

Supplementary Table S1 Gene numbers of plant YTH genes

Taxon	Name	Brief		YTHDF						YTHDC		
			TOTAL	DF total	DFA	DFB	DFCI	DFCII	DFCIII	DC total	DC1	DC2
Dicot	<i>Arabidopsis Thaliana</i>	At	13	11	4	3	2	1	1	2	2	
	<i>Capsella rubella</i>	Cr	12	10	3	3	2	1	1	2	2	
	<i>Boechera stricta</i>	Bs	12	10	3	3	2	1	1	2	2	
	<i>Brassica rapa</i>	Br	22	18	7	5	1	4	1	4	4	
	<i>Gossypium raimondii</i>	Gr	13	11	5	3	2	0	1	2	2	
	<i>Eucalyptus grandis</i>	Eg	6	4	2	1	1	0	0	2	2	
	<i>Populus trichocarpa</i>	Pt	17	14	3	5	2	2	2	3	3	
	<i>Salix purpurea</i>	Sp	20	18	5	7	2	3	1	2	2	
	<i>Linum usitatissimum</i>	Lu	15	12	2	5	2	0	3	3	3	
	<i>Manihot esculenta</i>	Me	14	12	5	4	1	1	1	2	2	
	<i>Glycine max</i>	Gm	18	14	5	2	4	2	1	4	4	
	<i>Phaseolus vulgaris</i>	Pv	11	9	3	1	2	2	1	2	2	
	<i>Medicago truncatula</i>	Mt	9	8	3	1	2	1	1	1	1	
	<i>Vitis vinifera</i>	Vv	10	8	2	3	1	1	1	2	2	
	<i>Solanum lycopersicum</i>	Sl	7	4	1	1	1	0	1	3	3	
	<i>Solanum tuberosum</i>	St	8	4	1	1	1	0	1	4	4	
	<i>Mimulus guttatus</i>	Mg	10	7	2	1	2	0	2	3	3	
	<i>Amaranthus hypochondriacus</i>	Ah	9	7	2	2	1	0	2	2	2	
	<i>Aquilegia coerulea</i>	Ac	7	6	2	1	1	1	1	1	1	
Monocot	<i>Zea mays</i>	Zm	15	15	5	5	2	2	1	0	0	
	<i>Setaria italica</i>	Si	13	12	4	3	3	1	1	1	1	
	<i>Panicum virgatum</i>	Pvi	22	20	8	6	3	2	1	2	2	
	<i>Panicum hallii</i>	Ph	12	11	4	3	2	1	1	1	1	
	<i>Brachypodium stacei</i>	Bst	11	10	3	1	3	1	2	1	1	
	<i>Oryza sativa</i>	Os	12	11	3	3	2	1	2	1	1	
	<i>Musa acuminata</i>	Ma	19	17	7	5	2	2	1	2	2	
	<i>Ananas comosus</i>	Aco	9	8	1	2	2	1	1	1	1	
	<i>Zostera marina</i>	Zma	8	7	1	1	1	3	1	1	1	
Basal Angiosperm	<i>Amborella trichopoda</i>	Atr	7	5	1	1	1	1	1	2	2	
Fern	<i>Selaginella moellendorffii</i>	Sm	3	1	1					2	2	

Liverworts	<i>Marchantia polymorpha</i>	Mpo	3	1	1	2	2	
Moss	<i>Physcomitrella patens</i>	Pp	4	2	2	2	2	
	<i>Sphagnum fallax</i>	Sf	5	3	3	2	2	
Algae	<i>Chlamydomonas reinhardtii</i>	Cre	1	0	0	1	1	
	<i>Dunaliella salina</i>	Ds	1	0	0	1	1	
	<i>Micromonas pusilla</i>	Mp	1	1	1	0	0	
	<i>Micromonas commoda</i>	Mc	1	1	1	0	0	

Supplementary Table S2 Gene numbers of animal and yeast YTH genes

Taxon	Latin	Brief		YTHDF				YTHDC		
			TOTAL	DF total	YTHDF1	YTHDF2	YTHDF3	DC total	DC1	DC2
Mammalia	<i>Homo sapiens</i>	Hs	5	3	1	1	1	2	1	1
	<i>Pongo abelii</i>	Pa	5	3	1	1	1	2	1	1
	<i>Macaca fascicularis</i>	Mf	5	3	1	1	1	2	1	1
	<i>Bos taurus</i>	Bt	5	3	1	1	1	2	1	1
	<i>Mus musculus</i>	Mm	5	3	1	1	1	2	1	1
	<i>Dipodomys ordii</i>	Do	5	3	1	1	1	2	1	1
	<i>Ornithorhynchus anatinus</i>	Oa	5	3	1	1	1	2	1	1
Aves	<i>Gallus gallus</i>	Gg	5	3	1	1	1	2	1	1
Amphibia	<i>Xenopus tropicalis</i>	Xt	5	3	1	1	1	2	1	1
Osteichthyes	<i>Carassius auratus</i>	Ca	5	3	1	1	1	2	1	1
	<i>Danio rerio</i>	Dr	5	3	1	1	1	2	1	1
	<i>Fundulus heteroclitus</i>	Fh	6	4	2	1	1	2	1	1
	<i>Nothobranchius furzeri</i>	Nf	6	4	2	1	1	2	1	1
	<i>Poecilia formosa</i>	Pf	5	4	2	1	1	1	1	
	<i>Oncorhynchus mykiss</i>	Om	11	8	4	2	2	3	2	1
	<i>Salmo salar</i>	Ss	11	8	4	2	2	3	2	1
Chondrichthyes	<i>Callorhinchus milii</i>	Cm	5	3	1	1	1	2	1	1
Cephalochordata	<i>Branchiostoma floridae</i>	Bf	2	1	1			1	0	1
Ascidiacea	<i>Ciona intestinalis</i>	Ci	3	1	1			2	1	0
Echinodermata	<i>Strongylocentrotus purpuratus</i>	Spu	3	1	1			2	1	0
	<i>Acanthaster planci</i>	Ap	3	1	1			2	1	1
Brachiopoda	<i>Lingula anatina</i>	La	3	1	1			2	1	1
Mollusca	<i>Octopus bimaculoides</i>	Ob	3	1	1			2	1	1
	<i>Mizuhopecten yessoensis</i>	My	3	1	1			2	1	1
	<i>Pomacea canaliculata</i>	Pc	3	1	1			2	1	1
	<i>Aplysia californica</i>	Aca	3	1	1			2	1	1
	<i>Crassostrea gigas</i>	Cg	3	1	1			2	1	1
	<i>Biomphalaria glabrata</i>	Bg	3	1	1			2	1	1
Insecta	<i>Drosophila hydei</i>	Dh	2	1	1			1	1	0
	<i>Drosophila melanogaster</i>	Dm	2	1	1			1	1	0
	<i>Stomoxys calcitrans</i>	Sca	3	1	1			2	1	0

	<i>Lucilia cuprina</i>	Lc	3	1	1	2	1	0
	<i>Habropoda laboriosa</i>	Hl	3	1	1	2	1	0
	<i>Pieris rapae</i>	Pr	3	1	1	2	1	1
	<i>Frankliniella occidentalis</i>	Fo	3	1	1	2	1	1
	<i>Hyposmocoma kahamanoa</i>	Hk	3	1	1	2	1	1
	<i>Bombyx mori</i>	Bm	3	1	1	2	1	1
	<i>Tribolium castaneum</i>	Tc	3	1	1	2	1	1
Priapulida	<i>Priapulus caudatus</i>	Pca	3	2	1	1	1	0
Nematoda	<i>Caenorhabditis elegans</i>	Ce	1	0	0	1	0	0
Platyhelminthes	<i>Clonorchis sinensis</i>	Cs	2	1	1	1	1	0
	<i>Opisthorchis viverrini</i>	Ov	2	1	1	1	1	0
	<i>Schistosoma haematobium</i>	Sh	2	1	1	1	1	0
Cnidaria	<i>Orbicella faveolata</i>	Of	3	1	1	2	1	1
	<i>Exaiptasia pallida</i>	Ep	3	1	1	2	1	1
	<i>Stylophora pistillata</i>	Spi	2	1	1	1	0	1
Porifera	<i>Amphimedon queenslandica</i>	Aq	2	1	1	1	1	0
YEAST	<i>Saccharomyces cerevisiae</i>	Sc	1	0	1	0	0	0
	<i>Schizosaccharomyces pombe</i>	Sp	1	0	0	0	1	0

Supplementary Table S3 YTH proteins
used in phylogenetic analysis

Species name	Accession number*	name code**	YTH motif
<i>Ananas Comosus</i>	Aco001739.1	AcoYT HDF1C	AK-----FFVIKSYSEDDVHK--SIKYSVWSSTVSGNRKLECAFE-----DARKR-SAG----- -----KTRNCP----VFLFFS-----VNASGQFC-----GVAEMVGPVDFHTDM- DFWQ-QD-----KW-SGCFPVKWHIIKDVSNAK-LRHIILENNENK-PVTNSRDTQEIP-----YNTGINMLKIF
	Aco003339.1	AcoYT HDF4C	AK-----FFMIKSFSEDDVQK--SIKYNVWASTTYGNKKLDMAFR-----DAQMV-VKE----- -----KGTKCP----IFLFFS-----VNTSGQFV-----GLAEMIGPVDFKKNM- EFWQ-QD-----RW-NGFFPLTWHIIKDIPNRH-FHSIKLENNDNQ-VVTFSRDTQEIG-----LPQGLKMLEIF
	Aco004279.1	AcoYT HDF1A	AK-----FFVIKSYSEDDVHK--SIKYNVWASTPNGNKKLDAGYQ-----EAQEK-A----- -----GGCP----VFLFFS-----VNTSGQFV-----GVAEMVGPVDFNKTV- EYWQ-QD-----KW-NGCFPVKWHIVKDVPSNI-LKHITLENNDNK-PVTNSRDTQEVK-----LEQGLEMLKIF
	Aco004441.1	AcoYT HDF2C	AL-----FFVIKSYSEDDIHK--SIKYNVWSSTPNGNRRLDNAFQ-----VGQEK-SRE----- -----KGTKCP----VFLFFS-----VNASGQFC-----GLAEMIGRVDFSKNM- DFWQ-QD-----KW-NGYFPVKWHIIKDIPNPQ-FRHLILENNDNK-PVTNSRDTQEVK-----FPQGTEMLSIF
	Aco007343.1	AcoYT HDF3C	AK-----FFIIKSYSEDDVHK--SIKYNVWSSTPNGNKKLDAAYE-----DAQRL-SAL----- -----KGVNCP----VFLFFS-----VNGSGRFC-----GVAEMLGRVDFQRDM- DFWQ-QD-----KW-SGSFSVKWHIIKDVPNTN-FRQITLENNENK-PVTHSRDTQEMY-----IP-GTTMLKIF
	Aco007480.1	AcoYT HDF2B	AM-----FFVIKSFSEDNIHK--SIKYGVWASTPSGNKKLDSAYH-----GAKER----- -----GDPCP-----VNASGHFC-----GVAEMIGPVDFEKSVD-FWQ- QN-----RW-SGCFPVKWRIVKDVNNL-FRHIVLENNDNK-PVSNSRDTQEVN-----LEQGLEMLNIF
	Aco008320.1	AcoYT HDF1B	AR-----FFIIKSYSEDNVHK--SIKYGVWASTANGNKKLDSAFH-----EAKER----- -----EDPYP----IFLFFS-----VNASGQFC-----GVAEMVGPVDFEKSVD- DYWQ-QD-----KW-TGQFPVKWHIVKDVNNL-FRHIILENNENK-PVTNSRDTQEVK-----LEQGLEMLTIF
	Aco008423.1	AcoYT HDC1A	SR-----YFIVKSCNRENLEI--SVQQGIWATQRSNEAKLNEAFE-----SSEN----- -----VILIFS-----INRTRHFQ-----GCAKMTSKIGGFIGG-GNWK-SA----- -----HGTAH-----Y-GRNFSVKWLKCELSFNK-THHLRNPYNDNL-PVKISRDCQELE-----PFIGEQLASLL
	Aco009712.1	AcoYT HDF2A	AK-----FFIIKSYSEDDVHK--SIKYNVWTSTPNGNKKLDAAYQ-----EAQAR-T----- -----GGCP----IFLFFS-----VNTSGQFV-----GVAEMVGLVDFNKTV- DYWQ-QD-----KW-HGCFSVKWHVVKDVPSNI-LKHITLENNDNK-PVTNSRDTQEVN-----LEQGLEMLKIF
<i>Amaranthus hypochondriacus</i>	AHYPO_001321-RA	AhYTH DF1B	AK-----FFIIKSFSEDNIHR--SIKYGVWASTPHGNRKLDAAYQ-----EAKEK----- -----GNCP----VLLFS-----VNASGQFC-----GVAEMVGPVDFDKNA- DYWQ-QD-----RW-TGQFAVRWHIIKDIPNSK-FRHILLENNNDHK-PVTHSRDSQEVN-----QEQGIDMLRIF
	AHYPO_001693-RA	AhYTH DF3C	AK-----FYVIKSYSEVNVYN--CIKYNVWSSTEYGNKKLDAAFR-----DAEIK-ANE----- -----TGVKCP----IFLFFS-----VNGSGQFV-----GVAEMIGKVDNFNKT- KFWQ-LD-----KW-SGFFPLKWHIVKDVPSNQ-LRHILLENNENK-PVTFTTRDTQEIG-----LKHGLEMLKIF

	AHYPO_003351-RA	AhYTH DF2B	AK-----FFIIKSFSEDNIHR--SIKYGIWASTPHGNRKLDAAAYQ-----EAKEK----- -----GDYP----VFLIFS-----VNASGQFC-----GVAEMTGPVDFEKNA-DYWQ- QD-----RW-TGQFTVRWHLIKDIPNSK-FRHILLENNDNK-PVTHSRDAQEVK-----LDLGIEMLKIF
	AHYPO_010570-RA	AhYTH DF1A	AK-----FFVIKSYSEDDVHK--SIKYNVWSSTPNGNKKLDLSYK-----EAQKK-S----- -----GGCP----VFLFFS-----VNTSGQFV-----GLAEMVGPVDFHKNV- EHWQ-QD-----KW-YGSFPVKWHIVKDVPNSL-LKHIILENNENK-PVTNSRDTQEVK-----LEQGLQILRIF
	AHYPO_011235-RA	AhYTH DF2C	AK-----FYVIKSYSEDDVHK--SIKYNVWSSTANGNKKLDAAFH-----DAEVK-ANE----- -----TGVKCP----IFLFFS-----VNGSGQFV-----GVAEMTGKVDFKKNM- GFWQ-QD-----KW-SGFFPVNWHIVKDVPNSQ-LRHILLENNDRK-PVTYTRDTQEIE-----LKEGLDMLKIF
	AHYPO_012466-RA	AhYTH DC1A	TR-----YFIVKSCNRENLEL--SVQQGVWATQRSNEAKLNEAFD-----SVEH----- -----VILIFS-----VNRTRHFQ-----GCAKMTSKIGETASG-GNWK- HA-----HGTAH-----Y-GRNFSVKWLKLCELSFNK-TRHLRNPYNENL-PVKISRDCQELE-----PSVGEQLASLL
	AHYPO_014122-RA	AhYTH DF1C	AK-----FFVIKSYSEDDVHK--SIKYNVWSSTPNGNKKLSIAYE-----DAQKL-AAG----- -----TPGGCP----IFLFFS-----VNASGQFC-----GVAEMVGPVDFDKDM- DFWQ-QD-----KW-SGSFSVKWHIIKDVPNPT-FRHIILENNEHK-PVTNSRDTQEIM-----LKQGLDMLKLF
	AHYPO_014607-RA	AhYTH DF2A	AK-----FFVIKSYSEDDVHK--SIKYNVWASTPTGNQKLDAAAYQ-----EAKGK-T----- -----DACP----VFLIFS-----VNASGQFV-----GLAEMVGPVDFNKNM- DFWQ-QD-----KW-TGCFPVKWHIVKDVPNSL-LKHITLENNDNK-PVTNSRDTQEVK-----LEQAVQVVKIF
	AHYPO_015768	AhYTH DC1B	TR-----YFIIKSLNHENIQL--SIERGIWATQVMNEPILEEAFY-----NCHK----- -----VILIFS-----VNSSGFFQ-----GYAQMMSSVGRRRD--NVWT-QG---- -----TGANN-----PW-GRSFRVKWLRSSNLAFHK-TLHLKNPLNEFK-PVKISRDCQELP-----PEIGEALCQLI
<i>Aquilegia corulea</i>	Aqcoe1G060600	AcYTH DF1A	AK-----FFIIKSYSEDDVHK--SIKYSVWASTPSGNKKLNAGYQ-----ESQEK-S----- -----GDCP----VFLCFS-----VNGSGQFV-----GLAEMVGPVDFDKSV- EYWQ-QD-----KW-NGCFPLKWHIVKDIPNSL-LKQITLENNDNK-PVTNSRDTQEVK-----LEQGLQMLKIF
	Aqcoe1G157200	AcYTH DF2C	AL-----FFVIKSYSEDDIHK--SIKYNVWASTPNGNKRLDSAYQ-----DAQEK-MGQ----- -----KGSKCP----VFLFFS-----VNASGQFC-----GVAEMIGRVDFNKNM- DFWQ-QD-----KW-NGFFPVKWHIIKDVPNPH-FRHIILENNDNK-PVTNSRDTQEVK-----FPQGLEMLNVF
	Aqcoe1G183700.1	AcYTH DC1A	SR-----YFVVKSCNRENLEL--SAQQGVWATQRSNEAKLNEAFD-----SAEN----- -----VILIFS-----VNRTRHFQ-----GCAKMTSKIGEISGG-GNWK- YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPYNDNL-PVKISRDCQELE-----PSIGQQLASLL
	Aqcoe2G257600	AcYTH DF1C	GK-----FFVIKSYSEDDVHK--SIKYNVWSSTPNGNKRLDSAYE-----DAQRI-ASG----- -----NSRGCP----VFLFFS-----VNASGQFC-----GVAEMVGRVDFNKDM- EFWQ-QD-----KW-SGSFPVKWHIIKDVPNTN-FRHIILENNENK-PVTNSRDTQEIK-----YRQGTEMLKIF
	Aqcoe6G010000	AcYTH DF3C	AK-----FFIIKSYSEDDIHR--SIKYDVWSSTPHGNKKLNAAFH-----DAATI-YSE----- -----TGTRCP----IFLFFS-----VNGSGQFL-----GFAEMIGPVDFEKDM- DFWQ-QD-----KW-NGFFPVTHVIKDIPNNR-LRHIILENNSK-PVTYTRDTQEVG-----LKQGLEMLSIF

	Aqcoe7G241300	AcYTH DF1B	GK-----FFVIKSYSEDNVHK--SIKYGVWASTPNGNKKLDAA YH-----EAKEK----- -----H--CP----VFL LFS-----VNASAQFC-----GVAEMVGPVDFDKSV- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIILENNDSK-PVTNSRDTQEVK-----LEQGLEMLNIF
	Aqcoe5G460600	AcYTH DF2A	AK-----FFIIKSYSEDDVHK--SIKYSVWASTPNGNKNLNAGYQ-----ESQEK-S----- -----GD CP----VFLCFS-----VNGSGQFV-----GLAEMVGPVDFDKSV- EYWQ-QD-----KW-NGCFPVKWHIVKDIPNSL-LKQITLENNDNK-PVTNSRDTQEVK-----LEQGLQMLKIF
Arabidopsi s thaliana	AT1G09810	ECT11 (AtYTH DF4C)	AK-----FFVIKSYSEDDVHK--SIKYSVWSSTINGNKKLDAAFR-----DAETK-TLE----- -----DGKKRP----IFLFFS-----VNASRQFV-----GLAEMVGYVDFNKDL- DFWQ-VD-----KW-SGFFPV EWHVVKDIPNWE-LRHIILDNNEDK-PVTHTRDTHEIK-----LKEGLQMLSIF
	AT1G27960	ECT9 (AtYTH DF2B)	AK-----FFVIKSYSEDNVHK--SIKHCVWASTKNGNKKLDAA YR-----EAKKK----- -----DVAC P----VFL LFS-----VNASSQFC-----GVAEMVGPVDFNTSV- EYWQ-QD-----RW-SGHFPVQWLIVKDVPNSL-FRHIIESNDNK-PVTNSRDTQEVG-----LEKGIEMLDIF
	AT1G30460	CPSF30 (AtYTH DC1A)	NR-----YFVVKSNNREN FEL--SVQQGVWATQRSNEAKLNEAFD-----SVEN----- -----VILIFS-----VNRTRHFQ-----GCAKMTSRIGGYIGG-GNWK- HE-----HGTAQ-----Y-GRNFSVKWLKLCELSFHK-TRNLRNPYNENL-PVKISRDCQELE-----PSVGEQLASLL
	AT1g48110	ECT7 (AtYTH DF2C)	AK-----FFVIKSYSEDDVHK--SIKYNVWSSTLHGNKKLQSAYE-----DAQRI-ATE----- -----KSCECP----IFLFFS-----VNASGLFC-----GMAEMTGPVSFDKDM- DFWQ-QD-----KW-SGSFPVKWHIIKDVPNSY-FRHIILQNNENK-PVTNSRDTQEIM-----LKQGLEVLKIF
	AT1G55500	ECT4 (AtYTH DF4A)	AK-----FFIIKSYSEDDVHK--SIKYNVWASTPNGNKKLDAA YQ-----EAQQK-S----- -----SGCP----VFLFFS-----VNASGQFI-----GLAEMKGPVDFNKNI- EYWQ-QD-----KW-TGSFPLKWHILKDVPNSL-LKHITLEYNENK-PVTNSRDTQEVK-----LEQGLKVVKIF
	AT1G79270	ECT8 (AtYTH DF3C)	AI-----FFVIKSYSEDDIHK--SIKYNVWSSTLNGNKKLDSAYQ-----ESQKK-AAD----- -----KSGKCP----VFLFFS-----VNASGQFC-----GVAEMIGRVDY EKSM- EFWQ-QD-----KW-TGYFPVKWHIIKDVPNPQ-LRHIILENNENK-PVTNSRDTQEV R-----LPQGNEVLNIF
	AT3G03950	ETC1 (AtYTH DF1A)	AK-----FFVIKSYSEDDVHN--CIKYGAWSSTPTGNKKLNAA YY-----EAKEN-S----- -----QECP----VYLLFS-----VNASGQFV-----GLAEMVGPVDFNKTM- EYWQ-QD-----KW-IGCFPVKWHIIKDIPNSL-LRHITLANNENK-PVTNSRDTQEVN-----LEHGTKIIKIF
	AT3G13060	ECT5 (AtYTH DF1B)	AK-----LFIKSYSEDNVHK--SIKYNVWASTPNGNKKLDAA YR-----EAKDE----- -----KEPCP----LFL LFS-----VNASSQFC-----GVAEMVGPVDFE KSV- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIILENNDNK-PVTNSRDTQEV-----
	At3g13460	ECT2 (AtYTH DF2A)	AM-----FFIIKSYSEDDVHK--SIKYNVWASTPNGNKKLAAAYQ-----EAQQK-A----- -----GGCP----IFLFFS-----VNASGQFV-----GLAEMTGPVDFNTNV- EYWQ-QD-----KW-TGSFPLKWHIVKDVPNSL-LKHITLENNENK-PVTNSRDTQEVK-----LEQGLKIVKIF
	AT3G17330	ECT6 (AtYTH DF1C))	AR-----FFVIKSYSEDDVHK--SIKYGVWSSTLNGNKKLQSVYE-----DAQRI-ATE----- -----KSRECP----IFLFFS-----VNSSGLFC-----GVAEMTGPVSFDRDM- DFWQ-QD-----KW-SGSFPVKWHIIKDVPNSY-FRHIILHNNENK-PVTNSRDTQEII-----LKQGLEVLKLF

	AT4G11970	ECT12 (AtYTH DC1B)	TR-----YFIIKSLNYDNIQV--SVEKGIWATQVMNEPILEGAFH-----KSGR----- -----VILIFS-----VNMSGFFQ-----GYAEMLSPVGWRRD--QIWS-QG--- -----GGKNN-----PW-GRSFKVKWLRLSELPFQK-TLHLKNPLNDYK-PVKISRDCQELP-----EDIGEALCELL
	AT5G58190	ECT10 (AtYTH DF3B)	AK-----FFIVKSFSEDNVHR--SIKYNVWASTPHGNKKLDTAYR-----DAEKM----- -----GGKCP----IFLFFS-----VNASGQFC-----GVSEMVGPDVFEKDA- GYWQ-QD-----RW-SGQFPVKWHIVKDIPNNR-FCHILLQNNDNK-PVTHSRDSQEVK-----LRQGIEMLRIF
	AT5G61020	ECT3 (AtYTH DF3A)	AK-----FYVIKSYSEDDIHK--SIKYSVWSSTPNGNKKLDASYN-----EAKQK-S----- -----DGCP----VFLIFS-----VNTSGQFV-----GLAEMVGPDVFNKTV- EYWQ-QD-----KW-IGCFPVKWHFVKDIPNSS-LRHITLENNENK-PVTNSRDTQEVK-----LEQGIKVIKIF
<i>Capsella rubella</i>	Carubv10003808m	CrYTH DC1B	AK-----FFVIKSYSEDDIHK--SIKYNVWSSTPNGNKKLDASYN-----EAKQK-S----- -----EGCP----VFLIFS-----VNTSGQFV-----GLAEMVGPDVFNKTV- EYWQ-QD-----KW-IGCFPVKWHFVKDIPNSS-LRHITLENNENK-PVTNSRDTQEVK-----LEQGMKVIKIF
	Carubv10008560m	CrYTH DF1C	AK-----FFIVKSFSEDNVHR--SIKYNVWASTPHGNKKLDTAYR-----DAEKM----- -----GGKCP----IFLFFS-----VNASGQFC-----GVSEMAGPDVFEKDA- GYWQ-QD-----RW-SGQFPVKWHIVKDVNNR-FCHILLQNNDNK-PVTHSRDSQEVK-----LRQGIEMLRIF
	Carubv10008570m	CrYTH DC1A	AM-----FFVIKSYSEDDIHK--SIKYNVWSSTLNGNKKLDSAYQ-----ESQKK-IAE----- -----KNVKCP----VFLFFS-----VNASGQFC-----GVAEMVGRVDYEKSM- EFWQ-QD-----KW-TGYFPVKWHMIKDVNPQ-LRHIILENNENK-PVTNSRDTQEVN-----LPQGNEVLNIF
	Carubv10008725m	CrYTH DF3B	AK-----FFVIKSYSEDDVHN--SIKYGAWSSTPTGNKKLNAAYY-----EAKEN-S----- -----QECP----VYLLFS-----VNASGQFV-----GLAEMVGPDVFNKTM- EYWQ-QD-----KW-IGCFPVKWHIHKDIPNSL-LRHITLENNENK-PVTNSRDTQEVN-----LDHGTKIIKIF
	Carubv10011018m	CrYTH DF4C	AK-----FFVIKSYSEDDVHK--SIKYGVWSSTLHGNNKKLQSVYE-----DAQRI-VTE----- -----KSCECP----IFLFFS-----VNASGLFC-----GVAEMTGPVSFNRDM- DFWQ-QD-----KW-SGSFPVKWHIHKDVPNSY-FRHIILQNNENK-PVTNSRDTQEIM-----LKQGLEVLKLF
	Carubv10013132m	CrYTH DF1B	AM-----FFIIKSYSEDDVHK--SIKYNVWASTPNGNKKLAAAYQ-----EAQK-P----- -----GGCP----IFLFFS-----VNASGQFV-----GLAEMTGPVDFNTNV- EYWQ-QD-----KW-TGSFPLKWHIVKDVPSL-LKHITLENNENK-PVTNSRDTQEVK-----LEQGLKIVKIF
	Carubv10013133m	CrYTH DF1A	AK-----LFIKSYSEDNVHK--SIKYNVWASTPNGNKKLDAAAYR-----EAKDE----- -----KEPCP----LFLIFS-----VNASSQFC-----GVAEMVGPDVFEKSV- DYWQ-QD-----KW-SGQFPVKWHIHKDVPNSQ-FRHIILENNNDNK-PVTNSRDTQEVK-----LEQGIEMLKIF
	Carubv10013212m	CrYTH DF3C	AK-----FFVIKSYSEDDVHK--SIKYSVWSSTINGNKKLDAAFR-----DAETK-TRE----- -----DGKKRP----IFLFFS-----VNASRQFV-----GLAEMAGYVDFKKDL- NFWQ-VD-----KW-SGFFPVEWHVVKDIPNWE-LRHIILANNEDK-PVTHTRDTHEVK-----LKEGLQMLSIF
	Carubv10013762m	CrYTH DF2A	AK-----FFVIKSYSEDNVYK--SIKYSVWASTKNGNKKLDAAAYR-----EAKTK----- -----DVACP----VFLIFS-----VNASAQFC-----GVAEMVGAVDFNTSV- EYWQ-QD-----RW-SGHFPVRWLIVKDVPSL-FRHIILENNNDNK-PVTNSRDTQEVG-----LEQGIEMLNIF

	Carubv10021946m	CrYTH DF2C	NR-----YFVVKSCNRENFEL--SVQQGVWATQRSNEAKLNEAFD-----SVEN----- -----VILIFS-----VNRTRHFQ-----GCAKMTSRIGGYIGG-GNWK- HE-----HGTAQ-----Y-GRNFSVKWLKLCELSFHK-TRNLRNPYNENL-PVKISRDCQELE-----PSIGEQLASLL
	Carubv10026226m	CrYTH DF2B	AK-----FFVIKSYSEDDVHK--SIKYNVWSSTLHGNKKLQSAYE-----DAQKI-ASE----- -----KSCECP----IFLFFS-----VNASGLFC-----GMAEMTGPVSFDKDM- DFWQ-QD-----KW-SGSFPVKWHIIKDVPNSY-FRHIILQNNENK-PVTNSRDTQEIM-----LKQGLEVLKIF
	Carubv10026294m	CrYTH DF3A	TR-----YFIIKSLNYENIQV--SVEKGIWATQVMNEPILEGAFH-----KSGR----- -----VILIFS-----VNMSGFFQ-----GYAEMLSPVGWRRD--HIWS-QG--- -----GGKNN-----PW-GRSFVKVWLRLSELPFQK-TLHLKNPLNDYK-PVKISRDCQELP-----EDIGEALCELL
<i>Drosophila melanogas ter</i>	sp Q9VZQ1	DmYT HDC1	TR-----FFLIKSNSDNVQL--SKNKSVWATLPQNDANLNQAFK-----EARN----- -----VLLIFS-----VNESGKFA-----GFARMAAPSRRDIPQ-VAWV- LP-----PSISPK-----AL-GGVIELDWICKELSFNA-TLHLHNTWNEGK-PVKIGRDGQEIE-----PKIGGELCRLF
	CG6422-RA	DmYT HDF1	AR-----FFVIKSYSEDDIHR--SIKYEIWCSTDHGNKRLDDAFK-----ERHEE----- -----GGN----IMLFFS-----VNGSGHFC-----GMAQMMTPVDYNSTS-SVWS- QD-----KW-RGKFKVKWIYVKDVPNGT-LRHIRLENNENK-SVTNSRDTQEVP-----NDKGIEVLQIL
<i>Chlamydo monas reinhardtii</i>	Cre12.g516400.t1.2	CreYTH DC1	IR-----YFIIRSNSLQNIFI---SVRTGAWATTRTNDPKLDAAFR-----SSRE----- -----VRLIFS-----VMGSNAFQ-----GYATMRTSVGAFPKP----- -----VIWENG-----QQFGRPFGVEWRVLFELPHDD-CNHIRNRLNDNK-VVYMARDCTELP-----QEQGDLLTTIM
<i>Dunaliella salina</i>	Dusal.0106s00010.1	DsYTH DC1	VR-----YFIIRSYNQENVDI---SINVGGWATTKHNEIKLNEAYA-----TCDE----- -----VRLVFS-----VNSSNCFQ-----GYAVMSTPVGQYRSI----- -----IWSNG-----KAFGNAFGVDWRCVFNLEVWN-VKHLLNPLNENK-PVHVARDGQEVP-----TRVGDELVSIM
<i>Homo sapiens</i>	sp Q9H6S0	HsYTH DC2	VR-----YFIMKSSNLRN--LEI--SQQKGIWSTTPSNERKLNRA--FW-----ESSI----- -----VYLVFS-----VQGSGHFQ-----GFSRM--SSEIGREKSQ----- -----DWGSA-----GL-GGVFKVEWIRKESLPFQF-AHLLNPWNDNK-KVQISRDGQELE-----PLVGEQLLQLW
	sp Q96MU7	HsYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNLA--FR-----SARS----- -----VILIFS-----VRESGKFQ-----GFARL--SSESHHGGSP-IHWV- LP-----AGMSAK-----ML-GGVFKIDWICRREL PFTK-SAHLTNPWNEHK-PVKIGRDGQEIE-----LECGTQLCLLF
	sp Q9BYJ9	HsYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDSA--FR-----CMSSK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSPVDYGTSA- GVWS-QD-----KW-KGKFDVQWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQEVP-----LEKAKQVLKII
	sp Q7Z739	HsYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDAA--YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--KSVVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQEVP-----LEKAKQVLKII
	NP_057342	HsYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHG NKRLDAA--YR-----SMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSAVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQEVP-----LEKAKQVLKII

<i>Eucalyptus grandis</i>	Eucgr.B03590.1	EgYTH DF1A	AK-----FFIIKSYSEDD--VHK--SIKYSVWASTPNGNKKLDAA---YR-----EAQEK-P----- -----GSSP----VFLFFS-----VNTSGQFV-----GLAEM---VGPVDFHKSV- EYWQ-QD-----KW-NGCFPVKWHIVKDVNSM-LKHITLENNENK-PVTNSRDTQEVK-----LVQGLKMIKIF
	Eucgr.B03591.1	EgYTH DF2A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YR-----EAQEK-A----- -----AGCP----IFLFFS-----VNTSGQFV-----GLAEM--- VGPVDFHKNV-EYWQ-QD-----KW-MGCFPVKWHIVKDVNNL-LKHITLENNENK-PVTNSRDTQEVK----- LPQGLKMIKIF
	Eucgr.D01949.1	EgYTH DC1B	IR-----YFIIKSLNHHN--LQL--SIEKGIWATQVMNEPILEEA--FH-----NSGK----- -----VILIFS-----VNMSGFFQ-----GYAQM---MSPIGWRRD--KVWS- QG-----NGRNN-----PW-GRSFKVKWLRLYDLPFQK-TLHLKNLLNDNK-PVKISRDCQELP-----QDVGEALCELL
	Eucgr.E02496.1	EgYTH DC1A	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA--FD-----SAAN----- -----VILIFS-----VNRTRHFQ-----GCAKM---TSRIGGAASG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCESFQK-TRHLRNPYNENL-PVKISRDCQELE-----PSVGEQLASLL
	Eucgr.H04096.1	EgYTH DF1C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLQSA---YE-----DAQKI-AAE----- -----KTTNCP----IFLFFS-----VNASGQFC-----GVAEM--- VGQVDFHKNM-DFWQ-QD-----KW-TGSFPVKWHIHKDVQNTA-FRHIILENNENK-PVTNSRDTQEIM----- QKQGLEMLKIF
	Eucgr.J03195.1	EgYTH DF1B	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDAA---YR-----EAKEK----- -----PDTCP----VFLFFS-----VNASAHFC-----GVAEM--- VGPVDFDRSF-DYWQ-QD-----RW-SGQFPVKWHVIKDV PNSQ-LRHIVLENNDNK-PVTNSRDTQEVK----- LEQGIEMLNIF
<i>Amborella trichopoda</i>	evm_27.model.AmTr_v 1.0_scaffold00001.426	AtrYTH DC1B	AF-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKRLDNA---YQ-----DAQQK-ALE----- -----KGSKCP----VFLFFS-----VNASGQFC-----GVAEM--- MGRVDFNQNM-DFWQ-QD-----KW-NGFFPVKWHVIKDV PNQ-FRHIILENNDNK-PVTNSRDTQEVK----- FPQGIEMLNIF
	evm_27.model.AmTr_v 1.0_scaffold00004.54	AtrYTH DF1A	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTANGNRKLDAA---YR-----ESKEK----- -----DGHCP----VLLFS-----VNASAQFC-----GVAEM--- MGPVDFEKS SV-DYWQ-QD-----KW-SGQFPVKWHIVKDV PNSQ-FRHIILENNDNK-PVTNSRDTQEVK----- LEQGLEILKIF
	evm_27.model.AmTr_v 1.0_scaffold00025.287	AtrYTH DF1B	AK-----FFIIKSYSEDD--IHK--SIKYSVWASTPNGNKKLDAA---YK-----EAQEK-T----- -----GGCP----VFLFFS-----VNASGQFL-----GVAEM--- VGPVDFNKNV-EFWQ-QD-----KW-NGCFPVKWHVVKDV PNQ-LKHIILENNDNK-PVTNSRDTQEVK----- FDQGIEILKIF
	evm_27.model.AmTr_v 1.0_scaffold00068.160	AtrYTH DF2C	TR-----YFVIKSLNHQN--IQL--SIEKGIWATQVMNEQILEEA--FH-----SSDR----- -----VILIFS-----VNMSGFFQ-----GYAQM---MSPVGWRRE-- NVWS-GS-----SGGSN-----PW-GRTFKVKWLQLNNLAFQK-TLHLKNPLNDYK-PVKISRDCQELT-----QEVGEALCELL
	evm_27.model.AmTr_v 1.0_scaffold00071.175	AtrYTH DF3C	AL-----FYVIKSFSEDD--VHK--SLKYNVWASTDFGNKKLDEA--FH-----GAQAK-LND----- -----NGSRCP----VFLFFS-----VNGSGQFV-----GLAEM---

			TCKVDFKKTL-DFWQ-GD-----VW-NGFFPVKWHIVKDVPNHL-LTHIILKDNENK-AVTYSRDTQEVT----- FSQGIEMLKIF
	evm_27.model.AmTr_v 1.0_scaffold00096.42	AtrYTH DF1C	SR-----YFIVKSCNREN--LEL--SVQKGIWATQRSNESKLNEA---FD-----SSEN----- -----VVLIFS-----INRTRHFQ-----GCAKM--TSKIGGYVGG- GGWK-YA-----HGTAH-----Y-GRNFSLKWLKLCELSFHK-TRHLRNPYNENL-PVKISRDCQELE-----PSIGEQLASLL
	evm_27.model.AmTr_v 1.0_scaffold00155.52	AtrYTH DC1A	AK-----FFVIKSYSEDD--VHK--SIKYHVWSSTPSGNNRLNTA---FE-----DAQRR-SGG----- -----KPGSCP----VFLFFS-----VNASGQFC-----GVAEM--- VGSVDFQKDM-DFWQ-QD-----KW-SGCFPVKWHFVKDVPNSY-FRHIILENNENK-PVTNSRDTQEIR----- FPQGIEMLAIF
<i>Glycine max</i>	Glyma.01G214100.1	GmYT HDC1B a	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDGA---FQ-----DAQKR-MEE----- -----KGCKCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDFNKSM-DFWQ-QD-----KW-NGYFPVKWHIIKDVPNPQ-LRHIILENNDHK-PVTSSRDTQEVs----- FPQGVEMLNIF
	Glyma.02G072000.1	GmYT HDF5A	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLENA---YE-----DAKKI-AAE----- -----KSEVCP----IFLLFS-----VNASGQFC-----GVAEM--- VGTVDfSKNM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNPn-FRHIILENNENK-PVTNSRDAQEIM----- YLKGLEMLKIF
	Glyma.05G166600.1	GmYT HDF2A	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNESKLNEA---FD-----SVEN----- -----VILVFS-----VNRTRHFQ-----GCAKM--TSRIGGSVAG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPYNENL-PVKISRDCQELE-----PSIGEQLASLL
	Glyma.07G000900.1	GmYT HDF2B	TK-----YFVIKSLNHQN--IHL--SIEKGIWATQIMNEPILQEA---YH-----NSGS----- -----VILIFS-----VNMSGSFQ-----GYAQM--MTSIGRGRD--NAWS- EG-----TGKSN-----PW-GRSFKVKWLCLNDLPFHK-TLHLKNPLNDYK-PVKISRDCQELS-----PDIGLALCKLL
	Glyma.07G233400.1	GmYT HDF2C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGN-KLENA---YE-----DAKKI-AAE----- -----KSEVCP----IFLFFS-----VNASGQFC-----GVAEM--- VGTVDfNKNM-DFWQ-QD-----KW-SGSFPLKWHIIKDVPNPn-FRHITLENNENK-PVTNSRDTQEIM----- YWKGLEMLKIF
	Glyma.08G124600.1	GmYT HDF1A	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNESKLNEA---FD-----SVEN----- -----VILIFS-----VNRTRHFQ-----GCAKM--TSKIGGSVAG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPYNENL-PVKISRDCQELE-----PSIGEQLASLL
	Glyma.08G162200.1	GmYT HDF6C	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDDA---YR-----QAMEK----- -----QDACP----IFLFFS-----VNAsAQFC-----GVAEM--- VGpVNFDKSV-DFWQ-QD-----KW-SGQFPLKWHIIKDVPNSQ-FRHIILENNDNK-PVTNSRDTQEVK----- LGQGVEMLTIF
	Glyma.08G226100.1	GmYT HDF1B	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDGA---FQ-----DAQKR-MEE----- -----KGCKCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDFNKSM-DFWQ-QD-----KW-NGYFSVKWHIIKDVPNPQ-LRHIILENNDHK-PVTNSRDTQEVs----- FPQGVEMLNIF

	Glyma.09G022200.1	GmYT HDC1A b	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTQNGNKKLDAA---YH-----EAQQK-P----- -----GGCP----VFLFFS-----VNTSGQFV-----GLAEM--- IGPVDFNKS SV-EYWQ-QD-----KW-NGCFPLKWHVVKDVPNNL-LRHITLDNNENK-PVTNSRDTQEV M----- LEPGLKLIKIF
	Glyma.09G031200.1	GmYT HDF4C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLQSA---HE-----DAKRI-ASG----- -----KFGSCP----IFLFFS-----VNASGQFC-----GVAEM--- IGPVDFNKM DM-DFWQ-QD-----KW-SGSFPVKWYI IKDVS NAN-FRHIILENNENK-PVTNSRDTQEIM----- YSKGLEMLKIF
	Glyma.11G027800.1	GmYT HDC1B b	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDAA---YL-----QAMEK----- -----QDACP----IFLFFS-----VNASAQFC-----GVAEM--- VGPNVFDKSV-DFWQ-QD-----KW-SGQFPVKWHI IKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEV K----- LTQGVEMLTIF
	Glyma.15G128500.1	GmYT HDC1A a	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTQNGNKKLDAA---YQ-----EAQQK-P----- -----GGTP----VFLFFS-----VNTSGQFV-----GLAEM--- IGPVDFNKS SV-EYWQ-QD-----KW-NGCFPLKWHIVKDVPNNL-LRHITLDNNENK-PVTNSRDTQEV M----- LEPGLKLIKIF
	Glyma.15G136400.1	GmYT HDF3C	AK-----FFVIKSYSEDD--IHK--SIKYK VWASTFNGNKKLDAA---YH-----ESKEK-P----- -----GD CP----VFL LFS-----VNTSGQFV-----GLAEM---VSPLDFGRTV- EYWQ-QD-----RW-SGCFSVKWHI IKDIPNSV-LRPITLENNENK-PVTNSRDTQEV K-----FEKGIQILKIF
	Glyma.15G265400.1	GmYT HDF5C	IK-----YFIIKSLNHQN--IHL--SIEKGIWATQIMNEPILEEA---FH-----NSGS----- -----VILIFS-----VNMSGSFQ-----GYAQM---MSSIGRGRD--NVWS- EG-----TGKSN-----PW-GRSFKVKWMCLNDLPFHK-TLHLKNPLNDYK-PVKISRDCQELS-----PDIGLALCELL
	Glyma.16G003200.1	GmYT HDF7C	AK-----FYVIKSFNEDD--VHK--SVKYNVWTSTPNGNKKLNAA---FL-----DAEAK-LRQ----- -----TGTKCP----VFLFFS-----VNASRQFV-----GVAEM--- LGPVDFKN DM-NFWK-LD-----KY-NGFFPIKWHI IKDVPNNQ-FVHIILPSNENK-PVTYTRDTQEIG-----LKEGLEMLNIF
	Glyma.16G041600.1	GmYT HDF4A	AK-----FFVIKSYSEDD--IHK--SIKYS AWASTPNGNKKLDSA---YQ-----EAKEK-P----- -----GGCP----IFLLFS-----VNTSGQFV-----GLAEM---LGPVDFGKTV- DYWQ-QD-----RW-TGCFSVKWHVI KDIPNSV-LRHITLENNENK-PVTNSRDTQEV K-----FEKGVQLVKIF
	Glyma.17G038400.1	GmYT HDF1C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLQST--HE-----DAKRI-ASG----- -----NFGSCP----IFLFFS-----VNASGQFC-----GVAEM--- IGPVDFNKM DM-DFWQ-QD-----KW-SGSFPVKWHI IKDVPNAN-FRHIILENNENK-PVTNSRDTQEIM----- YSKGLEMLKIF
	Glyma.19G110800.1	GmYT HDF3A	AK-----FFVIKSYSEDD--IHK--SIKYS AWASTPNGNKKLDAA---YQ-----EAKEK-P----- -----GGCP----IFLLFS-----VNTSGQFV-----GLAEM---LGPVDFGKTV- DYWQ-QD-----RW-TGCFSVKWHVI KDIPNSV-LRHITLENNENK-PVTNSRDTQEV K-----FEKGVQIAKIF
<i>Gossipium raimondii</i>	Gorai.002G031800.1	GrYTH DF2C	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTSTGNKKLDAA---FH-----ETKGN-P----- -----DICP----VFL LFS-----VNTSGQFV-----GLAEM---VGPVDFNKTV- EYWQ-QD-----KW-TGCFPVKWHI IKDVPNTS-LRHITLENNENK-PVTNSRDTQEV N-----FEQGVQILKIF

Gorai.002G182900.1	GrYTH DF3B	AK-----FFIIKSYSEDN--VHK--SIKYGWVASTPNGNKKLDAA---YR-----EAKEN----- -----QDPCP----VFLFFS-----VNASAQFC-----GVAEM--- VGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHFIKDVPNSQ-FRHIILENNDNK-PVTNSRDTQEVN----- LEQGIEMLNIF
Gorai.004G020600.1	GrYTH DF1A	AK-----FFIIKSYSEDN--VHK--SIKYGWVASTPNGNKRLDAA---YR-----EAMEN----- -----QDNCP----VFLFFS-----VNASAQFC-----GVAEM--- VGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-LRHIILENNDNK-PVTNSRDTQEVK----- LEQGLEMLSIF
Gorai.004G205800.1	GrYTH DC1B	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA---FD-----SAEN----- -----VILVFS-----VNRTRHFQV-----GCAKM--TSKIGGSVAG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPYNENL-PVKISRDCQELE-----PSVGEQLASLL
Gorai.004G244600.1	GrYTH DF3A	AK-----FFVIKSYSEDD--VHK--SVKYNVWASTSNGNKKLDAA---FH-----EAKKEE-P----- -----DGCP----VFLFFS-----VNTSGQFV-----GVAEM--- VDQVDFNKTV-EYWQ-QD-----KW-TGCFPVKWHIIKDVPNTL-LRHITLENNENK-PVTNSRDTQEVN----- FEQGIHILKIF
Gorai.005G070500.1	GrYTH DF1C	AM-----FFVIKSYSEDD--VHK--SIKYNVWASTSNGNKKLDAA---FR-----EAKEK-P----- -----DGCP----VFLFFS-----VNTSGQFV-----GLAEM--- VGPVDFNKTV-EYWQ-QD-----KW-TGCFPVKWHIVKDVPNAS-LRHITLKNENK-PVTNSRDTQEVN----- FEQGIQILKIF
Gorai.005G265300.1	GrYTH DF3C	AK-----FFVIKSYSEDD--VHK--SMKYNVWSSTPNGNRKLDAA---FH-----EAETR-ESE----- -----TGTKCP----IFLLFS-----VNGSGQFV-----GLAEM--- IGKVDFNKDM-DFWQ-LN-----KW-NGFFPVKWHVIKDIPNKE-LFHIILENNENK-PVTHSRDTQEIG----- LKQGLELLRIF
Gorai.007G288900.1	GrYTH DF2A	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLDSA---FE-----DAEKI-AAG----- -----KPSGCP----IFLFFS-----VNASGQFC-----GVAEM--- IGPVDFQKDM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNSH-FRHIILGNNENK-PVTNSRDTQEIM----- YKQGMEMPLKVF
Gorai.007G289200.1	GrYTH DF4A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNRKLDAA---FC-----EAKEK-P----- -----DGCP----IFLLFS-----VNTSGQFV-----GLAEM--- VGAVDFNRTV-EYWQ-QD-----KW-TGCFPVKWHIVKDVPNTS-LRHITLKNENK-PVTNSRDTQEVN----- FEQGMQILKIF
Gorai.008G046800.1	GrYTH DC1A	KR-----YFIIKSLNHQN--IQL--SIDKGIWATQVMNEPILEDA---FH-----NSGC----- -----VILIFS-----VNMSGFFQ-----GYAQM--MSSVGWRRD-- NVWS-QG-----SGKGN-----PW-GRSFKVKWLCLNHLPFQK-TLHLKNPLNDYK-PVKISRDCQELP-----QDIGEALCELL
Gorai.009G120700.1	GrYTH DF2B	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAQQK-S----- -----GHCP----IFLFFS-----VNTSGQFV-----GIAEM--- VGAVDFQKNV-EFWQ-QD-----KW-TGCFPVRWLIKDVPNNS-LKHITLENNENK-PVTNSRDTQEIK----- LDQGLKLLKIF

	Gorai.011G001700.1	GrYTH DF1B	AK-----FFVIKSYSEDN--VHK--SIKYGIWASTPIGNKKLDTA---YH-----EAKAI----- -----QGTCP----VLLFS-----VNSSAQFC-----GVAEM---VGPVDFDKSV- DYWL-QN-----KW-SGQFPVKWHIIKDVPNSQ-FRHILLESNDNK-PVTNSRDTQEVE-----FEQGIEMINIF
	Gorai.013G123200.1	GrYTH DF5A	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLDSA--FE-----DAQRI-AAG----- -----KPRGCS----IFLFFS-----VNASGQFC-----GVAEM--- IGSVDFQKAM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNSH-FRHIIVENNENK-PVTNSRDTQEIM----- FKQGVEMLKVF
<i>Zea mays</i>	GRMZM2G004997_T0 2	ZmYTH DF3B	AK-----FFVIKSYTEDH--VHR--SIKYNVWASTASGNRKLDSA---YR-----AAREK----- -----EEHCP----IFLFFS-----VNGSGQFC-----GVAEM---IGPVDFDRSV- NYWQ-QD-----KW-SGQFPVKWHIIKDVPNNL-LRHIILENNDNK-PVTNSRDTQEVK-----LEQGLQMLTIF
	GRMZM2G025488_T0 2	ZmYTH DF1B	AR-----FFIIKSYSEDN--VHK--SVKYGVWASTTNGNKKLDSA---YR-----EAKEK----- -----GEHCP----IFLLFS-----VNASAQFC-----GVAEM---IGPVDFEKS- DYWQ-QD-----KW-TGQFPVKWHIVKDVPNNL-FRHIILENNDNK-PVTNSRDTQEVK-----LEQGMEMLKIF
	GRMZM2G056573_T0 1	ZmYTH DF3C	AK-----FFVIKSIGEAD--VHK--SIKYGVWSSSSNGNIKLDSA--FR-----DADRI-SRR----- -----HSTKCP----VFLFFS-----VNGSGHFC-----GMAEM--- VGPVDFHKDM-DFWC-QD-----KW-TGCFPVRWHIVKDIPNGF-LQHITLQNNENK-PVTHSRDTQEIP-----YLPGISVIKIF
	GRMZM2G076062_T0 2	ZmYTH DF1A	AK-----FFVIKSYSEDD--IHK--SVKYNVWASTTNGNKKLDAA---YQ-----EAQSK-G----- -----SACP----IFLFFS-----VNTSGQFV-----GVAEM--- TGAVDFECTL-GYWQ-QD-----KW-NGSFSVKWHIVKDVPNNI-LKHIILENNENK-PVTNSRDTQEIH----- LEQGLQMLKIF
	GRMZM2G098174_T0 1	ZmYTH DF4C	AK-----FFVIKSIGEAD--VHK--SIKYGVWSSSSSGNSKLDSA--FR-----DADRI-SRR----- -----HSTKCP----VFLFFS-----VNGSGHFC-----GMAEM--- VGPVDFHKDM-DFWC-QD-----KW-TGCFPVRWHIVKDIPNGS-LQHITLQNNENK-PVTHSRDTQEV----- YLPGMSVINIF
	GRMZM2G102069_T0 1	ZmYTH DF4B	AR-----FYVIKSYTEDH--IHK--SIKYNVWASTPRGNRKLNAG---YH-----EAKAK----- -----EDHCP----IFLFFS-----VNSSGHFC-----GVAEM---IGPVNFDKSV- DYWQ-NE-----RW-NGQFPVKWHIVKDVPNNI-VRHIILENNENK-RVTNSRDTQEVK-----LKQGLQMLAIF
	GRMZM2G126338_T0 1	ZmYTH DF3A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAG---YR-----EAQEK-S----- -----SDCP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDFDKTV-EYWQ-QD-----KW-NGCFPLKWHIVKDVPNNT-LKHITLDNNDNK-PVTNSRDTQEVK----- LEQGLEMLKIF
	GRMZM2G127780_T0 1	ZmYTH DF2C	AL-----FFVIKSYSEDD--IHK--SVKYNVWASTPNGNKRLDNA---YR-----VAQER-IAE----- -----KGTKCP----VFLFFS-----VNASGQFC-----GVAEM--- VGPVDFNRNM-NFWQ-QD-----KW-NGFFSVKWHIIKDVPNPQ-FRHIILENNENK-PVTNSRDTQEVN----- FSQGTEMLNIF
	GRMZM2G144726_T0 1	ZmYTH DF4A	AK-----FFIIKSYSEDD--VHK--SVKYNVWASTPNGNKKLDAA---YQ-----EAKEK-S----- -----SETP----VLLFS-----VNASGQFV-----GLAEM---

			VGRVDFEKTVEHWQ-QD-----KW-TGCFPVKWHIVKDVPNSL-LKHIILENNENK-PVTNSRDTHEVK----- LEQGLQVLKIF
GRMZM2G169116_T01	ZmYTHDF1C	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDNA---YR-----LAQER-MAE----- -----KGTKCP----VFLFFS-----VNASGQFC-----GVAEM--- VGPVDFNRNM-NFWQ-QD-----KW-NGFFSVKWHIIKDVPNPQ-FRHIILENNENK-PVTNSRDTQEVK----- FSQGTEMLNIF	
GRMZM2G303312_T01	ZmYTHDF5C	AK-----FFMIKSYSEDD--IHK--GIKYNVWASTPNGNNKLDAA---YH-----EAQNL-M-D----- -----SGERCP----VFLFFS-----VNTSGQFV-----GLAEM--- LGPVDFKKTMDWE-ED-----KW-SGFFPIKWHIIKDIPNRL-FKHIILENNDNR-IVTFSRDTQEIG-----LPQGVQMLKIF	
GRMZM2G330019_T01	ZmYTHDF2A	AK-----FFVIKSYSEDD--IHK--SVKYNVWASTTNGNKKLDAA---YQ-----EAQSK-G----- -----SACP----IFLFFS-----VNTSGQFV-----GVAEM--- TGAVDFEKTLEYWQ-QD-----KW-NGSFSVKWHIVKDVPNNI-LKHIILENNENK-PVTNSRDTQEIR----- LEQGLQMLKIF	
GRMZM2G340130_T01	ZmYTHDF5A	AK-----FFIIKSYSEDD--VHK--SVKYNVWASTPNGNKKLDAA---YQ-----EAKEK-S----- -----SETP----VLLFS-----VNASGQFV-----GLAEM--- VGRVDFNKTVDHWQ-QD-----KW-TGCFPVKWHIVKDVPNSL-LKHIILENNENK-PVTNSRDTHEVK----- LEQGLQVLKVF	
Zm00008a020283_T01	ZmYTHDC1A	AK-----FFVIKSYTEDH--AHR--SIKYKVWASTASGNRKLDSS---YH-----AAKEK----- -----EEHCP----IFLFFS-----VNGSGQFC-----GMADM---IGSVDFDRSV- DYWQ-QN-----KW-SGQFPVKWHIIKDVPNNL-LWHIILENNDNK-PVTNSRDTHEVS-----LERPLCY----	
GRMZM2G442195_T01	ZmYTHDF2B	AK-----FFVIKSYTEDH--VHR--SIKYKVWASTASGNRKLDSA---YH-----AAKEK----- -----EEHCP----IFLFFS-----VNGSGQFC-----GVAEM---IGPVDFDRSV- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNNL-LRHIILENNDNK-PVTNSRDTQEVK-----LEQGLQMLTIF	
GRMZM2G363789	ZmYTHDF5B	AK-----FFVIKSYTEDH--AHR--SIKYKVWASTASGNRKLDSS---YH-----AAKEK----- -----EEHCP----IFLFFS-----VNGSGQFC-----GMADM---IGSVDFDRSV- DYWQ-QN-----KW-SGQFPVKWHIIKDVPNNL-LWHIILENNDNK-PVTNSRDTHEVS-----LERPLCY	
Musa acuminata	GSMUA_Achr1T10560_001	MaYTHDF5B	GK-----FFIIKSYSEAN--VHK--SIKYGVWSSTSAGNKKLNSA---YI-----EAQKK----- -----GHSSP----IFLFFS-----VNASGRFC-----GVAEM---IGPVDFEKS- DYWN-KD-----KW-TGQFPVKWHIVKDVPNSFR-FRHIILENNDNK-PVTNSRDTQEVK-----LEQGLEMLSIF
	GSMUA_Achr1T10590_001	MaYTHDF4B	AR-----FFIIKSYSEDN--VHK--SIKYGVWASTSNGNRKLNSA---YI-----EMREQ----- -----EHSYP----IFLFFS-----VNASGHFC-----GVAEM---IGPVDFEKS- DYWN-ED-----KW-TGQCPVKWHIVKDVPNTM-FRHIILEKNDNK-PVTNSRDTQEVK-----LEQGLEMLGIF
	GSMUA_Achr1T24980_001	MaYTHDF3C	AR-----FFVIKSYSEDD--VHK--SIKYNVWSSTHNGNRRLDGA---YE-----DAQSK-SVG----- -----RPRKCP----VFLFFS-----VNASGQFC-----GLAEM--- VGPVDFDKDM-NFWQ-QD-----KW-SGSFPVKWHIIKDVPNSS-LRHIILENNENK-PVTNSRDTQEIP----- YSAGIDMLKIF

GSMUA_Achr4T04600_001	MaYTH DF1B	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTSNGNKKLDSA---YH-----EAKKK----- -----EDPCP----VFLFFS-----VNASAHFC-----GVAEM---IGPVDFERSV- DYWQ-QD-----KW-SGQFPLKWHMVKDVPNNL-FRHIILENNENK-PVTNSRDTQEVK-----LEQGLEMLSIF
GSMUA_Achr4T11560_001	MaYTH DF2B	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTSNGNKKLDSA---YH-----EANKK----- -----EDPCP----VFLFFS-----VNASAHFC-----GVAEM--- IGPVDFEKSVDYWQ-QD-----KW-SGQFPVKWQIVKDVPNNL-FRHIILENNDNK-PVTNSRDTQEVK----- LEQGLEMLSIF
GSMUA_Achr4T12480_001	MaYTH DF3B	AM-----FFIIKSYSEDN--VHK--SIKYGVWASTSSGNRKLDSA---YH-----EAKQK----- -----EDPCP----VFLFFS-----VNASAHFC-----GVSEM---IGPVDFEKSVDYWQ-QD-----RW-SGQFPVKWHMVKDVPNNL-FRHIILENNENK-PVTNSRDTQEVK-----LEKGLEMLGIF
GSMUA_Achr4G14820_001	MaYTH DF7A	AK-----LFVIKAYSEDD--IHK--SIKYNVWASTGYGNKKLDAG---YQ-----EAQGK----- -----AGGCP----VLLFFS-----VNTSGQFV-----GVAEM----- -----DVPNSSILKHITLENNDNK-PVTNSRDAQEVM-----LEQGLRMLKIF
GSMUA_Achr4T21380_001	MaYTH DF1A	AK-----FFIIKSYSEDD--IHK--SIKYNVWASTPHGNKKLDAA---YQ-----ESKEK-T----- -----SGCP----VFLFFS-----VNTSGQFV-----GVAEM---VGPVDFNKTL-DYWQ-QD-----KW-VGYFPVKWHIVKDVPNNI-LKHITLENNDNK-PVTNSRDTQEVK-----LDQGLQLLKLF
GSMUA_Achr4T22630_001	MaYTH DF2A	AK-----FFIIKSYSEDD--IHK--SIKYNVWASTPHGNKKLDAA---YQ-----ESKEK-T----- -----NGCP----VFLFFS-----VNTSGQFV-----GVAEM---VGRVDFNKTL-DYWQ-QD-----KW-IGCFPVKWHIVKDVPNNI-LKHITLENNENK-PVTNSRDTQEVK-----LEQGLQLLKLF
GSMUA_Achr4T28430_001	MaYTH DF4A	AK-----FFIIKSYSEDD--IHK--SIKYNIWSSTPHGNKKLDAA---YQ-----ESKEQ-T----- -----SGCP----IFLFFS-----VNTSGQFV-----GVAEM---IGRVNFNRTF-GYWQ-QD-----KW-IGCFPVKWQIVKDVPNNI-LKHIILEDNENK-PVTNSRDTQEVK-----LDQGLQLLRLF
GSMUA_Achr5T02830_001	MaYTH DF3A	AK-----FFIIKSYSEDD--IHK--SIKYSIWASTPHGNKKLDAG---YQ-----ESKQK-T----- -----SGCP----VFLFFS-----VNTSGQFV-----GVAEM---VGQVNFNKTL-DYWQ-QD-----KW-VGCFPVKWHIVKDVPNSV-LKHITLENNDNK-PVTNSRDTQEVK-----LDQGLQLLKLF
GSMUA_Achr6T12810_001	MaYTH DF5C	AK-----FFMIKSYNEDD--VHK--SVKYNVWASTPNGNKKLDAV---FW-----DAERL----M----- -----KKGSKCP----IFLFFS-----VNASGQFV-----GLAEM--- IGPVDFNKNL-DFWQ-KE-----TW-NGFFPVKWHIIKDIPNRL-FQSIRLENNDNK- AVTFSKDTQEVSFSLSCIERFPIMQVLLGQQFTVIGLPQGLQMLHIF
GSMUA_Achr6T19820_001	MaYTH DC1Ab	SR-----YFIVKSCNREN--LEI--SVQQGVWATQRSNEPKLNEA---FE-----STEN----- -----VILIFS-----INKTRHFQ-----GCAKM---TSRIGGLVGG-GNWK-YS-----HGTAH-----Y-GRNFSVKWLKCELSFNK-THHLRNPYNDNL-PVKISRDCQELE-----PFIGEQLASLL
GSMUA_Achr6T26690_001	MaYTH DF2C	AL-----FFVIKSYSEDD--IHK--SIKYSVWASTPNGNKRVDNA---FQ-----VAQEK-MTE----- -----KGGNCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDFSKNM-DFWQ-QD-----KW-NGFFPVKWHIIKDVPNLQ-FRHIILENNDNK-PVTNSRDTQEVK----- FSQGIEMLSIF

	GSMUA_Achr7T01490_001	MaYTH DF5A	AK-----FFIIKSYSEDD--IHK--SIKYNVWASTLHGNKKLDAA---YL-----ESKEK-T----- -----SGCP----IFLFFS-----VNTSGQFV-----GVAEM---VGPVDFNCTL- DFWQ-QD-----KW-IGCFPVKWHIVKDVPNSI-LKHIKVENNDNK-PVTNSRDTQEVK-----LEQGLQLLKLF
	GSMUA_Achr7T27220_001	MaYTH DF6A	AR-----FFVIKSYSEDD--IHK--SIKYNVWTSTPNGNKKLDGG---YQ-----EAQEK-D----- -----GGCP----VFLFYS-----VNASGQFV-----GVAEM--- VGPVDFNKTV-DYWQ-QD-----KW-IGCFPVKWHIIKDVPNSL-LKHITLENNDNK-PVTNSRDTQEVN----- LEQGLQMLKIF
	GSMUA_Achr8T29890_001	MaYTH DF4C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPNGNKRLNSA---YE-----DAQRK-SAG----- -----KSRKCP----VFLFYS-----VNASGQFC-----GLAEM--- VGPVDFDQDM-DFWQ-QD-----KW-SGSFPVKWHVIKDVSNAS-LRHIILENNENK-PVTNSRDTQEIP----- YSTGINMLSIF
	GSMUA_Achr9T06180_001	MaYTH DF1C	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDNA---FQ-----VAQEK-MAE----- -----KNSKCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDFSKDM-DFWQ-QD-----KW-NGFFPVKWHIIKDVPNPQ-FRHIILENNDNK-PVTNSRDTQEVK----- FSQGTEMLSIF
	GSMUA_Achr9T30440_001	MaYTH DC1Aa	SRCLSCMNAVLSIMYFIVKSCNREN--LEI--SVQQGMWATQRSNEAKLNEA--FE-----STEN----- -----VILIFS-----INKTRHFQ-----GCGKM--- TSRIGGFVGG-GNWK-YS-----HGTAH-----Y-GRNFSVKWLKLCESFNK-THHLRNPYNDNL-PVKISRDCQELE----- PFIGEQLASLL
<i>Vitis vinifera</i>	GSVIVT01010494001	VvYTH DF2B	AF-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDGA---YQ-----EAKER-MGD----- -----RGSKCP----VFLFFS-----VNASGQFC-----GVAEM--- IGRVDFNKNM-DFWQ-QD-----KW-NGFFPVKWHIIKDVPNPQ-LRHIILENNDNK-PVTNSRDTQEVN-----FPQGIEILNIF
	GSVIVT01017649001	VvYTH DF1C	AK-----FFIIKSYSEDD--VHK--SIKYNMWASTANGNKKLDAA---YQ-----EAQGK-S----- -----GSCP----IFLLFS-----VNASGQFV-----GVAEM--- VGSVDFNRS�-EYWQ-QD-----KW-TGCFPVKWHVIKDIPNSL-LKHITLENNENK-PVTNSRDTQEVK----- FEQGIQVLKIF
	GSVIVT01019895001	VvYTH DC1B	AK-----FFIIKSYSEDN--VHR--SIKYSVWASTALGNRKLDAA---YQ-----KAKEI----- -----ETNCP----IFLCFS-----VNASSQFC-----GVAEM---VGPVNFEKDA- EYWQ-QD-----RW-SGLFPVKWHIIKDVPNSL-FRHILLENNENK-PVTHSRDTQEVN-----LEQGIEMLKIF
	GSVIVG01021617001	VvYTH DC1A	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDAA---YR-----EAKEK----- -----QAACP----VFLLFS-----VNASAQFC-----GVAEM--- VGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVK----- LEQGIEILNIF
	GSVIVT01023248001	VvYTH DF3C	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YR-----EAQEK-S----- -----AGCP----VFLFFS-----VNTSGQFV-----GLAEM--- VGHVDFHKNV-EYWQ-QD-----KW-NGCFSVKWHVVKDVPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLQMLKIF

	GSVIVT01025494001	VvYTH DF1A	AK-----FYVIKSFSEDD--IHK--CIKYDVWASTPNGNKKLDAA---FH-----DAEAK-ANE----- -----TGTKFP----IFLFFS-----VNGSGQFV-----GVAEM--- VGQVDFNKM-DFWQ-LD-----KW-NGFFPVKWHIVKDIPNSQ-LRHITLESNENR-SVTYTRDTQEIG----- LKQGVEMLKIF
	GSVIVT01029460001	VvYTH DF1B	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA---FD-----SVEN----- -----VILIFS-----VNRTRHFQ-----GCAKM---TSKIGGFVGG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPYNENL-PVKISRDCQELE-----PSIGEQLASLL
	GSVIVT01032236001	VvYTH DF3B	TR-----YFIIKSLNHHN--IQL--SMEKGIWATQVMNEPILEEA---FH-----NSGK----- -----VILIFS-----VNMSGFFQ-----GYAQM---MSSVGWRRD-- NVWS-QG-----SGGNN-----PW-GRSFKVKWLRHLDPFQK-TLHLKNPLNDYK-PVKISRDCQELS-----QEIGEALCELL
	GSVIVT01033395001	VvYTH DF2A	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPNGNKKLENA---YE-----DAQRI-ALG----- -----KRRGCP----IFLFFS-----VNASGQFC-----GVAEM--- IGPVDFHKDM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNTN-FRHIILENNENK-PVTNSRDTQEIR----- FKQGLEMLKIF
	GSVIVT01036696001	VvYTH DF2C	AK-----FFVIKSYSEDN--VHK--SIKYGVWVSTPNGNKRLNSA---FH-----EAKEK----- -----HGNCP----IFLLFS-----VNASAQFC-----GVAEM--- VGPVDYDKSV-DYWK-QD-----KW-TGQFPVKWHIIKDVPNSQ-FRHIILENNDNK-PVTNSRDTQEVE----- LEQGNEMLNIF
<i>Manihot esculenta</i>	Manes.02G029400.1	MeYTH DC1B	AF-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDSA---YQ-----DAQKK-IAE----- -----KGSNCP----VFLFFS-----VNASGQFC-----GVAEM--- IGQVDFNKNM-DFWQ-QD-----KW-NGYFPVKWHIIKDVPNPQ-LRHIILENNENK-PVTNSRDTQEVK----- FPQGMEMLNVF
	Manes.06G172700.1	MeYTH DF3A	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPNGNKKLQSA---YD-----DAQKI-AAG----- -----DAKACP----IFLFFS-----VNASGQFC-----GVAEM--- IGPVDFAKDM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNSS-FRHIILENNENK-PVTNSRDTQEIM----- YKQGLEMLKIF
	Manes.07G024100.1	MeYTH DF3C	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA---FD-----SAEN----- -----VILIFS-----VNRTRHFQ-----GCAKM---TSKIGASAVG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPYNENL-PVKISRDCQELE-----PSIGEQLASLL
	Manes.07G081200.1	MeYTH DF2A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAG---YQ-----EAQQK-S----- -----GGCP----VFLFFS-----VNTSGQFV-----GLAEM--- IGPVDFHKNV-EYWQ-QD-----KW-TGCFPLKWHIVKDVPNSL-LKHITLENNENK-PVTNSRDTQEVK----- MEQGLKMIKIF
	Manes.09G141700.1	MeYTH DF5A	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTPNGNRRLDAA---YS-----EAKEK----- -----QVPCP----VFLFFS-----VNASAQFC-----GVAEM--- VGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIAKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVK----- LEQGIEMLNIF

	Manes.10G067800.1	MeYTH DF4A	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTPNGNKKLDAA---YH-----EAKEK----- -----TGTSP----IFLLFS-----VNASAQFC-----GVAEM--- VGAVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVE----- LEHGVEMLKIF
	Manes.12G010500.1	MeYTH DF3B	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTLNGNKKLDGA---YH-----EAKER----- -----HGTSP----VFLIFS-----VNASAQFC-----GVAEM--- VGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVE----- LEHGVEMLKIL
	Manes.13G011300.1	MeYTH DF2B	AK-----IFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAQQK-S----- -----SGCP----VFLFFS-----VNTSGQFV-----GLAEM--- VGPVDFHKNV-EYWQ-QD-----KW-TGCFPLKWHIVKDIPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLKMFKIF
	Manes.14G000200.1	MeYTH DF1B	AK-----FFIIKSYSEDD--VHK--CIKYGVWASTPNGNKKLDAA---YH-----EAKET-P----- -----GSCP----VFLIFS-----VNASGQFV-----GLAEM--IGAVDFNKTV- GYWQ-QE-----KW-IGCFPVKWHFIKDVPNSS-LRHITLENNENK-PVTNSRDTQEVN-----LDKGIQILKIF
	Manes.14G012900.1	MeYTH DF1A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAQQK-S----- -----CGCP----MFLFFS-----VNTSGQFV-----GLAEM--- VGPVDFHKNV-EYWQ-QD-----KW-TGCFPLKWHIVKDIPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLKMVKIF
	Manes.14G122500.1	MeYTH DC1A	AK-----FYVIKSYNEDD--IHK--SIKYDVWASTPNGNKKLDAA--FR-----DAEQR-SDE----- -----TGSKCP----IFLFFS-----VNGSGQFV-----GIAEM--- VGQVDFDKDM-DFWQ-LD-----KW-NGFFPVKWHVIKDIPNSH-LRHIILENNERR-PVTFSRDTQEIG----- LKQGLEMLNIF
	Manes.15G003300.1	MeYTH DF1C	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAQQK-P----- -----GGCP----VYLFFS-----VNTSGQFV-----GLAEM--- VGPVDFHKNV-EYWQ-QD-----KW-TGCFPLKWHIVKDIPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLKMIKIF
	Manes.16G048600.1	MeYTH DF2C	TR-----YFIIKSLNHHN--IQL--SVEKGVWATQVMNEPILEEA--FH-----NSGK----- -----VILIFS-----VNMSGFFQ-----GYAQM--ISSVGWRRD-- NIWS-QG-----CGKSN-----PW-GRSFKVKWLRLNDLPFQK-TLHLKNPLNDYK-PVKISRDCQELP-----EDVGEALCDLI
	OAY33214	MeYTH DF4B	AR-----FFIIKSFSEDN--VHK--SIKYSVWASTPHGNKKLDVA---YR-----EAKES----- -----GSNCP----VFLIFS-----VNASGQFC-----GVAQM--- VGPVNFEKDA-DYWQ-QD-----RW-SGQFPVQWHIIKDVPNSR-FRHILLKNNDNK-PVTHSRDAQEVK----- LEQGIEMLKIF
<i>Marchanti</i> <i>a</i> <i>polymorph</i> <i>a</i>	Mapoly0007s0039.1	MpoYT HDC1B	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKRLEGA---YQ-----DAQTR----- -----Q-GPCP----VFFFFS-----VNASGQFC-----GVAEM--- TGPVDFNKSV-DYWQ-QD-----KW-NGRFPVKWHIIKDIPNCQ-FRHIILENNNDNK-PVTNSRDTQEVK----- FEQGVEMLNIF

	Mapoly0056s0030.1	MpoYT HDC1A	CR-----FFIVKSSNREN--LEL--SVERGLWATHRNNESKLNEA---YD-----SCDH----- -----VILIFS-----VNETRHFQ-----GCARM---MSKIGGVAGG- GGWK-YA-----HGTAH-----Y-GRNFRLKWLKLCELSFNK-TRHLRNPFNENL-PVKISRDCQELE-----PGVGEQLAQLL
	Mapoly0103s0072.1	MpoYT HDF1	TR-----YFIIKSLNHHN--IAK--SIENGIWATQAMNEPVLNEA---YE-----SSER----- -----VLLVFS-----VNMSGHFQ-----GYAQM---ASPIGRRRA-- NVWT-EG-----NEGTN-----PW-GGSFRVEWLRRLHDLPFQK-TVHLKNPLNFHK-PVKISRDCQELT-----LEIGDALCALI
<i>Medicago truncatula</i>	Medtr2g005840.1	MtYTH DF4C	DEFAFTVCRDQYNLPDFQTKYETAKFYMIKSFNEDDIHKGIKYDVWTSTPHGNKKLNAAFQNAEAKLSQTGTQCPIFLFFSVNASGQFVGVAEMLGPVDFKKD MKFWKLDKYNGFFPIKWHIIKDVPNRQFAHITLQINENKCVTFSRDTQEITLKEGLEMLKIFKSYPAKTSLDDDFDYENREKLCRSQRTEHTGW
	Medtr2g029540	MtYTH DC1A	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTQNGNKKLDAA---YQ-----EAQQK-S----- -----GGCP----IFLLFS-----VNTSGQFV-----GLAEM---TGPVDFNKS- EYWQ-QD-----KW-MGCFPLKWHIVKDVPNNV-LRHITLENNENK-PVTNSRDTQEIM-----LEPGLKLLKIF
	Medtr2g032660	MtYTH DF3C	AK-----FFIIKSYSEDD--VHK--SIKYSVWASTPNGNKKLDAA---YQ-----EA----- -----GGCP----IFLLFS-----VNTSGQFV-----GLAEM---TGPVDFDKTV- EYWQ-QD-----RW-TGCFNVKWHIIKDIPNGV-LRHITLENNENK-PVTNSRDTQEVK-----FEKGVQIVKIF
	Medtr2g063460	MtYTH DF2C	AK-----FFVIKSYSEDD--IHK--SMKYNVWTSTPNGNKKLDAA---YL-----EAKEK-S----- -----ADCP----IFLLFS-----VNTSGQFV-----GLAEM---VSPVDFDRTV- EYWQ-QD-----RW-TGCFSVKWRIIKDIPNNV-LRHITLENNENK-PVTNSRDTQEVK-----FEKGVEILKIF
	Medtr4g005110	MtYTH DF1B	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLQSA---YE-----DARRK-ATG----- -----KSGGCP----IFLFFS-----VNASGQFC-----GVAEM--- VGPVDFNKDM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNGN-FRHIILENNEFK-PVTNSRDTQEIM----- YRKGLEMLKIF
	Medtr4g123630	MtYTH DF1C	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDAA---YC-----QAKEK----- -----QDACR----IFLFFS-----VNASAQFC-----GVAEM--- VGPVNFDKSV-DFWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVK----- LQQGIEMLTIF
	Medtr6g032970	MtYTH DF3A	AL-----FFVIKSYSEDD--VHK--SIKYDVWASTPNGNKRLDNA---FQ-----DAQNR-MEE----- -----KGSKCP----VFLFFS-----VNASGQFC-----GVAEM--- IGRVDFNKSM-DFWQ-QD-----KW-NGYFPVKWHIIKDIPNPQ-LRHIILENNDHK-PVTNSRDTQEIH-----FPQGIEMLNIF
	Medtr7g085500	MtYTH DF2A	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTVHGNRKLGN---YE-----DTKKV-SAE----- -----KSGVCP----IFLFFS-----VNASGQFC-----GVAEM--- IGSVDFNKDM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNPN-FRHIILDNNENK-PVTNSRDTQEIM-----YSKGLEMLKIF
	Medtr8g088390	MtYTH DF1A	NRTSTPLPQGIS-RYFIVKSCNREN--LEL--SVQQGVWATQRSNESKLNEA---FD-----SVEN----- -----VILIFS-----VNRTRHFQ-----GCAKM--- TSRIGGSVAG-GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPYNEN-LPVKISRDCQELE----- PSIGEQLASLL
<i>Mimulus guttatus</i>	Migut.A00893.1	MgYTH DC1B	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPNGNKKLTTA---YQ-----DAHRT-TLG----- -----DLRGCP----IFLFFS-----VNASGQFC-----GVAEM--- TGPVDFHRDM-DFWQ-QD-----KW-SGSFPVKWHIIKDLPNSN-FRHIILENNENK-PVTNSRDTQEIC-----YEKGLEMLRIY

	Migut.B00769.1	MgYTH DF4C	AK-----FYVIKSYSEDD--VHK--CIKYDVWSSTPNGNQKLDAA--FS-----EAGAK-TRE----- -----TGVNCP----VFLFFS-----VNGSGQFV-----GVAEM--- IGQVDFSKNM-DFWQ-LD-----KW-NGFFPIKWHMIKDVPNTL-LRHIILENNENR-PVTYSRDTQEIG-----LKQGLEMLRIF
	Migut.D02575.1	MgYTH DF2A	AR-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----DAQQR-P----- -----GGCP----VFLFFS-----VNTSGQFV-----GVAEM--- TGPVDFNKNV-EYWQ-QD-----KW-VGCFPVKWHIVKDLPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LDQGLQVLKIF
	Migut.G00015.1	MgYTH DF2C	SR-----YFVVKSCNNEN--LEL--SVQQGVWATQRSNEAKLNEA--FE-----SVDN----- -----IILIFS-----VNKTRHFQ-----GCAKM---TSRIGGSISG- GNWK-NA-----HGTAH-----Y-GQNFSVKWLKLGELSFNK-TRHLRNPFNENL-PVKISRDCQELE-----PSIGEQLASLL
	Migut.H01337.1	MgYTH DC1Aa	AK-----FFVIKSFSEDN--IHK--SIKYSVWASTPLGNRKLDAA---YC-----ETKEM----- -----EGICP----VLLFS-----VNASGQFC-----GVAEM---IGPVDFENDA- DYWQ-QD-----RW-SGQFPVKWHIIKDVPNSR-FRHILLENNENK-PVTHSRDSQEVK-----LEQGIEMLQIF
	Migut.J00855.1	MgYTH DF1B	SR-----YFVVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA--FE-----SVEN----- -----IILIFS-----VNKTRHFQ-----GCAKM---TSRIGGSVGG- GNWK-HA-----HGTAH-----Y-GRNFALKWLKLCELTFDK-TRHLRNPYNENL-PVKISRDCQELE-----PSIGEQLASLL
	Migut.M01886.1	MgYTH DC1Ab	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPNGNKKLTTA---YQ-----DAHRT-GLG----- -----DLRGCP----IFLFFS-----VNASGQFC-----GVAEM--- TGPVDFHRDM-DFWQ-QD-----KW-SGSFPVKWHIIKDLPNSN-FRHIILENNENK-PVTNSRDTQEIC-----YKKGLEMLRIY
	Migut.N00538.1	MgYTH DF1A	AK-----FFIIKSYSEDD--VHK--SIKYNIWASTSNGNKKLEAA---YQ-----DAQQK-P----- -----GGCP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDFNKNV-EYWQ-QD-----KW-IGCFPLKWHIVKDLPNSS-LKHITLENNENK-PVTNSRDTQEVK----- LEPGLAVLKIF
	Migut.N00839.1	MgYTH DF3C	AK-----FYVIKSYSEDD--VHK--CIKYDVWSSTPNGNQKLDAA--FS-----EAGAK-TRE----- -----TGVNCP----VFLFFS-----VNGSGQFV-----GVAEM--- IGQVDFSKNM-DFWQ-LD-----KW-NGFFPIKWHMIKDVPNTL-LRHIILENNENR-PVTYSRDTQEIG-----LKQGLEMLRIF
	Migut.O00389.1	MgYTH DF1C	TR-----YFIIKSLNHEN--IQL--SVKKEIWATQVMNEPILEEA--FQ-----NSGK----- -----VILIFS-----VNMSGFFQ-----GYAQM---MSSVGWRRD--TIWS- QA-----SGKSN-----PW-GRSFKVKWLRLNDLAFQK-TLHLKNPWNDFK-PVKISRDCQELP-----GDIGRALCELL
<i>Oryza sativa</i>	Os01g22630	OsYTH DF3C	AK-----FFVIKSIGEDD--VHK--SIKYGVSSSSSGNSKLDIA--FK-----DANRI-AKR----- -----NSTKCP----VFLFFS-----VNGSGLFC-----GMAEM--- VGPVDFHKDM-DFWC-QD-----KW-TGSFPVRWHIVKDVPNYT-LQHILLQNNENK-PVTHSRDTQEIP----- YVPGISMLKIL
	Os01g48790	OsYTH DF1C	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDNA--FK-----LAQER-VAE----- -----KGTKCP----MFLFFS-----VNASGQFC-----GVAEM--- VGPVDFNRNM-NFWQ-QD-----KW-NGFFPVKWHIIKDVPNPQ-FRHIILENNENK-PVTNSRDTQEVK----- FPQGSEMLNIF

	Os03g06240	OsYTH DF1A	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTTNGNKKLDAA---YQ-----EAQAK-S----- -----SKCP----IFLFFS-----VNTSGQFV-----GVAEM--TGAVDFECTL- EYWQ-QD-----KW-NGSLSLKWHIVKDVPNNI-LKHIILENNENK-PVTNSRDTQEVN-----LDQGIQMLKIF
	Os03g20180	OsYTH DF2C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPNGNKRLDAA---YS-----DVQGR-ALG----- -----K---CP----IFLFFS-----VNASGQFC-----GVAEM--- VGPVDFHKDM-DFWQ-QD-----KW-SGSFPVKWHLVKDVPNST-FRHIILENNENK-PVTNSRDTQEIP----- FKSGTNMLKLF
	Os03g53670	OsYTH DF2A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAG---YR-----EAQEK-S----- -----SECP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDFEKTV-DYWQ-QD-----KW-NGCFPIKWHVVKDVPNNI-LKHITLDNNDNK-PVTNSRDTQEVK----- LEQGLEMLKIF
	Os04g04000	OsYTH DF5C	AK-----FFMIKSYSEDD--IHK--GIKYNVWASTPHGNNKLDAA---FR-----EAQIL-IKE----- -----KGKKCP----VFLFFS-----VNSSGQFV-----GLAEI--- LGPVDFKKTМ-DFWK-LD-----RW-NGFFPVTWHIIKDIPNRL-FKHITLENNDNR-IVTFSRDTQEIG-----LLQGLKMLKIF
	Os04g51940	OsYTH DF3B	AK-----FFVIKSYTEDH--VHK--SIKYGVWASTASGNRKLDAA---YR-----EAKEK----- -----EATCP----IFLFFS-----VNGSGQFC-----GVAEM--- IGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSL-LRHIILENNENK-PVTNSRDTQEVР-----LDHGLQMLTIF
	Os05g01520	OsYTH DF4C	AK-----FFMIKSYSEDD--VHK--GIKYNVWASTPNGNNKLDAA---FH-----EAQIL-MKE----- -----QGKRCР----IFLFFS-----VNTSGQFV-----GLAEM--- LGPVDFKKTМ-DFWQ-QD-----KW-NGFFPVMWHIIKDIPNRF-FKHITLENNEGK-VVTFSRDTQEIG-----LPQGLEMLKIF
	Os06g46400	OsYTH DC1A	SR-----YFIVKSCNREN--LEI--SVQQGIWATQRSNEAKLNEA---FE-----SIEN----- -----VILIFS-----INRTRNFQ-----GCAKM---TSRIGGYIGG-GNWK- SA-----HGTАH-----Y-GRNFSIQWLKLCELSFQK-THHLRNPYNDNL-PVKISRDCQELE-----PFIGEQLASLL
	Os07g07490	OsYTH DF3A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTSNGNKKLDAA---YQ-----EAKEK-S----- -----SDSS----VFLIFS-----VNASGQFV-----GLAEM--- VGRVDFNKTЛ-EHWQ-QD-----KW-TGCFPVKWHIVKDVPNSL-LKHIILENNENK-PVTNCRDTHEVK----- LEPGLQVLKIF
	Os08g12760	OsYTH DF2B	AK-----FFVIKSYTEDH--VHR--SIKYNVWASTASGNRKLDSA---YR-----LAKEK----- -----EDYCP----IFLFFS-----VNGSGQFC-----GVAEM---IGPVDFDKSV- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNNL-LRHIILENNDNK-PVTNSRDTQEVK-----LEHGLQMLTIF
	Os08g44200	OsYTH DF1B	AR-----FFIIKSYSEDN--VHK--SIKYGVWASTTNGNKKLDSA---YR-----EAKEK----- -----EEHCP----IFLLFS-----VNASAQFC-----GVAEM---IGPVDFEКСV- DYWQ-QD-----KW-TGQFPVKWHIVKDVPNNL-FRHIILENNDNK-PVTNSRDTQEVK-----LEQGMEMLKIF
<i>Panicum hallii</i>	Pahal.B00424	PhYTH DF2A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAG---YR-----EAQEK-S----- -----SDCP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDFDKTV-EYWQ-QD-----KW-NGCFPLKWHIVKDVPNNI-LKHITLDNNDNK-PVTNSRDTQEVK----- LEQGLEMLKIF

Pahal.C00997	PhYTH DF4C	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPSGNKKLDAA---YL-----EAKEK-S----- -----SSSP----VLLFS-----VNTSGQFV-----GLAEM--VGRVDFSKTV- EYWQ-QD-----KW-TGCFAVKWHIVKDIPNSL-LKHIILEYNENK-PVTNSRDTQEVK-----LDQGLQMLKIF
Pahal.C01447	PhYTH DF3C	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTTNGNKKLDAA---YQ-----EAQSK-G----- -----SACP----IFLFFS-----VNTSGQFV-----GVAEM--TGAVDFECTL- EYWQ-QD-----KW-NGSFSVKWHIVKDVNNM-LKHIILENNENK-PVTNSRDTQEIH-----LEQGLQMLKIF
Pahal.D00506	PhYTH DC1A	AK-----FFVIKSIGEAD--VHK--SIKYGVWSSSSNGNSKLDSA---FR-----DADRI-SRR----- -----NSTKCP----VFLFFS-----VNGSGHFC-----GMAEM--- VGPVDFHKDM-DFWC-QD-----KW-TGCFPVRWHIVKDIPNYF-LQHITLQNNENK-PVTHSRDTQEIP-----YIPGMSVLKIF
Pahal.E02120	PhYTH DF1C	AK-----FFVIKSYTEDH--VHK--SIKYNVWASTASGNRKLNTA---YR-----EAKDK----- -----EEYCP----IFLFFS-----VNGSGQFC-----GVAEM--- IGPVDFDKNV-DYWQ-ND-----RW-SGQFPVKWHIVKDVNNI-VRHIILENNEDK-RVTNSRDTQEVK----- LELGVQMLAIF
Pahal.F00398	PhYTH DF1B	AK-----FFVIKSYTEDH--VHR--SIKYSVWASTASGNRKLDSA---YR-----AAKEK----- -----EEHCP----IFLFFS-----VNGSGQFC-----GVAEM--IGPVDFDRSV- DYWQ-QD-----KW-SGQFPVKWHIIKDVNNL-LRHIILENNDNK-PVTNSRDTQEVK-----LEQGLQMLTIF
Pahal.F01360	PhYTH DF2B	AR-----FFIIKSYSEDN--VHK--SVKYGVWASTTNGNKKLDSA---YR-----EAKEK----- -----EEHCP----IFLLFS-----VNASAQFC-----GVAEM--IGPVDFEKS- DYWQ-QD-----KW-TGQFPVKWHIVKDVNNL-FRHIILENNDNK-PVTNSRDTQEVK-----LEQGLEMLKIF
Pahal.G02347	PhYTH DF3B	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDNA---YR-----LAQER-MAE----- -----KGTKCP----VFLFFS-----VNASGQFC-----GVAEM--- VGPVDFNRNM-NFWQ-QD-----KW-NGFFSVKWHIIKDVNPQ-FRHIILENNENK-PVTNSRDTQEVK----- FLQGTEMLNIF
Pahal.H01140	PhYTH DF2C	SR-----YFIVKSCNREN--LEI--SVQQGIWATQRSNEAKLNEA---FE-----STEN----- -----VILIFS-----INRTRHFQ-----GCAKM--TSRIGGYIGG-GNWK- SA-----HGTAH-----Y-GRNFSMQWLKLCESFQK-THHLRNPYNDNL-PVKISRDCQELE-----PFIGEQLASLL
Pahal.I00478	PhYTH DF1A	AK-----FFVIKSYDESD--VHK--SIKYGVWSTSSAGNQKLDTA---FR-----EAQAI-ASS----- -----TSTLCP----VLLFFS-----VNGSSNFC-----GVAEM--- VGPVDYQNDM-DFWC-KD-----KW-TGSFPVKWHIIKNVRNYT-FRSILLQNNEYK-PVTSSRDTQEIH----- YTPGTTMLELF
Pahal.I01354	PhYTH DF4A	AK-----FFMIKSYSEDD--IHK--GIKYNVWASTANGNDKLDAA---YH-----EAQIL-MKE----- -----NGENCP----VFLFFS-----VNTSGQFV-----GLAEM--- LGPVDFKKT-DFWK-ED-----KW-NGFFPIIWHIIKDIPNRL-FRHIILEHNDNR-PVTFSRDTQEIG-----LAQGMQMLKIF
Pahal.I01743	PhYTH DF3A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAKEK-S----- -----SESP----VLLFS-----VNASGQFV-----GLAEM--- VGRVDFNKT-ehwq-QD-----KW-TGCFPVKWHIVKDVNSL-LKHIILENNENK-PVTNSRDTHEVK----- LEQGLQVLKIF

<i>Populus trichocarpa</i>	Potri.001G002000.1	PtYTH DF2A	AK-----FFVIKSFSEDD--VHK--SIKYSVWTSTPNGNKKLDAA---YK-----QGKEN-P----- -----GDCP----VLLFS-----VNTSGQFV-----GLAEM--- VGPVDFNKTV-EYWQ-QD-----KW-TGCFPLKWHIIKDVPNGC-LRHITLENNENK-PVTNSRDTQEVI-----FEKGVQILKIF
	Potri.001G056100.1	PtYTH DF5B	AK-----FFIIKSFSEDN--VHK--SIKYSIWASTPHGNKKIDAA---YR-----EAKEK----- -----EGNCP----VLLFS-----VNASGQFC-----GVAEM---VGPVDFEKDA- DYWQ-QD-----RW-NGQFPVQWHIIKDVPNSR-FRHILLENNDHK-PVTHSRDSQEVK-----LEQGIEMLKIF
	Potri.001G113500.1	PtYTH DC1B	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDTA---YH-----EAKDK----- -----QDPCP----VLLFS-----VNASAQFC-----GVAEM--- VGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVK----- LEQGVEMLNIF
	Potri.001G357800.1	PtYTH DC1Aa	KL-----YFIVKSCNLEN--LEL--SVQQGVWATQRSNEPKLNEA---FD-----SAEN----- -----VILIFS-----VNRTRHFQ-----GCAKM---TSKIGASVGG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKCELSFHK-TRHLRNPFNENL-PVKISRDCQELE-----PSIGEQLASLL
	Potri.003G008400.1	PtYTH DF6C	AF-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLSA---YL-----DSQQK-IAQ----- -----IGCSCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDFNKNM-DFWQ-QE-----KW-NGYFPVKWHIIKDIPNPQ-LRHIILENNENK-PVTNSRDTQEVK-----FPQGIEILNIF
	Potri.003G222700.1	PtYTH DF1A	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLQTA---FE-----DAQKL-AVG----- -----RPRGCP----IFLFFS-----VNASGQFC-----GVAEM--- IGPVDLHRDM-DFWQ-QD-----KW-SGSFLVKWHIIKDIPNSS-FRHIILENNENK-PVTNSRDTQEIM-----YKQGLEMLKTF
	Potri.004G223800.1	PtYTH DF5C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLHSA---FE-----YAQKL-DLG----- -----RPRGCP----IFLFFS-----VNASGQFC-----GVAEM--- VGPVDFNRDM-DFWQ-QD-----KW-SGSFLVKWHIIKDIPNSS-FRHIILENNENK-PVTNSRDTQEIM----- YKQGLEMLKMF
	Potri.006G079900.1	PtYTH DF3B	AF-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLLDSA---YQ-----DAQQK-IAE----- -----KGNSCP----VFLFFS-----VNASGQFC-----GVAEM--- VGRVDFNKNM-DFWQ-QD-----KW-NGYFPVKWHIIKDVPNPQ-LRHIILENNENK-PVINSRDTQEVK-----FPQGIEILNIF
	Potri.007G002800.1	PtYTH DF2B	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDTT---YR-----EAKEK----- -----QDPCP----VLLFS-----VNASAQFC-----GVAEM--- TGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVK----- LEQGIEMLNIF
	Potri.008G080800.1	PtYTH DF4C	AK-----FFIIKSFSEDN--VHK--SIKYSVWASTPHGNKKIDAA---YR-----EAKEK----- -----EGNCP----VLLFS-----VNASGQFC-----GVAEM--- VGPVDFEKDA-EYWQ-QD-----RW-NGQFPVQWHIVKDVPNSR-FRHILLENNDNK-PATHSRDSQEVK----- LEQGIEMLKIF
	Potri.008G100200.1	PtYTH DF2C	AK-----FFVIKSYNEDD--IHK--SIKYDVWASTPNGNKKLDAA---FH-----NAEEV-SSE----- -----TGTKCP----IFLFFS-----VNGSGQFV-----GLAEM--- VGQVDFNKDM-DFWQ-ID-----KW-NGFFPVKWHVIKDIPNGQ-LRHIVLENNDGH-SVTFSRDTQEIG----- LEKGLEMLNIF

	Potri.010G152300.1	PtYTH DF1C	AK-----FFIIKSYSEDD--VHK--CIKYNVWASTPNGNKKLDAA---YQ-----EAEQK-S----- -----GGCP----VFLIFS-----VNTSGQFV-----GLAEM--- TGRVDFDKSV-EYWQ-QD-----KW-TGYFPVKWHIVKDVPSNF-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLKLIKIF
	Potri.010G175500.1	PtYTH DF3C	AK-----FFVIKSYSEDD--IHK--SIKYDVWASTPNGNKKLDAA---FH-----NAEEV-SSD----- -----TGYKCP----IFLIFS-----VNGSGQFV-----GFAEM--- VGQVDFNKDM-DFWQ-ID-----KW-NGFFPVKWHVVKDIPNGH-LRHIVLENNDGH-SVTFSRDTQEIV----- LKQGLEMLNIF
	Potri.011G089800.1	PtYTH DC1Ab	SQF-----VYFIVKSCNREN--LEL--SVQQGVWATQRSNEIKLNEA---LD-----SADN----- -----VILIFS-----VNRTRHFQ-----GCAKM--ASKIGASVGG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPFNENL-PVKISRDCQELE-----PSIGEQLASLL
	Potri.014G001000.1	PtYTH DF1B	TR-----YFIIKSLNQHN--IQL--SIENGIWATQVRNEPILEEA---FH-----NSGR----- -----VILIYS-----VNMSGFFQ-----GYAQM--ISSVGWRHD--NLWS- EG-----SGKSN-----PW-GRSFKVKWLRLNDLPFQK-TLHLKNPLNDYK-PVKISRDCQELP-----EDIGEALCELI
	Potri.018G149800.1	PtYTH DF4B	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTPNGNKKLDAA---YR-----EAKEN----- -----HGTCP----IFLLFS-----VNASAQFC-----GVAEM--- VGPVDFDKNV-DFWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVE----- LEQGAEMLGIF
	Potri.019G034300.1	PtYTH DF3A	AK-----FFIIKSYSEDD--VHK--CIKYNVWASTPNGNKKLDAA---YQ-----EAGQK-S----- -----GGCP----VFLIFS-----VNTSGQFV-----GLAEM--- TGRVDFDKSV-EYWQ-QD-----KW-TGYFPVKWHFVKDVPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLEMIF
<i>Physcomitr ella patens</i>	Pp3c10_17810V3.1	PpaYT HDF2	TR-----YFIIKSLNHHN--IEK--SIEKGIWATQAMNETVLNEA---FE-----TSEK----- -----VVLVFS-----VNMSSHQ-----GYALM--SSPIGQRRRA--NIWS- EA-----NEGAN-----PW-GGTFHVEWLRLYDLPFQK-TVHLKNPLNAFK-PVKISRDCQELT-----QAIGKALCALI
	Pp3c20_9290V3.1	PpaYT HDC1A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPVGNKRLDAA---YQ-----EALTK-CNG----- -----DTKSYP----VFLIFS-----VNASGQFC-----GMAQM--- TGRVDFSFSV-DYWQ-QD-----KW-NGRFPVTWHIIKDIPNCQ-FRHIILENNDNK-PVTNSRDTQEVK----- FEQGMAMLNIF
	Pp3c3_33560V3.1	PpaYT HDF1	CR-----YFIVKSSNREN--LEL--SVERGLWATHRNNEAKLNDA---FD-----SCEH----- -----VIFIFS-----VNETRHFQ-----GCARM--MSKIGGVAGG- GAWK-YA-----HGTAN-----Y-GRNFRLKWLKLCELSFYK-TRHLRNSYNENM-PVKISRDCQELE-----PSVGEQLALLL
	Pp3c8_11880V3.1	PpaYT HDC1B	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPVGNKRLDAA---YL-----EALAK-SNG----- -----DTKSFP----VFLIFS-----VNASGQFC-----GVAQM--- TGPVDFSFSV-DFWQ-QD-----KW-NGRFPVVWHIIKDIPNCQ-FRHIILENNDNK-PVTNSRDTQEVK-----FEQGFGMLNIF
<i>Saccharom yces cerevisiae</i>	Sacce1/1410	PHO92 (ScYTH DF1)	SR-----FFVIKSSSLKH--VKR--SFYNGIWSSTHFGNKRLSEA---YK-----KLNSG----- -----AK----VFLIFS-----INTSGRFC-----GVAEM---VSDLKMDLDT- SIWEDEQ-----KY-GKAFKVRWVIVRDINNRS-LKRFLIPSNEMK-PITHSRDTQEIP-----YSIGISIINLF

<i>Schizosacc haromyces pombe</i>	Schpo1/4324	MMI1 (SpYTH DC1)	SR-----YFIMLCDNETA--IAH--AKKTSIWAVKKDSSKRISDA---YK-----KAS----- -----VYFIFV-----AQQTYNAL-----GYAQV---VSDLNSTELP-- FWSDSS-----H-----AGGVRIKWIKTCNLFSAE-ISEIVSHMDHGS---EARDGMEMM-----YDEGSRLCTLI
<i>Setaria italica</i>	Seita.2G046200.1	SiYTH DF3A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAKEK-S----- -----SESP----VLLFS-----VNASGQFV-----GLAEM--- VGRVDFNKTV-EHWQ-QD-----KW-TGCFPVKWHIVKDVPNSL-LKHIILENNENK-PVTNSRDTHEVK----- LEPGLQVLKIF
	Seita.2G149700	SiYTH DF5C	AK-----FFVIKSYNEAD--IHK--SIKYGWSTSSVGNLKLDTA---FR-----DAQVI-AAS----- -----SSTLCP----VLLFFS-----VNGSSHFC-----GVAEM--- VGPDYQNDM-DFWCRKN-----KW-IGSFPVKWHIIKNVHNST-FRSISLQNNEDK-PVTSSRDTQEIH----- YTPGTTMLELF
	Seita.3G070000.1	SiYTH DF3C	AK-----FFMIKSYSEDD--IHK--GIKYNVWASTPNGNKKLDAA---YH-----DAQIL-MKE----- -----NGEKCP----VLLFFS-----VNTSGQFV-----GLAEM--- LGPVDFKKTm-DFWK-DD-----RW-SGFFPIIWHIIKDIPNRL-FRHIILEYNDNR-PVTFSRDTQEIG-----LLQGVQMLKIF
	Seita.4G262400.1	SiYTH DC1A	SR-----YFIVKSCNREN--LEI--SVQQGIWATQRSNEAKLNEA---FE-----STEN----- -----VILIFS-----INRTRHFQ-----GCAKM--TSRIGGYIGG-GNWK- SA-----HGTAH-----Y-GRNFMSQWLKLCELSFQK-THHLRNPYNDNL-PVKISRDCQELE-----PFIGEQLASLL
	Seita.5G156800.1	SiYTH DF2C	AK-----FFVIKSIGEAD--VHK--SIKYGWSSSSNGNSKLDSA---FR-----DADRI-SRR----- -----NSTKCP----VLLFFS-----VNGSGHFC-----GMAEM--- VGPDVDFHKDM-DFWC-QD-----KW-TGCFPVRWHIVKDIPNYS-LQHITLQNNENK-PVTHSRDTQEIP-----YIPGMSVLKIF
	Seita.5G271100.1	SiYTH DF1C	AL-----FFVIKSYSEDD--IHK--SIKYSVWASTPNGNKRLDNA---YR-----LAQER-MAE----- -----KGTKCP----VLLFFS-----VNASGQFC-----GVAEM--- VGPDVDFNRNM-NFWQ-QD-----KW-NGFFSVKWHIIKDVPNPQ-FRHIILENNENK-PVTNSRDTQEVK----- FPQGTEMLNIF
	Seita.6G022500.1	SiYTH DF1B	AK-----FFVIKSYTEDH--VHR--SIKYSVWASTASGNRKLDSA---YR-----AAKEK----- -----EDHCP----IFLFFS-----VNGSGQFC-----GVAEM---IGPVDFDRSV- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNNL-LRHIILENNDNK-PVTNSRDTQEVK-----LEQGLQMLTIF
	Seita.6G246600.1	SiYTH DF2B	AR-----FFIIKSYSEDN--VHK--SVKYGVWASTTNGNKKLDASA---YR-----EAKEK----- -----EEQCP----IFLLFS-----VNASAQFC-----GVAEM---IGPVDFEKSv- DYWQ-QD-----KW-TGQFPVKWHIVKDVPNNL-FRHIILENNDNK-PVTNSRDTQEVK-----LEQGLEMLKIF
	Seita.7G231300.1	SiYTH DF3B	AK-----FFVIKSYTEDH--IHK--SIKYNVWASTASGNRKLNAa---YR-----EAKER----- -----EDYCP----IFLFFS-----VNGSGQFC-----GVAEM---IGPVDFDKSV- DYWQ-ND-----RW-SGQFPVKWHTVKDVPNNL-VRHIILENNENK-RVTNSRDTQEVK-----LEQGVQMLAIF
	Seita.7G270400.1	SiYTH DF4C	AK-----FFVIKSYNEAD--IHK--SIKYGWSTSSVGNLKLDTA---FR-----DAQVI-AAS----- -----SSTLCP----VLLFFS-----VNGSSHFC-----GVAEM--- VGPDYQNDM-DFWCRKN-----KW-IGSFPVKWHIIKNVHNST-FRSILLQNNEDK-PVTSSRDTQEIH----- YTPGTTMLELF

	Seita.9G059600.1	SiYTH DF4A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPSGNKKLDAA---YV-----EAKEK-S----- -----SSSP----VFLIFS-----VNTSGQFV-----GLAEM---VGRVDFNKTV- EYWQ-QD-----KW-TGCFPVKWHIVKDIPNGL-LKHIILEYNENK-PVTNSRDTQEVK-----LDQGLQVLKIF
	Seita.9G092900.1	SiYTH DF2A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAG---YR-----EAQEK-S----- -----SDCP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDFDKTV-EYWQ-QD-----KW-NGCFPLKWHIVKDVNNI-LKHITLDNNDNK-PVTNSRDTQEVK----- LEQGLEMLKIF
	Seita.9G534000.1	SiYTH DF1A	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTTNGNKKLDAA---YQ-----EAQSK-G----- -----SACP----IFLFFS-----VNTSGQFV-----GVAEM---TGAVDFECTL- EYWQ-QD-----KW-NGSFSCLKWHIVKDVNNM-LKHIILENNENK-PVTNSRDTQEIH-----LEQGLQMLKIF
<i>Solanum lycopersic um</i>	Solyc01g028860.2.1	SIYTH DF1A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAQQN-S----- -----GGCP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDFNKNV-EYWQ-QD-----KW-VGCFPVKWHIVKDVNSL-LKHITLENNENK-PVTNSRDTQEVK----- VEQGLQVLKIF
	Solyc01g103540.2.1	SIYTH DF2C	AK-----FYIIKSYSEDD--IHK--CVKYDVWSSTPNGNKKLDTA---FV-----ESEAK-ASG----- -----TGSSCP----VFLFFS-----VNGSGQFL-----GVAEM--- VGQVDFNRNM-DFWQ-LD-----KW-SGFFPLKWHIVKDVPNTQ-FRHIILENNDNR-PVTYSRDTQEIG----- LKEGLEMLNIL
	Solyc02g021760.2.1	SIYTH DC1A	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA---FD-----SVEN----- -----VILIFS-----VNRTRHFQ-----GCGKM---TSRIGGAANG- GNWK-HE-----HGTAH-----Y-GRNFSCLKWLKCELSFQK-THHLRNPYNENL-PVKISRDCQELE-----PSVGEQLASLL
	Solyc02g070240.2.1	SIYTH DC1Ab	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA---FD-----SVEN----- -----VILIFS-----INRTRHFQ-----GLAKM---TSRIGGAAKG- GNWK-HE-----HGTAH-----Y-GRNFSVKWLKCELSFQK-TRHLRNPYNENL-PVKISRDCQELE-----ISVGEQLASLL
	Solyc05g032850.2.1	SIYTH DF1B	AK-----FFVIKSFSEDN--VHK--SIKYGVWASTPQGNRKLDAA---YA-----EAKEM----- -----NANCP----VFLFFS-----VNASGQFC-----GVAEM--- VGPIDFENSA-EYWQ-QD-----RW-SGKFPPVKWHVIKDV PNSQ-FRHILLEHNDNK-PVTHSRDSQEVK----- LPEGLEMLKIF
	Solyc08g007730.2.1	SIYTH DC1B	IR-----YFVIKSLNHEN--IQL--SVNRGIWATQAMNEAILDEA---FH-----NSSK----- -----VILIFS-----VNTSGYFQ-----GYAQM---ISSV-GLRRD-QVWS- QG-----NGGRN-----SW-GRSFEVNWRLRYDLPFQR-TLHLKNPWNQNK-PVKISRDCQELP-----PDIGEALCELL
	Solyc12g099090.1.1	SIYTH DF1C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPNGNKKLNSA---YE-----DAQRI-TPG----- -----NPRGCP----IFLFFS-----VNASGQFC-----GVAEM--- TGPVDFYKDM-DFWQ-QD-----KW-SGSFPVKWHFIKDVNPN-FRHIILENNENK-PVTNSRDTQEIR----- YKKGIEMLKVF
<i>Sphagnum fallax</i>	Sphfalx0029s0025.1	SfYTH DF1	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPVGNKRLDAA---FK-----DASGK----- -----AVGGCP----VFLFFS-----VNASGQFC-----GVAEM--- TGPVDFTQSV-EYWQ-QD-----KW-NGRFTVKWHIIKDIPNCQ-FRHIILENNDNK-PVTNSRDTQEV R-----FEQGIEMLSIF

	Sphfalx0037s0069.1	SfYTH DF2	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPAGNKRLDAA---FL-----ESQSK-AGG----- -----KQGSCP----VFLFFS-----VNASGQFC-----GVAEM--- VGPVDFGKSV-EYWQ-QD-----KW-NGRFTVKWHIIKDIPNCQ-FRHIILENNDNK-PVTNSRDTQEVK-----FEQAISMLNIF
	Sphfalx0040s0172.1	SfYTH DF3	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPAGNKRLDAA---FL-----EAQNKVASG----- -----KPGSCP----VFLFFS-----VNASGQFC-----GVAEM--- VGPVDFGKSV-EYWQ-QD-----KW-NGCFAVKWHIIKDIPNCH-FRHIILENNDNK-PVTNSRDTQEVK-----FEQAIGMLNIF
	Sphfalx0156s0007.1	SfYTH DC1B	TK-----YFIIKSLNHHN--LAK--SIEKGIWATQAMNEPVLNEA---FE-----TCER----- -----VVLVFS-----VNMSSHQ-----GYARM--ASPIGRRRA-- NIWS-EA-----NEGAN-----PW-GGTRFEWLCLYDLPFQK-TVHLKNPLNSFK-PVKISRDCQELT-----KEIGEALCALI
	Sphfalx0235s0015.1	SfYTH DC1A	CR-----YFIVKSNNREN--LEL--SVERGLWATHRNEAKLNEA---FD-----TCDH----- -----VILVFS-----VNETRHFQ-----GCARM--MSKIGGVIGG- GGWK-YA-----HGTAH-----Y-GRNFNLRWLKLCELSFNK-TRHLRNAYNENL-PVKISRDCQELE-----PSVGEQLASLL
<i>Zostera marina</i>	Zosma103g00140.1	ZmaYT HDF3C	AR-----FFVIKSYSEDN--VHK--SIKYGLWASTPNGNRKLDAA---YR-----EAKEK----- -----GGACP----VFLFFS-----VNSSAQFC-----GVAEM--- IGHVDFNKSVDYWQ-QD-----KW-SGNFPLKWHIVKDVPSM-FRHIILENNDKK-PVTNSRDTQEIK----- LKQGLEMLSIF
	Zosma105g00190.1	ZmaYT HDF2C	AR-----FFVIKSYSEDD--VHK--SIKYNMWSSTPSGNKRLDVA---YD-----GAKKI-SES----- -----KKMLCP----VFLFFS-----VNASGQFC-----GVSEM--- KGPVDFHKDM-DFWQ-QD-----KW-SGSFPVKWHIVKDVANSN-FRHIILENNENK-SVTNSRDTQ EVP----- YKAGVSMLNIF
	Zosma105g00770.1	ZmaYT HDF5C	AK-----FYIIKSYSEDD--IHK--SIKYNVWASTPNGNKKLDAG---YQ-----EAQEK-S----- -----GGLP----LFLFFS-----VNTSGQFV-----GVAEM--- VGNVDFNKTV-DYWQ-QD-----KW-NGCFPVKWHIVKDVPSNI-LKHITLENNDNK-PVTNSRDTQEVK----- FEQGIQLLKLF
	Zosma14g00600.1	ZmaYT HDF4C	SR-----YFIVKSCNREN--LEL--SVQQGAWATQRSNEAKLNGA---FE-----TTDN----- -----VILLFS-----INRTRHFQ-----GCAKM--TSKIGGYVGG- GNWK-YA-----HGTPH-----Y-GRNFSIKWLKLGELSFHK-TRHLRNPYNDNL-PVKISRDCQELD-----PFVGPQLATLL
	Zosma158g00160.1	ZmaYT HDC1A	AL-----FFIIKSYSEDD--IHK--SIKYNVWTSTSNGNKKLDNA---FH-----KIQEN-IGERG----- -----LSSSKCP----VFLFFS-----VNASGQFC-----GVAEM--- IGGVDFNKHWNFWQ-QD-----KW-NGSFPVKWHIIKDVPNSH-FRHIILANNSDK-PVTNSRDTQEIM-----FQQGSDMLSIF
	Zosma39g00650.1	ZmaYT HDF1A	AK-----FFMIKSYNEDD--VHK--SIKYNVWASTSSGNKKLND A---FR-----VVENI-FKE----- -----SSIKCP----IFLFFS-----VNTSGKFL-----GIAEM--- VGQVDFKKSM-DFWQ-EE-----RW-SGFFPLQWHIVKDV PNIN-FKNITLPNNDNR-LVYYSRDTQEIP-----LLQGLEMLKIF
	Zosma467g00180.1	ZmaYT HDF1C	AL-----FFIIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDAA---FQ-----SAQNQ-MKE----- -----KGCACP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDFNKNM-DFWQ-QD-----KW-NGYIPVKWHIIKDVPNPH-FRHIILENNDNK-PVTNSRDTQEV L----- FLRGSDMLKIF

	Zosma91g00280.1	ZmaYT HDF1B	AS-----FFVIKSYSEDD--IHK--SIKYNVWASTLNGNKILDSA---FQ-----TAEKMMKEE----- -----GNNHHP----IFLFFS-----VNASGQFC-----GVAEM--- IGRVDFNKNM-GFWQ-QD-----KW-NGFFPVKWHIIKDVPNPQ-LRHIKLENNDYK-PVTNSRDTQEVK----- LTQGSEMLNIF
<i>Bos taurus</i>	tr E1BAQ2 E1BAQ2	BtYTH DF1	GR-----VFIKSYSEDD--VHR--SIKYSLWCSTEHGNNRRLDSA---FR-----ALGSK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---KSPVDYGTSA- GVWS-QD-----KW-KGKFDVKWIFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKARQVLRII
	tr E1BH80 E1BH80	BtYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNNKRLDAA---YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---KSVVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	sp Q0VCZ3 YTHD2	BtYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHGNNKRLDAA---YR-----SMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---KSAVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_005208101	BtYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNVA---FR-----SARS----- -----VILIFS-----VRESGKFQ-----GFARL---SSESHHGGSP- IHWV-LP-----AGMSAK-----ML-GGVFKIDWICRREL PFTK-SAHLTNPWNEHK-PVKIGRDGQEIE-----LECGTQLCLLF
	NP_001179740	BtYTH DC2	IR-----YFIMKSSNLRN--LEI--SQQKGIWSTTPSNERKLNRA---FW-----ESSM----- -----VYLVFS-----VQGSGHFQ-----GFSRM---SSEIGREKSQ----- -----DWGSA-----GL-GGVFKVEWIRKESLPFQF-AHLLNPWNDNK-KVQISR DGQEIE-----PQVGEQLLQLW
<i>Dipodomys ordii</i>	tr A0A1S3GAX5 A0A1 S3GAX5	DoYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNNKRLDSA---FR-----AVASK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---KSAVDYGTSA- GVWS-QD-----KW-KGKFDVKWIFVKDVPNSQ-LRHIRLENNDHK-PVTNSRDTQ EVP-----LEKAKQVLKII
	tr A0A1S3EK84 A0A1S 3EK84	DoYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNNKRLDAA---YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---KSVVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	tr A0A1S3GQM8 A0A1 S3GQM8	DoYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHGNNKRLDAA---YR-----SMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---KSAVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_012864393	DoYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNLA---FR-----SARS----- -----VILIFS-----VRESGKFQ-----GFARL---SSESHHGGSP-IHWV- LP-----AGMSAK-----ML-GGVFKIDWICRREL PFTK-SAHLTNPWNEHK-PVKIGRDGQEIE-----LECGTQLCLLF
	XP_012871461	DoYTH DC2	VR-----YFIMKSSNLRN--LEI--SQQKGIWSTTPSNERKLNRA---FW-----ESSM----- -----VYLVFS-----VQGSGHFQ-----GFSRM---SSEIGREKSQ----- -----DWGSA-----GL-GGVFKVEWIRKESLPFQC-AHLLNPWNDNK-KVQISR DGQEIE-----PQVGEQLLQLW
<i>Callorhinc hus milii</i>	XP_007909300	CmYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNNKRLDSA---YR-----SMAGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---KSAVDYGTCA- GVWS-QD-----KW-KGKFDVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII

	XP_007894925	CmYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDAA---FR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---KSAVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_007893091	CmYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDSA---YR-----TMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---KSTVDYSTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_007902407	CmYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNTA---FR-----DARS----- -----VILIFS-----VRESGKFQ-----GFARL---SSESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIDWICRREL PFTK-TSHLVNLWNENK-PVKIGRDGQEIE-----PDCGTQLCLLF
	XP_007895610	CmYTH DC2	VR-----FFILKSSNLRN--LEI--SQQKGIWSTTPSNERKLNRA---FW-----ESSI----- -----VYLVFS-----VQGSGHFQ-----GFARM---ISEIGRERSQ----- -----EWGSA-----GL-GGVFRVEWIRKESLPFQY-AHLLNPWNDNK-KVQISR DGQELE-----PQVGEQLVQLW
<i>Xenopus tropicalis</i>	tr Q6P1V5 Q6P1V5	XtYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDSA---FR-----SMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---KSPVDYGTSA- GVWS-QD-----KW-KGKFDVKWLFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKLVLKII
	tr B1H2Z7 B1H2Z7	XtYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYTIWCSTEHG NKRLDAA---YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---KSVVDYNAYA- GVWS-QD-----KW-KGKFDVKWVFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_002934690	XtYTH DF2	GR-----VFIVKSYSEDD--IHR--SIKYNVWCSTEHG NKRLDAA---YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---RSAVDYNTCA- GVWS-QD-----KW-KGRFDVRWLFVKDVPNGQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKARQVLR II
	NP_001008121	XtYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA---FR-----SARS----- -----VILVFS-----VRESGKFQ-----GFARL---SSESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIDWICRREL PFTK-CVHLTNPWNEHK-PVKIGRDGQEIE-----PDCGTQLCLLF
	XP_004910524	XtYTH DC2	VR-----YFIMKSSNLRN--LEI--SQQKGIWSTTPSNERKLNQA---FW-----ESST----- -----VYLVFS-----VQGSGHFQ-----GFARM---TSEIGREKSQ----- -----DWGST-----SL-GGVFKVEWIRKESLPFQQ-AHLLNPWNDNK-KVQISR DGQELE-----TLVGEQLLLLW
<i>Ornithorhyn chus anatinus</i>	tr F7DG05 F7DG05	OaYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDSA---FR-----SMNSK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---KSPVDYGTSA- GVWS-QD-----KW-KGKFDVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	tr F6Q844 F6Q844	OaYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDAA---YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---KSVVDYNAYA- GVWS-QD-----KW-KGKFDVKWVFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_007662869	OaYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHG NKRLDAA---FR-----SLNAK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---CSAVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EAP-----LEKAKQVLKII

	XP_028929054	OaYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA--FR-----SARS----- -----VILIFS-----VRESGKFQ-----GFARL--SSESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIDWICRRELPTK-SAHLTNPWNEHK-PVKIGRDGQEIE-----LECGTQLCLLF
	XP_028912180	OaYTH DC2	VR-----YFIMKSSNSRN--LEI--SQQKGVWSTTPVNEGKLNQA--FF-----DSTT----- -----VFLVFS-----VQGS GHFQ-----GFSRM--ISEIGWEKSE----- -----DWGSS-----GL-GGMFKVDWIRKERLPFQQ-THLLNPWNENK-KVQISR DGQELE-----PQIGEQLLKLW
<i>Gallus gallus</i>	tr Q5F3J9 Q5F3J9	GgYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYTIWCSTEHG NKRLDSA--FR-----SMNSK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSPVDYGTSA- GVWS-QD-----KW-KGKFDVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQEVH-----LEKAKQVLKII
	tr Q5ZLM1 Q5ZLM1	GgYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDAA--YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--KSVVDYNAYA- GVWS-QD-----KW-KGKFDVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	tr A0A1D5P778 A0A1D5P778	GgYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCS TEHG NKRLDAA--YR-----SMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSAVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_025005417	GgYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA--FR-----SARS----- -----VILIFS-----VRESGKFQ-----GFARL--SSESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIDWICRRELPTK-SAHLTNPWNEHK-PVKIGRDGQEIE-----PECGTQLCLLF
	XP_004949328	GgYTH DC2	
<i>Mus musculus</i>	sp P59326 YTHD1	MmYT HDF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDGA--FR-----SMSSK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSPVDYGTSA- GVWS-QD-----KW-KGKFDVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	sp Q8BYK6 YTHD3	MmYT HDF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDAA--YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--KSVVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	sp Q91YT7 YTHD2	MmYT HDF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCS TEHG NKRLDAA--YR-----SMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSAVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LEKAKQVLKII
	sp E9Q5K9 YTHDC1	MmYT HDC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNLA--FR-----SARS----- -----VILIFS-----VRESGKFQ-----GFARL--SSESHHGGSP-IHWV- LP-----AGMSAK-----ML-GGVFKIDWICRRELPTK-SAHLTNPWNEHK-PVKIGRDGQEIE-----LECGTQLCLLF
	sp B2RR83 YTHDC2	MmYT HDC2	IR-----YFIMKSSNLRN--LEI--SQQKGIWSTTPSNERKLNRA--FW-----ESSM----- -----VYL VFS-----VQGS GHFQ-----GFSRM--SSEIGREKSQ----- -----DWGSA-----GL-GGVFKVEWIRKESLPFQF-AHLLNPWNDNK-KVQISR DGQELE-----PQVGEQLLQLW
<i>Macaca fascicularis</i>	tr A0A2K5U357 A0A2K5U357	MfYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDSA--FR-----CMSSK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSPVDYGTSA- GVWS-QD-----KW-KGKFDVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII

	tr A0A2K5VFW1 A0A2K5VFW1	MfYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDAA---YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--KSVVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	sp Q4R5D9 YTHD2	MfYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHGNKRLDAA---YR-----SMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSAVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_005555239	MfYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNLA--FR-----SARS----- -----VILIFS-----VRESGKFQ-----GFARL--SSESHHGGSP-IHWV- LP-----AGMSAK-----ML-GGVFKIDWICRREL PFTK-SAHLTNPWNEHK-PVKIGRDGQEIE-----LECGTQLCLLF
	EHH54445	MfYTH DC2	VR-----YFIMKSSNLRN--LEI--SQQKGIWSTTPSNERKLNRA--FW-----ESSM----- -----VYLVFS-----VQGSGHFQ-----GFSRM--SSEIGREKSQ----- -----DWGSA-----GL-GGVFKVEWIRKESLPFQF-AHLLNPWNDNK-KVQISRDGQELE-----PQVGEQLQLW
<i>Pongo abelii</i>	tr A0A2J8RB63 A0A2J8RB63	PaYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA--FR-----CMSSK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSPVDYGTSA- GVWS-QD-----KW-KGKFDVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	NP_001124613_YTHD F3	PaYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDAA---YR-----SLNGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--KSVVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_024105083	PaYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHGNKRLDAA---YR-----SMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--KSAVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_024101338	PaYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNLA--FR-----SARS----- -----VILIFS-----VRESGKFQ-----GFARL--SSESHHGGSP-IHWV- LP-----AGMSAK-----ML-GGVFKIDWICRREL PFTK-SAHLTNPWNEHK-PVKIGRDGQEIE-----LECGTQLCLLF
	sp Q5R746 YTHDC2	PaYTH DC2	VR-----YFIMKSSNLRN--LEI--SQQKGIWSTTPSNERKLNRA--FW-----ESSM----- -----VYLVFS-----VQGSGHFQ-----GFSRM--SSEIGREKSQ----- -----DWGSA-----GL-GGVFKVEWIRKESLPFQF-AHLLNPWNDNK-KVQISRDGQELE-----PQVGEQLQLW
<i>Poecilia formosa</i>	XP_007553615	PfYTH DF1a	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDAA---YR-----AMTAK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--RSPVDYGTSA- GVWA-QD-----KW-KGKFDVNWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_007557688	PfYTH DF1b	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA--FR-----AMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--RSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_007554569	PfYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA---YR-----SLCNK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--RSPVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFIKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKVI

	XP_007561175	PfYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCMSTEHGNKRLDAA---YR-----SLAGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--RSPVDYNTSA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LDKARQVLKII
	XP_007541776	PfYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA--FQ-----SARS----- -----VILVFS-----VRESGKFQ-----GFARL---SSESHHDGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIDWLCRRELPIK-TAHLFNPWNDNK-PVKIGRDGQEIQ-----PKVGAQLCALF
<i>Fundulus heteroclitus</i>	tr A0A146VPC4 A0A146VPC4	FhYTH DF1a	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDAA---YR-----AMNSK----- -----GP----VYLLFS-----VNGSGHFC-----GMAEM--RSPVDYGTSA- GVWA-QD-----KW-KGKFDVNWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	tr A0A146N3Z6 A0A146N3Z6	FhYTH DF1b	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA--FR-----AMNAK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--RSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	tr A0A146XRV8 A0A146XRV8	FhYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDAA---YR-----SLCNK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--RSPVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFIKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKVI
	XP_012720020	FhYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCMSTEHGNKRLDAA---YR-----SLAGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--RSPVDYNTSA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LDKARQVLKII
	XP_021169391	FhYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNSA--FQ-----AARS----- -----VILVFS-----VRESGKFQ-----GFARL---SSQSHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFRIDWLCRRELPIK-TAHLNPWNDHK-PVKIGRDGQEIA-----PKIGAQLCALF
	XP_012707270	FhYTH DC2	VR-----YFIMKSNSIRN--IEI--SQQKGIWSTTPSNETKLTQA--FL-----ANSF----- -----IILVFS-----VQGSGHFQ-----GYARM--TSMVRQDSCQ----- -----DWGFT-----GL-GGVFSVEWIIHKESLPPF-TQHILNPWNDNK-RVQVSRDGQELE-----PQAGSQLLSLW
<i>Nothobranchius furzeri</i>	XP_015824020	NfYTH DF1a	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA--YR-----AMNSK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--CSPVDYGTSA- GVWA-QD-----KW-KGKFDVNWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_015823582	NfYTH DF1b	GR-----IFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA--FR-----AMNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--RSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_015810707	NfYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA--YR-----SLGNK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--RSPVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKVI
	XP_015825357	NfYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCMSTEHGNKRLDAA---YR-----SLSGK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--RSPVDYNTSA- GVWS-QD-----KW-KGRFDVRWVFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LDKARQVLKII

	XP_015798763	NfYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA--FR-----SARS----- -----VILVFS-----VRESGKFQ-----GFARL--ASESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKINWLCRRELPIK-TAHLSPWNEFK-PVKIGRDGQEIQ-----PTVGAQLCALF
	XP_015829646	NfYTH DC2	VR-----YFVMKSSNARN--IDI--SQEKGIWSTTPSNETKLTKA--FM-----GHNL----- -----IILIFS-----VQGS GHFQ-----GYAHM--TSAASQESCQ----- -----DWGFV-----GL-GGGFSVEWVHKESLPFHL-TQHILNPWNDNK-KVQISR DGQELE-----PQTGSQ LVLLW
<i>Carassius auratus</i>	XP_026108152	CaYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDTA--FR-----GINGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--RSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_026057128	CaYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDGA--YR-----SLSAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--MSTVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_026141540	CaYTH DF2	GR-----IFIKSYSEDD--IHR--SIKYNIWCSTEHG NKRLDAA--YR-----SLANK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--RSPVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LDKARQVLKII
	XP_026110814	CaYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA--FR-----SARS----- -----VMLIFS-----VRESGKFQ-----GFARL--SSESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIDWICRREL PFTK-TAHLSPWNEHK-PVKIGRDGQEIE-----LDCGTQLCMLF
	XP_026099624	CaYTH DC2	IR-----YFIMKSSNMRN--IDL--SQQRGIWSTTPNNEHKLTRA--FI-----ESSA----- -----VFLIFS-----VQGS GHFQ-----GYARM--ASAVSGERCL----- -----DWGSS-----GL-GGVFGVEWIRKESLAFQL-TQQLLNPWNDNK-RVQISRDAQELE-----PQTGSQ LLQLW
<i>Salmo salar</i>	tr A0A1S3R6T3 A0A1S3R6T3	SsYTH DF1a	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDGA--FR-----GLNFK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--RSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	tr A0A1S3LGZ9 A0A1S3LGZ9	SsYTH DF1b	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDGA--FR-----SLNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--RSSVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQ VMKII
	tr A0A1S3LMH3 A0A1S3LMH3	SsYTH DF1c	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDSA--FR-----AINAK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--LSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	tr A0A1S3MGD6 A0A1S3MGD6	SsYTH DF1d	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDSA--FR-----AINAK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM--LSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_014015013	SsYTH DF3a	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHG NKRLDGA--YR-----SLGAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM--RSPVDYNAYA- GVWS-QD-----KW-KGKFEVKWAFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII

	XP_014036960	SsYTH DF3b	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDGA---YR-----SLGAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---RSPVDYNSYA- GVWS-QD-----KW-KGKFEVKWAFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_013979848	SsYTH DF2a	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHGNKRLDAA---YR-----SLGAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---RSPVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LDKARQVLKII
	XP_014065583	SsYTH DF2b	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHGNKRLDAA---YR-----SLGAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---RSPVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LDKARQVLKII
	XP_013994485	SsYTH DC1a	AR-----FFMIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA---FR-----SARS----- -----VILVFS-----VRESGKFQ-----GFARL---SSESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIDWICRREL PFTK-TAHLSNSWNEHK-PVKIGRDGQEME-----PEGIQLCVMF
	XP_014002672	SsYTH DC1b	TR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA---FR-----SARS----- -----VILVFS-----VRESGKFQ-----GFARL---SSESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIHWICRREL PFTK-TAHLNPWNEHK-PVKIGRDGQEIE-----PGCGMQLCMLF
	XP_013984132	SsYTH DC2	VR-----YFIMKSSNLRN--LDI--SQQKGIWSTTPSNELKLNRA---FL-----ESSL----- -----VFLVFS-----VQGS GHFQ-----GYARM---TSVIGQERCQ----- -----DWGST-----GL-GGVFSVEWTRKESLPFQC-THQLLPWNDNK-KVQISR DGQELE-----PQAGGQLLQLW
<i>Oncorhynchus mykiss</i>	XP_021422541	OmYT HDF1a	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDGA---FR-----SLNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---RSSVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVMKII
	CDQ89726	OmYT HDF1b	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDGA---FR-----SLNGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---RSSVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVMKII
	XP_021422899	OmYT HDF1c	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA---FR-----AINAK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---LSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_021472143	OmYT HDF1d	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA---FR-----AISAK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---LSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_021475945	OmYT HDF3a	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDGA---YR-----SLGAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---RSPVDYNAYA- GVWS-QD-----KW-KGKFEVKWAFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	XP_021418082	OmYT HDF3b	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDGA---YR-----SLGAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---RSPVDYNSYA- GVWS-QD-----KW-KGKFEVKWAFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII

	XP_021440084	OmYT HDF2a	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHGNKRLDAA---YR-----SLGAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---RSPVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LDKARQVLKII
	XP_021430447	OmYT HDF2b	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHGNKRLDAA---YR-----SLGAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---RSPVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LDKARQVLKII
	XP_021457161	OmYT HDC1a	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA---FR-----SARS----- -----VILVFS-----VRESGKFQ-----GFARL---SSESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIHWICRREL PFTK-TAHL SNPWNEHK-PVKIGRDGQEME-----PGCGMQLCVTF
	XP_021478131	OmYT HDC1b	SS-----LFAYTN-----SMPPVCSVLNMI-----CPP----- ---VCSVLN-----MVCPPVRA-----GFARL---SSESHHGGSP-IHWV-LP----- -----AGMNAK-----ML-GGVFKIDWICRREL PFTK-TAHL SNVNEHK-PVKIGRDGQEME-----PGCGMQLCVTF
	XP_021446650	OmYT HDC2	VR-----YFIMKSSNLRN--IDI--SQQKGIWSTTPSNELKLNRA---FL-----ESSL----- -----VFLVFS-----VQGSGHFQ-----GYARM---TSVIGQERCQ----- -----DWGST-----GL-GGVFSVEWTRKESLPFQC-THQLLN PWNDNK-KVQISR DGQELE-----PQAGGQLLQLW
<i>Danio rerio</i>	tr Q802Z0 Q802Z0	DrYTH DF1	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA---FR-----AINGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAEM---RSPVDYGTSA- GVWA-QD-----KW-KGKFDVDWLFVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	tr E7FAP0 E7FAP0	DrYTH DF3	GR-----VFIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDGA---YR-----SLSAK----- -----GP----LYLLFS-----VNGSGHFC-----GVAEM---KSTVDYNAYA- GVWS-QD-----KW-KGKFEVKWIFVKDVPNNQ-LRHIRLENNDNK-PVTNSRDTQ EVP-----LEKAKQVLKII
	NP_956544	DrYTH DF2	GR-----VFIKSYSEDD--IHR--SIKYNIWCSTEHGNKRLDAA---YR-----SLANK----- -----GP----PYLLFS-----VNGSGHFC-----GVAEM---RSPVDYNTCA- GVWS-QD-----KW-KGRFDVRWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----LDKARQVLKII
	NP_001007411	DrYTH DC1	AR-----FFLIKSNNHEN--VSL--AKAKGVWSTLPVNEKKLNAA---FR-----AARS----- -----VVLIFS-----VRESGKFQ-----GFARL---SSESHHGGSP- IHWV-LP-----AGMNAK-----ML-GGVFKIDWICRREL PFTK-TAHL ANPWNEHK-PVKIGRDGQEIE-----PECGTELCMLF
	XP_021332046	DrYTH DC2	VR-----YFIMKSSNPRN--IEL--SQQRSVWSTTPNNEQKLNRA---FQ-----NSSA----- -----VFLVFS-----VQGSGHFQ-----GYARM---TSAVSSERCL----- -----DFGSS-----GL-GGVFSVQWIHTESLAFQL-THKLLNPWNDNK-KVQISRDAQELE-----PHTGNQLLQLW
<i>Branchiostoma floridae</i>	XP_002601468	BfYTH DF	SR-----FFVIKSYSEDD--IHR--SIKYHIWCSTEHGNKRLDQA---FR-----ERKGK----- -----GP----IYLFFS-----VNGSGHFC-----GVAQM---MSEVDYNADT- GVWS-QE-----KW-KGKLEVKWIFVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----PEKGKQVLKIL
	XP_002609689	BfYTH DC2	NR-----YFILKCNNQRN--LDI--AMNQSIWATTPSNEKKLNKA---FK-----DCQN----- -----VYL VFS-----VQGSGHFQ-----GYARM---ASSISKDKVP----- -----EFSSA-----SL-GGAFQIEWIKRMSIPFQA-AHLLNPWNENK-KVQISR DGQEI E-----PQVGEQLLKAW

<i>Ciona intestinalis</i>	XP_002130883	CiYTH DF	AR-----FFVIKSYSEDD--IHR--SIKYNIWCSTDHGNKRLDAA---FR-----EQQGH----- -----GP----VILLYS-----VNGSGHFC-----GVAEM---LTQIDYSKRA- GVWA-QD-----KW-KGKFQVKWIYAKDVPNSQ-LRHIRLENNENK-PVTNSRDTQEVP-----AEKGRQVLKII
	XP_002127950	CiYTH DC1	AH-----FYLIKSNNHEN--VAL--AKARGVWSTPPSNEAKLNRS---FR-----EARN----- -----VILIYS-----VRESGAFQ-----GFARL---ATEAKHNLSP- IDWV-LP-----AGLSAK-----AL-GGVFKIDWLCKRELSFAK-TTDIYNTFNGNK-PVKIGRDGQEVE-----PNAGKVLCLF
<i>Strongyloce ntrotus purpuratus</i>	XP_011684124	SpuYT HDF	SR-----IFIKSYSEDD--IHR--SIKYGIWCSTEHGKNKRLDAA---MR-----ERQSK----- -----GP----VYLIYS-----VNGSGHFC-----GVAEM---MSEVDYTTNT- GVWA-QD-----KW-KGRFDVRWVYVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQEVL-----LDKAKQVMKII
	NW_022145609	SpuYT HDC1	AR-----YFLIKSNNHEN--IAL--AKAKGVWSTLPYNEQRLNAA---FR-----EARN----- -----VLLIFS-----VKESGKFQ-----GFARM---RCESRRDGQP- INWV-LP-----NGMNRS-----IL-GGVFKVDWITRNELPFTK-TTHLYNPWNSDK-PVKIGRDGQEIE-----SKCGESVCRLF
<i>Acanthaster planci</i>	XP_022109588	ApYTH DF	SR-----MFIKSYSEDD--IHR--SIKYGIWCSTEHGKNKRLDSA---FR-----ERANK----- -----GP----VYLLYS-----VNGSGHFC-----GVAEM---MSPVDYNVNT- GVWM-QD-----KW-KGRFDVRWVYVKDVPNSQ-LRHIRLENNDNK-PVTNSRDTQEVS-----LDKGRQVVKII
	XP_022105412	ApYTH DC1	AR-----YFLIKSNNHEN--VAL--AKARGVWSTLPNNEQMLNQA---FR-----ESRN----- -----VLLIFS-----VKESGKFQ-----GFARM---RSESRRDGPN- INWV-LP-----NGMSRS-----VL-GGVFKIDWITRQELAFSK-TGHLFNSWNDNK-PVKIGRDGQEVE-----TRCGEALCRLF
	XP_022100852	ApYTH DC2	VR-----FFIVKCNNAMN--IDL--SYSNGLWCVSPSTGQILSNA---FK-----TSQA----- -----IFLIFS-----VQGSGQFE-----GFGRM---TSDLQYKQTI--DW--- -----RDSCM-----RN-GAEFGVQWMKRASVSFDQ-TRAILNPWNDNL-RVHVSRDGQELE-----PSVGQNLLQLW
<i>Lingula anatina</i>	XP_013381791	LaYTH DF	SR-----FFIIKSYSEDD--IHR--SIKYSIWCSTDHGNKRLDTA---YR-----QQEGK----- -----GP----VYLLFS-----VNGSGHFC-----GVAQM---LSPIDYNRTS- GVWA-QD-----KW-KGQFEVKWIYVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQEVP-----LEKGKQVMKIL
	XP_013407344	LaYTH DC1	AT-----YFIIKSNNHEN--VAL--AKAKGVWSTPPQNEFRINKA---YR-----ESRN----- -----VILIFS-----VRESGKFQ-----GYARV---ASESDKDHPP- IRWV-LP-----PGLSAK-----AL-SGVFKLDWVTRRDLPFTK-TAHLNPWNDNK-PVKIGRDGQPVE-----PRCGEALCRMF
	XP_013406748	LaYTH DC2	CC-----YFVIKCNDKQ--LDA--SFNRGIWGPQIQTERKLVKA---FR-----EGKV----- -----VYLIFS-----VQGSGHFQ-----GFAKM---LAEPIKEKAP----- -----EFNYP-----GL-GGTLSIQWIKRANLPFKN-THHLTNPWNENR-RVQISRDGQEIE-----PSIGAQLIQLW
<i>Octopus bimaculoide s</i>	XP_014787225	ObYTH DF	AR-----FFIIKSYSEDD--IHR--SIKYNIWCSTEHGKNKRLDGA---YR-----EREGK----- -----GP----VYLFYS-----VNGSGHFC-----GMAQM---MSPVDYSTNS- GVWA-QD-----KW-KGQFEVKWIYVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQEVP-----PEKGKQVLKIL
	XP_014768358	ObYTH DC1	AR-----FFLIKSNNHEN--VAL--AKAKGVWSTPPQNEARLNQA---FR-----EADN----- -----VILVFS-----VKESGKFQ-----GFARL---SAESTRDHPP- IRWV-LP-----PGLSAR-----AL-SGVFKLDWINRRDLQFTK-TTHLHNPWNENK-YVKIGRDGQEIE-----PTVGEALCKLF

	XP_014778535	ObYTH DC2	TSNNQRN--LDT--SFSKSIWTTSPNNEKKLNKA---FQ-----DGKT----- VYLIFS-----IQGSGCFQ-----GYAKM--LSTFSKDRSA----- EYSMP-----GL-GATCTVDWLKRGNIPFHN-VQHLSNPWNDNK-RIQVSRDCQEIE-----PFVGETLLKQW
<i>Mizuhopecten yessoensis</i>	OWF49575	MyYTH DF	AR-----FFVIKSYSEDD--IHR--SIKYSIWCSTEHGNKRLDSA--YK-----ERESK----- -----GP----IYLFYS-----VNGSGHFC-----GMAQM--MSTLDYNRSP- GVWA-QD-----KW-KGQLDVKWIYVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----PEKGKQVLKLL
	XP_021370725	MyYTH DC1	AR-----YFLIKSNNHEN--VAL--AKAKGVWSTPPQNEAKLNQA--FR-----SCDN----- -----VILIFS-----VKESGKFQ-----GFARI--VEESTKDHPP- IRWV-LP-----PGLSAR-----AL-SGVFKLDWINRRELSFTK-TSHLHNSWNDNK-PVKIGRDGQEIE-----ARCGETVCKMF
	XP_021349616	MyYTH DC2	FFVMKCNNQSK--VDL--SMNKGVWATNKSNNKKLSV--FQ-----EGNT----- -----VYLVFS-----VQGSGHFQ-----GYAKM--KSEFVDKKVQ----- -----DSSYH-----GL-DYCCDVEWIKRANLSFQS-TLQLLNPWDDNR-KVQTSRDGQEIE-----PHVGETLIKLW
<i>Pomacea canaliculata</i>	XP_025090552	PcYTH DF	AR-----FFIIKSYSEDD--IHR--SIKYNIW CSTEHGNKRLDQA--FR-----EREGK----- -----GP----VYLIYS-----VNGSGHFC-----GIAQM--VSPVDYNKNS- GVWA-QD-----KW-KGQFEVKWVYVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----PEKGKQVLKIL
	XP_025111582	PcYTH DC1	AR-----FFLIKSNNHEN--VAL--AKAKGVWSTPPQNEARLNQA--FR-----ECDN----- -----VILVFS-----VKESGKFQ-----GFARL--AAESTKDHPP- IRWV-LP-----QGMNSR-----AL-SAVFKLDWVCRREL PFTK-TNHLHNPWDDK-PVKIGRDGQEID-----PRCGESLCKLF
	XP_025077319	PcYTH DC2	CR-----YFVMKCNNQRN--LDI--SQSKGIWATSPANQAKMNRA--FR-----DGKT----- -----VYLIFS-----IQGSGHFQ-----GYAKM--LTEIGRHKSP----- -----DFASP-----GL-TGTF AVEWIKRANIPFMS-THHLYNTWNENR-KVQVSRDGQELE-----PGVGEALVKLW
<i>Aplysia californica</i>	XP_005091424	AcaYT HDF	AR-----FFIIKSYSEDD--IHR--SIKYNIW CSTDHGNKRLDQA--FR-----EREGK----- -----GP----VYLIYS-----VNGSGHFC-----GIAQM--MSPVDYNKSA- GVWA-QD-----KW-KGQFTVKWVYVKDVPNST-LRHIRLENNENK-PVTNSRDTQ EVP-----PEKGKQVLRIM
	XP_005104889	AcaYT HDC1	AR-----FFLVKSNNHEN--VAL--AKAKGIWSTPPQNEARFNQA--FK-----ECEN----- -----VILIFS-----VKESGKFQ-----GFARL--AEESTKDHPP- VRWV-LP-----PGMTSR-----AL-SGVFKLDWVSRKDLEFIK-TNHLFNLWNDNK-RVKIGRDGQEIE-----PRCGENLCKLF
	XP_005089719	AcaYT HDC2	FFIMKAANHKL--LEI--SQTKNFWATSTGHEGKLSKA--YM-----SGRV----- -----VYLIFS-----VQGSGHFQ-----GFAKM--TSSIARTKSP----- -----DFPSP-----GL-SAIFSVEWLKSAHLPFQL-CHHLLNPWNENK-KVQESRDGQELE-----AHVGSQLLKLW
<i>Crassostrea gigas</i>	XP_011456337	CgYTH DF	AR-----FFIIKSYSEDD--IHR--SIKYSIWCSTDHGNKRLDQA--FK-----ERDNK----- -----GP----IYLFFS-----VNGSGHFC-----GMAQM--MSSLDYGKQA- GVWA-QD-----KW-RGQFEVKWIYVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQ EVP-----PEKGKSVLKIM
	XP_011447601	CgYTH DC1	AR-----YFLIKSNNHEN--VAL--AKAKGVWSTPPQNEIRLNNA--YK-----SCDN----- -----VILIFS-----VRESGKFQ-----GFARI--ADESTKDHPP- IRWV-LP-----PGLSAR-----AL-SGVFKLDWINRKEL AFTK-TQHLHNAWNDNK-PVKIGRDGQ EVE-----PRCGEALCKMF

	XP_011425711	CgYTH DC2	VK-----YFVVKPNNQKA--LDI--ALSNSVFATTPKSETKFNKA---IQ-----DGKE----- -----VYLIFS-----MIDSAQFQ-----GYAKV---TAQSSQDKCP----- -----DMSGD-----GL-GGTFKIEWMKKTPVPFRA-TQNICNSWNENK-KVQYSKDGQELE-----YSCGERLIQVL
<i>Biomphalar ia glabrata</i>	XP_013083543	BgYTH DF	AR-----FFIIKSYSEDD--IHR--SIKYNIW CSTDHGNKRLDQA--FR-----EREGK----- -----GP----VYLIYS-----VNGSGHFC-----GIAQM---MSPVDYNKSA- GVWA-QD-----KW-KGQFVVKWVYVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQEV-----PEKGKQVLRIV
	XP_013071333	BgYTH DC1	AR-----FFLVKSNNHEN--VAL--AKAKGVWSTPPQNEARFNQA--FR-----ECDN----- -----VILIFS-----VKESGKFQ-----GFARL---SEESTKDHP- IRWV-LP-----PGMTSR-----AL-SGVFRLDWITRRDLDFQK-TNHLFNAWNDNK-RVKIGRDGQEIE-----PRCGESLCKLF
	XP_013089748	BgYTH DC2	GR-----YFLMRCNNQKI--VDV--SETKGIWATSVSNETKLNRA--FN-----SGKP----- -----VYLIFS-----VPGNANFQ-----GYAKM---TSLISKNRSP----- -----DFPGS-----GL-TGTFSVSWVKRATIPFSN-TNFLNNPWNENR-RVHTGRDGQEIE-----PKIGLELIKW
<i>Drosophila hydei</i>	XP_023169635	DhYTH DF	AR-----FFVIKSYSEDD--IHR--SIKYEIWCSTDHGNKRLDDA--FK-----ERQKE----- -----GGN----VLLFFS-----VNKSGYFC-----GMAQM---MTSVDYNSTS- SVWS-QD-----KW-KGKFKVKWIYVKDVPNGE-LRHIRLENNDNK-SVTHSRDTQEIP-----NTKGIEVLQIL
	XP_023173281	DhYTH DC1	TR-----FFLIKSNNSDN--VQL--SKNKS VWATLPQNDANLSQA--FK-----EARN----- -----VLLIFS-----VNESGKFA-----GFARM---AAPSRRDIPQ- VAWV-LP-----PSISPK-----AL-GGVIELDWICKELSFNA-TLHLHNTWNEGK-PVKIGRDGQEIE-----PKIGAELCRLF
<i>Stomoxys calcitrans</i>	XP_013113692	ScaYTH DF	AR-----FFVIKSYSEDD--IHR--SIKYEIWCSTDHGNKRLDDA--FK-----ERHKD----- -----GGN----ILLFFS-----VNGSGHFC-----GMAQM---MTPVDYNSTS- SVWS-QD-----KW-KGKFKVKWIYVKDVPNNK-LRHITLENNENK-PVTNSRDTQEV-----NAKGIEVLQIL
	XP_013118835	ScaYTH DC1	TR-----FFLIKSNNADN--VTL--SKNKNVWATLPQNDANLTQA--FK-----ESRN----- -----VLLIFS-----VNESGKFA-----GFARM---SASSSRDIPQ- PDWV-LP-----SSISAK-----AL-GGVIEIDWICKELSFNC-TSHLYNSWNEGK-PVKIGRDGQEIE-----PKVGAELCRLF
<i>Lucilia cuprina</i>	XP_023298015	LcYTH DF	AR-----FFVIKSYSEVD--VHR--SIKYEIWCSTDHGNKRLDDA--FK-----ERSKD----- -----GGN----ILLFFS-----VNGSGHFC-----GMAQM---MTSVDYNSTS- SVWS-QD-----KW-RGKFKVKWIYVKDVPNKE-LRHITLENNENK-PVTNSRDTQEV-----HAKGIEVLQIL
	XP_023292455	LcYTH DC1	
<i>Habropoda laboriosa</i>	KOC65487	HIYTH DF	AR-----FFVIKSYSEDD--IHR--SIKYEIWCSTE HGNKRLDQA--YR-----EASRE----- -----GAP----LYLFFS-----VNGSGHFC-----GMAQM---VSPVDYKSNS- SVWS-QD-----KW-KGQFRVRWIYVKDVPNVQ-LRHIKLENNENK-PVTNSRDAQEV-----HAKGVTVLRIL
	XP_017789685	HIYTH DC1	AR-----FFIIKSNN AEN--VTL--SKAKGVWSTLPQNEANLNQA--YR-----ESRN----- -----VLLVFS-----VKESGKFA-----GFARL---STESRRDGAP- ISWV-LP-----PGLSAK-----AL-GGVFKVDWICKELPFTA-TLHL YNPWNDGK-QVKIGRDGQEIE-----PRVAEELCRLF
<i>Pieris rapae</i>	XP_022130163	PrYTH DF	TR-----FFVIKSYSEDD--IHR--SIKYEIWCSTE HGNKRLDSA--FR-----DRERE----- -----GGS----VYLFFS-----VNGSGHFC-----GMARM---VSAVDYNSNS- SVWS-QD-----KW-KGQFRVRWIYVKDVPNGQ-LRHIKLENNENK-PVTNSRDTQEV-----HAKGLQVLRIM

	XP_022113565	PrYTH DC1	TR-----FFLIKSNNNAEN--ITL--SKAKGVWSTLPQNEANLNQA---YR-----ESRN----- -----VLLIFS-----VKESGKFA-----GFARL--GSESRRDVPA- VSWV-LP-----PGLSAK-----VL-DGVFKVDWICKELPFSS-TLHLYNPWNEGK-PVKIGRDGQEIE-----PKVAEELCRLF
	XP_022129346	PrYTH DC2	SR-----YFIVKADDLHS--VEM--AQASGSYPFTQNTIKKLQKA--KQ-----EGSR----- -----VIMIFS-----CAGASKIT-----GAAAL-----GEA----- -----AS--PLDWISNNHIPFHM-LRHITNGLAGGA-RVTGARDGTELC-----STSGRGLLAAL
<i>Frankliniella occidentalis</i>	XP_026290617	FoYTH DF	AR-----FFVIKSYSEDD--IHR--SIKYEIWCSTEHGKRLDEA---YR-----EREAE----- -----GGI----VLLFFS-----VNGSGHFC-----GMAQM--ISPLDYNASS- SVWS-QD-----KW-KGQFGVRWIYVKDVPNVQ-LRHIRLENNENK-PVTNSRDTQEV-----FEKGRQVLRIM
	XP_026272952	FoYTH DC1	AR-----FFVIKSNNNAEN--VTL--SKAKGVWSTLPQNETKLNQA--FK-----ESRN----- -----VLLIFS-----VKESGRFA-----GFARL--NGESRHDVAP- ISWV-LP-----PGLSAK-----AL-GGVFKVDWVCRKELPFTA-TMHLYNPWNEGK-PVKIGRDGQEIE-----PRVAEELCRLF
	XP_026287428	FoYTH DC2	R-----YFIKAGNPRA--INA--SLRENVWAFTATTENKLITV---FR-----EGFA----- -----VMLIFS-----IHGSGNFQ-----GVASL---VSDVSDVRDSGKVHV- Q-----DMAGP-----NL-CSPLPIKWLYGDIPFHA-TRNIMNPYNENR-NIQTSRDGQEVE-----PHVASQLCKLW
<i>Hypoasmoco ma kahamanoa</i>	XP_026323400	HkYTH DF	AR-----FFVIKSYSEDD--IHR--SIKYEIWCSTEHGKRLDAA---FR-----ERERE----- -----GGM----VYLFFS-----VNGSGHFC-----GMARM--MSAVDYNSSNS- SVWS-QD-----KW-KGQFRVKWIYVKDVPNVQ-LRHIKLENNENK-PVTNSRDTQEV-----HAKGLQVLRIM
	XP_026316753	HkYTH DC1	TR-----FFLIKSNNNAEN--ITL--SKAKGVWSTLPQNEANLNQA---YR-----ESRN----- -----VLLIFS-----VKESGRFA-----GFARL--ASESRRDVPP-ISWV- LP-----PGLSAK-----VL-DGVFKVDWICKELPFNS-TLHLYNPWNEGK-PVKIGRDGQEIE-----PKVAEELCRLF
	XP_026333402	HkYTH DC2	VR-----YFVVKTDDIHS--VEAA-AQNNGTFAFSPNTAKKLQKV---KQ-----EGHR----- -----VVLFFS-----CAASSKFV-----GCASL-----LDP-- -----NG--TLDWAHAHQLPFHM-VRHISNSLAGGA-RIAGARDGTELC-----PASGRALYAAL
<i>Bombyx mori</i>	XP_004924605	BmYTH DF	TR-----FFVIKSYSEDD--IHR--SIKYEIWCSTEHGKRLDAA---YR-----EREKE----- -----GGM----VYLFFS-----VNGSGHFC-----GMARM--MSAVDYNSSNS- SVWS-QD-----KW-KGQFRVKWIYVKDVPNAQ-LRHIKLENNENK-PVTNSRDTQEV-----HPKGLQVLRIM
	XP_004931496	BmYTH DC1	TR-----FFLIKSNNNAEN--ITL--SKARGVWSTLPQNEANLNQA---YR-----ESRN----- -----VLLIFS-----VKESGKFA-----GFARL--GSESRRDVPP-ISWV- LP-----PGLSAK-----VL-DGVFKVDWICKELSFNS-TLHLYKPWNEGK-PVKIGRDGQEIE-----PKVAEELCRLF
	XP_012544932	BmYTH DC2	AK-----QFMIVDELHA--LEA--AYSTGSYVFAQNIAKRLQKA--KM-----EGHR----- -----VTVFFS-----CPSANKFV-----GCANL-----LDV-- -----SG--ALEWISTQHVPYHM-VRH---SCGGA-RGCVWREG-ELC-----GAGGGALLAHS
<i>Tribolium castaneum</i>	XP_015835734	TcYTH DF	AR-----FFVIKSYSEDD--IHR--SIKYEIWCSTEHGKRLDQA---YR-----EREAH----- -----GA----VYLFFS-----VNGSGHFC-----GMAQM--VSPVDYNANS- SVWS-QD-----KW-KGQFKVRWIYVKDVPNVQ-LRHIRLENNENK-PVTNSRDTQEV-----HAKGLQVLRIM

	XP_969804	TcYTH DC1	AR-----FFVIKSNNAEN--ITL--SKAKGVWSTLPQNEANLNKA---YR-----ESRN----- -----VLLIFS-----VKESGKFA-----GFARL--HSESRHDTVPA- ISWV-LP-----PGLSAK-----AL-GGVFKVDWICKELPFSN-TMHLYNPWNDGK-PVKIGRDGQEIE-----PRVAEELCRLF
	XP_008198757	TcYTH DC2	SV-----FLLIKVKQECs--VKI--AFDSNKWIFSPQTEKQVMAL--DNGGMN----- -----VYLVYT-----VQKLNAFY-----GIAKY--LT----- FDTT-----RH-KTSAAIEWIFKSCVPYKS-VSHLRNALNNNR-LIYDGLDGQEIE-----MGAALQLW
<i>Priapulus caudatus</i>	XP_014679284	PcaYTH DFa	SR-----FFVIKSYSEDD--IHR--SIKYSIWCSTEHGKNKRLDTA---FK-----ERDSK----- -----GS---VYLFFS-----VNGSGHFC-----GLAEM--LTPIDHDTKS- SVWA-QD-----KW-KGQFQVRWIYVKDVPNSA-LRHIRLENNENK-PVTNSRDTQEVp-----ADKGKQVLKIM
	XP_014672005	PcaYTH DFb	AR-----FFIIKSYSEDD--IHR--SIKYSIWCSTEHGNNRRLDQA---FK-----ERHGK----- -----GP---VYLLFS-----VNGSGHFC-----GVAQM--LSEVDYDTQS- GVWA-QS-----KW-KGQFQVKWIYVKDVPNSQ-LRHIRLENNENK-PVTNSRDTQEVp-----FEQGKQVLKII
	XP_014667135	PcaYTH DC1	SA-----YFLIKSNNHEN--ISL--AKAKGVWSTPPQNEAKLNKA---FK-----ECRN----- -----VILVYS-----VKESGKFQ-----GYARL--SSESRHDIAP- PQWV-LP-----PGMTSR-----AL-GGVFKIDWVNRKELAFSK-TLHLHNSWNENK-PVKIGRDGQEIE-----HNCGESLCRLF
<i>Clonorchis sinensis</i>	RJW65808	CsYTH DF	AR-----FFVIKSFSEDD--IHR--SIKYSVWCSTELGNKKLDSA---YV-----GANNQ----- -----YP----IYLFFS-----VNGSGHFC-----GMAEM--TSRVDYDTRV- RVWA-QD-----KW-QGAFSVRWIFVKDVPNTA-LRHIRIESNENK-PVTHSRDATELP-----LERGRQVMEVF
	RJW63992	CsYTH DC1	AR-----YFMIKSNNYEN--VEI--AKTRNVWSTTKGNETRLNKA---FF-----DCPN----- -----VFLIFS-----VRESGKFQ-----GFAQI--IASSDPRI-K-VNWV- LP-----PRMDIN-----LL-SNPFRIKWISKRDLPFSK-VNHLTNPWNENK-PVKIGRDGQEIE-----GVCGEALCRLl
<i>Opisthorchi s viverrini</i>	OON14740	OvYTH DF	AR-----FFVIKSFSEDD--IHR--SIKYSVWCSTELGNKKLDSA---YV-----GANNQ----- -----YP----IYLFFS-----VNGSGHFC-----GMAEM--TSRVDYDTRV- RVWA-QD-----KW-QGAFSVRWIFVKDVPNTA-LRHIRIESNENK-PVTHSRDATELP-----LERGRQVMEVF
	XP_009167386	OvYTH DC1	AR-----YFMIKSNNYEN--VEI--AKTRNVWSTTKGNETRLNKA---FF-----DCPN----- -----VFLIFS-----VRESGKFQ-----GFAQI--IASSDPRI-K-VNWV- LP-----PRMDIN-----LL-SNPFRIKWISKRDLPFSK-VNHLTNPWNENK-PVKIGRDGQEIE-----GVCGEALCRLl
<i>Schistosoma haematobiu m</i>	XP_012796317	ShYTH DF	AR-----FFVIKSFSEDD--IHR--SIKYSIWCSTELGNKKLDTA---FA-----EANHA----- -----YP----IYLFFS-----VNGSGHFC-----GMAEM--VSRVDYNARA- SVWA-QD-----KW-QGKFsvRWIFVKDVPNTA-LRHIRIETNDNK-PVTHSRDTTELP-----LERGKQVMEVL
	XP_012801596	ShYTH DC1	TK-----YFLIKSNNFEN--IEI--AKSRNVWATTKGNETRLNKA---FF-----DyNN----- -----VLLIFS-----VRESGRFQ-----GFARI--IASSDPRI-K-VDWV- LS-----SRMSTG-----LL-SNPFRIKWISKSDLPFTK-TGHLLNAWNEDK-PVKIGRDGQEIE-----PTCGEALCRCF
<i>Orbicella faveolata</i>	XP_020606490	OfYTH DF	AR-----FFIIKSYSEDD--IHR--SIKYSVWTSTEHGNNRRLNEA---FK-----EQQGA----- -----KAP----IYLLFS-----VNGSGHFC-----GIAMM--MSEVDLEIET- GIWS-QD-----KW-KGKFEVKWFYVKDVPNNA-LRHIRLENNDNK-PVTNSRDTQEVp-----PEKGKQVLKII

	XP_020617190	OfYTH DC1	AR-----YFVMKSNNHEN--VAL--SKAKGVWSTPKANEKKLNAT---FK-----RYKN----- -----VILIFS-----VKESGKFQ-----GFARL---ASEAKHGGQP- MPWV-LP-----PGMSAK-----AL-GGVFKLEWLNRRRELWFSK-CLHLRNPWNDNK-EVKICRDGQEVE-----PSVGEALCRLF
	XP_020627768	OfYTH DC2	AR-----YFIMKCNNQRN--LDI--SMAKGIWATTLANEKKLNRA---FK-----ETKL----- -----VILVFS-----VQGS GHFQ-----GYAQM---TSPIGKDKSP----- -----EFGSS-----SL-SGVFSVEWIKKASIPFQQ-AHHLVNPWNDHK-KVQISR DGQELE-----PKIGEDLCKLW
<i>Exaiptasia pallida</i>	XP_020892001	EpYTH DF	AR-----FFIIKSYSEDD--IHR--SIKYSVWTSTEHGNRRLNEA---FK-----EQSKS----- -----GP----IYLIFS-----VNGSGHFC-----GIAQM---MSDVDFDIET- GIWS-QD-----KW-KGKFDVKWFYVKDVPNNA-LRHIRLENNDNK-PVTNSRDTQEIP-----PDKARQVVKII
	XP_020896581	EpYTH DC1	AR-----YFVMKSNNNAEN--VLL--SKAKGVWSTPRTNEKKLSSA---FR-----RYKN----- -----VIVIFS-----VKESGKFQ-----GMARL---MGEATYGGPQ- IPWV-LP-----PGMSAK-----AL-GGVFPIKWLN RQDLWFSK-CTHLRNPWNDNK-EVKICRDGQEVE-----PTVGEQLCRLF
	KXJ22716	EpYTH DC2	AR-----YFIIKCNNQRN--LSI--SMAKGIWATTIANEKKLNRA---FR-----ECKK----- -----IVLIFS-----VQGS GHFQ-----GFAHM---ASPIGKDKSP----- -----EFGSS-----SL-GGVFKVDWIKKANIPFQE-AHHLVNPWNDHK-KVQISR DGQELE-----PTVGADLCKLW
<i>Stylophora pistillata</i>	XP_022806830	SpiYTH DF	AR-----FFIIKSYSEDD--IHR--SIKYSVWTSTEHGNRRLNDA---FK-----EQQSS----- -----KAP----IYLLFS-----VNGSGHFC-----GIAMM---TSEVDIEIET- GIWT-QD-----KW-KGKFDVKWFYVKDVPNNA-LRHIRLENNDNK-PVTNSRDTQ EVP-----PEKGKQVLKII
	PFX31771	SpiYTH DC2	AR-----YFIMKCNNQRN--LDI--SMAKGIWATTLANEKKLNKA---FK-----ESKH----- -----VMLVFS-----VQGS GHFQ-----GYAQM---TSPIGKDKSP----- -----EFGSS-----SL-SGVFSVEWMKKASIPFQQ-AHHLVNPWNDHK-KVQISR DGQELE-----PKIGEELCMLW
<i>Amphimedo n queenslandi ca</i>	XP_003386824	AqYTH DF	AR-----FFVIKSYAEDD--VHR--SIKYNVWCSTDHGNRRLDTA---FK-----EQKSK----- -----GGG----VYLLFS-----VNGSGHFC-----GVAQM--- MSEVELSTD T-GIWT-QD-----KW-KGRFDIRWIYVKDVPNNQ-LRHIRLENNENK-PVTNSRDTQ EVP-----VDKGKLVIKII
	XP_019850317	AqYTH DC1	TR-----YFVIKSNNYEN--VDI--AKSKNVWSTLPYNEKKLNKA---YR-----DCRN----- -----VLLIFS-----VKESGGFQ-----GFAKL---VSESRS DVPR- VHWV-LP-----PSMSAS-----QL-SHVFKLDWIIHKGTLAFNL-CQDLKNPW NENK-PVKIGR DGQEIE-----PSVGEKLCKLW
<i>Selaginella moellendorf fii</i>	XP_024531733	SmYTH DC1B	TR-----YFIIKSLNHQN--LSK--SVERGVWATPAVNEDILNEA---FQ-----TSER----- -----VVLVFS-----VNMSGYFQ-----GYAEM---TSRPGR RKD-- NLWN-DA-----NDGSS-----PW-GGVFSVDWLKLHDLPFQE-TSHLKNPLDDNK-PVKISKDCQELP-----REVGESLCALI
	XP_024516925	SmYTH DC1A	SR-----YFIVKSSNREN--LEL--SVRRGVWATHRNNEAKLNEA---LE-----SCEH----- -----VILIFS----- VNETRHFQVSSLSTFFPSLFHDPFVSLRNQHKLCCVFLRLCCSQGCARM---MSKAGGA AHGTAGWK-QS-----HGMGS-----Y- GRNFRLKWLKLCELSFHK-TRHLHNPYNENL-PVKISRDCQEVE-----PSVGQELAE LL
	XP_002961786	SmYTH DF1	AK-----FFIIKSYSEDD--VHK--SIKYG VWASTPNGNKRLDAA---YK-----EAAGE----F----- -----P----IFLFFS-----VNGSQFC-----GVAEM---SGPMDFLRSV- DFWQ-QD-----KW-TGRFSVKWHFIKDITNGH-FRHIILENNDNK-PVTNSRDTQ EVQ-----LDQGLEMLRIF

Phaseolus vulgaris	Phvul.002G152600	PvYTH DC1B	IK-----YFIIKSLNREN--IDL--SIKKGIWATQIMNERILEEA---FH-----NSGC----- -----VILIFS-----VNMSGSFQ-----GYAQM--MSSIGRGRD--NVWS- EG-----IGKSN-----PW-GRSFKVQWLCFNDLPFYK-TLHLKNPLNDYK-PVKISRDCQELS-----PDIGLALCELL
	Phvul.006G130200	PvYTH DC1A	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNESKLNEA---FD-----SVEN----- -----VILIFS-----VNRTRHFQ-----GCAKM--TSRIGGSVAG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPYNENL-PVKISRDCQELE-----PSIGEQLASLL
	Phvul.006G121600	PvYTH DF1C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLENA---YE-----DAKKI-AAE----- -----KSGVCP----IFLFFS-----VNASGQFC-----GVAEM--- IGTVDFNKNM-DFWQ-QD-----KW-SGSFPVKWHFIKDVPNPN-FRHIILENNENK-PVTNSRDTQEIV-----YLKGLEMLKIF
	Phvul.003G119300	PvYTH DF2C	AK-----YFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLQNA---YE-----DAERI-AAG----- -----KSGGCP----VFLFFS-----VNASGQFC-----GVAEM--- AGPVDFNKDM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNAN-FRHIILENNENK-PVTNSRDTQEIM----- YGKGLEMLKMF
	Phvul.004G132700	PvYTH DF3C	AL-----FFVIKSYNEED--IHK--SIKYNVWASTPNGNKRLDGA---YQ-----DAQKR-MED----- -----KGCKCP----VFLFFS----- -----VKWHIIKDVPNPQ-LRHIILENNNDHK-PVTN----MN-----FPQGVEILNIF
	Phvul.005G045600	PvYTH DF4C	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDGA---FQ-----DAQKR-MEE----- -----KGCKCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDFNKSMM-DFWQ-QD-----KW-NGYFPVKWHIIKDVPNPQ-LRHIILENNNDHK-PVTNSRDTQEVN-----FPQGVEILNIF
	Phvul.010G165400	PvYTH DF1B	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDAA---YR-----QAMEK----- -----QEACP----IFLFFS-----VNASAQFC-----GVAEM--- VGPVNFDKSV-DFWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVK----- LPQGIEMLTIF
	Phvul.006G218800	PvYTH DF5C	AK-----FYVIKSFNEDD--VHK--GVKYNVWTSTPNGNKKLNIA---FL-----DAEAK-LRQ----- -----TGTKCP----VFLFFS-----VNASRQFV-----GVAEM--- VGPVDFKKDM-SFWK-LD-----KY-NGFFSIKWHIIKDVPNNQ-FVHIILPSNENK-PVTFTTRDTQEIG-----LKQGLEMLNIF
	Phvul.002G247000	PvYTH DF1A	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTQNGNKKLDAA---YQ-----EAQQK-P----- -----GGCP----VFLFFS-----VNTSGQFV-----GLAEM--- VGSVDFNKSV-EYWQ-QD-----KW-NGCFPLKWHIVKDVPNNL-LRHITLDNNENK-PVTNSRDTQEVN----- LEPGLKLIKIF
	Phvul.004G080300	PvYTH DF2A	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTLNGNKKLDAA---YH-----EAKEK-P----- -----GDGP----VFLFFS-----VNTSGQFV-----GLAEM---VSPVDFGRTL- EYWQ-QD-----RW-TGCFSVKWHIIKDIPNSV-LRHITLENNENK-PVTNSRDTQEVN-----FEKGIQVLKIF
	Phvul.001G110200	PvYTH DF3A	AK-----FFVIKSYSEDD--IHK--SIKYSVWASTPNGNKKLDAA---YQ-----EAKEK-T----- -----GGCP----IFLLFS-----VNTSGQFV-----GLAEM---LGPVDFGKSV- DYWQ-QD-----RW-TGCFSVKWHVIKDIPNSV-MRHITLENNENK-PVTNSRDTQEVK-----FEKGVQIVKIF

<i>Solanum tuberosum</i>	XP_006352991	StYTH DC1Ba	IR-----YFVIKSLNHEN--IQL--SVNRGIWATQAMNEAILDEA---FH-----NSSK----- -----VILIFS-----VNMSGYFQ-----GYAQM--ISSVGLRRD--QVWS- QG-----NGGRN-----PW-GRSFEVNWLRLYDLPFQR-TLHLKNPWNQYK-PVKISRDCQELP-----PDIGEALCELL
	XP_006358382	StYTH DC1Bb	IR-----YFVIKSLNHEN--IQL--SVNRGIWATQAMNEAILDEA---FH-----NSSK----- -----VILIFS-----VNMSGYFQ-----GYAQM--ISSVGLRRD--QVWS- QG-----NGGRN-----PW-GRSFEVNWLRLYDLPFQR-TLHLQNPWNQYK-PVKISRDCQELP-----PDIGEALCELL
	XP_006343481	StYTH DC1Aa	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA---FD-----SVEN----- -----VILIFS-----VNRTRHFQ-----GCGKM--TSRIGGAANG- GNWK-HE-----HGTAH-----Y-GRNFSVKWLKLCELSFQK-THHLRNPYNENL-PVKISRDCQELE-----PSVGEQLASLL
	XP_006359103	StYTH DC1Ab	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA---FD-----SVEN----- -----VILVFS-----INRTRHFQ-----GLAKM--TSRIGGAAKG- GNWK-HE-----HGTAH-----Y-GRNFSLKWLKLCELSFQK-TRHLRNPYNENL-PVKISRDCQELE-----ISVGEQLASLL
	PGSC0003DMG400004607	StYTH DF1C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPNGNKKLNSA---YE-----DAQRI-TAG----- -----NPRGCP----IFLFFS-----VNASGQFC-----GVAEM--- TGPVDFYNDM-DFWQ-QD-----KW-SGSFPVKWHFIKDVPNPN-FRHIILENNENK-PVTNSRDTQEIR----- YKKGIEMLKVF
	XP_006338126	StYTH DF1B	AK-----FFVIKSFSEDN--VHK--SIKYSVWASTPQGNRKLDAA---YA-----EAKEM----- -----NANCP----VFLFFS-----VNASGQFC-----GVAEM--- VGPIDFENNA-EYWQ-QD-----RW-SGKFPVKWHVIKDVPNSQ-FRHILLEHNDNK-PVTHSRDSQQVK----- LPEGLEMLKIF
	PGSC0003DMG400024891	StYTH DF2C	AK-----FYIIKSYSEDD--IHK--CVKYDVWSSTPNGNKKLDTA---FV-----EAEAK-SSG----- -----TGSSCP----VFLFFS-----VNGSGQFL-----GVAEM--- VGQVDFNRNM-DFWQ-LD-----KW-SGFFPLKWHIVKDVPNTQ-FRHIILENNDNR-PVTYSRDTQEIG----- LKEGLEMLNIL
	PGSC0003DMG400024008	StYTH DF1A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDA---YQ-----EAQQN-S----- -----GGCP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDFNKNV-EYWQ-QD-----KW-VGCFPVKWHIVKDVPNSL-LKHITLENNENK-PVTNSRDTQEVK----- VEQGLQVLKIF
<i>Brassica rapa</i>	Brara.B02704	BrYTH DC1Ba	TR-----YFIIKSLNYDN--IQL--SVERGIWATQVMNEPILEGA---FH-----NSGR----- -----VVLIFS-----VNMSGFFQ-----GYAEM--LSPVGWRRD-- HIWS-QG-----GGKNN-----PW-GRSFKVKWLRLSELPFQK-TLHLKNSLNDYK-PVKISRDCQELP-----GDIGEALCELL
	RID51204	BrYTH DC1Bb	TR-----YFIIKSLNYDN--IQL--SVERGIWATQVMNEPILEGA---FH-----NSGR----- -----VVLIFS-----VNMSGFFQ-----GYAEM--LSPVGWRRD-- HIWS-QG-----GGKNN-----PW-GRSFKVKWLRLSELPFQK-TLHLKNPLNDYK-PVKISRDCQELP-----GDIGEALCELL
	Brara.H01885	BrYTH DC1Aa	NR-----YFVVKSNNSEN--FEL--SVQQGVWATQRSNEAKLNEA---FD-----TVNN----- -----VILIFS-----VNRTRHFQ-----GCAKM--TSRIGGYIGG- GNWK-NE-----HGTQQ-----Y-GGNFSVKWLKLCELSFHK-TRNLRNPYNENL-PVKISRDCQELE-----PSVGEELASLL

Brara.G00734	BrYTH DC1Ab	NR-----YFVVKSCNLEN--FEL--SVQRGVWATQRSNEAKLNEA---FD-----SVAN----- -----VILIFS-----VNRTRHFQ-----GCAKM--TSRIG---G- ENWK-HE-----HGTAQ-----F-GRNFSVKWLKLCELSFHK-TRNLRNPYNENL-PVK
Brara.F00450	BrYTH DF1C	AK-----FFVIKSYSEDD--VHK--SIKYSVWSSTLHGNKKLQSA---YE-----DAQRI-ATE----- -----KSCECP----IFLFFS-----VNASGLFC-----GMAEM--- TGPVSFEKDM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNSY-FRHIILHNNENK-PVTNSRDTQEIM-----MKQGLEVLKIF
Brara.G03650	BrYTH DF2C	AM-----FFVIKSYSEDD--IHK--SIKYSVWSSTLNGNKKLDNA---FQ-----ESQKK-VAE----- -----KGGTCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDYETSM-DFWQ-QD-----KW-TGYFPVKWHIIKDVPNPQ-LRHVILENNENK-PVTNSRDTQEVN----- LPQGNEVLNIF
XP_009124755	BrYTH DF3C	AM-----FFVIKSYSEDD--IHK--SIKYNVWSSTLNGNKKLDSA---YQ-----ESQKK-VAE----- -----NGGTCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDYEKSM-EFWQ-QD-----KW-TGYFPVKWHIIKDVPNPQ-LRHVILENNENK-PVTNSRDTQEVN----- LPQGNEVLNIF
Brara.B02362	BrYTH DF4C	AM-----FFVIKSYSEDD--IHK--SIKYNVWSSTLNGNKKLDSA---YQ-----ESQKK-VAE----- -----KGGTCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDYEKSM-EFWQ-QD-----KW-TGYFPVKWHIIKDVPNPQ-LRHVILENNENK-PVTNSRDTQEVN----- LPQGNEVLDIF
Brara.G02088	BrYTH DF5C	AM-----FFVIKSYSEDD--IHK--SIKYNVWSSTLNGNKKLDSA---YQ-----ESQKK-VAE----- -----KGGTCP----VFLFFS-----VNASGQFC-----GVAEM--- TGRVDYEKSM-EFWQ-QD-----KW-TGYFPVKWHIIKDVPNPQ-LRHVILENNENK-PVTNSRDTQEVN----- LPQGNEVLNIF
Brara.E02805	BrYTH DF1B	AK-----LFIKSYSEDN--VHK--SIKYNVWASTANGNKKLDAA---YR-----EAKEE----- -----KEPCP----VLLFS-----VNASSQFC-----GVAEM--IGPVDFEKS- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIILENNDNK-PVTNSRDTQEVK-----LEQGIEMLKIF
Brara.A03292	BrYTH DF2B	AK-----LFIKSYSEDN--VHK--SIKYNVWASTPNGNKKLDAA---YR-----EAKEE----- -----KEACP----VLLFS-----VNASSQFC-----GVAEM--IGPVDFEKS- DYWQ-QD-----KW-NGQFPVKWHIIKDVPNSQ-FRHIILENNDNK-PVTNSRDTQEVK-----LEQGIEMLKIF
Brara.H02025	BrYTH DF3B	AK-----FFVIKSYSEDN--VYK--SMKYCVWASTKNGNKKLDAA---YR-----EAKTK----- -----EVACP----VLLFS-----VNASAQFC-----GVAEM--- VGPVDFETSV-EYWQ-QD-----RW-SGHFPVKWVIVKDVPNSL-FRHIIEDNDNK-PVTNSRDTQEVG-----VEQGIEMINIF
Brara.B01161	BrYTH DF4B	AK-----FFIVKSFSEDN--VHR--SIKYNVWASTPHGNKKLDTA---YR-----DAEKM----- -----GGKCP----IFLFFS-----VNASGQFC-----GVSEM--- VGPVDFEKDA-GYWQ-QD-----RW-SGQFPVKWHILKDVPNNR-FSHILLQNNDNK-PVTHSRDSQEVK----- LRQGIEMLRIF
Brara.C01152	BrYTH DF5B	AR-----FFIVKSFSEDN--VHR--SIKYNVWASTPHGNKKLDTA---YR-----DAEKM----- -----GGKCP----IFLFFS-----VNASGQFC-----GVAEM---

			VGPVDFEKDA-AYWQ-QG-----KW-NGQFPVKWHIVKDVPNNR-FSHILLQNNSDK-PVTHSRDSQEVK----- LRQGIEMLRIF
Brara.F00638	BrYTH DF6C	AT-----FFVIKSYSEDD--VHK--SIKYSVWSSTVNGNKKLDAA---YR-----DAEAK-TLV----- -----DGKKRP----IFLFFS-----VNASRQFV-----GLAEM--- VGYVDMNKDL-DFWQ-VD-----KW-CGFFPVEWHVVKDVPNWE-LCHIVLHNNEGK-AVTHTRDTQEIK----- LKEGLQMLSIF	
Brara.C03469	BrYTH DF1A	AM-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLAAA---YQ-----EAQQK-P----- -----GGCP----IFLFFS-----VNASGQFV-----GLAEM--- TGPVDFDTNV-DCWQ-QD-----KW-TGSFPLKWHIVKDVPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLKIVKIF	
Brara.A03258	BrYTH DF2A	AM-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLAAA---YQ-----EAQQK-P----- -----GGCP----IFLFFS-----VNASGQFV-----GLAEM--- TGPVDFDTNV-EYWQ-QD-----KW-TGSFPLKWHIVKDVPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLKIVKIF	
Brara.E02771	BrYTH DF3A	AM-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLAAA---YQ-----EAQQK-P----- -----GGCP----IFLFFS-----VNASGQFV-----GLAEM--- TGPVDFNTNV-EYWQ-QD-----KW-TGSFPLKWHIVKDVPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLKIVKIF	
Brara.B02570	BrYTH DF4A	AK-----LFVIKSYSEDD--IHK--SIKYNVWSSTPNGNKKLDAA---YN-----EAKEK-SN----- -----GSCP----VFLMFS-----VNTSGQFV-----GLAEM--- VGPVDFNQTV-EYWQ-QD-----KW-IGCFPVKWHIVKDIPNSS-LRHITLENNENK-PVTNSRDTQEVT-----LEQCMKVIKIF	
Brara.G02587	BrYTH DF5A	AK-----LFVIKSYSEDD--VHK--SIKYNVWSSTPNGNKKLNAA---YN-----EAKDK----- -----SCP----VFLIFS-----VNTSGQFV-----GLAEM---VGPVDFNQTV- EYWQ-QD-----KW-VGCFPVKWHIVKDIPNSS-LRHITLENNENK-PVTNSRDTQEVK-----IEQGVKVIKIF	
Brara.A03796	BrYTH DF6A	AK-----FFVIKSYSEDD--VHN--SIKYGMWSSTPTGNKKLNAA---Y-----QES-S----- -----QDCP----VYLLFS-----VNASGQFV-----GVAEM---TGPVDFNKTM- EYWQ-QD-----KW-IGCFPVKWRIIKDVPNSL-LRHITLVNNENK-PVTNSRDTQEVK-----LEDGIKIIKIF	
Brara.E03479	BrYTH DF7A	EK-----FFVIKSYSEDD--VHN--SIKHGVWSSTPTGNKKLNAA---YY-----EAQES-C----- -----CP----VYLLFS-----VNASGQFV-----GVAEM---TGPVDFNKTV- EYWQ-QD-----KW-IGCFPVKWHIIKDVPNSF-LRHVTIANNENK-PVTNSRDTREVS-----VEDGTKIIKIF	
Boechera stricta	Bostr.25463s0115	BsYTH DC1B	TR-----YFIIKSLNYEN--IQV--SVEKGIWATQVMNEPILEGA---FH-----KSGR----- -----VILIFS-----VNMSGFFQ-----GYAEM---LSPVGWRRD--HIWS- QG-----GGKNN-----PW-GRSFRVKWLRRLSELPFQK-TLHLKNPLNDYK-PVKISRDCQELP-----EDIGEALCELL
	Bostr.15697s0342	BsYTH DC1A	NR-----YFVVKSCNREN--FEL--SVQQGVWATQRSNEAKLNEA---FD-----SVEN----- -----VILIFS-----VNRTRHFQ-----GCAKM---TSRIGGYIGG- GNWK-HE-----HGTAQ-----Y-GRNFSVKWLKLCELSFHK-TRNLRNPYNENL-PVKISRDCQELE-----PSIGEQLASLL
	Bostr.19424s0931	BsYTH DF1C	AK-----FFVIK--SEDD--VHK--SIKYGVWSSTLHGNKKLQSV---YE-----DAQRI-ATE----- -----KSCKCP----IFLFFS-----VNASGLIC-----GVAEM---

			TGPVYLDRDM-DFWQ-QD-----KW-SGSFPVKWYIIKDVPNSY-FRHIILHNNENK-PVTNSRDTQEIM----- LKQGLEVLKLF
Bostr.15654s0023	BsYTH DF2C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTLHGNNKKLQSA---YE-----DAQKI-ATK----- -----KSCECP----IFLFFS-----VNASGLFC-----GMAEM--- TGPVSFDKDM-DFWQ-QD-----KW-SGSFPVKWHIIKDVPNSY-FRHIILQNNENK-PVTNSRDTQEIM-----LKQGLEVLKIF	
Bostr.20129s0365	BsYTH DF3C	AI-----FFVIKSYSEDD--IHK--SIKYNVWSSTLNGNKKLDSA---YQ-----ESQKK-IAE----- -----KSVKCP----VFLFFS-----VNASGQFC-----GVAEM--- VGRVDYKKSM-EFWQ-QD-----KW-TGYFPVKWHIIKDVPNPQ-LRHIILENNENK-PVTNSRDTQEVN----- LPQGNEVLNIF	
Bostr.3640s0080	BsYTH DF1B	AR-----LFIKSYSEDN--VHK--SIKYNVWASTPNGNKKLDAA---YR-----EAKDE----- -----KEPCP----LFLFFS-----VNASSQFC-----GVAEM---VGPVDFEKS- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSQ-FRHIILENNDNK-PVTNSRDTQEVK-----LEQGIEMLKIF	
Bostr.15697s0116	BsYTH DF2B	TK-----FFVIKSYSEDN--VHK--SIKYCVWASTKNGNKKLDAA---YR-----EAKTK----- -----DVACP----VFLFFS-----VNASAQFC-----GVAEM--- VGPVDFNTSV-EYWQ-QD-----RW-SGHFPVRWLIVKDVPNSL-FRHIIENNDNK-PVTNSRDTQEVG-----LEQGIEMLNIF	
Bostr.26833s0433	BsYTH DF3B	AK-----FFIVKSFSEDN--VHR--SIKYNVWASTPHGNKKLDTA---YR-----DAEKM----- -----GGKCP----IFLFFS-----VNASGQFC-----GVSEM--- VGPVDFDKDA-GYWQ-QD-----RW-SGQFPVKWHIVKDVPNNR-FCHILLQNNNDNK-PVTHSRDSQEVK----- LRQGIEMLRIF	
Bostr.25494s0041	BsYTH DF4C	AK-----FFVIKSYSEDD--VHK--SIKYSVWSSTPNGNKKLDAA---FR-----DAETK-TLE----- -----DGKKRP----IFLFFS-----VNASRQFV-----GLAEM--- VGYVDFKKDL-DFWQ-QD-----KW-SGFFPVEWHVVKDIPNWE-LRHIILDNNEDK-PVTHTRDTHEIK----- LKEGLQMLSIF	
Bostr.3640s0139	BsYTH DF1A	AM-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLAAA---YQ-----EAQKQ-P----- -----GGCP----IFLFFS-----VNASGQFV-----GLAEM--- TGPVDFNTNV-EYWQ-QD-----KW-TGSFPLKWHIVKDVPNSL-LKHITLENNENK-PVTNSRDTQEVK----- LEQGLKIVKIF	
Bostr.26833s0133	BsYTH DF2A	AK-----FFVIKSYSEDD--IHK--SIKYNVWSSTPNGNKKLDAS---FN-----EAKQK-S----- -----DSCP----VFLFFS-----VNTSGQFV-----GLAEM---VGPVDFNKT- EYWQ-QD-----KW-IGCFPVKWHFVKDIPNSS-LRHITLENNENK-PVTNSRDTQEVK-----LEQGIKVVKIF	
Bostr.2570s0314	BsYTH DF3A	AK-----FFVIKSYSEDD--VHN--SIKYGVWSSTPTGNKKLNAA---YY-----EAKEN-S----- -----QECP----VYLLFS-----VNASGQFV-----GLAEM--- VGPVDFNKT- EYWQ-QD-----KW-IGCFPVKWHIIKDIPNSL-LRHITLANNENK-PVTNSRDTQEVN-----LEHGTKIIF	
<i>Linum usitatissimu m</i>	Lus10006706.g	LuYTH DC1Ba	TR-----YFIIKSLNHHN--LQL--SVDEGIWATQVMNEPILEEA---FN-----NSGK----- -----VILIFS-----VNMSGFFQ-----GYAQM---VSSIGLRHD--HIWS- QG-----SGKSG-----SW-GRSFKVKWLQLNDLPFQR-TLHLKNPLNEYK-PVKISRDCQELP-----EDIGETLCRLI

Lus10007048.g	LuYTH DC1Bb	TR-----YFIIKSLNHHN--LQL--SVDEGIWATQVMNEPILEEA--FN-----NSGK----- -----VILIFS-----VNMSGFFQ-----GYAQM--VSSIGLRHD--HIWS- QG-----SGKVG-----SW-GRSFKVKWLQLNDLPFQR-TLHLKNPLNEYK-PVKISRDCQELP-----EDIGEALCRLI
Lus10023254.g	LuYTH DC1A	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEAKLNEA--FD-----SAEN----- -----VILVFS-----VNRTRHFQ-----GCAKM--TSKIGATIGG- GNWK-YQ-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPYNENL-PVKISRDCQELE-----PSVGEQLASLL
Lus10017111.g	LuYTH DF1C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTLHGNNKKLQSA---YE-----DAQKI-AAE----- -----KVTSCP----VFLFFS-----VNASGQFC-----GVAEM--- IGPVDLKKDM-DFWQ-QD-----KW-SGSFPVKWHMIKDVQNTS-FRHIILENNEHK-PVTNSRDTQEVL----- LKQGLQMLKIF
Lus10018343.g	LuYTH DF2C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTLHGNNKKLQSA---YE-----DAQKI-AAE----- -----KATSCP----VFLFFS-----VNASGQFC-----GVAEM--- IGPVDLKKDM-DFWQ-QD-----KW-SGSFPVKWHMIKDVQNTS-FRHIILENNEHK-PVTNSRDTQEVL----- LKQGLQMLKIF
Lus10034792.g	LuYTH DF1B	AK-----FFIIKSYSEDN--VHK--SIKYGIWASTPNGNKKLDAA---YA-----DAKTK----- -----EDPCP----VFLIFS-----VNASAQFC-----GVAEM--TGPVNFEKSV- DYWQ-QD-----KW-SGQFPVKWHMIKDV PNSQ-FRHIVLENNDNK-PVTNSRDTQEVK-----LEQGIEMLSIF
Lus10033335.g	LuYTH DF2B	AK-----FFIIKSYSEDN--VHK--SIKYGIWASTPNGNKKLDAA---YA-----DAKTK----- -----EDPCP----VFLIFS-----VNASAQFC-----GVAEM--TGPVNFEKSV- DYWQ-QD-----KW-SGQFPVKWHMIKDV PNSQ-FRHIVLENNDNK-PVTNSRDTQEVK-----LEQGLEMLSIF
Lus10037028.g	LuYTH DF3B	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTQNGNKKLDAA---YS-----EAQEK----- -----QRAPP----VFLIFS-----VNASAQFC-----GVAEM--- VGPVDFEKS SV-NYWQ-QD-----KW-TGQFPVKWHIIKDV PNSQ-FRHIILENNDNK-PVTNSRDTQEVQ----- LDHGIEMLNIF
Lus10015778.g	LuYTH DF4B	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTQNGNKKLDAA---YS-----EAQET----- -----QRAPP----VFLIFS-----VNASAQFC-----GVAEM--- VGHVDFEKS SV-NYWQ-QD-----KW-TGQFPVKWHIIKDV PNSQ-FRHIILGNNDNK-PVTNSRDTQEVQ----- LDHGIEMLNIF
Lus10027582.g	LuYTH DF5B	AK-----FFIIKSFSEDN--VHK--SVKYGVWASTPHGNKKLDAA---YN-----QAKEI----- -----DPKCP----IFLIFS-----VNASGQFC-----GVAEM--LGPVDFGKDA- DYWQ-QD-----RW-SGQFPVRWHIVKDVPNPR-FRHILLENNENK-PVTHSRDCQEVK-----LKHGIEILKIF
Lus10037365.g	LuYTH DF3C	AK-----FYVIKSYNEDD--IHK--SIKYNVWASTPNGNRKLDEA---YR-----SAQEK-LSE----- -----SGVNSP----IFLFFS-----VNGSGQFV-----GIAEM--- VGQVDFNKDM-DFWQ-LN-----KW-NGFFPVKWHVVKDIPNNQ-LRHIILENENK-PVTFSRDTQEIG----- MKQGLEMLSIF
Lus10035790.g	LuYTH DF4C	AK-----FYVIKSYNEDD--IHK--SIKYNVWASTPNGNRKLDES---YR-----SAQEK-LSE----- -----TGVKSP----IFLFFS-----VNGSGQFV-----GIAEM---

			VGQVDFNKDM-DFWQ-LN-----KW-NGFFPVKWHIVKDIPNNQ-LRHIILENNENK-PVTFSRDTQEIG----- MKQGLEMLSIF
	Lus10037364.g	LuYTH DF5C	AK-----FYVIKSYSEDD--IHK--SIKYNVWSSTPNGNKKLDAA---FR-----DSEEK-SSE----- -----SGTKCP----VFLFFS-----VNGSGQFV-----GLAEM--- TGLVDFNKDM-DFWQ-VD-----KW-SGFFPLKWHIVEDIPNTQ-LRHIVLENNDNR-PVTFSRDTQEIG-----LKQGLEMLTIF
	Lus10002624.g	LuYTH DF1A	AK-----FFVIKSYSEDD--VHK--SIKYGVWTSTPNGNKKLDAA---YR-----EASAK-A----- -----ARCP----VLLFS-----VNTSGQFV-----GLAEM--- TGPVDFDKTV-EYWQ-QD-----KW-TGCFAVKWHIIKDVPNST-LRHITLENNENK-PVTNSRDTQEIH-----IEKGIEVLKIF
	Lus10020269.g	LuYTH DF2A	AK-----FFVIKSYSEDD--VHK--SIKYGVWTSTSNGNKKLDAA---YR-----ESSAK-A----- -----AQCP----VLLFS-----VNTSGQFV-----GLAEM--- VGPVDFDKTV-EYWQ-QD-----KW-TGCFAVKWHIIKDVPNST-LRHITLENNENK-PVTNSRDTQEVH-----IEKGIEVLKIF
<i>Salix purpurea</i>	SapurV1A.0260s0290	SpYTH DC1B	TR-----YFIIKSLNHHN--IQL--SIENGIWATQVRNEPILEEA---FR-----NSGR----- -----VILIYS-----VNMSGFFQ-----GYAQM--LSSVGWRHD--NLWS- EG-----SGKSN-----PW-GRSFKVKWLQLNDLPFQK-TLHLKNPLNDYK-PVKISRDCQELP-----EDIGEALCELI
	SapurV1A.0030s0120	SpYTH DC1A	SR-----YFIVKSCNREN--LEL--SVQQGVWATQRSNEIKLNEA---LD-----SSDN----- -----VILIFS-----VNRTRHFQ-----GCAKM--TSKIGASVGG- GNWK-YA-----HGTAH-----Y-GRNFSVKWLKLCELSFHK-TRHLRNPFNENL-PVKISRDCQELE-----PSIGEQLASLL
	SapurV1A.0114s0500	SpYTH DF1C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLHSA---YE-----DARKL-DLG----- -----RPRGCP----IFLFFS-----VNASGQFC-----GVAEM--- VGPVDFNRDM-DFWQ-QD-----KW-SGSFFVKWHIIKDIPNSS-FRHIILENNENK-PVTNSRDTQEIM----- YRQGLEMLKMF
	SapurV1A.0072s0540	SpYTH DF2C	AK-----FFVIKSYSEDD--VHK--SIKYNVWSSTPHGNKKLQTA---FE-----DAQKL-AAG----- -----RPRGCP----IFLFFS-----VNASGQFC-----GVAEM--- IGPVDLHRDM-DFWQ-QD-----KW-SGSFLVKWHIIKDIPNSS-FRHIILVNNEsk-PVTNSRDTQEIM-----YKQGLEMLKIF
	SapurV1A.0149s0560	SpYTH DF3C	AF-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKRLDSA---YQ-----DAQQK-IAE----- -----KGNSCP----VFLFFS-----VNASGQFC-----GVAEM--- IGRVDFNKTM-DFWQ-QD-----KW-NGCFPVKWHIIKDVPNPQ-LRHIILENNENK-PVTNSRDTQEVK-----LPQGIDILNIF
	SapurV1A.0164s0020	SpYTH DF4C	AF-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKRLDIA---YQ-----DAQQK-IAE----- -----KGNSCP----VFLFFS-----VNASGQFC-----GVAEM--- IGRVDFNKTM-DFWQ-QD-----KW-NGCFPVKWHIIKDVPNPQ-LRHIILENNENK-PVTNSRDTQEVK-----LPQGIDILNIF
	SapurV1A.0093s0340	SpYTH DF5C	AF-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDNA---YI-----DSQLK-IAE----- -----KGCSCP----VFLFFS-----VNASGQFC-----GVAEM--- IGRVDFNKRM-DFWQ-QD-----KW-NGCFPVKWHIIKDVPNLH-LRHIILENNENK-PVTNSRDTQEVK-----FPQGIEILNIF
	SapurV1A.2058s0020	SpYTH DF1B	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDTA---YS-----EAKDK----- -----QDPCP----VLLFS-----VNASAQFC-----GVAEM--- VGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSR-FRHIVLENNDNK-PVTNSRDTQEVK----- LKHGVEMLNIF

SapurV1A.1769s0060	SpYTH DF2B	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDTA---YS-----EAKDK----- -----QDPCP----VFLIFS-----VNASAQFC-----GVAEM--- VGPVDFDKSV-DYWQ-QD-----KW-SGQFPVKWHIIKDVPNSR-FRHIVLENNDNK-PVTNSRDTQEVK----- LKHGVEMLNIF
SapurV1A.1485s0090	SpYTH DF3B	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDTT---YR-----EAKEK----- -----QDPCP----VFLIFS-----VNASAQFC-----GVAEM--- TGPVDFDKSV-DYWQ-QD-----KW-NGQFPVKWHLIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVK----- LEQGIEMLSIF
SapurV1A.0703s0020	SpYTH DF4B	AK-----FFIIKSYSEDN--VHK--SIKYGVWASTPNGNRKLDTT---YR-----EAKEK----- -----QDPCP----VFLIFS-----VNASAQFC-----GVAEM--- TGPVDFDKSV-DYWQ-QD-----KW-NGQFPVKWHLIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVK----- LEQGIEMLSIF
SapurV1A.1271s0080	SpYTH DF5B	AK-----FFVIKSYSEDN--VHK--SIKYGVWASTPNGNKKLDAA---YR-----EAKEN----- -----HGTCQ----IFLIFS-----VNASAQFC-----GVAEM--- VGPVDFDKNV-DFWQ-QD-----KW-SGKFPVKWHIIKDVPNSQ-FRHIVLENNDNK-PVTNSRDTQEVE----- LEHGVEMLGIF
SapurV1A.0430s0170	SpYTH DF6B	AK-----FFIIKSFSEDN--VHK--SIKYSIWASTPHGNKKIEAA---YR-----EAKEK----- -----EGNCP----VFLIFS-----VNASGQFC-----GVAEM---VGPVDFEKDA- DYWQ-QD-----RW-NGQFPVQWHIIKDVPNSR-FRHMLLENNDNK-PVTHSRDSQEVK-----LEQGIEMLKIF
SapurV1A.0001s2340	SpYTH DF7B	AK-----FFIIKSFSEDN--VHK--SIKYNVWASTPHGNKKIDAA---YR-----EAKEK----- -----EGNCP----VFLIFS-----VNASGQFC-----GVAEM--- VGPVDFEKDA-EYWQ-QD-----RW-NGQFPVQWHIVKDVPNSR-FRHILLENNDNK-PATHSRDSQEVK----- LEQGIEMLKIF
SapurV1A.0470s0280	SpYTH DF6C	AK-----FFVIKSYNEDD--VHK--SIKYDVWASTPNGNKKLDAA---FH-----NAEUV-SSE----- -----TSTKCP----IFLIFS-----VNGSGQFV-----GLAEM--- VGQVDFNKDM-DFWQ-ID-----KW-NGFFPVKWHVIKDIPNGQ-LRHIVLENNDGH-SVTFSRDTQEIG----- LEKGLEMLNIF
SapurV1A.0081s0640	SpYTH DF1A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAEQK-S----- -----GCCP----VFLIFS-----VNTSGQFV-----GLAEM--- TGRVDFDKSV-EYWQ-QD-----KW-TGYFPVKWHIVKDVPNSF-LKHITLDNNENK-PVTNSRDTQEVK----- LEEGLKLIKIF
SapurV1A.0699s0200	SpYTH DF2A	AK-----FFIIKSYSEDD--VHK--CIKYHVVWASTPNGNKKLDAA---YQ-----EAEQK-S----- -----GGCP----VFLIFS-----VNTSGQFV-----GLAEM--- TGRVDFDKSV-EYWQ-QD-----KW-TGYFPVKWHFVKDVPNSL-LKHITLNNENK-PVTNSRDTQEVK----- LEHGLKVIKIF
SapurV1A.0308s0100	SpYTH DF3A	AK-----FFVIKSFSEDD--VHK--SIKYSVWTSTPNGNKKLDAA---YK-----QAKEN-Q----- -----SDCP----VFLIFS-----VNTSGQFV-----GLAEM--- VGPVDFNKTV-EYWQ-QD-----KW-TGCFPLKWHIIKDVPNGC-LRHITLNNENK-PVTNSRDTQEVI-----FEKGVQILKIF

	SapurV1A.0668s0150	SpYTH DF4A	AK-----FFVIKSFSEDD--VHK--SIKYCVWTSTANGNKKLDAA---YK-----QAKEN-PG----- -----GGCP----VFLIFS-----VNTSGQFV-----GLAEM--- TGHVDFNKTV-EYWQ-QD-----KW-TGCFPLKWHIIKDVPNGC-LRHITLENNENK-PVTNSRDTQEVM----- FEKGVQILKIF
	SapurV1A.2122s0020	SpYTH DF5A	AK-----FFVIKSFSEDD--VHK--SIKYCVWTSTANGNKKLDAA---YK-----QAKEN-PG----- -----GGCP----VFLIFS-----VNTSGQFV-----GLAEM--- TGHVDFNKTV-EYWQ-QD-----KW-TGCFPLKWHIIKDVPNGC-LRHITLENNENK-PVTNSRDTQEVM----- FEKGVQILKIF
<i>Brachypodi um stacei</i>	Brast07G208500	BstYTH DC1A	TR-----YFIVKSCNREN--LEI--SVQQGIWATQRSNEAKLNEA---FE-----SMEN----- -----VILIFS-----INRTRNFQ-----GCAKM---TSRIGGYIGG- GNWK-SA-----NGTAH-----Y-GRNFSLQWLKLCELSFQK-THHLRNPYNDNL-PVKISRDCQELE-----PFIGEQLASLL
	Brast02G160500	BstYTH DF1C	AK-----YFVIKSYSEDD--VHK--SIKYNVWSSTPNGNRRLDAA---YS-----EAQGR-NPW----- -----K---CP----IFLFFS-----VNTSGQFC-----GVAEM--- VGLVDFHKDM-DFWQ-QD-----KW-SGSFPVKWHLVKDVPNST-FRHIILENNENK-PVTNSRDTQEIP----- YKSGINMLALF
	Brast01G183400	BstYTH DF2C	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDNA---YK-----VAQER-MAG----- -----KGTKCP----VFLFFS-----VNASGQFC-----GVAEM--- VGPVDFNRNM-NFWQ-QD-----KW-NGFFPVKWHIIKDVPNPQ-FRHIILENNENK-PVTNSRDTQEVK----- FLQGAEMLNIF
	Brast08G195000	BstYTH DF3C	AK-----FFVIKSWGEAN--VHK--SVKYGVWSSSLQGNKKLDRA---FS-----DAQLI-AAS----- -----SSTKCP----VFLFFS-----VNQSNHFC-----GVAEM--- VGPVDFQKNM-DFWS-QD-----RY-VGSFPVRWHIIKNIPNFA-LQYIVLQNNENK-PVTFSRDTQEIP-----YGPGTSMLKIF
	Brast01G273700	BstYTH DF4C	AK-----FFVIKSIGEAD--IHK--SIKYGVWSSSSSGNSKLDGA---YR-----DADRI-ARR----- -----NSTKCP----VFLFFS-----VNGSGHFC-----GLAEM--- VGPVDFHKDM-DFWC-QD-----KW-SGSFPVRWHIIKDVPNYT-LQHILLQNNENK-PVTHSRDTQEIP-----YIPGISMLKIL
	Brast03G001600	BstYTH DF1B	AK-----FFVIKSYTEDH--VHR--SIKYNVWASTASGNRKLD SA---YR-----AAKEK----- -----EDHCP----IFLFFS-----VNGSGQFC-----GVAEM---IGPVDFDRSV- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNNL-LRHITLENNDNK-PVTNSRDTQEVK-----LEYGLQMLTIF
	Brast09G011900	BstYTH DF5C	AK-----FYMIKSYSEDD--IHK--GIKYNVWASTRNGNSKLDAA---FH-----EAQNL-MKE----- -----TGSKCP----VFLFFS-----VNTSGQFV-----GLAEM--- LGPVDFKKT M-EFWQ-QD-----KW-NGFFPVIWHIVKDIPNRL-FKHITLENNDNR-PVTFSRDTQEIH-----LPQGLELLKIF
	Brast04G276500	BstYTH DF6C	AK-----FYMIKSYSEDD--IHK--GIKYNVWASTPNGNSKLNAA---FH-----EAQNL-MEE----- -----KGSKCP----VFLFFS-----VNTSGQFV-----GLAEM--- LGPVDFNKT M-DFWQ-QD-----KW-NGFFPVIWHIVKDIPNRL-FKHITLENNDNR-PVTFSRDTQEIH-----LPQGLELLKNF
	Brast02G048000	BstYTH DF1A	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTTNGNKKLDAA---YQ-----EAQAK-S----- -----SSCP----IFLFFS-----VNTSGQFV-----GVAEM---TGPVDFECTL- EYWQ-QD-----KW-NGSFSVKWHIVKDVPNNI-LKHIILENNEGK-PVTNSRDTQDIN-----LEQGTQMLKIF

	Brast10G020600	BstYTH DF2A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDSG---YR-----EAQEK-S----- -----SECP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDFDKTV-DYWQ-QD-----KW-NGCFSIKWHIVKDIPNNI-LKHITLDNNDNK-PVTNSRDTQEVK----- LEQGLQMLKIF
	Brast02G336900	BstYTH DF3A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDTA---YQ-----AANDE-S----- -----SKSP----VFLFFS-----VNTSGQFV-----GLAEM--- VGPVDFNKTV-EYWQ-QD-----KW-TGCFPVKWHIVKDIPNNL-LKHIILEYNENK-PVTNSRDTQEVK----- LEQGLQVLKIF
<i>Panicum virgatum</i>	Pavir.Db00395	PviYTH DC1Aa	SR-----YFIVKSCNREN--LEI--SVQQGIWATQRSNEAKLNEA---FE-----STEN----- -----VILIFS-----INRTRHFQ-----GCAKM--TSRIGGYIGG-GNWK- SA-----HGTAH-----Y-GRNFSMQWLKLCESFQK-THHLRNPYNDNL-PVKISRDCQELE-----PFIGEQLASLL
	Pavir.Da00064	PviYTH DC1Ab	SR-----YFIVKSCNREN--LEI--SVQQGIWATQRSNEAKLNEA---FE-----STEN----- -----VILIFS-----INRTRHFQ-----GCAKM--TSRIGGYIGG-GNWK- SA-----HGTAH-----Y-GRNFSMQWLKLCESFQK-THHLRNPYNDNL-PVKVC
	Pavir.Ea02386	PviYTH DF1C	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDNA---YR-----LAQER-MAE----- -----KGTKCP----VFLFFS-----VNASGQFC-----GVAEM--- VGAVDFNRRNM-SFWQ-QD-----KW-NGFFSVKWHIIKDVPNPQ-FRHIILENNENK-PVTNSRDTQEVK----- FPQGTEMLNIF
	Pavir.Eb02750	PviYTH DF2C	AL-----FFVIKSYSEDD--IHK--SIKYNVWASTPNGNKRLDNA---YR-----LAQER-MAE----- -----KGTKCP----VFLFFS-----VNASGQFC-----GVAEM--- VGPVDFNRRNM-NFWQ-QD-----KW-NGFFSVKWHIIKDVPNPQ-FRHIILENNENK-PVTNSRDTQEVK----- FPQGTEMLNIF
	Pavir.J03441	PviYTH DF3C	AK-----FFVIKSYNESD--VHK--SIKYGVWSTSSVGNRKLDAA---FR-----EAQAI-AAS----- -----SSTLCP----VFLFFS-----VNESFNFC-----GVAEM--- VGPVDYQNDM-DFWC-KD-----KW-TGSFPVKWHIIKNIRNYT-FRSILLQNNYK-RVTWSRDTQEIH----- YTPGTTMLELF
	Pavir.Eb02265	PviYTH DF4C	AK-----FFVIKSIGEAD--VHK--SIKYGVWSSSSNGNSKLDSA---FR-----DADRI-SRR----- -----NSTKCP----VFLFFS-----VNGSGHFC-----GMAEM--- VGPVDFHKDM-DFWC-QD-----KW-TGCFPVRWHIVKDIPNYC-LQHITLQNNENK-PVTHSRDTQ EVP----- YIPGMSVLKIF
	Pavir.Ea01248	PviYTH DF5C	AK-----FFVIKSIGEAD--VHK--SIKYGVWSSSSNGNSKLDSA---FR-----DADRI-SRR----- -----NSTKCP----VFLFFS-----VNGSGHFC-----GVAEM--- VGPVNFHKDM-DFWC-QD-----KW-TGCFPVRWHIVKDIPNYC-LQHITLQNNENK-PVTHSRDTQEIP-----YIPGMSVLKIF
	Pavir.J39541	PviYTH DF1B	AR-----FFIIKSYSEDN--VHK--SVKYGVWASTTNGNKKLDSA---YC-----EAKEK----- -----EEHCP----IFLLFS-----VNASAQFC-----GVAEM---IGPVDFEKS V- DYWQ-QD-----KW-TGQFPVKWHIVKDVPNNL-FRHIILENNDNK-PVTNSRDTQEVK-----LEQGLEMLKIF

Pavir.Fa00200	PviYTH DF2B	AR-----FFIIKSYSEDN--VHK--SVKYGVWASTTNGNKKLDSA---YR-----EAKEK----- -----EEHCP----IFLLFS-----VNASAQFC-----GVAEM--IGPVDFEKS DYWQ-QD-----KW-TGQFPVKWHIVKDVPNNL-FRHIILENNENK-PVTNSRDTQEVK-----LEQGLEMLKIF
Pavir.Fa01762	PviYTH DF3B	AK-----FFVIKSYTEDH--VHR--SIKYSVWASTASGNRKLDASA---YR-----AAKEK----- -----EEHCP----IFLFFS-----VNGSGQFC-----GVAEM--IGPVDFDRSV- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNNL-LRHIILENNDNK-PVTNSRDTQEVK-----LEQGLQMLTIF
Pavir.Fb00853	PviYTH DF4B	AK-----FFVIKSYTEDH--VHR--SIKYSVWASTASGNRKLDASA---YR-----AAKEK----- -----EEHCP----IFLFFS-----VNGSGQFC-----GVAEM--IGPVDFDRSV- DYWQ-QD-----KW-SGQFPVKWHIIKDVPNNL-LRHIILENNDNK-PVTNSRDTQEVK-----LEQGLQMLTIF
Pavir.J38606	PviYTH DF5B	AK-----FFVIKSYTEDH--IHK--SIKYNVWASTATGNRKLNA---YR-----EAKDK----- -----EELMA----VV-----TGQFC-----GVAEM--IGPVDFDMSV- DYWQ-ND-----RW-SGQFPVKWHIVKDVPNNL-VRHIILGNNKDK-RVTNSRDTQEVK-----LEQGVQMLAIF
Pavir.J11462	PviYTH DF6B	AK-----FFVIKSYTEDH--VHK--SIKYNVWASTARGNRKLNA---YR-----EAKDK----- -----EEYCP----IFLFFS-----VNGSGQFC-----GVAEM--- IGPVDFDKSV-DYWQ-ND-----KW-SGQFPVKWHIVKDVPNNL-VRHIILENNEDK-RVTNSRDTQEVK----- LEQGVQMLAIF
Pavir.Ca00545	PviYTH DF6C	AK-----FFMIKSYSEDD--IHK--GIKYNVWASTANGNDKLDAA---YH-----EAQIL-MKE----- -----NGENCP----VFLFFS-----VNTSGQFV-----GLAEM--- LGPVDFKKTMDFWK-GD-----KW-NGFFPIWHIIKDIPNRL-FKHIILEHNDYR-PVTFSRDTQEIG-----LAQGMQMLKIF
Pavir.Ia04185	PviYTH DF1A	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTTNGNKKLDAA---YQ-----EAQSK-G----- -----SACP----IFLFFS-----VNTSGQFV-----GVAEM--TGAVDFEKT EYWQ-QD-----KW-NGSFSVKWHIVKDVPNNI-LKHIILENNENK-PVTNSRDTQEIH-----LEQGLQMLKIF
Pavir.Ib00367	PviYTH DF2A	AK-----FFVIKSYSEDD--IHK--SIKYNVWASTTNGNKKLDAA---YQ-----DSQSK-G----- -----SACP----IFLFFS-----VNTSGQFV-----GVAEM--TGAVDFEKT EYWQ-QD-----KW-NGSFSVKWHIVKDVPNNI-LKHIILENNENK-PVTNSRDTQEIH-----LEQGLQMLKIF
Pavir.Ca01254	PviYTH DF3A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAG---YR-----EAQEK-S----- -----SDCP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDLDKTV-EYWQ-QD-----KW-NGCFPLKWHIVKDVPNNI-LKHITLDNNDNK-PVTNSRDTQE
Pavir.J30385	PviYTH DF4A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAG---YR-----EAQEK-S----- -----SDCP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDLDKTV-EYWQ-QD-----KW-NGCFPLKWHIVKDVPNNI-LKHITLDNNDNK-PVTNSRDTQE
Pavir.Ia00570	PviYTH DF5A	AK-----FFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAG---YR-----EAQEK-S----- -----SDCP----VFLFFS-----VNTSGQFV-----GVAEM--- VGPVDFDKTV-EYWQ-QD-----KW-NGCFPLKWHIVKDVPNNI-LKHITLDNNDNK-PVTNSRDTQEVK----- LEQGLEMLKIF
Pavir.J01552	PviYTH DF6A	AK-----IFVIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAG---YR-----EAQEK-S----- -----SDCP----VFLFFS-----VNTSGQFV-----GVAEM---

			VGPVDFDKTV-EYWQ-QD-----KW-NGCFPLKWHIVKDVPNNI-LKHITLDNNDNK-PVTNSRDTQEVK----- LEQGLEMLKIF
	Pavir.Ba03744	PviYTH DF7A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAKEK-S----- -----SETP----VFLLFS-----VNASGQFV-----GLAEM--- VGRVDFNKTIV-EHWQ-QD-----KW-TGCFPVKWHIVKDVPNSL-LKHIILENNENK-PVTNSRDTHEVK----- LEQGLQVLKIF
	Pavir.J38005	PviYTH DF8A	AK-----FFIIKSYSEDD--VHK--SIKYNVWASTPNGNKKLDAA---YQ-----EAKEK-S----- -----CESP----VFLLFS-----VNASGQFV-----GLAKM--- VGRVDFNKTIV-EHWQ-QD-----KW-TGCFPVKWHIVKDVPNSL-LKHIILENNENK-PVTNSRDTHEVK----- LEQGLQVLKIF
<i>Micromona s pusilla</i>	MicpuC2.fgenesh1_pg. C_scaffold_8000034	MpYTH	VR-----FFVIKSFAEED--VRK--SVKHGCWTSTSQGNARLDAA---WRGEDVFTFEPHGD-----DEN-GDDERERE----- REGEGETAAAAAAAAAADSSSGSGSGSGSDPASDAEPA-SDSDEPSVRSVDTQTPGPPLLDDATPATAESATKTTIAPCSRPGSSGAPPSKPRVILFFS----- -----VNSSGHFC-----GVAEM---TSPVD-----DDAVDATLLP-----PAAA----- ASW-PGRFAVKWHIVKDVPNTA-LRHIRVCAGDKK-PVPNSRDAQEIE-----PAQGALVLNIF
<i>Micromona s commoda</i>	EuGene.1100010578	McYTH	VR-----FFVMKSHGEDD--VHR--SLRYGWWSSTQAGNARLYAA---FRGLDAGEGESLGDLPKTLDESCGMDDLDRAFIVNAVKEDGDETEVLAP----- ---DLSDISRDSEESDSPSPAGPL-----EASTADAAAADRAT----SKDRAETP---RVVLFFS----- VNCSGHFC-----GVAEM---IGPVE---RI-DPTAPRDAHLRSGGGGGGGGGGGGGGGGGPRRFPAASMLTNGFALA- DGRFKVRWHWVKDVPNTV-LRHIRLVAGNEK-PVTNSRDAQEVE-----PGQGAMVLSVF

*All accession numbers relate to the Uniprot, NCBI, and Phytozome databases

** In cases when a name was already attributed to a protein, this name was kept with the new name, refering to the species of origin and to the phylogenetic classification of the protein, added in parenthesis

Supplementary Table S4 the relative expression level of 77 organismal-development-related genes used for heatmap analysis.

gene_id	gene symble	Log2FC		
		osythdf1a	osythdf2a	osythdf3a
LOC_Os02g13310		-9.5619	-1.0855	-4.1578
LOC_Os03g51710	<i>OSH3</i>	-8.9869	-1.3526	-7.0396
LOC_Os01g46870		-8.9168	-1.5943	-5.3881
LOC_Os04g45330	<i>OsYABBY5; OsYAB3; TOB1</i>	-8.615	-1.2943	-4.3509
LOC_Os12g36890	<i>OsCSLD4; NRL1; NDI; sle1; DNL1; OsCD1</i>	-8.0836	-1.1736	-5.0574
LOC_Os09g34930		-7.8626	-1.2858	-3.9654
LOC_Os03g14080	<i>OsAUX2</i>	-7.7898	-1.3768	-4.9957
LOC_Os07g03250	<i>Crl-5</i>	-7.7566	-1.3525	-4.6714
LOC_Os01g33040	<i>DBS1; OsNACK</i>	-7.5488	-1.2459	-3.6439
LOC_Os04g48510	<i>OsGRF12</i>	-7.4847	-1.2526	-4.1748
LOC_Os04g51000	<i>RFL; APO2</i>	-7.3429	-2.1784	-6.2554
LOC_Os10g05690	<i>OsAUX4</i>	-7.318	-1.1632	-3.9296
LOC_Os04g56850	<i>OsARF11; OsMP; OsARF5</i>	-7.3041	-1.0846	-4.1656
LOC_Os01g67100	<i>FSM; CAF-1</i>	-7.1895	-1.0183	-3.4899
LOC_Os10g26340	<i>PLA1</i>	-7.0451	-1.0395	-7.8152
LOC_Os08g40170	<i>CDKB2;1; cdc2Os3</i>	-6.9668	-1.1371	-3.5603
LOC_Os08g41360		-6.9401	-3.3398	-2.7567
LOC_Os01g62605		-6.7356	-1.1936	-4.7526
LOC_Os04g28620		-6.6957	-5.648	-7.9919
LOC_Os11g04190	<i>OsPIN1c; OsPIN1b</i>	-6.5802	-1.191	-3.375
LOC_Os03g10040		-6.2745	-1.7185	-4.2933
LOC_Os02g03120		-6.2414	-2.663	-2.3359
LOC_Os03g56050		-6.1617	-1.3587	-5.2617
LOC_Os06g10310	<i>OsGRF2</i>	-6.1049	-1.2917	-5.0023
LOC_Os12g10670		-6.0781	-1.3261	-3.8577
LOC_Os05g27980		-6.0617	-1.3375	-3.7453
LOC_Os02g28850		-5.9803	-1.1244	-3.4852
LOC_Os03g41600		-5.8846	-2.1204	-1.9548
LOC_Os03g11600	<i>DL; OsYABBY</i>	-5.8114	-1.7158	-3.8138
LOC_Os04g38570	<i>OsABCB14</i>	-5.7616	-1.4281	-3.2766
LOC_Os12g38400	<i>OsMYB91</i>	-5.7002	-1.2739	-4.2461

LOC_Os03g49880	<i>OsTB1; FCI; SCM3</i>	-5.5398	-1.7117	-6.3093
LOC_Os04g02640		-5.3723	-1.5771	-6.279
LOC_Os04g33560		-5.3588	-1.0619	-3.1647
LOC_Os08g42600	<i>OsRBR1; PIS1</i>	-5.3002	-1.0986	-3.0869
LOC_Os04g28260		-5.2725	-1.0827	-2.8998
LOC_Os06g36680		-5.2476	-1.8521	-3.2175
LOC_Os12g03130		-4.9757	-1.1114	-3.9286
LOC_Os01g15480		-4.6478	-1.1559	-3.0775
LOC_Os04g13140		-4.363	-1.2208	-2.5563
LOC_Os01g07480	<i>OsCrll4</i>	-4.0908	-1.1631	-1.6119
LOC_Os04g43300		-4.0777	-1.0175	-2.418
LOC_Os07g49140		-3.9888	1.3961	-3.0252
LOC_Os09g36160		-3.8437	-1.1961	-4.6417
LOC_Os09g25100		-3.741	-1.2983	-5.5075
LOC_Os01g55560		-3.7138	-1.5581	-3.2888
LOC_Os07g07920		-3.5831	1.4895	-2.6613
LOC_Os04g46580	OSSPL7	-3.4951	-1.635	-3.2
LOC_Os10g25620		-3.3118	-4.0817	-2.3927
LOC_Os02g46970		-3.2992	-1.1604	-4.2757
LOC_Os06g49830		-3.1737	-1.2646	-5.8352
LOC_Os08g31030		-2.9736	1.087	-1.2371
LOC_Os07g17210		-2.7093	2.2462	-1.8848
LOC_Os03g02800	<i>RIM1</i>	-2.645	1.0142	-2.1354
LOC_Os06g15020		-2.2586	1.6406	1.5527
LOC_Os01g12440		-2.2399	-1.8037	-2.0165
LOC_Os01g34560		-2.2126	1.3549	-1.1105
LOC_Os01g66100	<i>sd1; OsGA20ox2; qSD1-2; qPAI</i>	-2.1301	-1.0491	-1.9423
LOC_Os03g58600	<i>OsMEL1</i>	-2.1155	1.2839	-2.1407
LOC_Os02g58490	<i>OsAGO1c</i>	-1.8356	-1.2321	-1.1439
LOC_Os04g47080		-1.7186	1.081	2.543
LOC_Os05g44090		-1.5961	-1.6446	-2.3388
LOC_Os01g66590	<i>OsCrll3; OsIG1; OsAS2</i>	-1.5556	-1.0164	-2.4638
LOC_Os06g11330		-1.2077	-1.1194	-1.0372
LOC_Os11g35710		-1.0678	3.5252	-1.6476
LOC_Os01g18360		1.1451	1.7689	2.0873
LOC_Os01g25010		1.3611	1.1524	1.8913
LOC_Os04g40140		1.4495	2.645	1.5658

LOC_Os06g19540		1.5108	1.6758	1.6269
LOC_Os01g58860	<i>OsPIN9</i>	1.5857	2.1314	1.4208
LOC_Os02g12350		1.6883	2.0187	2.0254
LOC_Os03g59600		1.8122	2.3614	1.9622
LOC_Os01g58194		1.8911	1.3941	1.3227
LOC_Os08g29660		2.2899	1.0293	1.0592
LOC_Os01g50100		2.8393	1.6911	1.4538
LOC_Os01g64470		2.9377	1.9662	1.4414
LOC_Os04g12960		2.9503	3.1572	1.1924

Supplementary Table S5 Primers used in this study

Primer used for qPCR analysis	
RT-DF3C-2F	GTGAAGCCACAGGGTAGTAATG
RT-DF3C-2R	GTCTGTTCTCTTTCCCGTCATC
RT-DF1C-1F	TCCTCGAAGACTGCAAACAAGGC
RT-DF1C-1R	ATGCACCGCAAAC TTGCTAGAC
RT-DF1A-1F	AGCCGTGACACACAAGAGGTAAAC
RT-DF1A-1R	TCCTGCATCAACTTCTGACGGTTC
RT-DF2C-2F	GAAGCGAAAGGCAATGGTAATG
RT-DF2C-2R	GGCTCACCTGCCACATTTA
RT-DF2A-1F	AAGCTGATGCAGGAGAAGAGAGC
RT-DF2A-1R	CATTGTCAAGAGAGCCCTGTCC
RT-DF5C-2F	GAGGCACATCCACAGCTAAA
RT-DF5C-2R	GCCCATCTTGAACCTCTGATTA
RT-DF3B-1F	CATTGGCTTCTGGAATGCATCAGG
RT-DF3B-1R	TTGCTGCCGTGCCTTGTATGAC
RT-DF4C-2F	TCAGCAAGGTTCCATCTCTTC
RT-DF4C-2R	GGTCAGCCTTTGTGCATTTC
RT-DC1A-1F	GGTGAGCAATTGGCTTCACTGC
RT-DC1A-1R	GCTGCAATTAGTATAGCCGTCAGC
RT-DF3A-1F	AGACGTCGTTACTGGATGACTTTG
RT-DF3A-1R	GCAGCTTCTCATCAACGACCTTC
RT-DF2B-2F	AGAAAGCCTTGCAGGAGAATAG
RT-DF2B-2R	GTCTGAGATGTGGGCCATAAG
RT-DF1B-2F	CTGATAACCCTGAAGAGCAGAC
RT-DF1B-2R	GCTTGTCCCTTCACTTGGTAGAT
RT-DF3C-1F	TCTAGTGGAACAGCAAAC TGGAC
RT-DF3C-1R	AGAAGAGCCCACTACCATT CACG
RT-OE-2-F	CTGAGATGGTCGGTCCGGTAGAT
RT-OE-2-R	TCCCTGCTGTTTGT CACAGGTTT
RT-OE-3-F	GGCAGTTTGT TGGTGTTGCTGAA
RT-OE-3-R	CGGCTATTTGTCACTGGCTTG TTC
RT-DF2C-1F	AGGAAGAGCTCTGGGAAAGTGTC
RT-DF2C-1R	AACTGCCCCGCTAGCATTAACAG
RT-OE-7-F	GATGATTGGACCTGTGGACTTCG
RT-OE-7-R	AGGCTGTTCGGGACATCCTTGAT

RT-OE-8-F	CAGTGGGCAGTTTGTAGGATTAG
RT-OE-8-R	AACCGATTTGGAATGTCCTTTATA
Primer used for vector construction	
DF3C-CF	AGATGATCCGTGGCA TTATCCGTATGGTTATACGTTTTAGAGCTATGC
DF3C-CR	GCATAGCTCTAAAACGAAAATAGATGTCTTGGCCTGAGCCTCAGCGCAGCAGCTTA
DF1C-CF	AGATGATCCGTGGCA ATATCCATTTTCATACCCGTTTTAGAGCTATGC
DF1C-CR	GCATAGCTCTAAAACGATTTTGTTACGAAGTATCTGAGCCTCAGCGCAGCAGCTTA
DF1A-CF	AGATGATCCGTGGCACGTCGCGCCGCCTCAGGTCCGTTTTAGAGCTATGC
DF1A-CR	TTCTAGCTCTAAAACGGACCTGAGGCGGCGCAGCGCTGAGCCTCAGCGCAGCAGCTTA
DF2C-CF	AGATGATCCGTGGCA ATCACACTAATTTTGTGGGTTTTAGAGCTATGC
DF2C-CR	GCATAGCTCTAAAAC TATTGTATTGGTCAGGATCTGAGCCTCAGCGCAGCAGCTTA
DF2A-CF	AGATGATCCGTGGCAGTCGATCACTCCCCTGCTCCGTTTTAGAGCTATGC
DF2A-CR	TTCTAGCTCTAAAACAACAGTTGGGACAGGAGAACCTGAGCCTCAGCGCAGCAGCTTA
DF5C-CF	AGATGATCCGTGGCATATCATTCAGAAGAACGCGTTTTAGAGCTATGC
DF5C-CR	GCATAGCTCTAAAACGTATCTTGGATCTTGTGCTGAGCCTCAGCGCAGCAGCTTA
DF3B-CF	AGATGATCCGTGGCATCTTCCCATTGACCCAGAGTTTTAGAGCTATGC
DF3B-CR	GCATAGCTCTAAAACGTGCAGATGGAAGTATGCTGAGCCTCAGCGCAGCAGCTTA
DF4C-CF	AGATGATCCGTGGCAACCAACATCCTCAGTGCAGTTTTAGAGCTATGC
DF4C-CR	GCATAGCTCTAAAAC TTGCATTCTGGTCAGTGGCTGAGCCTCAGCGCAGCAGCTTA
DC1A-CF	AGATGATCCGTGGCAGCACTCGTCCGACCCCGGTTTTAGAGCTATGC
DC1A-CR	GCATAGCTCTAAAACGGGGATGGCGGCGGGCACCTGAGCCTCAGCGCAGCAGCTTA
DF3A-CF	AGATGATCCGTGGCATCCACATACCTGAGCCATGAGTTTTAGAGCTATGC
DF3A-CR	TTCTAGCTCTAAAACGAAGTTGAATAACCATATGGCTGAGCCTCAGCGCAGCAGCTTA
DF2B-CF	AGATGATCCGTGGCAAGAGTGCTGCTAAAGAGCGTTTTAGAGCTATGC
DF2B-CR	GCATAGCTCTAAAACGGAGATAACATGATTGACCTGAGCCTCAGCGCAGCAGCTTA
DF1B-CF	AGATGATCCGTGGCATATCAATCTACCAAGTGAGTTTTAGAGCTATGC
DF1B-CR	GCATAGCTCTAAAACC TTGTGTTGGGTCAATCGCTGAGCCTCAGCGCAGCAGCTTA
SacIL-DF2CF	TTCTGCACTAGGTACAGGCCTGTTTCAGCCCACCACAGATTTCA
SacIR-DF2CR	CTGACGTAGGGGCGATAGAGCTCTGTTGCTTTGCCTTGTCCACT
SnaBIR-DF2CF	CGGGGATCCGTCGACTACTTCAGCCCACCACAGATTTCA
SnaBIL-DF2CR	AGGTGGAAGACGCGTTACTGTTGCTTTGCCTTGTCCACT
SacIL-DC1AF	TTCTGCACTAGGTACAGGCCTGGCATACAAGCACTCCTACGACGAT
SacIR-DC1AR	CTGACGTAGGGGCGATAGAGCTCCGACGAGCCATTTGGAACAGA
SnaBIR-DC1AF	CGGGGATCCGTCGACTACGCATACAAGCACTCCTACGACGAT
SnaBIL-DC1AR	AGGTGGAAGACGCGTTACCGACGAGCCATTTGGAACAGA
DF3C-dn-F	TCCGGAGCTAGCTCTAGAATGCGAGTGGA CTATCCCTTT

DF3C-dn-R	CCTCGAGACGTCTCTAGACTTCACTTTGATAGCCTT
DF1C-dn-F	TCCGGAGCTAGCTCTAGAAATGGTTACGAAGTATGATCAA
DF1C-dn-R	CCTCGAGACGTCTCTAGATTTACATGAAAAGTTCTT
DF1A-dn-F	TCCGGAGCTAGCTCTAGAAATGCCTGTCCAATATGATGAT
DF1A-dn-R	CCTCGAGACGTCTCTAGACTTACTGACATGCTCCTT
DF2C-dn-F	TCCGGAGCTAGCTCTAGAAATGCCTGTTGATCATCCAGAT
DF2C-dn-R	CCTCGAGACGTCTCTAGATGTCAATGGGCCATCCTT
DF3B-dn-F	TCCGGAGCTAGCTCTAGAAATGGTTATTGAGTATGAGGAT
DF3B-dn-R	CCTCGAGACGTCTCTAGACTCGACCTCATGGTTCTT
DF4C-dn-F	TCCGGAGCTAGCTCTAGAAATGACAGTTCAGTATGAGCAT
DF4C-dn-R	CCTCGAGACGTCTCTAGATCCCTGGTGATATGCCTT
primer used for PCR sequencing	
CRAC-DF2B-F	CGACTCTGGGTAATCGGAGGAGG
CRAC-DF2B-R	TAGGAGAGGCTGGTGGCTGGTAGT
CRAC-DF3C-F	TTGACTTTTCCAGGTTACCAAACCTT
CRAC-DF3C-R	AACAGGAGGAACTGAGGGTAATG
CRAC-DF1B-F	GGATTCGCAGGAGCCAAGAGTTG
CRAC-DF1B-R	TGAGGTGAAGCCGCAGGTGATG
CRAC-DF1C-F	GCCATATCTGTGGCATCAGGATT
CRAC-DF1C-R	AAGGTTTGGACGCCTCCTATTCT
CRAC-DF2C-F	CAGGGTCTTTATTATCCAGCAAC
CRAC-DF2C-R	ACAGGCTTGTTCTCGTTATTCTC
CRAC-DF5C-F	AAATGTCATCGGGAAGTGGGTAT
CRAC-DF5C-R	GGATTACATGCAAGAAAATGAGGAC
CRAC-DF3B-F	TTGGGTAAAGGTGGAGAACAACA
CRAC-DF3B-R	CCCAGGAGTTGGTGAATACAGAAG
CRAC-DF4C-F	AAGCCAGGACACTTGGAAGAGTATA
CRAC-DF4C-R	CAAAGGAGGGATGGCATTATTCT
CRAC-DC1A-F	GTCCCAAGTCCCAACTCCCAAC
CRAC-DC1A-R	CTCCAACCCAAGAGCTAACAAACG

Supplementary Table S6 Log2 expression changes of abiotic response genes in OsYTH mutants.

gene_id	gene symble	Log2FC									
		<i>osythdf1a</i>	<i>osythdf2a</i>	<i>osythdf3a</i>	<i>osythdf1b</i>	<i>osythdf2b</i>	<i>osythdf3b</i>	<i>osythdf1c</i>	<i>osythdf3c</i>	<i>osythdf4c</i>	<i>osythdf5c</i>
LOC_Os11g04020	OsTOM1	3.2792	7.4229	4.4971	-10.2747	-7.1067	-1.8743	-10.7481	-8.1509	-1.2217	-8.441
LOC_Os11g26790	RAB21; Rab16A	-0.7541	0.655	-4.6795	-2.1252	-6.0341	-4.334	-0.9926	-3.8629	-6.5668	-7.2578
LOC_Os01g72370	OsIRO2	-1.0762	4.1649	3.7685	-3.4543	-3.26	0.1071	-6.3446	-6.929	0.1176	-2.3838
LOC_Os03g17790	OsRCI2-5	0.3925	0.7344	-0.7367	-4.1495	-5.0063	-2.5996	-3.7051	-2.0998	-3.9781	-1.8866
LOC_Os03g12820	OsSRO1c; BOC1	0.2927	0.9939	-1.0999	-4.1682	-3.8594	-2.9352	-3.3651	-4.2107	-4.9093	-2.6602
LOC_Os02g10760	OsWR1	-0.1569	1.6293	0.2219	-2.7727	-1.758	-1.0787	-4.462	-0.3951	-1.1819	-1.0965
LOC_Os04g28420	rFKBP65	-0.0126	1.9587	1.2482	-1.9999	-1.9103	-1.6581	0.0152	-0.7631	-2.3771	-0.5023
LOC_Os12g39400	ZFP252; RZF71	-0.8923	-0.3044	-1.9578	-2.7631	-1.7294	-1.0259	-2.4661	-2.6747	-1.319	-2.3747
LOC_Os01g04800	OsRAV2	0.798	-0.272	-0.7896	-2.0584	-1.0062	-1.7092	-0.2974	-2.1543	-2.1038	-2.4577
LOC_Os05g34830	OsNAC52	1.0026	-0.0645	-0.0199	-2.9351	-1.6469	-1.1573	-0.1372	-3.4641	-2.1139	-1.4226
LOC_Os03g44380	OsNCED3	2.0449	-2.3295	1.1522	-1.3779	-0.0272	-0.7932	0.868	-3.2871	-4.9982	0.3461
LOC_Os03g32230	bsr-d1; ZOS3-12	6.1221	2.1551	1.6753	-1.112	-1.3549	-4.0854	1.9422	-2.2745	-3.5644	-1.0873
LOC_Os02g41510	OsMYB30	5.2242	1.7389	1.669	-0.3266	0.7217	-3.2884	2.0153	-1.1565	-0.518	-1.2932
LOC_Os01g61080	OsWRKY24	3.7233	0.1532	1.1274	-0.8505	0.7542	-1.4353	3.2491	-1.8999	-2.7649	-1.7122
LOC_Os07g26640		2.0774	3.1019	2.0239	1.5806	4.3036	0.2312	1.7276	3.3047	3.4691	-1.2601
LOC_Os02g55890	OVP3	0.7099	2.2184	0.8049	2.6642	2.6268	-1.1854	1.3301	3.3235	3.3431	0.0764
LOC_Os07g26660		1.2386	2.0218	0.9646	1.1967	2.1181	-2.6716	-2.2566	2.9063	0.5398	0.3232
LOC_Os03g20370	OsCam1-1	1.2014	-0.4156	0.5156	1.5053	1.0869	-1.1379	1.4713	1.4145	-0.3582	0.6861
LOC_Os02g47470	OsABA8ox1	2.0725	-1.1284	0.3294	1.0176	2.7681	-1.5304	3.2839	2.6201	-0.2035	0.3795
LOC_Os06g29790	OsPHO1;3	1.3371	-0.0175	0.4666	1.4351	1.2341	1.4791	0.7457	0.7633	0.1743	0.2197
LOC_Os05g51830	OsHDT1;HDT701	-0.5294	-0.5258	-0.4	2.5687	1.6139	0.1734	1.5598	2.6592	1.0175	1.756
LOC_Os02g53130	OsNR2; qCR2	0	-1.6365	0.5677	2.0279	4.1125	-1.5243	4.0553	2.1721	-3.1336	2.7605
LOC_Os04g51820	OsHKT1;1; OsHKT4	4.0549	1.4687	3.1727	0.314	1.3998	-0.9731	1.8912	0.1022	-0.6739	1.5438
LOC_Os06g48800	OsHKT2;4; OsHKT9	3.1048	-0.1044	2.5841	-0.0156	1.255	0.9039	1.8172	-1.6154	-1.2601	1.5969
LOC_Os02g52150	OsHSP24.1	1.4966	1.7964	1.6875	0.0918	0.3772	-0.9207	1.802	0.6593	-0.6719	1.2121
LOC_Os02g07830	OsHKT1;3; OsHKT6	1.7307	1.0571	1.8045	0.38	0.776	0.2489	1.4869	-0.3678	-0.5899	1.3482
LOC_Os02g10780	OsSPX2	2.3781	1.6273	1.7887	0.5156	0.5315	0.1733	0.2543	-1.5674	-0.5151	1.1946
LOC_Os04g01740	OsHSP1	-4.1178	1.5218	-1.864	-1.5222	-4.3195	-0.4964	-1.3461	-2.0332	-2.078	-2.3704
LOC_Os02g56920	OsGL1-6	-5.5386	-0.3876	-2.648	-1.8512	-3.6289	1.0069	-5.2235	-0.1738	0.3328	1.4248
LOC_Os06g40150	OsWR2	-7.1935	0.3689	-3.9251	-1.7815	-1.4235	-1.5792	-6.3569	-0.1031	-0.7874	-1.3909
LOC_Os01g15830	OsPOX1; ddOs319	-2.9293	0.2039	-1.7504	-1.0154	-1.7262	-1.1592	-2.573	0.7427	0.2868	-0.3067

LOC_Os06g12230	OsTCP19	-2.373	-1.6345	-2.4699	-0.2134	-1.2238	0.4586	-0.7745	0.6985	0.7167	-0.4599
LOC_Os03g06970	OsSDI1	-2.8728	1.0974	-2.9134	-0.7493	-0.9865	0.7087	-1.5789	-1.506	0.7097	-1.1904
LOC_Os02g58220	OsRPA2	-7.2101	-0.7715	-3.5271	1.995	-1.3754	-0.072	-4.3319	2.3253	1.4308	-2.4158
LOC_Os12g38400	OsMYB91	-5.7002	-1.2739	-4.2461	1.2356	0.0297	0.2821	-0.263	1.8048	0.8423	0.558
LOC_Os05g01730	OsDi19-6	-3.9695	-0.1226	-3.0293	2.1234	-1.0876	-1.1294	-1.6512	1.8631	0.3397	-0.4102
LOC_Os02g18410		-5.9437	-0.3254	-4.3456	2.4406	1.4235	-1.6656	0.237	3.3962	1.4854	0.5697
LOC_Os02g41904	CAL1	-8.2648	-1.4899	-3.6824	5.8619	-0.0508	-2.0616	-2.6434	5.5899	5.2243	-3.1448
LOC_Os01g56940	OsEXO1	-5.418	-1.4427	-3.7897	3.7485	-1.23	1.0147	-1.0311	3.8296	3.0369	-1.2945
LOC_Os10g05690	OsAUX4	-7.318	-1.1632	-3.9296	4.6849	-0.6765	0.4562	-2.3334	4.6487	3.8861	0.9784

Supplementary Table S7 Log2 expression changes of biotic-response genes in OsYTH mutants.

gene_id	gene symble	Log2FC									
		<i>osythdf1a</i>	<i>osythdf2a</i>	<i>osythdf3a</i>	<i>osythdf1b</i>	<i>osythdf2b</i>	<i>osythdf3b</i>	<i>osythdf1c</i>	<i>osythdf3c</i>	<i>osythdf4c</i>	<i>osythdf5c</i>
LOC_Os09g25070	OsWRKY62	0.0533	1.5696	0.8971	-4.9948	-2.0432	1.0718	-3.6035	-3.4029	2.0691	-1.7991
LOC_Os12g12010		-2.9448	-0.6273	-0.1078	-1.7396	-1.3692	-2.5783	-0.7713	-1.8189	-1.7731	-0.5742
LOC_Os12g11370		-0.4841	0.0032	-0.1538	-1.3639	-2.0095	-2.8819	-1.5858	-1.2705	-1.8403	-1.4848
LOC_Os12g17490		0.0447	0.0132	0.3972	-2.0656	-2.7488	-3.1688	-2.4434	-2.5546	-2.3857	-2.1736
LOC_Os12g12130		3.3146	0.8731	0	-3.4064	-3.4094	-3.7111	-2.8352	-3.4961	-3.3526	-3.21
LOC_Os02g14430	OsPrx30	1.1716	-2.573	-0.7368	-1.8581	-1.6216	-2.7997	-3.0237	-4.0243	-1.8807	-2.8318
LOC_Os10g10130	OsWAK112d	0.8629	-1.0833	0.2204	-3.275	-1.789	-0.1616	-2.0453	-4.9201	-2.8534	-3.2814
LOC_Os08g39840	OsHI-LOX; RLL; OsLOX9	3.5757	1.7762	1.5257	-4.5029	-2.5147	-1.7191	-0.8563	-7.079	-5.7451	-4.5283
LOC_Os08g04500	OsTPS3	2.5124	-1.0556	2.5999	-0.8625	-0.0785	0.7725	1.3457	-4.3147	-4.9098	0.6238
LOC_Os10g25230	OsJAZ13; OsTIFY11e	3.9878	-1.7234	1.7672	-1.071	0.6581	-3.9918	1.6437	-4.6038	-5.0541	-1.1949
LOC_Os06g44010	OsWRKY28	3.7097	0.8182	0.948	-1.3869	1.2229	-1.8984	4.3396	-2.2113	-2.1322	-1.3793
LOC_Os03g32230	bsr-d1; ZOS3-12	6.1221	2.1551	1.6753	-1.112	-1.3549	-4.0854	1.9422	-2.2745	-3.5644	-1.0873
LOC_Os04g48850	OsACS2	3.9619	1.3443	0.6496	-3.5308	-1.3392	-2.1932	0.8451	-2.9741	-3.2949	-3.6599
LOC_Os11g32170		1.5952	2.0732	2.3441	0.3862	0.6695	-2.2404	1.2968	2.3036	0.0886	-1.8319
LOC_Os09g14100		2.1577	2.3398	1.9147	-0.5393	0.458	-0.6742	-1.0567	1.1318	1.9078	-1.0003
LOC_Os02g02640		1.5195	1.6044	1.1555	0.0285	0.3489	-0.0797	-0.2442	0.4534	1.6391	-0.2275
LOC_Os05g31570		4.3948	3.2984	4.2185	-0.1273	0.365	-0.1255	0.5004	-0.4252	-0.7325	-0.0983
LOC_Os11g12320		3.2207	1.592	2.7703	0.3338	1.1138	-0.8846	1.0601	-0.4016	-0.0646	0.3713
LOC_Os03g40194		2.0885	1.1023	1.578	0.1987	0.4965	0.8544	1.0377	-0.3525	-0.5318	0.068
LOC_Os11g12340	OsRSR1	2.681	1.4543	1.6456	-0.6367	0.0562	-0.5726	0.4214	-1.476	-0.6402	-0.2096
LOC_Os06g03500	Bph37	1.5276	1.268	1.134	-1.1488	-0.183	-0.4523	-0.9153	-0.9927	0.2505	0.1083
LOC_Os02g57720	OsPIP1;3	2.1219	2.064	1.5316	0.0339	-0.9566	-0.8947	0.2744	-0.389	0.4598	0.5573
LOC_Os11g45930		1.2586	1.012	1.218	-0.1468	-0.162	-0.4333	0.0102	-0.3373	0.1015	0.0017
LOC_Os12g32790		1.8052	1.9369	1.5339	0.148	0.34	-0.3752	0.3794	-0.0775	0.6808	-0.5421
LOC_Os11g45980		2.3116	2.8606	2.0794	2.9145	3.5974	0.1262	2.5974	3.8378	4.4043	0.5905
LOC_Os12g17430		2.2495	1.5356	2.2386	0.9074	2.7378	-0.8021	3.6279	1.4286	0.6058	2.3035
LOC_Os11g17330		1.8625	0.8071	2.5702	1.7217	3.6142	1.6105	3.9774	1.2419	-0.3212	2.0683
LOC_Os06g41670		0.0035	1.9885	-0.726	1.4024	2.0834	1.1616	2.083	2.5013	2.7577	1.9742
LOC_Os11g37880		-0.0012	0.2702	-1.4369	1.899	2.2075	-1.0239	1.9016	1.848	1.3864	1.3358
LOC_Os04g53050		-0.5266	1.2766	2.6819	2.8468	0.6451	0.2638	1.9436	3.4479	1.3325	1.6121
LOC_Os06g41640		0.4664	0.7308	1.7911	1.2202	1.2075	1.2275	1.4034	1.0466	1.3801	0.5835
LOC_Os11g44690		2.009	1.5379	1.287	1.0705	1.6759	0.1046	0.7787	1.314	0.3598	0.896
LOC_Os11g12050		1.4215	1.2248	1.3999	0.9463	0.7931	-0.0516	1.8656	1.3945	0.4936	0.4415

LOC_Os12g12120		1.0621	-0.0887	2.3987	1.3462	2.001	1.366	1.9394	0.1504	1.6269	1.8123
LOC_Os11g11950		0.177	-0.0337	0.1847	1.9865	1.9501	1.3158	2.0103	1.7775	1.9052	2.1946
LOC_Os11g45050		-0.0906	0.1635	0.0323	1.3649	1.2672	1.497	1.1865	0.7384	0.5668	1.5341
LOC_Os05g01140	OsJMT1	-4.251	2.0644	-3.5894	-1.7733	-1.153	-0.3508	-4.3423	0.7307	-0.1277	-0.4646
LOC_Os04g39150		-6.2474	0.4748	-2.8745	-1.488	-1.2672	-1.8819	-4.4468	0.4178	-0.0273	-1.324
LOC_Os01g28450	OsPR1b	-2.569	-3.1894	-1.8784	1.8782	0.4103	1.5161	0.5027	-0.4447	-2.7678	-3.2751
LOC_Os07g48020	Perox4	-4.3273	-1.4594	-1.4255	0.2657	0.5262	-1.5043	1.1996	0.4785	-0.5642	0.9936
LOC_Os03g36920		-1.8449	-1.393	-2.3	2.3622	0.9559	-0.1088	-0.5613	2.3346	1.3954	1.2536
LOC_Os04g08390	Bph40	-2.8048	1.2703	-2.8307	0.7215	0.137	-1.5462	-2.4981	1.4766	1.2483	-0.8018
LOC_Os02g58490	OsAGO1c	-1.8356	-1.2321	-1.1439	0.4068	-0.7631	0.0094	-0.9028	0.5015	0.7344	-0.303
LOC_Os10g04090		-2.6957	-1.1651	-1.9781	-1.0469	-0.8866	-0.2167	-2.0348	0.2643	0.3574	-0.5123
LOC_Os11g39280		-2.4754	-1.3968	-2.2923	-0.357	-1.2445	-0.2769	-0.998	-0.0195	0.5501	-1.0456
LOC_Os11g30060		-3.9156	-1.6799	-4.8419	5.8175	1.1582	1.6569	1.7997	5.8305	5.2439	3.0626
LOC_Os03g63240		-4.6272	1.5095	-2.3512	3.4646	2.9732	0.9981	2.2794	3.1816	3.3442	4.2558
LOC_Os12g11930		-1.7147	-1.9645	-1.5875	3.972	2.8508	2.378	2.7183	3.8027	3.4394	2.5465
LOC_Os12g10870		-0.612	0.2568	-0.1824	6.5847	6.7623	6.1674	6.7061	6.0332	5.4152	5.3463
LOC_Os12g11860		1.8083	0.1971	0.8463	7.6367	7.6215	5.1893	7.9751	5.8773	7.2298	8.0244
LOC_Os12g11680		0.4401	0.4996	0.8306	6.9993	6.8344	6.5209	7.3262	6.5152	6.9686	7.2723
LOC_Os11g11810	RGA5	0.0357	-0.2446	0.2108	7.7418	7.8081	7.6888	7.6922	7.7285	7.873	7.691
LOC_Os11g44960		1.2039	2.4188	1.4243	5.2452	2.9167	4.3807	4.1847	5.1518	4.824	1.8113
LOC_Os11g11770		0.3173	-0.2071	0.2119	4.5139	4.1224	3.266	4.3221	4.4308	3.8725	3.7848
LOC_Os11g45180		0.5342	0.4286	0.6771	4.8407	4.1713	5.0359	5.1678	4.2584	3.3372	3.2896