRVLPSPRTGISSTSEIWL	122
	OsATG4	52	I---FEAHQDSSA-----NRSLKPHSGSYAWSRFLRRRIA-CTGSMWRF---LG---ASKALTS	110
	ZmATG4	65	I---FEGQQQSSSPACDARSTKSSSGSYGLSRILRRFV-GSSMWRL---LG---CGRVLTSSDVWFL	128
	HvATG4	116	LSSEE-SSSDSDSEGGHVAFLEDFSSRIWI TYRKGFDAISDSKLTSDVNWGCVMVRSSQMLVAQAL	189
	AtATG4a	120	ISADE-NSGETDTGTVLAALQLDFSSKILMTYRKGFEPFRDTTYTSDVNWGCMIRSSQMLFAQALL	193
	AtATG4b	123	ISEGE-SSSEADAGRVLAAFRQDFSSLILMTYRRGFEPIGDTTYTSDVNWGCMLRSQMLFAQALL	196
	OsATG4	111	LSSEE-LSNSDCESGNAAFLEDFSSRIWI TYRKGFDAISDSKYTSDVNWGCVMVRSSQMLVAQAL	184
	ZmATG4	129	VSPREEESGDSGSHAFLDFSSRIWI TYRKGFDAISDSKLTSDVNWGCVMVRSSQMLVAQAL	203
	HvATG4	190	KPAQNPSPNPEHIRILHLFGDSEVCAFSIHNLQAGKSYGLAAGSWVGPYAMCRAWQTLIRTNREQPEVIN	264
	AtATG4a	194	KKSELP-EQEYLETLEPFGDSEPSAFSIHNLIIAGASYGLAAGSWVGPYICRAWESLACKKRKQTD--	265
	AtATG4b	197	KKDSEPADEKYLEILELFGDTEASAFSIHNLILAGESYGLAAGSWVGPYAVCRSWESLARKNKEETD--	269
	OsATG4	185	KPSQKPSPSEYIGILHMFGDSEACAFSIHNLQAGKSYGLAAGSWVGPYAMCRAWQTLVCTNREH	259
	ZmATG4	204	KPPEKPYNPDIYGLHLFGDSEACAFSIHNLQAGRNYGLAAGSWLGPYAMCRAWQTLIRTNREQADAV	278
	HvATG4	265	PMALYVVSVDGEDGERGGAPVVCIDVAAQLCYDFNKGQSAWSPILLVPLVLGLDKINPRYIPLLK	339
	AtATG4a	266	PMAVHIVSGSEDGERGGAPILCIEDATKSCLEFSKGQSEWTPILLVPLVLGLDSVNPRYIPSL	340
	AtATG4b	270	SMAVHIVSGSEDGERGGAPILCIEDVTKTCLFSEGETEWPPILLVPLVLGLDRVNPRYIPSL	344
	OsATG4	260	PMALYVVSVDGEDGERGGAPVVCIDVAAQLCCDFNKNQSTWSPILLVPLVLGLDKLNPRYIPLLK	334
	ZmATG4	279	PMALYVVSVDGEDGERGGAPVVCIDVAAQLCSDFNKGPSTWSPILLVPLVLGLDKINPRYIPLLK	353
	HvATG4	340	ILGGKPGASTY-----	350
	AtATG4a	341	ILGGKPGASTYIVGVQEDKGFYLDPHEVQVTVNKETPDVDTSSYHCNVLRYPVLES	412
	AtATG4b	345	ILGGKPGASTYIVGVQEDKGFYLDPHDVQVTVVKENQDVDTSSYHCNTLRYPVLES	416
	OsATG4	335	ILGGKPGTSTYIAGVQDDRALYLDPHEVQLAVDIAADNLEAGTSSYHCSTVRDLALDLIDPSLA	409
	ZmATG4	354	ILGGKPGTSTYIAGVQDDRALYLDPHEVQMTVDIALDNLEADTSSYHCSVVRALALEQIDPSLA	425
	HvATG4		-----	
	AtATG4a	413	-----DDFDDFCRLALKLAEESSNGAPLFTVTQTHTAINQS-----	447
	AtATG4b	417	-----DDFDDFCIRATKLAGDSNGAPLFTVTQSHRRNDCGIAETSS-----	457
	OsATG4	410	LLPDKMLGHHLSSLQSWFSYLLCL SAYVDDFDDFCRSASELVDKANGAPLFTVVQSVQPSKQMYNEESSGDG-M	483
	ZmATG4	426	-----DDFDDFCRSASELAEKANGAPLFTVVQSIEPSKQMYKQDDGLGCSGS	472
	HvATG4		-----	
	AtATG4a	448	--NYGFADDDSEDEREDDWQML	467
	AtATG4b	458	--STETSTEISGEEHEDDWQLL	477
	OsATG4	484	DSINVEGLDGSGETGEEEWQIL	505
	ZmATG4	473	SMANDDDL DGSGE--AEEWQIL	492

E

HvATG5 1 MAAAPWDKEAAWSEEAARLVWGGAVPLQVHLHDADVTALPPPPFLT LGPR-----IGYFPLL VST IKAHFS 69
HsATG5 1 -----MTDDKDVLRDWWFGRIPTCFTLYQDEITERE-AEPYYLLLP-----VSYLT LVT DKVKKHFQ 57
MmATG5 1 -----MTDDKDVLRDWWFGRIPTCFTLYQDEITERE-AEPYYLLLP-----VSYLT LVT DKVKKHFQ 57
ScATG5 1 -----MNDIKQLLWNGELNVLVSDPSFLMKGSPREIAVLRIRVPRETYLVNMYPLIWNKIKSFLS 61
DmATG5 1 -----MAHDREVLRIWEGQIGICFQADRDEIVGIK-PEFFYLMISR-----LSYLP LVT DKVRKYFS 57
AtATG5 1 -----MAKEAVKYVWEGAIPLOIHLHKS DVASHAPPPALV LAPR-----IGYLP LL IPL IKPYFK 56
OsATG5 1 ---MAAQRDDEAGWSAEAAARRVWGGAVPLQVHLHDADVTALPPPPFLT LGPR-----IGYLP LL VPI IKAHFS 66
BdATG5 1 ---MAARDEEA EWSEEAARWLWEGAVPLQVHLHDADVTALPPPPLL ILGPR-----LGYP LL VSR IRAHFS 66
SoATG5 1 ---MAAPHDEAAAWSEEAARRVWAGAVPLQVHLHDADVTALPPPPFLT LGPR-----IGYLP LL IPI IKAHFS 66
ZmATG5 1 ---MAAPHDEAAAWAEAAARRVWAGAVPLQVHLHDADVTALPPPPFLT LGPR-----IGYLP LL IPI IRAHFS 66
SbATG5 1 ---MAAPHDEAAAWSEEAARRVWAGAVPLQVHLHDADVTALPPPPFLT LGPR-----IGYLP LL IPI IKAHFS 66
RcATG5 1 -----MEAQKNVWGAIPLOIHLHESEVTT HQRP PPA LI LGPR-----IGYLP LL IPI IKPHFS 54

HvATG5 70 SSLPPGVDT--VWFEYKGLPLKWWYIPIGVLFDLLCAD-PERPWNLT VHFR-----GYPADILSPCE 127
HsATG5 58 KVMRQEDIS-EIWF EYEGT PLKWHYPIGLLFDLLASS-SALPWNITVHFK-----SFPEKDLLHCP 116
MmATG5 58 KVMRQEDVS-EIWF EYEGT PLKWHYPIGLLFDLLASS-SALPWNITVHFK-----SFPEKDLLHCP 116
ScATG5 62 FDP L T DSEK-YFWFEHNKTPIPWNYPVGVLF DCLAGKSATFTTSFENQVKDVLTFRLRIHLVMGDSLPTTIPIAS 135
DmATG5 58 RYISAEHQDGAYWVDFNGT PLRLHYPIGVLYDLLHPEEDSTPWCLTIHFS-----KFPEDMLVKLN 118
AtATG5 57 DSLPPGEDS--IWF DYKGF PLKWWYIPIGVLF DCLCAE-PERPWNLT I HFR-----GYPCNLIIPCE 114
OsATG5 67 STLPPGIDT--VWFEYKGLPLKWWYIPIGVLYDLLCAD-PERPWNLT VHFR-----GYPSEILTLCD 124
BdATG5 67 STLPPGIDT--VWFEYKGLPLKWWYIPIGVLF DCLCAD-PERPWNLT VHFR-----GYPGEVLSPCE 124
SoATG5 67 SALPPGVDT--VWFEYKGLPLKWWYIPIGVLF DCLCAD-PERPWNLT VHFR-----GYPSEILSPCE 124
ZmATG5 67 NALPPGVDT--VWFEYKGLPLKWWYIPIGVLF DCLCAD-PERPWNLT VHFR-----GYPSEILSPCE 124
SbATG5 67 NALPPGVDT--VWFEYKGLPLKWWYIPIGVLF DCLCAD-PERPWNLT VHFR-----GYPSEILSPCE 124
RcATG5 55 STLPPGSDT--VWFDYHGLPLKWWYIPIGVLF DCLCAQ-PERPWNLT VHFR-----GYPNNLIIPCE 112

HvATG5 128 GEDSVKWNYNNSLKEAFAIITGNSKNVMNMSQADQLAMWESVRKGDLSYMNISTKLKLGPF EEDFLVRTSSLEP 202
HsATG5 117 SKDAIEAHFMSCKEADALKHKS-QVINEMQKKDHQQLWMGLQNDRF DQFWA INRKLMEYPAEENGFR-----183
MmATG5 117 SKDAIEAHFMSCKEADALKHKS-QVINEMQKKDHQQLWMGLQNDRF DQFWA INRKLMEYPAEENGFR-----183
ScATG5 136 SKTQAEKFWFHQWQVCFILNGSSKAIMSLSVNEARKFWG SVITRNFQDFIEISNKISSSRPR-----198
DmATG5 119 SKELLESHYMSCLKEADVLKHRG-LVISAMQKKDHQQLWLGLVNEKFDQFWAVNRRLM EPGDLESFK-----185
AtATG5 115 GEDSVKWNFVNSLKEAQYIINGNCKNVMNMSQSDQEDLWTSVMNGDL DAYTRLSPKLMKGTVEDEFSRKTSLSSP 189
OsATG5 125 GEDSVKWSYMNLSLKEAFAIITGNSKNVMNMSQADQ GALWQSVMKGNLDGYMNI STRLKLGPFEEDCLVRTSSVEG 199
BdATG5 125 GEDSVKWSYMNLSLKEAFAIITGNSKNVMNMSQADQVAMWESVMKGNLDGYMNVSTRLKLGPFEEDCVVRTSSAER 199
SoATG5 125 GEDSVKWSYMNLSLKEATFIITGNSKNVMNMSHADQVALWESVMKGNVDGYKNI STRLKLGPFEEDGLIRTASAER 199
ZmATG5 125 GEDSVKWSYMNLSLKEATFIITGNSKSVMNMSHADQVALWESVMKGNLDGYKNI STRLKLGPFEEDDLVRTASVER 199
SbATG5 125 GEDSVKWSYMNLSLKEATFIITGNSKSVMNMSHADQVALWESVMKGNLDGYKNI STRLKLGPFEEDGLVRTASAER 199
RcATG5 113 GEDSVKWSFINSLKEADYIINGNCKNVMNMSQSDQVELWRSVMNGNLEAYMHAS SKLKLGTIDEFTLKPDCSCP 187

HvATG5 203 --RQGSDEPESPGSVKPCRV PVRLYVRRVQQDLEYLEDAIPVSDWESVSYINRPFEIRKEGGRSYIALEHALET L 275
HsATG5 184 -----YIPFRIYQ-----TTTERPFIQKLFRPVAADGQ-----LHTLGD L 218
MmATG5 184 -----YIPFRIYQ-----TTTERPFIQKLFRPVAADGQ-----LHTLGD L 218
ScATG5 199 -----HILTIQTSR-----TSGTFRISQPTISMTG-----VNPTLKD I 232
DmATG5 186 -----NIPLR IY-----TDDDFTYTQKLISPI SVGGQ-----KKS LAD L 219
AtATG5 190 QSQQVVPETEVAGQVKTARI PVRLYVRSLNKDFENLEDVPEIDTDDDISYLNRPFEFLKEEGK-CFTLRDAIKSL 263
OsATG5 200 --RQGSDEPESPGSGKPCRV PVRLYVRSVQEDLYDLEDALPVGDWESISYINRPFEVRREEGRSYITLEHALKTL 272
BdATG5 200 --RQGSDEPESPGSSKPCRV PVRLYVRSVQEDLEYLEDAIPVSDWEGVSYINRPFEIRKREGRIYITLQDALET L 272
SoATG5 200 QRQQNSDEPESPGSSKLCRV PVRLYVRNVQEDLEYIEDAVPVSDWEGVSYINRPFEIRKVEGRSYITLEHALQTL 274
ZmATG5 200 QRQQNSDEPESPGSSKPCRV PVRLYVRNVQEDLEYIEHAVPVSDWENVSYINRPFETRKAEGRSYITLEHALQTL 274
SbATG5 200 QRQQNSDEPESPGSSKPCRV PVRLYVRNVQEDLEYIEDAVPVSDWEGVSYINRPFEIRKVEGRSYITLEHALQTL 274
RcATG5 188 KSHKTTGDVDMAGHVKTGKI PVRLYIWTVSEDFELEDIPKIDSWDKISYINRPFEFHREEGK-CFSLHDALKTL 261

HvATG5 276 LPEFFSSKPAARAADPEPAATTDPSEPKDSDTSPSTH--HDEKPPASPQETDAVAKTK---LKLVRVQGI E LDM 345
HsATG5 219 LKEVCPSAIDPEDGEK-----KNQVMIHGIEPML 247
MmATG5 219 LREVCPSA VAPEDGEK-----RSQVMIHGIEPML 247
ScATG5 233 EGDILDVKEGINGND-----VMVICQGI EIPV 259
DmATG5 220 MAELS-TPVRRAVG-----CRTHGIDLHE 242
AtATG5 264 LPEFMGDRAQTSGEERSIDD-----TEEADGSR E MG-----EIKLVRIQGI E M K L 308
OsATG5 273 LPEFFSSKASRIPDDSETAPQAPDSAPNDDSDVTPRSCEKLESSASSSPQEANVANKGKI--VKLVRVQGI E VDM 345
BdATG5 273 LPEFFSSKPAVATAESEPAETS-DSAPDDSDTS-----RPALSSQRESSATKNAK--VKLVRVQGI E PKM 334
SoATG5 275 LPEFFSSKPAGSADGSQHAGAL-DSTADSSNTTNSSS-SQEAKQALASPREAGASKES--GEAGKVQGI E L GH 344
ZmATG5 275 LPEFFSSKPPGSADGSQHAGAM-DAAADSSDATNSSRSQAEQALASPAEAGSAKRAK--VKLVRVQGI E LDM 345
SbATG5 275 LPEFFSSKAASRADGSHAGAL-DSAADSSDATNSSRSKAEQALASPREVGA AKTK--VKLVRVQGI E LDM 345
RcATG5 262 MPEYLADKSLIDEEPFRVEDEEFPFRVEDDEQKVSSEEASSNRKAADGGEISSQSAHSYGAAEIKLVRIQGI E PKL 336

HvATG5 346 DIPFLWANNLKNPERFLHVCVYVSA-----371
HsATG5 248 ETPLQWLSEHLSYPDNFLHISII PQPTD-----275
MmATG5 248 ETPLQWLSEHLSYPDNFLHISII PQPTD-----275
ScATG5 260 HMLLYDLYSKLR SFDGFLYITLVP IKGDKASSEL 294
DmATG5 243 ETQLQWMSEHLSYPDNFLHLSVDYKDV-----269
AtATG5 309 EIPFSWVVNNLMNPEFYLHISVLVKAQR-----337
OsATG5 346 DIPFLWANNLKNPECYLHICVYVGTRKREP K DGR 380
BdATG5 335 SIPFLWANNLKNPEHYLHVCVYVASPRI-----363
ZmATG5 345 DHPFLLVAHNLENPGYYP---TFGLRRP-----369
SbATG5 346 DIPFLWVADHLKNPEYVHICVYVGTRKQ-----374
RcATG5 346 DIPFLWANNLKNPEYVHICVYVGTRKQ-----374
337 EIPFSWVVNNLKNPEHFLHICVYVKFPNVKSF---368

Gene	Protein	Accession	Length
HvATG6	1	-----	14
OsATG6-1	1	MSVTVCSDDDESVP TLFHRLRLRFDLGRHEIGASGRRKSRVEREDHVSVERGVVDSGD	73
OsATG6-2	1	-----	14
OsATG6-3	1	-----	14
ScATG6	1	-----	14
AtATG6	1	-----	14
HvATG6	15	GRGVDPSLPFRFKCQECHELRALVVVGVESFP-DRLPAHANSGMHASSVQGSIMGASRMDSSYVVL	88
OsATG6-1	74	AGGVDPSPFRFKCQECHELRALVVVGVDSSFAADKLPAQATS-GHVSSVHGSIMGASRMDNSYVVL	147
OsATG6-2	15	GGGVDPSPFRFKCQECHELRALVVVGVESFT-DKLPAHANSGMNVSSVQGSIMGASRMDNSYVVL	88
OsATG6-3	15	AGGVDPSPFRFKCQECHELRALVVVGVDSSFA-DKLPAQATS-AHASSVHGSIMGASRMDNSYVVL	87
ScATG6	15	SLEGLSLTQRNLLLSNNSIITATNENVISNKGIEAADNCGPQIPKERLRLLEIQNIKDLNLKDDKLITDSFVFL	89
AtATG6	1	-----	20
HvATG6	89	PRPPSAAA---RHVEPNQSTRAMEGSYIMLPAAASIIYKTSTSEGGGAHLSPPNLNSTSPSPGNNSG	160
OsATG6-1	148	PRPPSAAA---PHIEPNQPTTRAMEGSYIVLPAAASIIYKTSTSEGGGAQLPPPSINSSSLLTGNS--	217
OsATG6-2	89	PRPPSAGI---PRAEPNQPTTRAMEGSYIVLPAAASIIYKTSAEGGGAQLSPTSMNPGSPLPGNN--	158
OsATG6-3	88	PRPPSAAA---PHIEPNQPTTRAMEGSYIVLPAAASIIYKTSTSEGGGAQLPPPSINSSSLLPGNS--	157
ScATG6	90	NHDDDDNANITNSREDQRYGNANGNDNKKANSDTSDGTSTFRDHDEEEQEATDEDENQIQLNSKTLSTQV	164
AtATG6	21	PRPRGASS---PQPDATQSGKAMEESFVYVYKSEP-----VSDSGSHNLSELVGQNGPLHSNTSG	86
HvATG6	161	KRAFEIASQTQVEQPLCLECMRVLSDKMDKEIEDVNTDIKAYDAQLRLEQESYNILSET-----	229
OsATG6-1	218	KRAFEIATSTQVEQPMCLGCMRLSDKMDKEIEDVNADIKAEVACLQHLQESYNVLS DAG-----	286
OsATG6-2	159	KRAFEIATSTQTIQEQPLCLDCMRLSDKMEKEIEDVNTDNKAYEACLQRLQEQSYNILSET-----	227
OsATG6-3	158	KRAFEIATSTQVEQPMCLDCMRLSDKMDKEIEDVNADIKAYEACLQHLQESHTVLS DAG-----	226
ScATG6	165	TNVFNILSSOTNIDFPIQDCCNILINRLKSEYDDAIKERDTYAQFLSKLESQNKESISNKQKQYSHNLSE	239
AtATG6	87	TRAFDIAARTQTQVEQPLCLECMRVLSDKLEKEVEDVTRDVEAYEACVQRLEGETQDVLSEAD-----	155
HvATG6	230	IEEEEKKLKAAIEEAQKQYSEVSSEMKDLETKSKQFEELLEERYWHEFNSFQFQLTSHQEERDAVM	304
OsATG6-1	287	IEEEEKKLNAAIEEAQKQYSEISSEMKDLETKSKQFEELLEERYWHEFNSFQFQLTSHQEEREAIL	361
OsATG6-2	228	IEEEEKKLKAAIEEAQKQYSEISSEMCKLETKSKQFEELLEERYCHDLNSFQFQWISHQEERDAVLA	302
OsATG6-3	227	IEEEEKKLNAAIEEAQKQYSEISSEMKDLETKSKQFEELLEERYWHEFNSFQFQLTSHQEERDAI	301
ScATG6	240	LKKEEERLLDQLRLLEMTDDDLDGELVRLQEKKVQLENEKQLKLSQDNLMDLNNIQFNKNLQSLKLQ	314
AtATG6	156	IEEEERKLVAIEETEKKQNAEVNHQLKELEFGKGNRFNELEDRYWQEGNFFQFQLIAHQEERDAI	230
HvATG6	305	ELLKRTNVLNDAFYISHDGVIGTINSFRLGRLPNVQVEWDEINAAWGQAALLHTMAQY-FPKFQY	378
OsATG6-1	362	ELLKRRNVLDNAFYISHDGVIGTINNFRGLRPLNVQVEWDEINAAWGQAALLHTMAQYFTPKFEY	436
OsATG6-2	303	ELLKRTNVLNDAFYISHDGVIGTINNFRGLRPLNVQVEWDEINAAWGQAALLHTMAQYFFPKFEY	377
OsATG6-3	302	ELLKQTNVLNDAFYISHDGVIGTINNFRGLRPLNVQVEWDEINAAWGQAALLHTMAQYFTPKFEY	376
ScATG6	315	DKLRKINIFNATFKISHSGPFATINGLRLGSIPEVSVPWKEINAAALGQLILLLATINKNLKINLVD	388
AtATG6	231	ELLNKTNVLIADFPINRDGEFGTINNFRGLRPLAIKVEWDEINAAWGQAALLHTMCNIFYRPFKQY	296
HvATG6	379	YPRVTDINSNTYEL-----FGPVNLFWSTFRFDKAMTWFLTCLQEFSEFAISLDKENVVPAEKS	436
OsATG6-1	437	YARVTDIHKNNTYELYIMLTRFGPVDLFWSTFRFDKAMTWFLTCLQDFAEFAISLDKENVVPEKS	500
OsATG6-2	378	YPRVTDINQNTYEL-----FGPVNLFWSTFRFDKAMTWFLTCLQEFADFAVSLDKENVVPPDKS	435
OsATG6-3	377	YPRVTDIHKNNTYEL-----FGPVNLFWSTFRFDKAMTWFLTCLQDFAEFAISLDKENVVPEKS	434
ScATG6	389	FSKIKKRMVNSVEYN-NSTTNAPGDWLILPVYYDENFNLGRIFRKETKFDKSLLETTLEIISITRQL	462
AtATG6	297	-----PYN-----YLTVL--FLILPFLFDSVDCI-----	318
HvATG6	437	-----LKLPHYIDGDKVGSYITFLS-FNKNLENWTKALKYMLCNLKWLYWYIGNT	485
OsATG6-1	501	-----LKLPHYIDGDKVGSHTIFLS-FNKVENWTKALKYMLCNLKWLY-----	543
OsATG6-2	436	-----LKLPHYIEGDKVGSYITFLS-FNKNLENWTKALKYMLCNLKWLYWYIGNT	484
OsATG6-3	435	-----LKLPHYIDGDKVGSHTIFLS-FNKVENWTKALKYMLCNLKWLYWYIGNT	483
ScATG6	463	SQTLTTSQDESSMNNANDVENSTSI LELPHYIMNKDKINGLSVKLHGSSPNLEWTAMKFLLTINVKWLA	537
AtATG6	-----	-----	-----
HvATG6	486	SFAPPSASLYLAQSPNKKG-----	504
OsATG6-1	-----	-----	-----
OsATG6-2	485	SFAPPSGSLHVAQSS--KG-----	501
OsATG6-3	484	SFAPPSGSLCAAQSSKR-----	500
ScATG6	538	SKSITLSPTVNYNDKTIIGN-----	557
AtATG6	-----	-----	-----

G	HvATG7	1	MAPK - AEVRPRPLRPLMVEAITS CVETPFGEALRLKLDVLGTDDSPIITGYTPTCTHPKVSGSLRLSPESLV	74
	OsATG7	1	MAAR - AEA - AAAAPRPLQAAAIGVCAETGFWDALRRLKLDVLGTDDSPIITGYTPTCTHPKVSGSLRLSPESLV	73
	ScATG7	1	MSSER - - - - - VL SYAPAFKSLFDTSTFFQELSRLLKLDVLKLDSTCQPLTVNLDLHNIPKSADQVPLFLTNRSL	66
	AtATG7	1	MAEK - ETP - - - - - AII LQFAPLNSVDEGFWSHFSLLKLDKLGIDDSPIISITGFIYGPCHGPQVSNHLLTLESSELP	69
	HvATG7	75	PP - - - - - SANSFGSRNYCPVPGTLINTNNIRGFGQNLDEYLLREEAKKILHDIMSGKIEEGPSLLLRFLVISFAD	144
	OsATG7	74	PP - - - - - SANSFGDRNNCVPVPGTLINTNNMRGFGQNLDRALLKAEAKKILHDIKSGKVEENPALLRFLVISFAD	143
	ScATG7	67	FEK - - - - - HNNKRTNEVPLQGSIFNFNVLDEFKNLDKQLFLHQRALCEWEDG - - - - - IKDINKCVSFVVISFAD	130
	AtATG7	70	LDEQSLIASTSHGNRNKCPVPGI L YNTNTVESFNKLDKQSLKAEANKIWE DIQSGKAL EDPSVLP RFLVISFAD	144
	HvATG7	145	LKNWKIYYSVAFPSLVFKSEMTLLSLRSASLVLSQEKAKSLSKSLKEWRSSNETTVLPFFWVDMSSDSSIVIRQL	219
	OsATG7	144	LKNWKVYYNVAFP SLIFDSKITLLSLKLASQVLKQEEATSLSNAFTEWRKSSETTVVPFFLINISPSSATIRQL	218
	ScATG7	141	LKKYRFYYWLGVP CFQ - - - - - RPSSTVLHVRPEPSLKGLFSKQKWFVNYSKWVCILDADD - - - - - E I	189
	AtATG7	145	LKKWSFRYWFAPAFVLDPPVSLIELKPASEYFSS EEAESVSAACNDWRSDLT TDVPFFLVSVSSD SKASIRHL	219
	HvATG7	220	KDWKDCQDSGQKLLFGFYDNGYRQDYPGWALRNYIAFLSLRWK - MEKVQFLCYRERGSEPDLEKSLIGEASFPPP	293
	OsATG7	219	KDWKACQGNQKLLFGFYDHGNGR - FPGWALRNYIAFVSLRWK - IEKVHFFCYREKRGKRPDIQQLSLVGEASFPP	291
	ScATG7	190	VNYDKG IIR - KTKVLAIRDSTSTMENVP SALTKNFLSVLQYDVPDLIDFKLLIIRQNEG - - - - - SFALNATFASI	257
	AtATG7	220	KDLEACQGDHQKLLFGFYDPCHLPSNPGWPLRNYLALIRSRWN - LETVWF CYRESRGFADNLNLVGVQASITLS	293
	HvATG7	294	HG - WDDSDYVPAAGWEGEKPGDGRKEKKLKEINLE - SMSPERRDEEHQLHLKLMGWRQFP - VDLKKLSSFRCL	365
	OsATG7	292	HAGWDEPDYVPEAGWEGETAGKESKMKPKEIDLS - SINPASQDEEKQLMHLKLMGWRHFP - VNLDKLAGVRCL	364
	ScATG7	258	LLGAGTLGCYVSRAIAWGVKRI FVDNGTYSVSNPVRAALYNFEDG - - - - - GKKPAELAAASLKRIFFLMDATGVK	328
	AtATG7	294	SG - - - - - ESAETVPNSVGWELNKG - - - - - KRVPRSISLANSMDPTRLAVSAVDLNLKLMRWRALPSLNLNLVSSVKCL	361
	HvATG7	366	LLGAGTLGCEVSRLLMTWGVKRLTVVDGGHVSMSDVLKQSLYVDKDC - - - - - GVPRTAIVPHLKERCPAVDVEA IQ	437
	OsATG7	365	LLGAGTLGCEVARLLMTWGVKRLTVVDGGCVSMSDVLKQSLYTDKDC - - - - - GVPRTAIVPHLKERCSPAVEVEG IQ	436
	ScATG7	329	LLGAGTLGCYVSRAIAWGVKRI FVDNGTYSVSNPVRAALYNFEDG - - - - - GKKPAELAAASLKRIFFLMDATGVK	400
	AtATG7	362	LLGAGTLGCQVARTLMGWGIRNITFVDYGVKAMSNPVRQSLYNFEDCLGRGEFKAVAAVKSLLKQIFPAMETSGVV	436
	HvATG7	438	M - - - - -	
	OsATG7	437	MGIPKLEYNISASKISSITDDCKRLQTLVDSNDVVFLNETWEGMWLPTLLCADKNKIAITVLLGYDNYLVMRHG	511
	ScATG7	401	LS - - - - -	402
	AtATG7	437	M - - - - -	
	HvATG7		- - - - -	
	OsATG7	512	AGPGTKSGGMDEGIAQIENLSTQDALGRQRLGCCFCSDTTSLVNSDHNGALDQQSAVILPGLTTSVASGKAVELFA	586
	ScATG7		- - - - -	
	AtATG7		- - - - -	
	HvATG7		- - - - -	
	OsATG7	587	RMLHHPDEIHAPGDIAGTDEHQLGLLPHQMGSLSKCVLSTVLCNSSSNCIACSNVLSSEYRRRGFDFTQAIT	661
	ScATG7		- - - - -	
	AtATG7		- - - - -	
	HvATG7		- - - - -	
	OsATG7	662	CPTYLKDLTGISDLKKPFASKISASIPVSKTSASIPVNLEKLSSARCLLLGAGTLGCDVARILMDCGVKRLTVVD	736
	ScATG7		- - - - -	
	AtATG7		- - - - -	
	HvATG7	439	- - - - - EIPTPGNPVS - - - - - TSVLDDCERLQTLVA	463
	OsATG7	737	SGRVVSNLARQSLYTSDDRDSPKASAILGRLKERCPSVDAKGIKMEIPMPGHPVSPNEAVSVLEDCKRLQELVS	811
	ScATG7	403	- - - - - IPMIGHKLVN - - - - - EEAQHDKDFDLRALIK	428
	AtATG7	438	- - - - - AIPMPGHPIS SQEEDSVLGDCKRLSELIE	466
	HvATG7	464	SSNVVFLTDTWESRWFPTLLCANENKMAITAALGYDSYFAMRHGAGPGTVAEGSDMVAAMSKLSAEDVLGRQRL	538
	OsATG7	812	SHDAVFLTDTRESRWLPTLLCANENKIAITAALGYDSYLVMRHGAGPGTNCGSPDVVAADTL SAEDVLGRQRL	886
	ScATG7	429	EHDIIFFLLVDSRESRWLPSLLSNIENTVINAAALGFD SYLVMRHGNRD - - - - - EQSSKQL	483
	AtATG7	467	SHDAVFLTDTRESRWLPSLLCANANKIAINAALGFD SYMVMRHGAGP - - - - - TSLSDMQNLIDINKTN - TQRL	534
	HvATG7	539	GCYFCNDVIAPVDSVSNRRLDQQCTVTRPGLASIASGHAADLFTRLLNHPDGIHAPGDIA - - - - - GTNSEGPSGL	608
	OsATG7	887	GCYFCNDVVAPVDSVSNRRLDQQCTVTRPGLSSITSGCAADLFTRLNHPDGIHAPGEIA - - - - - GTSSSEGPLGL	956
	ScATG7	484	GCYFCHDVVAPTDSLTDRLDQMCTVTRPGVAMMASSLAVELMTSLLTQTKY - - - - - SGSETTVLGD	544
	AtATG7	535	GCYFCNDVVAPQDSMTDRLDQQCTVTRPGLAPIAGALAVELLVGVLOHPLGINAKGDNSSLNNTGNDDSPGLI	609
	HvATG7	609	LPHQIRGSVSQYNLLTLMGYSSSSCIACSNVREYRSRGLDFVMQVIN EPTYLEDLTGLTELMKSAADYSRVEWV	683
	OsATG7	957	LPHQIRGSLSQYNLLTLMGYSSSSNCTACSNVLSYHRRGMDFVMQVIN EPTYLEDLTGLTDLMKSAAYSQVEWI	1031
	ScATG7	545	IPHQIRGFLHNFSILKLETPAYEHCPACSPKVI EAFTDLGWEFVKKALEHPLYLEEISGLSVIKQEVERLGNDVF	619
	AtATG7	610	LPHQIRGSVSQFSQITLLGQASNSCTACSETVISEYRERGNSEIFLEA INHPTYLEDLTGLTELMKKAANSFNLDWE	684
	HvATG7	684	DEADDDEEFADM -	695
	OsATG7	1032	DEVDDDDDEMDI - -	1042
	ScATG7	620	EWEDDESDEIA - -	630
	AtATG7	685	DDDTDDDDVAVDL	697

H

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

1 MERDEYQLPNSHGKNTFLSRIFGLQSDDEVNPSLNSQEMSNFPLPDIERGSSLLHSTNDSREDVDENDLRVPESDQ 75

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

76 GTSTEEEDDEVDEEQVQAYAPQISDGLDGDHQLNSVTSKENVLETEKSNLERLVEGSTDDSVPKVGQLSSEEEEDN 150

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

1 MMSFPSKDTNSQP-----VFKWPWR-RESPLSAQLLIDIPPEIELSDYRRLPSSG 49
1 MMSFRSKDRNVQP-----RFNWPWR-SESPLSAQLLIDIPPEIELSDYRRLPGSG 49
1 MMSFLPKGKTTQT-----AFKWPWR-GESQLSAHLLIDIPPEIELSDYRRLPSG 49
151 EFINNDFDDDTPLFQKSKIHEFSSKKSNTIEDGKRPLFRHILQNNRPQRDTQKLFSSNAIHHDKDKSANNPG 225
1 MMSSGHKGNVNRN-----FEKWRGESSSLTTGLLHNESHEIELSNYGGIPSPG 50

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

50 SESPSGLLHGEVKE-----EPI 67
50 SESPSGLLHGEFKD-----EPI 67
50 NESPSGLLHGEFKD-----EVI 67
226 RNINGNQKHGTYFGSATQPRFTGSPLNNTNRFTKLFPLRKPNNLSNISVLNNTPEDRINTLSVKERALWKWANV 300
51 SESPSGLLNGESLNV-----QPI 68

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

68 PDLDIFFERLYEYFCAKGLRCIVTKWIEILNVLFTVCCIGFFFLFVDWDTL IHLKCGVEALESGEKPCDLM EAI 142
68 ADLDIFFERLYEYFCAKGLRCIVTKWIEILNVLFMVCCIGFFFLFVDWDTL IHLKCGVEALESGEKPCDLMQV 142
68 PDLDIFFERLYEYFCAKGLRCIVTKWIEILNVTFMVCCIGFFFLFVDWDTL IHLKCGVEALESGEKPCDLMK 142
301 ENLDFLQDVYNYLNGFYCIILEKILNICTLLFVVFSTYMGHCVDYSKLP-----TSHRVSDIIIDK 365
69 ADLDFVERLYSYRDKGLWCIVKWKAVELL SLGFIICFSGFFLLYVDWDTL IHLKCGMDAVESGTPKCDLVKEA 143

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

143 KH-NPLVPFTFPKMVTGSMVILVTYGLINFLKFFVQLKSTLNARDFYNSLKITDLEIQTISWPRIIEKVVLQ 216
143 KH-NPLVPFTFPKMITIGSMVILVTYGLINFLKFFVQLRSTLNIRDFYCNSLKITDLEIQTISWPKIEKVVLQ 216
143 KY-RPLDPFTFTKFIIGSMVILVTYGLINFLKFFVQLRSTLNIRDFYCNSLKITDLEIQTISWPRVVEKVVLQ 216
366 CYSNSITGFTK-----FFLWMFYFFVILKIVQLYFDVQKLSLQNFYKYLINISDDELQTLPLWQNVIQQLMYLK 434
144 IHPHPLSPFTLTATAIIVGYLALFSVYWFCLFRFFAQLKDTLDFRHFYNNLHVTDNEILTMPWATVLEKVVLQ 218

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

217 KS-----KKLCVVRDLSEHDIIMRIMRKENYLIGMVNKGIIISFPIRPWLPAGAPTVKSHVHDDRHHVLPKAL 284
217 KS-----QKLCVVRDLSEHDIIMRIMRKENYLIGMVNKGIIISFPIRPWLPAGAPTVKSHLQNNRRNHLIPKAL 284
217 KS-----QRLCVVKDLTEHDIIMRIMRKENYLIGMVNKGIIIALPISWLPAGVGTPTSSRMHGKKSYLEPKAL 284
435 DQNAMTANVVEVKAKNRIDAHDVANRIMRKENYLIALYNSDILNLSLPIPLFRTN-----VLTKTL 495
219 SS-----QCLCVVKDLSEHDMVMRLMRKENYLIGMLNKGLLSFPISHWIPGAGPAVKSPADGTQYHLVLT 286

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

285 EWTNLNWCIFQSMFDSKFCVRKDFLSP-----AALKKRLVFGIAMLILSPCLVIFPLVYLILRHAEEIYNHPS 349
285 EWTNLNWCIFQSMFDSKFCVRKDFLTSP-----AVLKKRLVFGIAMLILSPCLVIFPLVYLILRHAEEIYNHPS 353
285 EWTNLNWCIFQTMFDRKFCVRKDLTSP-----SLKKRLVFMGIAMFLSPCLVIFPLVYLILRYAEEFYNHPS 353
496 EWNINLCVMGFVFNESGFIKQSLKPSQREFTREELQKRFMLAGFLNIIAPFLVTYFVLLYFRFYNEYKTSFG 570
287 EWTNLNWCILQSMFDCNFRVRRDFVSNP-----TTLKKRLVFGVGLAMLLSPFLVIFMLVYLILRHAEEFYNHPS 355

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

350 TASSRRWSNLSRWILREYNEVDQFFRHRMNSAVHSLNLYLKQFPTPLISIMAKFISFVSGGLAAGIRHRGFLG-E 423
354 TASSRRWSNLSRWIFREYNEVDHFFRHRMNSAVHSLNLYLKQFPTPLISIMAKFISFVSGGLAGALLIIGFLG-E 427
354 TASSRKWSNLSRWILREYNEVDHFFKHLRNNSSVNSNLYLKQFPTPLVSIIAKFISFVSGGLAGILLILGFLG-E 427
571 SIGARQYTPIAEWKFREYNELYHIFKKRISLSTTLANKYVDQFPKEKTNLFLKFSVFCGSFVAILAFLTVFDPE 645
356 TASSRRWSNLSKWLFRFNEVDHLLFKHRISSVHVHASEYLKQFSPISIIIAKFISFVSGGFAAVLIIIAFLLE-E 429

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

424 SLEGHIFG-RNLFWYTIIVFGTIAAISRKVVADELQVIDPEGAMCLVVQQTTHYMPKRWGKESNELVRKEFETLF 497
428 SVLEGHIFG-RNLFWYTIIVFGTIAAISRKVVADELQVIDPEGAMCNVVQQTTHYMPKRWGKESNELVRKEFETLF 501
428 SILEGHIFG-RNLLWYTIIVFGTIAATVSRNVVVADELQVIDPEGAMSFVLQQTTHYMPKRWGKESNELVRKEFETLF 501
646 NLFNFEITSDRSVIFYITILGAIWSVSRNTITQEYHVFDPETLKELEYETHYLPKEWEGRYHKEEIKLEFCKLY 720
430 SLEGHIFG-RNLFWYAAVFGTITAIISRAAISDELLVLDPVGTMSLVVQNTTHYMPKRWGKENKDDVRLLETLF 503

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

498 QYTIIVMLLEEMASIFITPYLLIFEVPKRVDDILHFIISDFTIYVDGVGDVCSLSLFDERRHGKNKYGSPFDAPKN- 571
502 QFTIIVMLLEEMASIFISPYLLIFEVPKRVDDILRFIISDFTIYVDGVGDVCSLSLFDERRHGKNKYGSPFDALKT- 575
502 QYTIIVMLLEEMASIFITPYLLIFVVPKRVDDILRFIISDFTIYVDGVGDVCSLSLFDERRHGKNKYGSPHNAVKS- 575
721 NLRIVILLRELTSMLITPFLVWFLSPSSAGRIVDFFRENSEYVDGLGYVCKYAMFMNMKNIDGEDTHSMDEDSLT 795
504 QYTGMMMLLEEIASIFITPFLLMFVVPKRVDDILQFIKDFITVDIEGVGHVCSFSAFYFENHGNIKYGSPhNATRRE 578

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

572 LRSSQGKMEKSLFSFQSVYPSLASNADGKQFLHNLQKFKEKQIRQQAVAQYQAMEASGFVDST-GQRDDIFHQLL 645
576 LRSSQGKMEKSLFSFQSVYPSWEPNAEGKQFLTNLQKFKEKQIRQQALAQYQAMEASGFVASTRGHRDDIFHQLL 650
576 MRSSQGKMEKSLFSFQSTYTSWEPNADGKKEICNLQKFKEKQIRQHT--FQTTSSQLGLSCRGQTA-VFHRLL 646
796 KIAVNG-----SHTLNSKRRSKFTAEDHSDKDLANNKMLQSVYV-----FMDYSNSENLTGKYQLPAKKG 857
579 QRSSQGKMEKSLFSFQSSYPSSWESDSLKGQFLSNLRTFRDRKLHEIN-----TRHSSPSRAWRESTNTPALYRDI 648

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

646 PSIIIRNHAEAFPPAGYNLDPLGLLDTDQRIHPYILDWYIMRHSPLDRTEAPLFDEASLEAGQNSNQ-LARETSE 719
651 PSDIHNRAEASPAVYNLGLPLGLLDTDQRSHPIYLDWYVCHPPHLDRTAPYFNEVFPETSENTGS-AAFKASE 724
647 PRNIYPNGV-----FNFDPLGLLDTDQRCAPYILDWYITQHNTREAGSSSHLNEASPEQEEIWPPLSKPLTE 717
858 PNN-----EGDSFLNNKYSWRKQFQPGQKPELFRIGKHALGPGHNIISPAIYSTR 906
649 PRNPLAS-----GNHTDSMWLIDPDQRNHPYILDWYITSQAHNRTDHPIERANEILTANQNATDCWPPDLGIR 716

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

720 LEEEDENYYS DLYG-----RVQSHMGASTSSTLFQQAS--TKHDGNEDS-----SAGNWNQGP 770
725 IEARGWDS DMVPPPRADRDEWNFNHERVSHHMASTSSNLFFHAG--VEHHDGK-----NIIDWWDQAP 788
718 IEDEQIWDSDLYR-----RARSYLEASTSSAFFRQATTFRKHGREQNS-----TSHQWAAQAS 770
907 NPGKN-----WDNNNNGDDIKNGTNNATAKNDNN-----GNND 940
717 GEDSR-----DLLN-----MEASTSGQFFRESILRHDQPEGEDSYGSQHPLDGRNQWVGRGN 768

HvATG9
OsATG9-1
OsATG9-2
ScATG9
AtATG9

771 ASPLDP-----QGSFLEPPAFGYHNMAAGNSHSHHSGDISSEGSEGLQ-----QGDN 817
789 EHSTGQ-----QGSFLEPPAFGNRYVAGN-RSSYHSGDVSDGSVEELE-----RSDN 834
771 RQQADPRNSFQGGPPQDSFLEPPDFRNHLEASHDSSHQSDCRLTSRRSTDQDQSFVEPPDFGDYMSCHSSSYHGD 845
941 HEYVLT-----ESFLDSGAFPNHDVIDH----- 963
769 HSQISTAHP---ATTNSFIEPPDFINRYTAGNLLDNSWSRRSIEEEDEEEE-----ELDW 820

<i>HvATG9</i>	818	RSSST - - - - - SSWRNPPRALSKTRYMDDS - - YIEEGLGLHFADVLKDGDDERPGV - AADAYDRTPAGLPVRI	882
<i>OsATG9-1</i>	835	RSS - - - - - SSWRRP-QDLSTTRYMDDS - - DIEEGLNLPFADLPQKD - EDARHG - - TSDTNDPTPVGLPVRI	894
<i>OsATG9-2</i>	846	TS DGNSELDQSNNSWRSP - HALSKTRYMGDDDLLEQGSPSFHFTDAPQKDSGSEGDGHGVANIYSSTPASLPVRI	919
<i>ScATG9</i>	964	- - - - - NKMLNSNYNGNG - - ILNKGGVLGLVKEYYKK - - - - - SDVGR - - -	997
<i>AtATG9</i>	821	EENAR - - - - - RNLSTRITTFMDDN - - DIEAGIDLHFDVYSSR - - - - - PQETSTSSTTLR -	866
<i>HvATG9</i>	883	IPRSSDPV	890
<i>OsATG9-1</i>	895	IPRSSDPV	902
<i>OsATG9-2</i>	920	IPRSSDPV	927
<i>ScATG9</i>		- - - - -	
<i>AtATG9</i>		- - - - -	

Protein	Sequence	Position
HvATG10	1 -MGGSSVCDGTLSDLDFNASAKALVTKWSGI--DVDNALPDWEWRPCRK--MGVPSETEGFVALEGVYRIGAGSQ	70
AtATG10	1 MDSAREVSDGRLTVEGFVSASRAFADQWKIH---NQSFPPWSVYPLINRTLLYSKKEEGYLSLEKIIILSSLEE	71
ScATG10	1-----MIPYQEWKSQLSLYDSQIFHNWALQD--VHLNDEKDGLLLR---LIPTRQ	47
OsATG10a	1 MGGSTTVRDGTLSHGDFVASAKALIEKWKIEI--DVDDALPDWRWKPCCK--MGVPSEEEGYLALLEGVYRNHGGSSQ	71
ZmATG10	1 -MGGSPVWDGTLSPDSEFNTSAAALVKRWKEI--EVDDSLPEWTWKPCSK--LGVPSEVEGYLALERVYRSCGTSQ	70
HvATG10	71 SEESDDDP-V-----PDDVVEHDTWVSF-----GYSYSNVICFCYQHVAV--LHCSA---PQPFHFVRLFIS	126
AtATG10	72 EIPEDESLNVATDCLKEKETVDHTILVPTMENEAHYYDFHIVYSASYKVPVLYFRGYCSG--GEPLALD-----	138
ScATG10	48 LQKNTERI-----EN-----KLLNHIELYLTYSKVYNEPLLLLRIWEEKSIDGIPMTKL-----	96
OsATG10a	72 V-----QSCSGNLHFYDYHVVSFSYKVPVLYFQGHQSG--GQLLTLD-----	112
ZmATG10	71 EQIEEMKFD-----GAGDVAWVESSDNVHVYDFHAVYSFSYKVPVLYFRGYHTS--GQLLTLD-----	127
HvATG10	127 YIYKNKILTVSPNSVCV-----	142
AtATG10	139 -----VIKKDVPCSVSL--LESKWTFITQEEHPYLNRPWFKLHPCGTEDWIKLLSQSSSSSSGQMPVLYLVVSW	207
ScATG10	97 -----MLPTDIESLLDVQGGFQLGLDTIINLEGSVWYSFHPCDTSCIVGDAQAEFMST-YLRRWVSIFIFSW	161
OsATG10a	113 -----EIKEDLPSSLKLL--GESRWTFITREEHPHFSRPWFTLHPCGTSDCMKLLLEGMQ--D-KDQQVRYLPW	178
ZmATG10	128 -----EVKEGLPSHSQKVL--SESKWTFITQEEHPHLKPLWALHPCATSGWMKLLLEETEATD-KEHSVQYLPW	195
HvATG10	-----	
AtATG10	208 FSVVGQVVGLRIPLEMLN--	225
ScATG10	162 LGYEDS-----	167
OsATG10a	179 LTVVGQAVGLKIPGLHCNS	198
ZmATG10	196 LSVVGQAVGLKIPLELHNS	217

J

HvATG11	1	MSSGSAVTAGSGGGGAAGAALGQKLMVHVAENGHSMFEFCGGTRVEAIIQRAIEHVCGVPPADQQLLLC-GNIPLD	64
AtATG11	1	-----MSGSFTESFADDGKLLLCVAENGHSFEFCQSETTSVESVVMRFVESVSGIALSDQLLLS-LDMKLE	64
ScATG11	1	MADADEYSTAP--TQQEITPLQTTATIIINAISGECITTNVDFVSLDKFKQFIARKWKIIPDQLLILLPYGNKLG	73
OsATG11			
HvATG11	75	GANHLA-HYNLRDDREVFLYNKARLHADSPPP-----APESIDIPEPS--IPPP-----	122
AtATG11	65	PQKLLS-AFGLPASDREVFVFNKAMLQSNHPP-----SPEDVDLQDVADALPPAS-----	114
ScATG11	74	PSMFKELLINRSFTLNDFYVYDRRLFSLVSKPTPTNLLTSKDSNPMNSPNSNDLTETLEYLIKNSHISQYQGS	148
OsATG11			
HvATG11	123	---RPQDATALVVSADPALKALVSYEVFRYDFQVANALYQSSVAKYEVCRRLLEWQVQERALDMARSNLEQAF	194
AtATG11	115	---LHEHHPLDDASDPALKALPLYERQFRYHFHKGRTIYNCTVVKHENCERLTREQKVQGRAVEVATRNLEQY	186
ScATG11	149	IMIKPMPSPLEDAVDL-----SRLNY--HSVTSLLTNTL-----GWL---SALEID---VHYFK	195
OsATG11			
HvATG11	195	KPSLRYSNFRVSFTQQHGRGYVEVLSTFERDVQRLRAIKL-----HPHLQCEGRRCLLDLMD-----	250
AtATG11	187	VIIYQNFLFEMKRYKHQHRLHSDLLMNFGRDIEKLSAKI-----HPYLQTESRKCLLDFVK-----	242
ScATG11	196	SLIPDIIAHIKRIFDGLTVCSQYLKLYCFDVESLYNSNVQFLNQLVDNGMTSKWEKCFNDTL SKLTALE	270
OsATG11			
HvATG11	251	-----E---NRLRLADEYLSSQKGFEDFVSPLKAKFLELKRRVESLLNSMSSSAWKDL	301
AtATG11	243	-----E---DNLKKAVENCASSHRQFENKIAQFQMFVEVKRKVEELFACRASLSMKNL	293
ScATG11	271	FINIESLLENEKSVKILNHSINGKLNKIKREIDENASFRDIIITVNI DRLRQMFTPNESKFELE-DQM---	340
OsATG11			
HvATG11	302	EALIKEHHRVIGDQKSIMQSLSKDVT SKKLVDCECSRQLSASVRPHDAVSAVGRIYEVHEKDN---LPSVR	372
AtATG11	294	EVTVKDHERFIDEKSI MQSLSKDVNTVKLVDDCMSSQVSSSLRPHDAVSAALGPMYEVHDKNH---LPKMQ	364
ScATG11	341	EVLVSE-----MRTRSRN-----VLDKE-----EEEFNSQEFLLKSMNVMLEKDKKESVKTLFTIS	393
OsATG11			
HvATG11	373	DHMLTNLLQCKTKKNETNTLVHVCVKGVKSQAIDII--KDMMSQFIIYEAEIDSRDKEFSYLLKLGGLGHAY	444
AtATG11	365	YNSISELDDQCKNKKENNFVHGYMQKIITYVTYII--KDAK-LQFPVFREAMVRQDDL FADKLVRGVGPAY	439
ScATG11	394	YSQIGELIDLKSLQKHAV--AILGNIAFTQMEILGIRKLLNECKNDLELYKKYEV--EFAQVEDLPLIYG	461
OsATG11	1	-----MNTLVHVSQMRVKSQAIVI--KEMM-NELHAFQEVMGHQDKIFDSLKLASGMGHAYR	54
HvATG11	445	ACLAEVVRRHSFKLYTGLAGQLAEKLAEREVEIRRREVFLRTWRKYIR--GEIMGSMGL-----FG---	508
AtATG11	436	ACLAEVVRRKASMKLYMGAGQLAEKLAAMKRETVRKREELFKTLGFPFV--RDVLASMGL-----YD---	496
ScATG11	462	LYLIEKYRRLSWFQYLQISFNQDLLEFKQNELRTNKKWKNFSGIATVFCDDLSSDFKRLNEYHSHTSPP	539
OsATG11	55	ACLAEVVRRKSSFKLYTGLAGQLAEKLATERAEVRRREAFRTWSKYIP--EDIMGSMGL-----FD---	118
HvATG11	509	-----QCDVNIAPFDCDLLPID-----VDDLEKLAPQSLVGSLLKPERSQQHKSSSSDSSTTGNTFNA	566
AtATG11	500	-----QCDVNVAPYDTSLLNIE-----ISDVDRYAEFLVGLHKSIA---LKSSLLTMSGDSSLSAEP	554
ScATG11	537	NEDEEDENENSIANYRQDLVKVQAIDNYMTQIKETDVSEPIIDL SKTLFETKRFHIIYSNFKN--NNNS	609
OsATG11	119	-----QCDVTVAPFDCNLLSID-----VDDVEKLAPQSLVGSFLKSERSQLPKSSLSNSGTSGNLSKS	176
HvATG11	567	EQNSLNTDGKMSQDFFGGCDTVDITGTSVLEVENARLKAELASAIAVLCTFGAEYTHESIDEG---QNDNV	638
AtATG11	555	EEIGIDTFDKDNFDDILAASELIEIAGTSKMEVENAKLKADLASAISRICSLGPQFEEYVLDES---EVEN	626
ScATG11	610	NSISPEGSIALKSDVVVKGY-----KTRIKKLESLLHEFYQSDIGHWPPQGVNLTHLKP	662
OsATG11	177	EQYPPNADDKMDQDFLGGFDSVDIAGTSKLEVENARLKAELASAIAVLCFSGAEYGYSIDEG---QIDNV	248
HvATG11	639	AREKTAQALSAKDEYANQLQSMLEKTK-----QEQCMSFEKRIQELEEQLANQYMHGQMVSQKSADS	703
AtATG11	627	AADKTAELAQAKDEYEKHLMLLEK-----QMHCDSYEKRIELEQLRSDLEYMQQRHNKNDVSGNL	694
ScATG11	663	FRGSA-TSINKK-KFLGAS-VLEPANISEVNI DSVSQANNHQIQELESNVDDLHLQLQLL-----	720
OsATG11	249	AREKTAALSAKDEYANHLQAML TAK-----QNQNL SYEKRIQELEEQLANQYIQGHVIGSKDASD	313
HvATG11	704	-STFKGNDCNL--DGGRQTHLRDESSVAMDET-----SSTSEQPSKQTEGGDENMTDVSGALNLQL	771
AtATG11	695	VSEYKAEAS-SDVE-GNKTHVS--GSEPMDEVSCVSNLTSQPCAKAREGMDENMVDSVQLSPLD---	756
ScATG11			
OsATG11	314	-SAFKANDCNLHISGGRQTQVRDESSVAMDEA---SSTSEQPSKQTEGGDENMTDISGALNLQLLDPI	383
HvATG11	772	APMAEFSQDNEHKVNIIDKEGQMLTLTMVDTSDIPVEGP-----QGLNSDNEHHTLEFRNNELFVSEL	839
AtATG11	757	SSMLESQQNNEKGGK-SEAGEMGVFLSNSS-----QKSLDDNVAATRGLDKDGSDGIDIELRN	819
ScATG11	721	-----KEENNRKSMQISEMGKKISDL--EVEKTA YRETTLNLNQELARLTNNEEQSHRTEIFTL	786
OsATG11	384	AFMAELPPDSEHKIVDSQKEGQVLTQFTTTDTSGVPIEDP-----LGILNSRTNEHHTSELRNKELL	451
HvATG11	840	TIDIKAKLLDEASKLSTVMGE-----VNSLKEELEN-----ARVLLDES---QIN	882
AtATG11	820	ELMEKSKNLSMESKLNGAMEE-----VNSLSRELET-----NQKLLAES---QMN	862
ScATG11	787	IISQDN-----EKIEKLTGDYDDVSKSRERLQMDLDESNNKHEQEVNLLKADIERLGKQIVTSEK	857
OsATG11	452	TLEDKSKRLDETESKLNALVDE-----VNSLKEELEH-----TQGLLDESQVSQMN	497
HvATG11	883	CAHLENCLHEAREEARTNKCSADRRAVE--YDALRSS--ALRIHGLFERLN-----	929
AtATG11	863	CAHLENCLHEAREEATHLCAADRASQ--YALRAS--AVKMRGLFERFR-----	909
ScATG11	858	KGEKFETIPLAEDPGRENISAYTQTLQDRIFDIISTNIFILNGLLTLFDNNNNIQUIRRVKG	932
OsATG11	498	CVQLENCLHEAREEARTNKCSADRRAVE--YDALRSS--ALRIHGLFERLN-----	544
HvATG11	930	-----NCV-TTPGMSGFADSLRSLALSLARYHVSICIRLYVY-----CRCVST	972
AtATG11	910	-----SSVCAGSGIADFADSLRTLAQALANSVNEENDDGTTFF-----RKCI	953
ScATG11	933	DESTQMLDAHNSLISKSPVFQKLKDEYELI-KSVANG--SEKDTQQSIFLGNITQLYDNKLYEVA	1004
OsATG11	545	-----NCV-TAPGMSGFADSLRALSLASAKKDEGDTT-IQF-----QQCI	

HvATG11	- - - - -	
AtATG11	1018 VHEIAAFVLNQAGHYE - - - - AINR - - - - -	1037
ScATG11	1035 IGDLALFLPTRENVNSVGSMSSSTSSLSSSFSSVDLSTPPPLDAMS IQSSPSV IHSNVI NQAS I SGRDKNKLMP	1109
OsATG11	655 VHELAVFVRNPAGHYE - - - - AINR - - - - -	674
HvATG11	- - - - -	
AtATG11	1038 - - - - - NCPNYLSSSEALFTDHLPSRPTYIVGQIVHIERQIVKLPSQLSASASPEAGKTHHLCSDQGSRTL	1104
ScATG11	1110 WAAFTAFEESTRYFLKDE - - - - KGLTKGKEWFGVGRIVTLEHFVA - - - - -	1149
OsATG11	675 - - - - - NCSNYLSEESVALFTEQHPRHPAYIIGQIVHIERRIAKLPSHGDQMEASR - - - - - LDSG - - - -	729
HvATG11	- - - - -	
AtATG11	1105 ASSSISTSTSATTTSNPYGLSSGCEYFIVTIAMLPDTA IHQQAS	1148
ScATG11	1150 - - - - - DSPSNNPFRLPKGSVWFQVTAVVVS YQGV - - - -	1178
OsATG11	730 - - - - - GRRSPASMLNPYNLPVGCEYFLVTVAMIPDNIR - - - -	762

K	<i>HvATG12</i>	-----	
	<i>AtATG12a</i>	-----	
	<i>AtATG12b</i>	-----	
	<i>OsATG12</i>	-----	
	<i>ScATG12</i>	1 MSRI LESENETESDESS I I STNNGTAMERSRNNQELRSSPHTVQNRLELFSRRLSQLGLASD I SVDQQVEDSSSG	75
	<i>HvATG12</i>	1 -----MAGS-----EAEQKVVVHV RSTGNAP I L KQDKFK I SGRDKFLRV I EFLRRQLHQDTLFVYV	56
	<i>AtATG12a</i>	1 -----MATESSSPSSVRKVVVHLRATGGAP I L KQSKFK I PGTDKFAKV I DFLRRQLHSDSLFVYV	60
	<i>AtATG12b</i>	1 -----MATE--SPNSVQK I VVHLRATGGAP I L KQSKFKVSGSDKFANV I DFLRRQLHSDSLFVYV	58
	<i>OsATG12</i>	1 -----MAAV---AAEQKVVVHFRSTGNAPQLKQSKFK I GGNEKFLK I I DFLRRQ I HQDTVELYV	57
	<i>ScATG12</i>	76 TYEQEET I KTNQTSKQKSHKDEKN I QK I Q I K FQ P I G S I G Q L K P S V C K I S M S Q S F A M V I L F L K R R L K M D H V Y C Y I	150
	<i>HvATG12</i>	57 NSSFSPSPDELVIDLYNNFA I DGKLVVNYALSAAWG	92
	<i>AtATG12a</i>	61 NSAFSPNPDESVIDLYNNFGFDGKLVVNYACSMAWG	96
	<i>AtATG12b</i>	59 NSAFSPNPDESVIDLYNNFGFDGKLVVNYACSMAWG	94
	<i>OsATG12</i>	58 NSAFSPNPDEL I I DLYNNFG I DGQLVVNYASSMAWG	93
	<i>ScATG12</i>	151 NNSFAPS PQQNIGELWMQ FKTNDEL I VSYCASVAFG	186

L

HvATG13 1 MASLSDSGGAGGGGGRSGAELMVPPQHFLKALHAILAARVPPPVAS-----ASASAA-VRRRDRWFHL 61
OsATG13-1 1 MATLSDSAG-GGGGGRAGAEMLVPPQHFLKALHAILAVRAPRPLAA-----APAPAAFRRRDRWFHL 61
OsATG13-2 1 -----MAAAAEPMPVEQVITEFFAKSLHIILESRRPYESSRNFT-----PSPSSPLSGSQPRDRWFNL 60
AtATG13-1 1 -MSSSHNRSNNNNSEGAKEQIIFFFAKSLHIILESRTPFMSSRNFSGEQMI CSPSSSSSSSSSVRPRDKWFNL 74
AtATG13-2 1 ----MDFPENLPSDIGRLQIVSHFFPKALHIVLNSRIPLQSRGRTR-----ERL SGLNVRKSDKWENL 61
ScATG13 1 -----MVAEEDIEKQVLQLIDSFFLKTTLLICSTESSRYQSS-----TENIFLFD TWFEDHSEL 55

HvATG13 62 PLHAPP---AAEH IPEPALGEPVVVDVYL APSAV-----SGGGEEEEVVERWTVACEPWAAGER----- 117
OsATG13-1 62 PLHAPP PPPASAEHLPEPSGPEPLVVDVYLTPS-----GGGGGAEEAVVERWTVSCEPWSAGARGG----- 120
OsATG13-2 61 ALRDCPAVLENF DLWRQSNLEPLVIDIVLCRDSTS-----NTAAGSGKIIERWWIQYEARKSGGGNGNGSKNNGR 131
AtATG13-1 75 ALRECPAALESF DIGRRSSLEPLVVDVYL VVRPLVG-----DQSGKRELIRNFSGKDYQSGWNSDQDELGCETKNE 145
AtATG13-2 62 VMGDRPAALEKLHSWHRNILDMSIIDIIIVHPISND-----NLDDDD--HSDSVVRSAAETVIERWVVQYENP-- 127
ScATG13 56 VSELPEIISKWSHYDGRKELPLPLVVETYL DLRLNSSLVRLKDHEGHLWNVCKGTTKKQEIVMERWLI ELDNSSP 130

HvATG13 118 -----AAAEAGEGLAVNRAYKRCITLLRSLYATLRLLPAYRVFRTL CASGGQGYNYEMGHR 172
OsATG13-1 121 -----GGAAASGEGLAVNRAYKRCITLLRSVYTALRLLPAYRVFRTL CASGGQAYNYEMGFR 176
OsATG13-2 132 -----KSRNSSAEDHSLYRATYQGSTVLLRSLHLLVRLLPAYSLFRELNSSGRIRPLNL SHK 188
AtATG13-1 146 QIIERWVVQYDNRKIRESVTTSSRRSSSNKLQVMYKKATILLRSLFVMVRLLPAYKIFRELNSSGQIFKFKLVPR 220
AtATG13-2 128 -----LIMSPQSSDSATRYQKVYKKSIIILRLSLYAQTRLLPAYRVSRQLSSSLASSGYDL IYK 185
ScATG13 131 -----TFKSYSEDET DVNELSKQLVLLFRYLLTLIQLLPTTELYQLLIKSYNGPQNEGSSN 186

HvATG13 173 -----VGSFAAPFSRA-DEAAMRTRGFPAVETQLGRLVVSQYLYPT 212
OsATG13-1 177 -----VGSFAAPFTRA-EEAAMSTRRFAPVETQLGRLVVSQYLYPS 216
OsATG13-2 189 -----ISSEVEPFTRA-EDAEMKHYAFAPLETFLGRLSLSVSYVPV 228
AtATG13-1 221 -----VPSIVEPFTRK-EEAEMQKFSFTPVETICGRLCLSVLYRSL 260
AtATG13-2 186 -----VSSFSDIISGP-VTETMKEFRFAPVEVPPGRLCASVTRYSD 225
ScATG13 187 PITSTGPLVSI RTCVLDGSKPILSKGRIGLSKPIINTYSNALNESNLP AHL DQKKITPVWTKFGLLRVSVSYYRSD 261

HvATG13 213 LAAYNFEIT-SLSSAMLITDYVGSPAAEPMSRFPSSL-TEAASSALPLPSRRP-----NSWASPAAYWPQSPGQH 281
OsATG13-1 217 LAAFNLEIC-SLAPAMLITDYVGSPAADPMRAFASL-TEAASSAPAFPPRRP-----NSWA-PSPAPWPYTPGQQ 284
OsATG13-2 229 LEVVAASEPTSPMPEIITDYVGSPTTDFLKKFNSLP-SAGIAPACAAMTRRHSWSIEHGAGTSVSPSPSTKQA 302
AtATG13-1 261 SDVSCHESS-TPMSPTFITDYVGSPLADPLKRFPSLP-LSYGSPLLPFQRRHSWSFDRYKASPPSVSCSPSPTR 332
AtATG13-2 226 LSDFNLAGH-ITLPPRIITDYVGSPATDPMRFFPSPG-RSVEGHSFTGRAGRPPLTGSSAERPHSWTSGFHRPPA 298
ScATG13 262 WKFEINNTNDELFSARHASVSHNSQGPQNQPEQEQSDQDIGKRQPFQQQQQPQQQQQQQQRQHQQVQTQQ 336

HvATG13 282 AKFSPPTLYASPTPSPPTFGGGYLQSRLSGETAPMSIPQ-----AGGGRGPVQYRNMSDPSRGFMLPPPS 348
OsATG13-1 285 AKFSPPPALYASPTPSPPTFAGGYLQSRLSGETAPMIIP-----GGGRGPVHNRNMSDPVRGFMLPPPS 349
OsATG13-2 303 SRGSPQLGVPLHVSLKTC SHPQNASSSGQKKYTPFEECYP-----SPPLSPSPSQSPSANYPKNPLFRYESAP 370
AtATG13-1 333 SDSHALVSHPCSRLHP--PHPSDIP-TGRRKESYP EEYS-----CQDFSPSPSPSAPKHAVPRGITRTEAP 397
AtATG13-2 299 QFATPNQSFSPAQSHQLSPGLHDFHWSRTDAFGDNHQLSPP-----FSPSGSPSTPRYISGNSPRINVRPGTAP 368
ScATG13 337 RQIPDRRSLSLSPCTTRANSFEPQSWQKKVYPI SRPVQPFKVGSI GSQSASRNPSSNSFFNQPPVHRPSMSSNYGP 411

HvATG13 349 KS-VRGEARS-----HESLTENSRSFRKAEGIRMTDLYANLP-----AAP--KIKDSREESGRFSGVF 403
OsATG13-1 350 KN-IRGDSGG-----HETPMETGR-----TGIRMA DLYTNLP-----SVPKIKIKDSRDESGRFSGVF 401
OsATG13-2 371 VT-IPTLKS-----GGGSGLPPSPCSKGKHQFSSHNDNL A--HSPDHNSNVRKDLVRLGEFEKDMALQ 432
AtATG13-1 398 VR-IPAPTFQ-----SKENVVAPSAHLKLSRHASLKPVRNLG--PGESGAAIDKLFYGRDDFRPSGVR 459
AtATG13-2 369 VT-IPSSATLNRYVSSNFS EPGRNPLPPFSPKSTRRSPSSQDSLPGIALYRSSRSGESPSGLMNQYPTQKVMLLT 442
ScATG13 412 QMNIEGTSVG-----STSKYSSSFGNIRRHSSVKT TENAEKVSKAVKSPLQPQESQEDLMDVFVKLLEKPDLTIKK 482

HvATG13 404 SSSGSPRHG-----ISRSSSRFSTQDDTDDAY-----LPFAVDDVDAPDSRPG 446
OsATG13-1 402 SSSGSPRLG-----FSRSSRSLSMQDDTDDLD-----FPFAVDDVDTPDSRPG 444
OsATG13-2 433 KVL SYSKYDLGYFHG-----LKLTRTSSKLFIMDELDEHE-----LVFAWEDRDTIIDQLN 483
AtATG13-1 460 PSSSSSPR-----ISFSRSSRSFQDDFDDPDF-----PCPF DVEYDDITDRNS 503
AtATG13-2 443 SYVSCSMQEKYHYIFKYDSGRFSGVLSSSDSPRAF SRSPSRLSSQDDLDDPD-----CSCPFDFDDVDESGQL 511
ScATG13 483 TSGNPPNINISDSLIRYQNLKPSNDLLSEDL SVLSMDPNHTYHGRSDSHSPLPSISPSMHYGSLNSRMSQA 557

HvATG13 447 SS-----GGK--EDQSGSSS-----HKSQDAAVGYLVHLLRSARPLRDPSSSLT-----SRAES 494
OsATG13-1 445 SS-----GGKDVGDQASSS-----HKSQDAAVGYLVHMLKSARPLRDSSNSPLT-----SRVES 494
OsATG13-2 484 RADISDRE-----EQKNQDAGSSS-----TRSPAAAIGALVHLLKTAPSLREGLOSDAAAVVP--QEPSSVQKVVE 548
AtATG13-1 504 RPGSDFHRGDIHEPFDSSGSYP-----KKSQDAAVGALVRLMKAPPLRQDVSESSRPEICSNNNKPAGAHEIAVA 574
AtATG13-2 512 YSHSLDRRKTS SSIQS LPLGR-----RSSQDAAVGYLVHMLKTAPPLRQDSSTYMASMSG-----VQREGS 573
ScATG13 558 NASHLIARGGGSST SALNSRRNSLDKSSNKQGMGSLPPIFGGESTSYHHDNKIQKYNQLGV EEDDDDDENDRLLN 632

HvATG13 495 TEADNTSSFMSRRTSDAFEELES-----FKDIKENLLSRSRSRMQDSLDRS- 540
OsATG13-1 495 VEGGNVSSFMSRRTSDALEELES-----FKEIKENLLARSRRSRMQESLDKSL 541
OsATG13-2 549 EHGSIASSSTPVTATDALEELKK-----YREV KESILNRGKTQVSGTNLGEK 595
AtATG13-1 575 SITASGIALASKTTADALEELRS-----YKEMKNHLLLGQSTSNPSSVTITS 621
AtATG13-2 574 VSGTESEFSMARSTDALEELRN-----YKQLKDLLSKSKSGSGPTRVH-- 618
ScATG13 633 QMGNSATKFKSSISPRSIDSISSSFIKSRIPIRQPYHYSQPTTAPFQAQAKFHKPAKLI DNGNRSDNNNNHNG 707

HvATG13 ----- 542
OsATG13-1 542 RHS----- 544
OsATG13-2 596 LT DGEP----- 601
AtATG13-1 622 PFDV----- 625
AtATG13-2 -----
ScATG13 708 NDAVGVMHNDEDDQDDDLVFFMSDMNLSKEG 738

M	<i>HvATG16</i>	1 MTQAEADAGKAAIRRALRSLRRRHLEEGAH ^{RP} AI ^{EAL} NR ^{PF} AAHALEWKE ^K AEKN ^{ELE} LQQCYKAQSRLSEQLV	75
	<i>OsATG16</i>	1 MTMVEAEAGKEAIRRALRSLRRRHLEEGAH ^{RP} AI ^{EAL} AR ^{PF} AAQAVEWKE ^K AEKH ^{ELE} LQQCYKAQSRLSEQLV	75
	<i>AtATG16</i>	1 - -MVQEEKAMEAINDALRALRK ^{RHLL} EEGAH ^{AP} AI ^{SAL} SK ^{PL} ISQGS ^{EWKE} TEKL ^{ETE} LQQCYKAQSRLSEQLV	73
	<i>ScATG16</i>	1 - - - - -MGNF ^I ITE ^R KKAK ^E ERSN ^P QTD ^S MD ^{DL} LIRRLTDRND ^K - - -EAH ^L NELFQDN ^S GAIGGNI	57
	<i>HvATG16</i>	76 SEINEAKTSK ^{ALL} KEKEALIT ^{TL} LQSEL ^{GQ} TREENVQL ^{KES} LEEKT ^{NAL} DLLIQ ^{EH} QA ^{AK} AELER ^{VL} TKLKAVE ^{HE}	150
	<i>OsATG16</i>	76 TEIEEGKASK ^{ALL} KEKETLIT TM QTELE ^Q TREENTQL ^{KQ} SLEEK ^T SAL ^{DL} IIQ ^{EH} QAVKAELE ^Q ALT ^{KQ} KVAE ^{DE}	150
	<i>AtATG16</i>	74 IEVAESRTSK ^{AIL} QEKELLIND ^L LQKEL ^{TQ} RED ^{CTR} LQEEL ^E EKT ^{KT} VDVLIA ^{EN} LEIR ^{SQ} L ^E EMTSRVQKA ^{ETE}	148
	<i>ScATG16</i>	58 VSHDD- - - -ALLN- - - -TLA ^I LQKEL ^K SKQE ^E IRRL ^E KEVIAL ^{KN} KNTERL ^{NDE} LISGT ^I ENNV ^L QQ ^{KL} SDLK ^{KE}	123
	<i>HvATG16</i>	151 NTQLVERLMQAKMVEAE ^{KL} NEANAMY ^E EMVLKLKAAGLGAGGIQHNAQ ^E ADGVIRRSEAGYVDIMETPI ST CR	225
	<i>OsATG16</i>	151 NRNLIDRWMLEKMKDAERLNEANAMY ^E EMVLKLKSAGVG- -GIQHNA ^L Q ^E ADGIIRRSEAGYMDIMETPI ST CR	223
	<i>AtATG16</i>	149 NKMLIDRWMLQKMQDAERLNEAN ^D LYE ^E MLAKLKAN- - - -GLETLARQQVDGIVRRNEDGTDHFVESTIP ST CA	218
	<i>ScATG16</i>	124 HSQ ^L VAR ^{WL} KKTEKET ^E AM ^N SEIDG ^{TK} - - - - -	150
	<i>HvATG16</i>	226 VTIRAHDGGCGSII ^{FQ} NNTDKLI ^{SGG} QDQTVKI ^{WSA} HTGALTSTLQGC ^L GTVNDLAVTNDNK ^{FV} IAACSSN ^{KL} FV	300
	<i>OsATG16</i>	224 ITIRAHDGGCGSII ^{FQ} HNTDKLI ^{SGG} QDQTVKI ^{WSA} HTGALTSTLQGC ^L GSVNDLAVTNDNK ^{FV} IAACSSN ^{KL} FV	298
	<i>AtATG16</i>	219 NRIHAHEGGCGSIV ^{FE} YNSGTLFTGGQDRAVKMWD ^T NSGTLIK ^{SL} Y ^G SLGNI ^L DMAVTHDNK ^{SV} IAATSSN ^{NL} FV	293
	<i>ScATG16</i>	- - - - -	
	<i>HvATG16</i>	301 WEINGGRPRHTLTGHTKNVCSVGASWAKSLVIASS ^S NDRTIKI ^{WDL} QTGFCKSTIM ^S ASNPNTLAF- IHGDS ^I CS	374
	<i>OsATG16</i>	299 WEVNGGRPRHTLTGHTKNVSSVDASWVKSCVLA ^S SSNDHTIKI ^{WDL} QSGFCKSTIM ^S GSNANSLAF- IDGVT ^L CS	372
	<i>AtATG16</i>	294 WDVS ^S GRVRHTLTGHTDKVCAVDVSK ^F SSRHVVSAAYDRTIKL ^{WDL} LHKGYCTNTVLFTSNCNAICLSIDGLTV ^F S	368
	<i>ScATG16</i>	- - - - -	
	<i>HvATG16</i>	375 GHRDGS ^L KFHDIRSGKCFATVAGH-ADVSSVCVTRSKNHVLS ^S GRDGVHKLFDVRMPTEVVEICGTFRAPSNRLI	448
	<i>OsATG16</i>	373 GHRDGH ^L RLWDIRSAKCTSQTF ^{AH} -LDVSSVSVSRNRNFI ^L TSGKDNVHNLFD ^{PRT} - - -MEVCGK ^F KAMGNRVV	442
	<i>AtATG16</i>	369 GHMDGNLRLWDIQ ^T GKLLSEVAGHSSAVTSVSLSRNGNRIL ^T SGRDNVHN ^V FD ^{TRT} - - -LEICGTLRASGNRLA	439
	<i>ScATG16</i>	- - - - -	
	<i>HvATG16</i>	449 GSWGRACISP ^D ENCIAAGCSDGSVCI ^{WSR} SKNEG-PTILEGHSLPVVTS ^A WSEFG-PLATADKN-HIHIWA	516
	<i>OsATG16</i>	443 SSWGRPCISP ^D ENSIAAGANDGSVYI ^{WSR} LKKDGVPTILQGHSSSVVSSSWCGLG-PLATADKH-HIYIWT	511
	<i>AtATG16</i>	440 SNWSRSCISP ^D DDYVAAGSADGSVHVWS-L ^{SK} GNIVSILKEQTSPILCCSWSGIGKPLASADKNGYVCTWT	509
	<i>ScATG16</i>	- - - - -	

N

<i>HvATG101</i>	1	-----MNCETCHLNELLEPLEIKDVLRCILHT	28
<i>OsATG101</i>	1	MFC-SSGAVGYQSPEYFCGNPTGFLSLYII RNFIWLRLL IRRFGVAEMNCETCOLKELELEPREIKDVLRCILHT	74
<i>AtATG101</i>	1	MMKQAYEKVSPN-PPKTI GEKKGESVSC---KF-----QQGRSEE ILEKSENSLTREVESFEIREVLRCILHT	64
<i>MmATG101</i>	1	-----MNCRSE-VLEVSVEGRQVEEAMLAVLHT	27
<i>HvATG101</i>	29	IFFHRTL T-----LVRPKDVDCDL FEITYVQCGLAELEKEVDEKINQFI AWA EK-HPNRKSQVCLSF	89
<i>OsATG101</i>	75	IFFHRTL S-----LVRPKDFDCDFE I TYVQCGLPELEKEVDEKINQFVAVVEK-HPNRSSQVCLSF	135
<i>AtATG101</i>	65	IVFHRLG-----LIRPKDIDL E LFEITYVQCGEI EVEKKIDEKIEQFINWIEK-HPNKKSQICLSF	125
<i>MmATG101</i>	28	VLLHRSTGKFHYKKEGTYSIGTVGIQDVDCDFIDFTYVRVSSEELDRALRKVVGEFKDALRNSGGDGLGQMSLEF	102
<i>HvATG101</i>	90	FDEKNKHPGW FSSKTERVYWEQWF INLHVTNPKGQ--GKSRGSKAPASTKGQALEETSSRRDAL SLL IQEVL FQI	162
<i>OsATG101</i>	136	FDEKNKLPSWFGNKTERIYWEQWF INLHVISPKRH--GKSHSSKALTNIGGQALEESSRRRAALES SIHEVL FQI	208
<i>AtATG101</i>	126	YEVKSKQPSWFT-KIERLYWEQWY INLNVLPQTKPPVGKSHH SKL-VMDPGEASEERSRRTLLEQSLQEVL FQI	198
<i>MmATG101</i>	103	YQKKKS--RW-PFSDECIPWEVWTVKVVHVVALATEQERQICRE----KVGE-----KLCEK I NI	155
<i>HvATG101</i>	163	INYANEKKDHI PPISDRIF--NHEILVPSSSDSVFGWNADVLRRALSSGHSYSLN-----	215
<i>OsATG101</i>	209	INFANEKKDHI PPIDRIF--NHEISIPSSSDSMFGWNTDVLRRVLNSGHPYSL-----	260
<i>AtATG101</i>	199	IKFVNEKKDHPPIINDGV IYYPFEITIPSSSDSAFGM--DMFKRILHSGHP SMLG-----	251
<i>MmATG101</i>	156	VEVMS-RHEYL PKMPT-----QSEVDNVF-----DTGLRDVQPYLYKISFQITEALGTSVTTTMRRL	211
<i>HvATG101</i>		-----	
<i>OsATG101</i>		-----	
<i>AtATG101</i>		-----	
<i>MmATG101</i>	212	IKDTLAL	

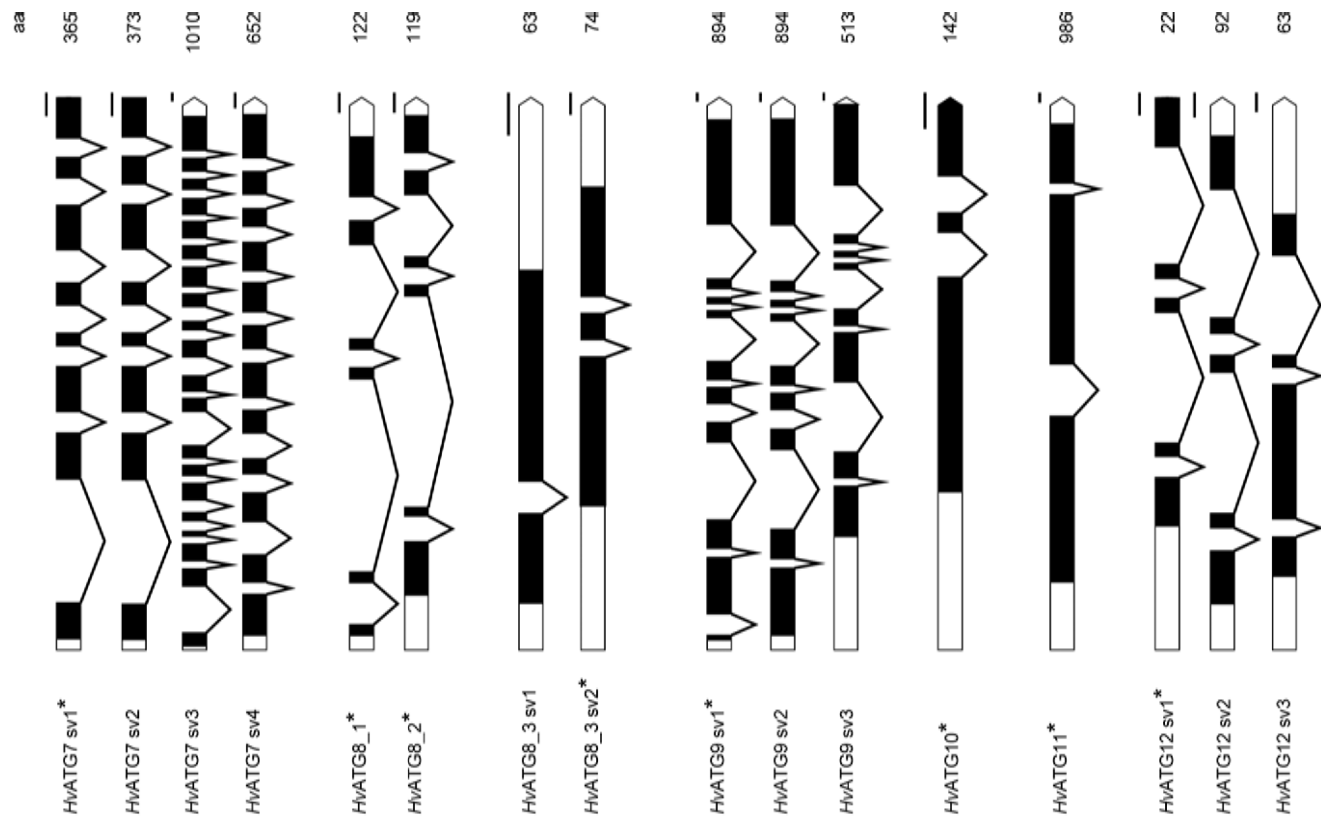
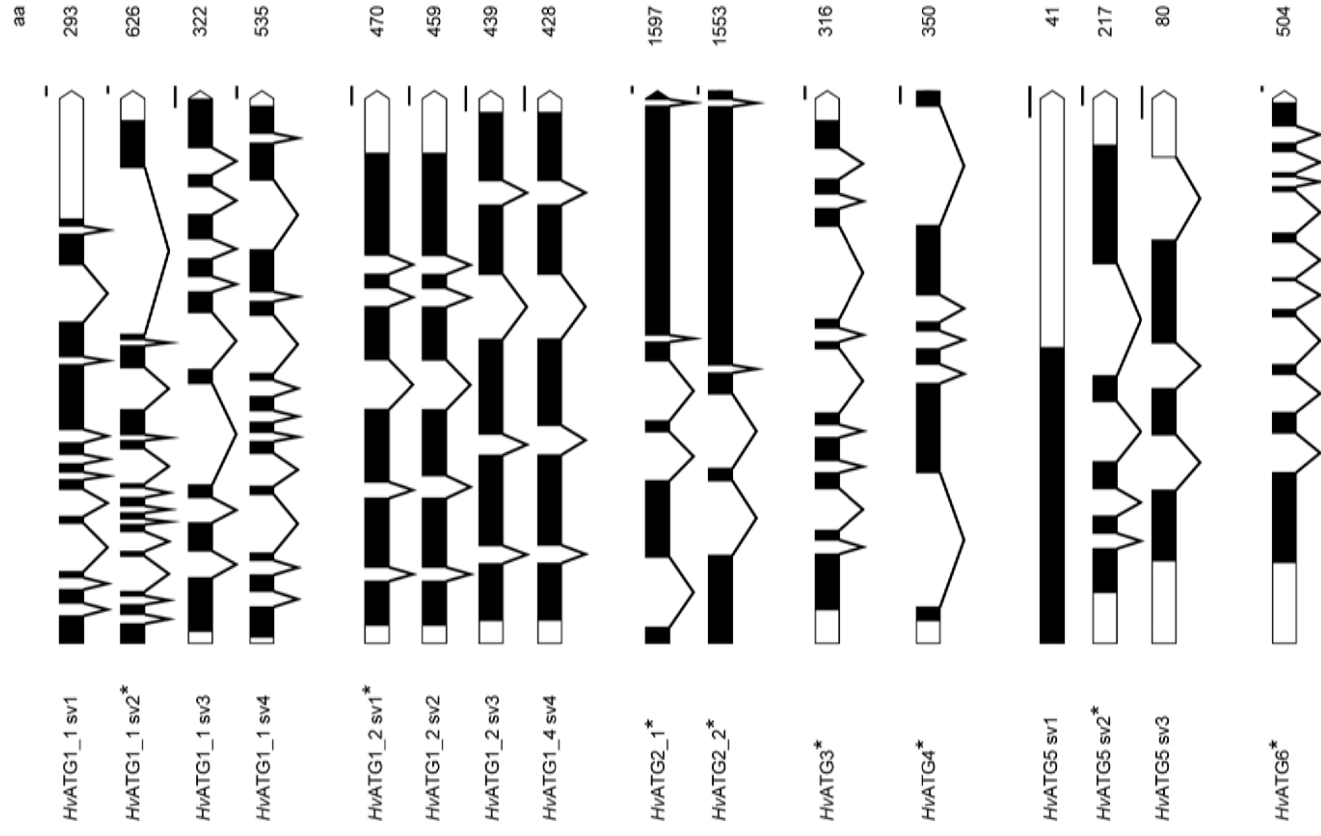
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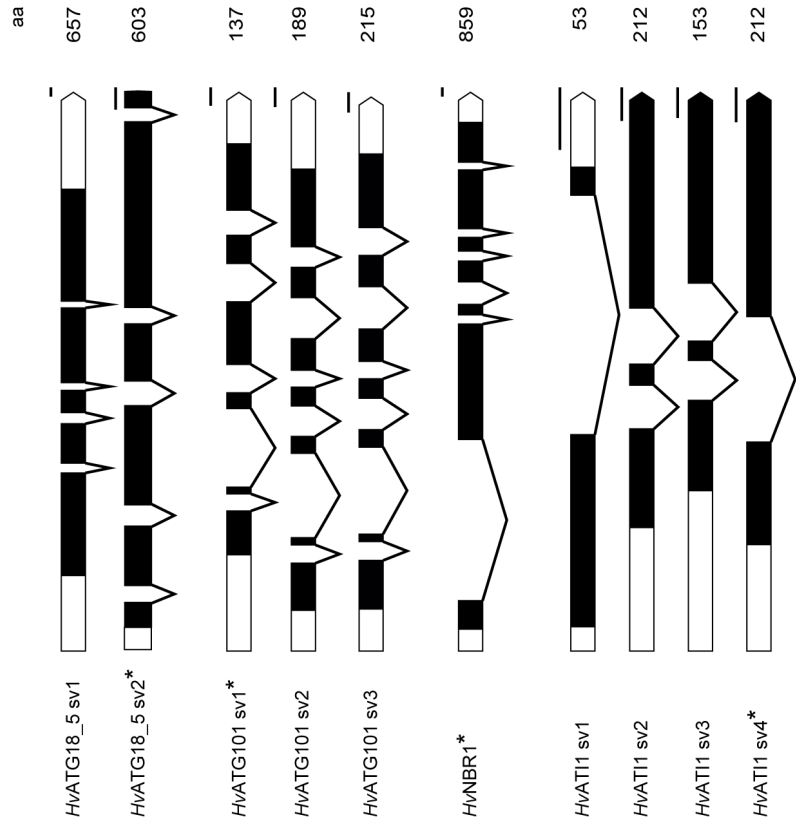
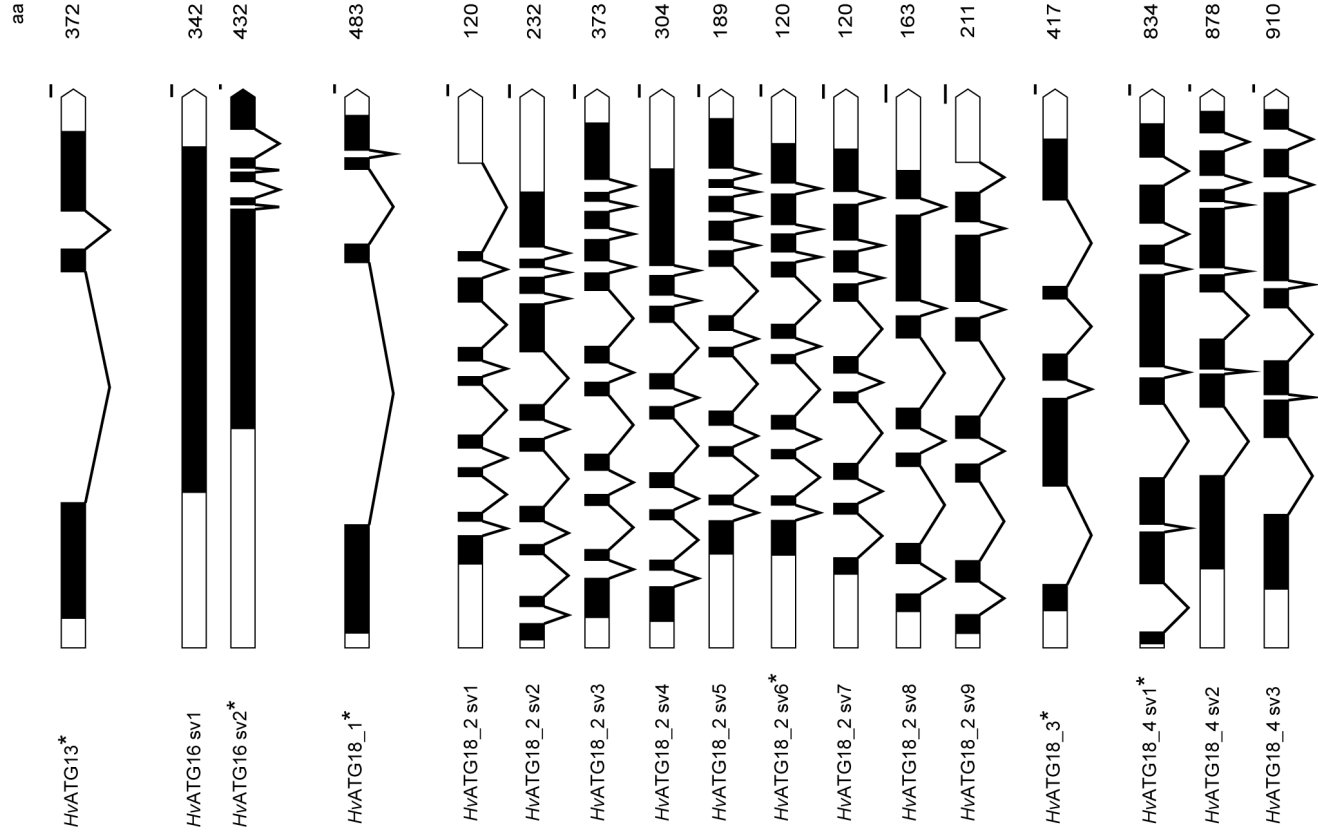
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OsAT11	1	MADND-KEAAGEGATPRGADWEVVTLTASAYAAAPGGGAGDRPAAETKGLDASQEGDQTKGLDGSQEGRGSESA	74
ZmAT11-1	1	MEDD----NEVTGESPVADWDMLSLTSSIYASPLFRRGFDPIN---LPGYG-----N-----VINIQEGTQTG	57
ZmAT11-2	1	MADN--EKEVGEGTTPRGADWEVVTLTASAYEAAAPGPV RTEVKPVNENQ-----EHSSSNA	54
AtAT11-1	1	MANN-----EEHPPRGNEWVVSLTSSAYAAAPGPYNVES--RDVRKYDAYY-----GAETSRD	52
AtAT11-2	1	MADK-----DEAATRGNDWEVVS LTASAYAAAPGPKPVVDSKDDDHKEVTPCY-----EAETSHP	55
HvAT11	58	LLMSDHFVFPPSEHENL--PIETALLEPQUESTSV----DAAAAAFKNVGGGY---DDDGSETVKYYDEGKSLSV	122
OsAT11	75	LFMSGHFVFPPSEHENL--PI DAGFDDIQHKDAQEASTSVEDEGFKNVGGNY--G-AGLERIQFYDEGRNLSA	143
ZmAT11-1	58	LVMSDGFVFPPSEHENL--PIEPEHEDLP IEPGHDESNTNSV-EKESS-----CAGNDDDDWCHVSPEEI-	119
ZmAT11-2	55	LLMSDHFVFPPSEHENL--PIQTSFDEIQPEKDVQKPSTTVEDYSIKNVV-----GSERVQFDDEGKDLSD	118
AtAT11-1	53	LYMSEHFVFPPSEHENL--PIDESLFVAEQRKDGRDLMLEG--QGLSDQFHY----EAGNNQQS IYGESALGSS	118
AtAT11-2	56	LYMSRHFVFPP TGQLENTSDL TEASLTGSHCKEGSDLSLKG--LDLSDDFGGLEFSEDKGKKEENIYTTAMSSL-	127
HvAT11	123	HD AEMMMGDVAE---FYAEDDGRGFVVFHDD-----DSQDKSGAPQDTSGSSSKGRGSGAPQCWLKKHMSCL	186
OsAT11	144	NDVEMMMGDAAEHGSFHAQDEEQG-----LDDDNDFDDSHDKSDLPSE-SADSKSRDSGAPCKCWLKKHMSCL	210
ZmAT11-1	120	DDV-----SN-----ENLADNSDL----PTASEATVPDSQPT E INAKREKD HRTCKADHTCERWWKKKTTYL	177
ZmAT11-2	119	DDVEMRDDT-PGYGSSHTDDAHGFVVLDDGVESGEDF--DEKSGHPSD-PADSRSCDTGASCKCWLKKHMTCL	188
AtAT11-1	119	RHM-----ESFGSES AVYEHGLV--DAEGNLDLHSD--GEGEKDVKKSTHNLPC EAWWKRRASIM	174
AtAT11-2	128	DDE-----RAIG-GSHVYEPVEEPT EPVSPSDVTLD--LNP IKDDEVANSPPSEEA WKKRSVASL	184
HvAT11	187	YDQAKETNTI WGAVVVAALVGLVILW-----SGSTVRG-----	212
OsAT11	211	YHQAKETNALWSVVVAAALVGLVILG-RWHKDKLHLKNLKWRS	258
ZmAT11-1	178	FHHIKGVTTLC SVVAAGAVVG FVVMGQRWQQDHWHLHQFKFSV--SGESMNRVIGAFSRLKDGLPGSEQLRSMLP	250
ZmAT11-2	189	YNQAKETNAIWSVVVAAALVGLVILG-RWHKDKLHLNQLKWRS	236
AtAT11-1	175	YSRTREANA IWSLFFAAAVTGLVVLGQRWQQRWQVLQLKWQSSISSEKLGRVLEPLSRLKDVIVRSNPQASLVR	249
AtAT11-2	185	IAQAKETNTVWSICIAAAVMGIVILGQHWQQRWQILQQKWESSIGNEKAGRLMGPI SRLKQAFVGGQRRDSFIR	259
HvAT11		-----	
OsAT11		-----	
ZmAT11-1	251	TRVLPQQPLSA	261
ZmAT11-2		-----	
AtAT11-1	250	SGSSSEV----	256
AtAT11-2	260	ASAQNDR----	266

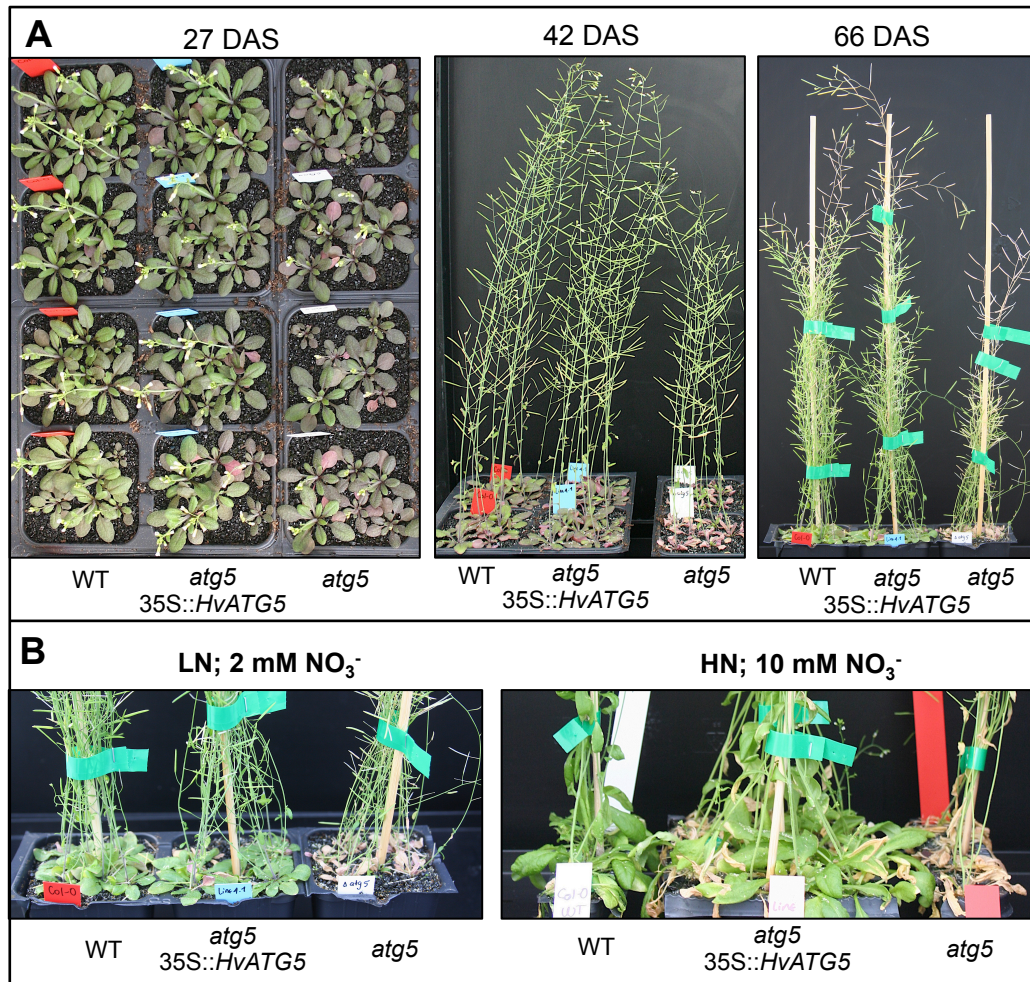
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	ZmNBR1	1	MSDWSSPAAPTFPFPGQAEGWDVTFVKVYGDTLKRFYGCAN-GSHFDMNLSALRARIDTAFKFGPDVDFVLTYYT	74
	OsNBR1	1	---MSGRSSPMYEGLASRPDEWVVLVKVYGETLKRFGGYVQ-GPQFSLNLSALRSKIASAFKFGSDVDFILTYT	71
	AtNBR1	1	-----MESTANALVVKVSYGGLRRFRVPVKANGQLDLEMAGLKEKIAALFNLSADAELSLTYS	59
	MmNBR1	1	-----MEPQVTLNVTFK	12
	HvNBR1	72	DEGDV VMLDDDEDLHDAI HQKLNPLRIN VQVKNSHADASHINRQDSRPKPVRT-TQDPLAQIKSVIDEALKP	145
	ZmNBR1	75	DEGDI VMLDDDDDLDAALRQRLNPLRITVQLKKNQPTKEK-----DTSAPVK-SAAQDPLSQLMSAIEG-LKP	142
	OsNBR1	72	DEGDI VMLDDDDDLHDAI HQKLNPLRIN VQLNNSHTAAPQAKQDSDNIPLRSTTTEDPLAHIKSVIDEVLKP	146
	AtNBR1	60	DEGDV VALVDDNDFDVT-NQRLKFLKINVNAGVSTNSAAPESSGSSTP-----AGMPNPVSKIQKGINDV LMA	128
	MmNBR1	13	NETQSFLVSDPENTTWA-----	29
	HvNBR1	146	I SEPLRSTAREDLAHLKSALDEAMKSIHEPVPESLAKLSREVLDA-----PPQLTDLI---KPFVNLITSTNSSQ	214
	ZmNBR1	143	-----VQEDSLAHIKSAIGEAIKSIPEIPDALAKLSHEILDAA---PPPLAELM---KPFQALMAPNNNGN	203
	OsNBR1	147	IS-----MKS IQEPVPETLAKLSHEVLEAA---SPQLAELI---KPFVKLVTPSNNNP	193
	AtNBR1	129	VPNPMR-----DTISKVYMDLASKASTSSPVVGEMLDICISKLGLSIPQESSP	176
	MmNBR1	30	-----DVEAMVKVSFD-----	40
	HvNBR1	215	--SAGHAESS--PVSSGVQQAQV DLKANDQPKVDS SLGSS-----ETRGLKSVLA EVPA-AVITEASQG--	273
	ZmNBR1	204	GPSDVHAEGSSSS--SSAQVPAEAKNEPKVRPSLGLK-----TVLKEAAGVPVNAGASQV--	256
	OsNBR1	194	--SNGHADGSCSSSTGLPQTQVDPKTNDEPKIDTSLGSQPLDTQNSKSSGARGLKTLVSEAPA-TSGVKSSQG--	263
	AtNBR1	177	CSP-VTKPGS--SGA-----SLSRDV-----	194
	MmNBR1	41	-----LNTIQI--KYLDEENEEISINSQ-----GE---YEEA---LKMANIKQGNQ	78
	HvNBR1	274	---QQGSLYPSVEDL LFT---SNSGGNSSGCKGMSNAESKCKSVMPSAEP---LSRSTVPNFRF SHPNASGY--	336
	ZmNBR1	257	---QQPLMYPVSEEMLF---CNSVDKSVCKGKIDAQSKGKSVTSSGIQ---PAPHSLRTHAPPPPHPCIS--	318
	OsNBR1	264	---QQASLYPSIEEL LFSPFLPNSGDDKSASKGIDSAQSKGKSVMTSATP---PTPPAAPAFRFPAPP IPSLN--	329
	AtNBR1	195	-----PSAGGK---DISERTQTRKPVNLNEP-----TGAHSKTS-----	227
	MmNBR1	79	LQM QVHEGYHVVDEALPKNVVENQA-----ARTGKKPLAHYSSSLVRVLGSDMKTTTEEPA-PEQCSSAP	141
	HvNBR1	337	-EWYQPRRSTDGWSQPKSIWQPEANVKPASDPGWRVPMYKAPHSP-----PVPHAPLGYGHSQFPYPGR	401
	ZmNBR1	319	-EWSRAQRSQHR-----QLKFEDNAKATNDSRWIRPMYKMPYAP-----PPPAVPPPGYVSPHFPYPGR	377
	OsNBR1	330	-DWSQPPARG--STFYPSIWQSEADPKANSDSRWVPLCRAGHPFQPHAPLSRPPPPMPAPMSYGPSPHFPYPGR	401
	AtNBR1	228	--GHVPNSSGLGANFNECPF-----SGSTMN-----YSCP N-----PVNLNKHPRRVCHSK	271
	MmNBR1	142	CDTDQPPQDK-----PPDWFTSYLEMFREQVVKETVE-----KLEQRLQEKLVLQKP	187
	HvNBR1	402	LLSAG--RLHGNLSNNSERSP-RISHRWIQCDGCGVQPIVGPRYKSNVKEDYDLCDTCFRRMGSEVE---YTRID	470
	ZmNBR1	378	LLSSG--HPYGDLAGNMENSAPHSLHRWIQCDGCGAQPIVGPRYKSNVKEDYDLCDSCFQRMGNEME---YTKID	447
	OsNBR1	402	LLSSG--HLHGD LGNNIENSPARTFHRWIQCDGCGVQPIVGPRYKSKTKEDYDLCDACFHRMGNEVE---YTRID	471
	AtNBR1	272	KSTNG--D-----YWTSLGVFHKGRCDGCGVLPITGPRFKSKVKEDYDLCTICYSVMGNEGD---YTRMD	332
	MmNBR1	188	LLSSSPTEVSMPISEETLFLPENQFSWHIACHCQ-KRIVGVRYQCCLCPSYNICEDCEAGPYTHDTNHVLLKLR	261
	HvNBR1	471	KPILPHKLSRDLNLC-----R-----KI H--	489
	ZmNBR1	448	KPILPHRFLRDPHVY-----R-----KVH--	466
	OsNBR1	472	KPLL PQRLLRDPTLC-----R-----PVDQV-----KI H--	490
	AtNBR1	333	KPVSVQHLHPFRGPFQTQFPNPWL SHVP-----RAT--	363
	MmNBR1	262	RPVV--ISSEFFFYSKYSAPRLPAALEQVRLQKQVDKNFVKA EKQRLRAEKKQRKA EVKELKKQLKLHRKIH LW	333
	HvNBR1	490	-----SRVSMK-----SKREKLESRFILDVTVLDGTLMS PSSPFTKIWRMHNNGSIMW	537
	ZmNBR1	467	-----HPRVLMK-----SRREKLESRFILDVTVLDGTLMT PSTPFTKIWRMHNNGSVVW	515
	OsNBR1	491	-----SRAAMK-----SKREKLESRFILDVTVLDGTLMAPSTPFTKIWRMHNNGSIMW	538
	AtNBR1	364	-----NGGAPLR-----CTRPKLSRFVLDVNVIDGT VVAPSAPFTKIWKMRNSGSLVW	412
	MmNBR1	334	NSIHGLQSPKSP LGRPESLLQSN TLM LPLQPCAPVMPTL-SAAFVDENLPDGT HLQPGTKFIKHWRMKNTGNVKW	407
	HvNBR1	538	PLGTQLIWVGGDQFALQTSVPLEIPLNGFPVDQEMDVA VDFVAPARPGRYISYWRLASPSGQKFGQRVWVHIQVE	612
	ZmNBR1	516	PRGTQLVWVGGDQFALQTSVPLEIPVDGFPVDKEIDVPVDFVAPTRPGRYISYWRLASPSGQKFGQRVWVHIQVE	590
	OsNBR1	539	PLGTQLIWVGGDQFALQTYVPLEIPVDGFPVDQEIDVA VDFVAPARPGRYISYWRLASPSGQKFGQRVWVHIQVE	613
	AtNBR1	413	PQGTQIVWIGGDRFCNSLSDVLIQKEGVPIYSELDVKVDFVAPELPGRYISYWRMATSDGAKFGQRVWVLIHVD	487
	MmNBR1	408	NTDTKLKFMWGNLTASTE-KKDVLPCLKAGHVGVSVVEFIAPTLEGTYSHWRLS-HKQQQFGPRVWCSIIIVD	480
	HvNBR1	613	DPSFVSDN-KTAAVN LNQPQESNI-----TN--TSSL-P-----QE-----SDI	647
	ZmNBR1	591	DPSFVNDNNRNAAI NLNLPPESY-----S	614
	OsNBR1	614	DPSFVSN-RTAAI NLNLPPESN-----I	636
	AtNBR1	488	ASLKNSVVNEFHGLNLNASPSLDE-----NF--PSEF-LGIMNYESAQPG-----SSS	532
	MmNBR1	481	PFPSSESPDNVEGDRISSSKADDFSCQEAEFLLAEEIPLGEVTKQTEGTGASASQKTRRAASERELYIPSVDL	555
	HvNBR1	648	TNAS-----NLIDVNVE-----PANQV-----LDE---	667
	ZmNBR1	615	SNTT-----NLIDVNI-----PADSA-----LSA---	634
	OsNBR1	637	TNTS-----NLIDVNI-----PVDQV-----FNQ---	656
	AtNBR1	533	VNPG-----TVKGTD-----LEG---	545
	MmNBR1	556	LTAQDLLSFELLDINIVQELERVPHNTPVDMTPCMSPLPHDSPLIEKPGLGQIQEESEGAGFKAPPDSTVSAKRK	630
	HvNBR1	668	-----HVNDTRI-----ELLEPLIYR-EAAEPKKSPSASAAAP-----L-----	700
	ZmNBR1	635	-----HAKRTKE-----FHF--CST-DFPEPSKSVPTLATTS-----LS-AAA-----	669
	OsNBR1	657	-----HVNSTNK-----ELLEHLIHH-QIDEPKNPEAPLPVPI---VSSTSL-----	696
	AtNBR1	546	-----EVGETQA-----VEKENLLVG-----EAH-----	564
	MmNBR1	631	AETPASVEETFEEDLSGTQFVCE TVIRSLTLDAAPDHNPPCRQRS PQRELQLYSTEGQQPLVLPGF CRKDS SLKFA	705
	HvNBR1	701	-----YPK--VDVPSSSE-NAAGFV--P-----SVNVLAPE-	726
	ZmNBR1	670	-----PTNQTGDVPMSS-TAAACL--P-----SVNVPMHE-	697
	OsNBR1	697	-----HPIIDVDVPSS-S-TAAAFV--P-----VFDEPAPE-	723
	AtNBR1	565	-----PAIPHGHSPSSSS-SSFNMV--D-----FPSMPAVE-	592
	MmNBR1	706	LPEEGPRGDEREEIVHIVEEEVVEEEVEEQDEEVQSQSSASSEDYIIILPECFDTSRPLGDSMYSSALSQGLER	780

<i>HvNBR1</i>	727	-----V I P E P S A T T P - A E V P T S L L T S ----- I P V D ----- L T V	753
<i>ZmNBR1</i>	698	-----V V T T H T P S P I T P V L P T T I H F S A P V S A P A I A P E ----- L A S	732
<i>OsNBR1</i>	724	-----P A V T P ----- V P P T ----- V N V	735
<i>AtNBR1</i>	593	-----V L S G G S S ----- S	600
<i>MmNBR1</i>	781	G A E G E P G I E S G L E P T E A R E R L P E R E S Q P Q E Q S I S D I L T T S Q P L D T V P L V P E V A G L P A A L S R S A P C G Q C E S S G V D S	855
<i>HvNBR1</i>	754	- A A T A P V - - - D V A S A L L D I - D R L T E E K L L Q E L E E M G F K Q V D L - - - - - N K E I L - - R Q N K Y N L - - - - - E	803
<i>ZmNBR1</i>	733	G A V G V P P P V S A V V P E L S E L - D V H N E E K L L R E L E E M G F R Q V D L - - - - - N K E I L - - R Q N N Y N L - - - - - E	786
<i>OsNBR1</i>	736	P A G N A P A S V G A S S D H H G I - D N L T E E K L L K E L E E M G F R Q V D L - - - - - N K E I L - - R Q N K Y N L - - - - - E	789
<i>AtNBR1</i>	601	T T K D V P V P L Q - - - - - E D I E K N D V E I T M L K E L E E M G F K E I D L - - - - - N K E I L - - R D N E Y N L - - - - - E	649
<i>MmNBR1</i>	856	P G V D S P A T M H E V P P A P D D I R G E P R G S T - - - G L A N S R Q R S C D H S R H H N G S S I A G G L V K G A L S V A A S A Y K A L F S G P P	927
<i>HvNBR1</i>	804	Q S V D D L C G V N E W D P L L A E L S E M G F D D R E T N K E L L A K N G G S I K R A V M D L I A R E K K D K - - - - -	859
<i>ZmNBR1</i>	787	Q S V D D L C G V N E W D P L L A E L E E M G F D D T E M N K E L L A K N E G S I K R A V M E L I A R E K K D K - - - - -	842
<i>OsNBR1</i>	790	Q S V D D L C G V S E W D P L L E E L Q E M G F E D T E I N K E M L E K N G G S I K R A V M D L I A R E K K D Q - - - - -	845
<i>AtNBR1</i>	650	Q S V D A L C G V S E W D P I L E E L Q E M G F C D D V T N K R L L K K N G S I K G V V M D L L T G E K E A - - - - -	704
<i>MmNBR1</i>	928	V T A Q P I V S E D Q T T A L M A H L F E M G F C D R Q L N L R L L R K H N Y N I L Q V V T E L L Q V N N N D W Y S H R Y	988

Supplementary Figure 4. Diagram of predicted splice variants of barley ATG genes. Data is according to genomic assembly database EnsemblPlants (<http://plants.ensembl.org/>). White boxes (□) represent untranslated regions, black boxes (■) represent coding regions and solid lines (V) represent introns. The predicted amino acid (aa) length for each of the corresponding proteins is shown at right. See table 1 for EST and cDNA sequences supporting each gene. The upright bars represent a scale of 0.1 Kb. Asterisks and red boxes indicate gene models found in this study. sv1 to sv9 name extension indicate the different splice variants described on *Ensemblplants* web site. The * splice variants represent the most likely DNA coding sequence of the HvATG putative proteins.







Supplementary Figure 5. The *atg5* 35S::*HvATG5* transformants are less senescing and less sensitive to nitrate limitation than *atg5* mutants. Wild type, *atg5* mutant and *atg5* 35S::*HvATG5* transformant (4.1; 2.3 and 3.1) were grown under low (A and B left panel) and high (B right panel) nitrate conditions. They displayed late senescence and bigger biomass than the *atg5* mutants under the different conditions; In A, phenotypes of the 4.1 plants 27, 42 and 66 days after sowing (DAS) are shown. Early leaf senescence was observed in *atg5* but not in *atg5* 35S::*HvATG5* plants under both low (2 mM) and high (10 mM) nitrate conditions. Planting was repeated two times including three independent transformants that showed similar recovery phenotypes. Only one is shown here.

Supplementary Table 1. Yeast, Arabidopsis and rice *ATG* genes used as query.

Gene in <i>S. cerevisiae</i>	Systematic gene name	No. of AA residues	Gene in <i>A. thaliana</i>	TAIR locus	No. of AA residues	Gene in <i>O. sativa</i>	TIGR locus	No. of AA residues	Identity <i>Sacc.</i>	<i>O. sat.</i> to <i>A. thal.*</i>
ATG1	YGL180W	897	ATG1	AT2G37840 AT3G53930 AT3G61960	733 711 626	ATG1a ATG1b ATG1t	Os03g0122000 Os03g16130 OsJNBa0070M12	652 714 275	28% 28% 32%	43% 44% 49%
ATG2	YNL242W	1592	ATG2	AT3G19190	1839	ATG2	Os06g15700	1920	12%	32%
ATG3	YNR007C	310	ATG3	AT5G61500	313	ATG3a ATG3b	Os01g10290 Os10g41110	314 314	27% 13%	72% 36%
ATG4	YNL223W	494	ATG4a ATG4b	AT2G44140 AT3G59950	467 477	ATG4a ATG4b	Os03g27350 Os04g58560	474 478	18% 19%	45% 48%
ATG5	YPL149W	294	ATG5	AT5G17290	337	ATG5	Os02g02570	380	12%	48%
ATG6	YPL120W	557	ATG6	AT3G61710	517	ATG6	Os03g15290 Os03g44200 Os01g48920	544 502 501	15% 19% 17%	32% 36% 36%
ATG7	YHR171W	630	ATG7	AT5G45900	697	ATG7	Os01g42850	1043	20%	34%
ATG8	YBL078C	117	ATG8a	AT4G21980	137	ATG8a ATG8b ATG8c ATG8d ATG8e	Os07g32800 Os04g53240 Os08g09240 Os11g01010 Os02g32700	120 120 121 119 87	71% 72% 71% 33% 51%	82% 83% 84% 31% 51%
			ATG8b	AT4G04620	122					
			ATG8c	AT1G62040	133					
			ATG8d	AT2G05630	164					
			ATG8e	AT2G45170	122					
			ATG8f	AT4G16520	121					
			ATG8g	AT3G60640	121					
			ATG8h	AT3G06420	119					
			ATG8i	AT3G15580	115					
ATG9	YDL149W	997	ATG9	AT2G31260	866	ATG9 ATG9 ATG10a ATG10b	Os03g14380 Os10g07994 Os04g41990 Os12g32210	903 927 199 223	13% 14% 15% 14%	48% 47% 40% 42%
ATG10	YLL042C	167	ATG10	AT3G07525	226	ATG11 ATG12	Os02g0179800 Os06g10340	1140 94	21% 32%	50% 72%
ATG11	YP9499C	1178	ATG11 ATG12a	AT4G30790 AT1G54210	1148 96	ATG13 ATG13 like ATG16	Os11g06320 Os02g43040 Os03g53510	602 544 510	10% 10% 5%	24% 32% 54%
ATG12	YBR217W	186	ATG12b	AT3G13970	94					
ATG13	YPR185W	738	ATG13 ATG13	AT3G49590 AT3G18770	618 625					
ATG16	YMR159C	150	ATG16	AT5G50230	509	ATG18a ATG18b ATG18c ATG18g ATG18 like ATG18 like	Os01g70780 Os02g54910 Os01g07400 Os05g33610 Os01g57720 Os05g07710	458 375 418 769 871 383	7% 17% 20% 20% 21% 6%	6% 61% 49% 49% 21% 6%
ATG18	YFR021W	500	ATG18a	AT3G62770	425					
			ATG18b	AT4G30510	312					
			ATG18c	AT2G40810	393					
			ATG18d	AT3G56440	391					
			ATG18e	AT5G05150	374					
			ATG18f	AT5G54730	763					
			ATG18g	AT1G03380	959					
			ATG18h	AT1G54710	927					
Gene in <i>M. musculus</i>	Systematic gene name	No. of AA residues	ATG101	AT5G66930	251	ATG101	Os12g0428200	260	26%	54%
ATG101	Q9D826	218								
Nbr1	U73029	988								
-	-	-								
-	-	-	ATI1 ATI2	AT2G45980 AT4G00355	256 266	ATI1	Os04g0165300	258	-	38%

Sequences compared with the single gene product in yeast and the a isoform from Arabidopsis*
AA. Amino acids.

Supplementary Table 2. Primers used for transcript amplification of *HvATG* genes by RT-qPCR

Gene	Accession	Sequence 5'-3'		Source	Amplification size (bp)
<i>HvATG3</i>	AK252967	Fwd	GAAACAGACCTCCCAACCCA	This work	
		Rev	ATCAAAGCAGAAAAGTGGGGC		
<i>HvATG5</i>	AK362511	Fwd	GCCGATCCTGAACCTGCGGC	This work	101
		Rev	GGGCTCGCTGGAGGTGGTTT		
<i>HvATG6</i>	AK362923, AM075824	Fwd	GAATGCAGCGTTGTTTGTCAT	This work	
		Rev	ATTAAGGAGGGTGGAGCCAG		
<i>HvATG7</i>	AK367931	Fwd	GACTGGCCTCCATAGCATCT	This work	212
		Rev	CTGTATTACGCACTACCGC		
<i>HvATG8_1</i>	AK251678	Fwd	CGCGTCGCAAACCCTCGTCC	This work	123
		Rev	CGGTTAGCCTCCGCCTGCCT		
<i>HvATG8_2</i>	AK248733	Fwd	ACCGAGCACCCCCTGGAGAG	This work	249
		Rev	CGAAGCAGTCGGTGGCAAGGT		
<i>HvATG8_3</i>	AK250515	Fwd	CTGTCTCCAGGAACGGCGCT	This work	357
		Rev	ACGCCCATGCTTCCAGAGG		
<i>HvATG13</i>	AK365609	Fwd	CGCGATTCAAAACCACGAAC	This work	86
		Rev	GAAGGAGGAGTTCGTTCCGA		
<i>HvATG16</i>	AK361491	Fwd	AGCTTAATGAGGCCAATGCG	This work	
		Rev	GCTTCAGACCGACGAATGAC		
<i>HvATG18_1</i>	AK364793	Fwd	ATCAGGGTCGAGCACTATGG	This work	
		Rev	CTCAGCGGCATTGAAGATCC		
<i>HvATG18_2</i>	AK371787	Fwd	TTTCCTGCTGTGAGGACTGT	This work	
		Rev	TGAAGGAACGTGGTCGGTAA		
<i>HvATG18_3</i>	AK364502	Fwd	GATCCGACAAGCAGCATCAG	This work	
		Rev	CGATCAGATTGATGAGCTTCAGA		
<i>HvATG18_5</i>	AK362065, AK371649	Fwd	GGAGGGGTTTTGCCTTCAG	This work	
		Rev	CGCGGCATGACTTTATTCCA		
<i>HvGS2</i>	AK360336	Fwd	AAGCTGGCGCTGAAGGTATGAAGG	Goodal <i>et al</i> , 2013	124
		Rev	GACGGAACCACAGGATCAACAAGAATG		
<i>HvNAC13</i>	AK376297	Fwd	ATGCCGCCGCACATGATGTAC	Christiansen <i>et al</i> , 2011	
		Rev	ACAGGTCGCCGGAATTAGCG		
<i>HvActin</i>	AY145451	Fwd	CGACAATGGAACCGGAATG	Rapacz <i>et al</i> , 2012	
		Rev	CCCTTGGCGCATCATCTC		
<i>HvGAPDH</i>	AAA32956	Fwd	GCTCAAGGGTATCATGGGTTACG	Hebelstrup <i>et al</i> , 2010	98
		Rev	GCAATTCCACCCTTAGCATCAAAG		
<i>AtActin</i>		Fwd	GCCATCCAAGCTGTTCTCTC		
		Rev	CCCTCGTAGATTGGCACAGT		