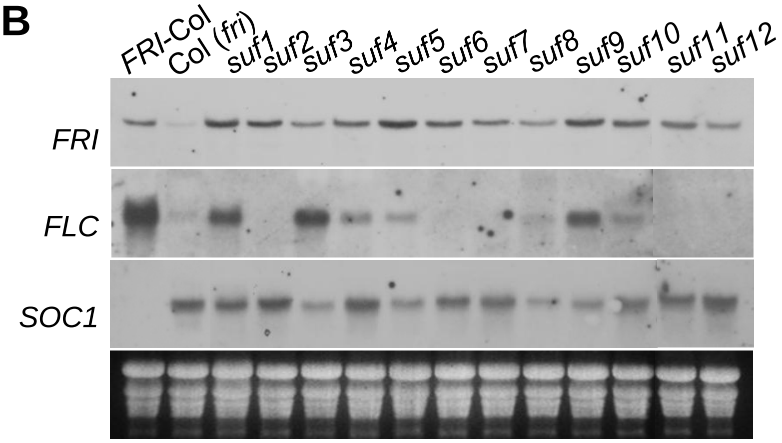
A

Group	FN alleles
flc	17, 102, 116, 215
fri	13, 14, 221, 233, 236
suf1/hua2	8, 109, 208, 234
suf2/abh1	4, 223
suf3/arp6	6, 7, 19, 24, 108, 115, 202, 225
suf4	25
suf5/flx	22
suf6	15
suf7	16
suf8/frl1	103
*suf*9	126
suf10/efs	207
suf11/vip5	204, 224
suf12/vip4	212

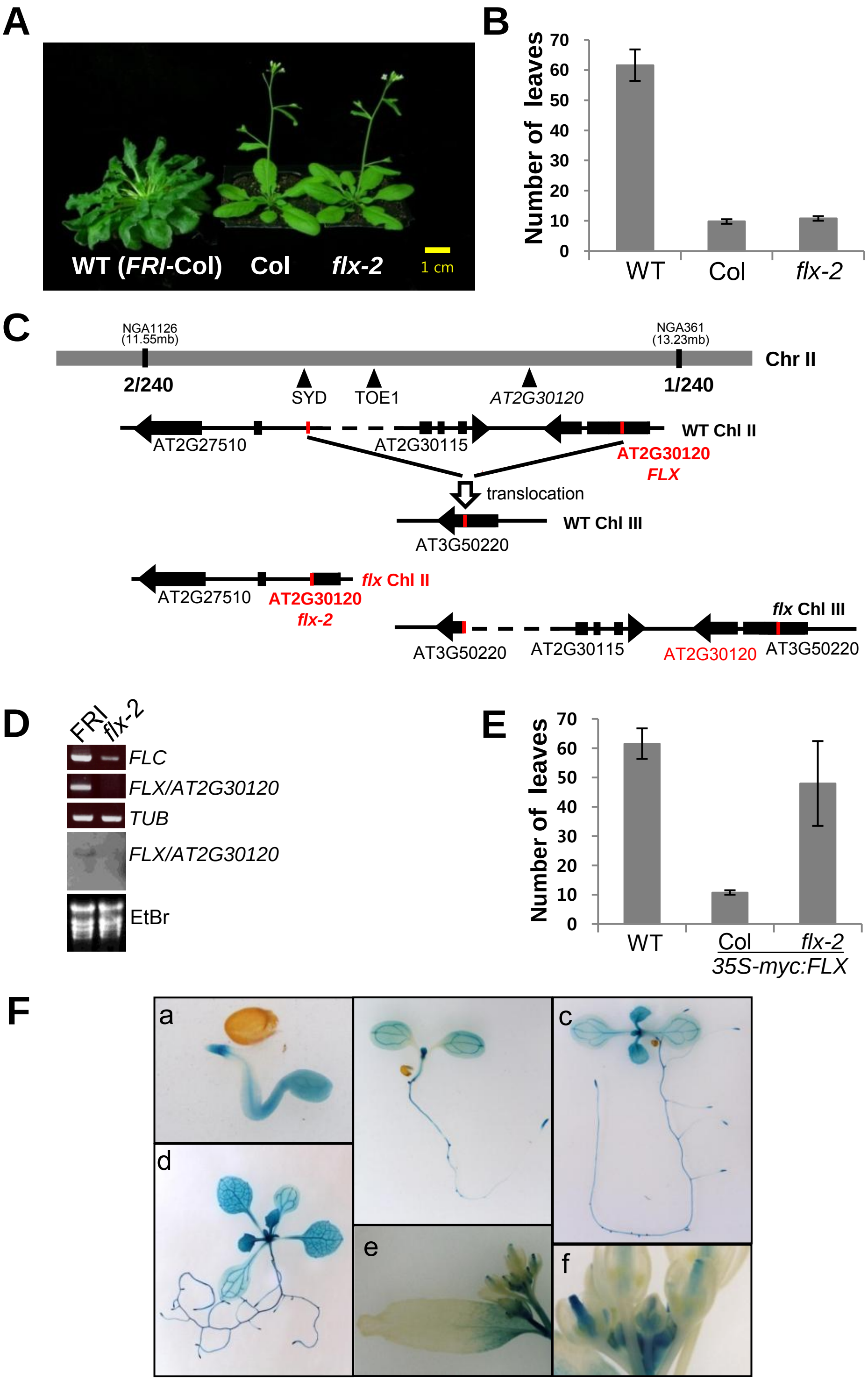
B



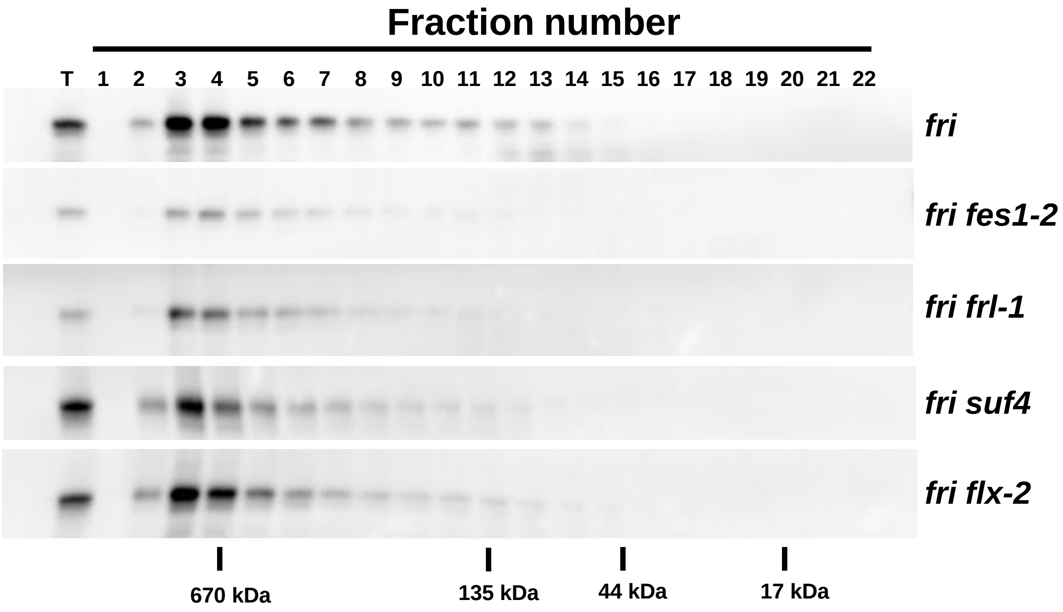
Supplemental Figure 1. Grouping of *suf* mutants and *FLC* expression

(A) Grouping of the *suf* mutants. The *suf* mutants were grouped into 12 loci.

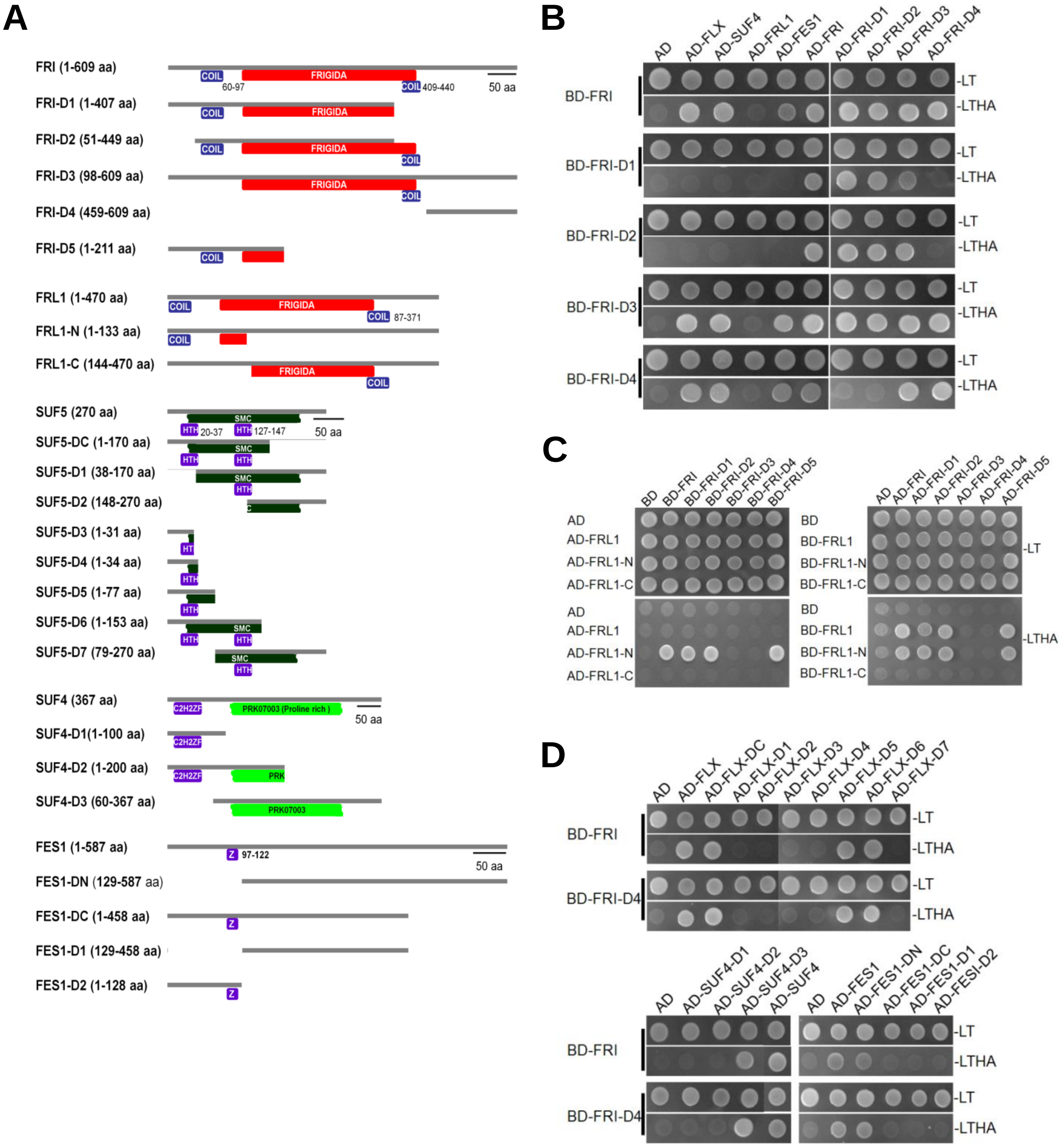
(B) The RNA blots showing the expression of *FRI*, *FLC*, and *SOC1* in *suf* mutants. All of the *suf* mutants showed reduced *FLC* expression and, as a consequence, an increase in the expression of *SOC1,* a flowering pathway integrator, resulting in the early flowering of *suf* mutants*.* The *suf4, suf5/flx, suf8/frl1* and *suf10/efs* show a small level of transcription, similar to Col, while *suf2*, *suf6*, *suf7*, *suf11* and *suf12* did not produce detectable RNA transcripts. The *suf1, suf3* and *suf9* mutants still maintain approximately 30 % of the *FLC* transcripts.



Supplemental Figure 2. Characterization of *flx-2* and the expression patterns of *FLX*
(A) Phenotype of wild type plants (*FRI*-Col), Col, and *flx-2* grown for 40 or 30 days under long days.
(B) Flowering time of wild type, Col, and *flx-2* plants .
(C) Map-based cloning and chromosomal structure of *flx-2.*
(D) RT-PCR analysis of *FLC* and *FLX* and RNA blot of *FLX* in wild type and *flx-2* mutant.
(E) Flowering time of transgenic plants expressing myc tagged FLX in the *flx-2* and Col backgrounds.
(F) Expression patterns of *FLX* in transgenic plants expressing translational fusion, GUS-FLX. GUS detections in transgenic plants grown for 3 days after germination (DAG) (a), 6 DAG (b), 9 DAG (c), and 12 DAG (d). GUS detections in the axillary bud and flowers (e), and inflorescence and flower (f).



Supplemental Figure 3. Gel filtration analysis of myc:FRI proteins expressed in the *fes1*, *frl1*, *suf4* and *flx* mutant backgrounds Homozygotes of *35S-myc:FRI fri* (Col) were crossed with each double mutant of *fri fes1-2, fri frl1-2*, *fri suf4*, and *fri flx-2.* The homozygotic F3 plants of *35S-myc:FRI fri* in each mutant background were selected and used for gel filtration analysis. The T of first lane indicates the input control in the protein gel blots.



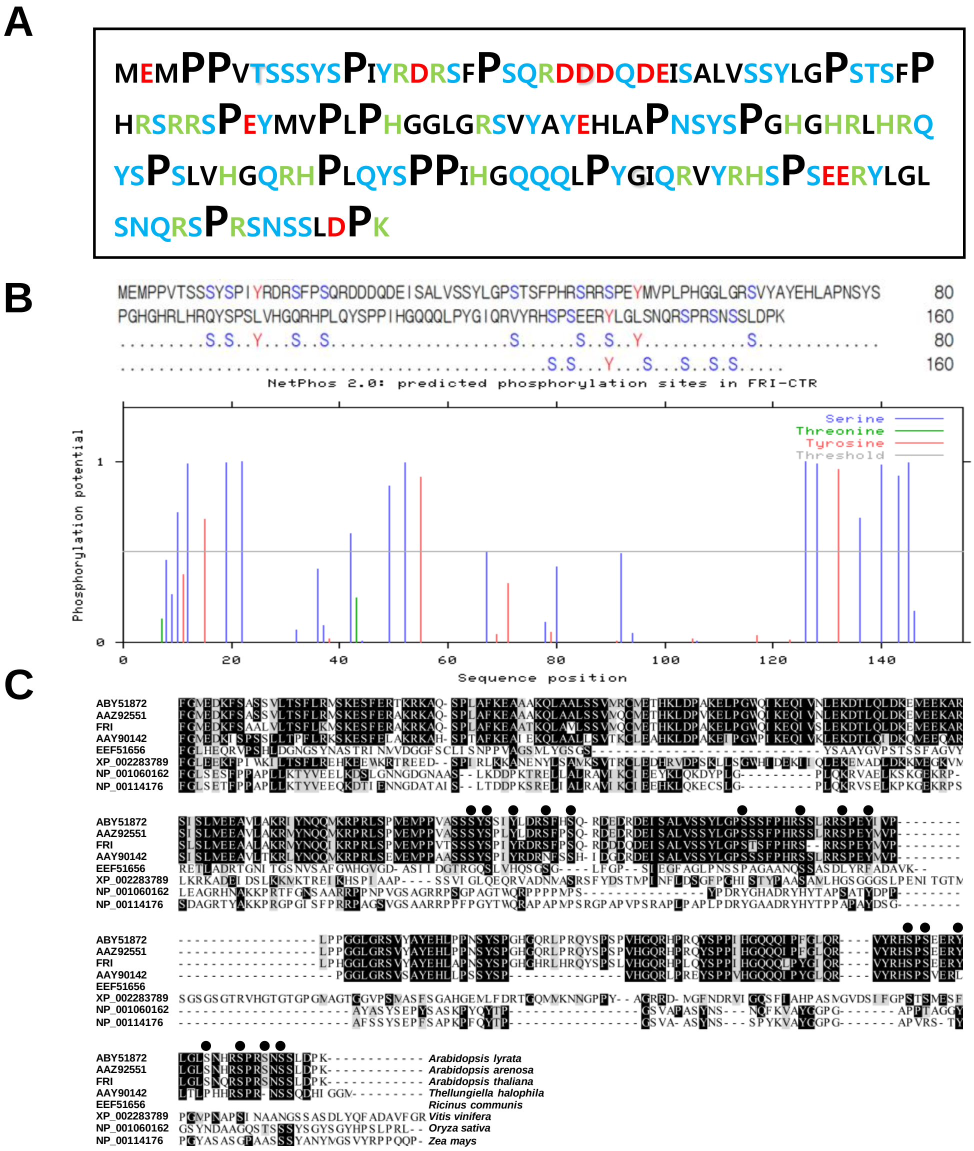
Supplemental Figure 4. Yeast two hybrid interaction analyses among the deletion forms of FRI, FRL1, FLX, SUF4, and FES1

(A) Diagrams of the secondary structures of FRI, FRL1, FLX, SUF4 and FES1, showing the specific domains and truncated regions that were used in the Y2H analysis (B-D). The blue colored COIL indicates the coiled-coil motifs in FRI and FRL1. The FRIGIDA domain is shown in red. In FLX, the SMC motif is shown in dark green and the HTH domain is shown in purple. In SUF4, two C2H2 type zinc finger motifs are shown in purple, and the proline-rich region PRK07003 is shown in green. In FES1, the CCCH type zinc finger motif is shown in purple.

(B) The C-terminal region of the FRI protein binds to FLX, SUF4, and FES1.

(C) The interaction between FRI and FRL1 requires their N terminal coiled-coil motifs.

(D) The N-terminus of FLX and the C-termini of SUF4 and FES1 physically interact with FRI-CTR.

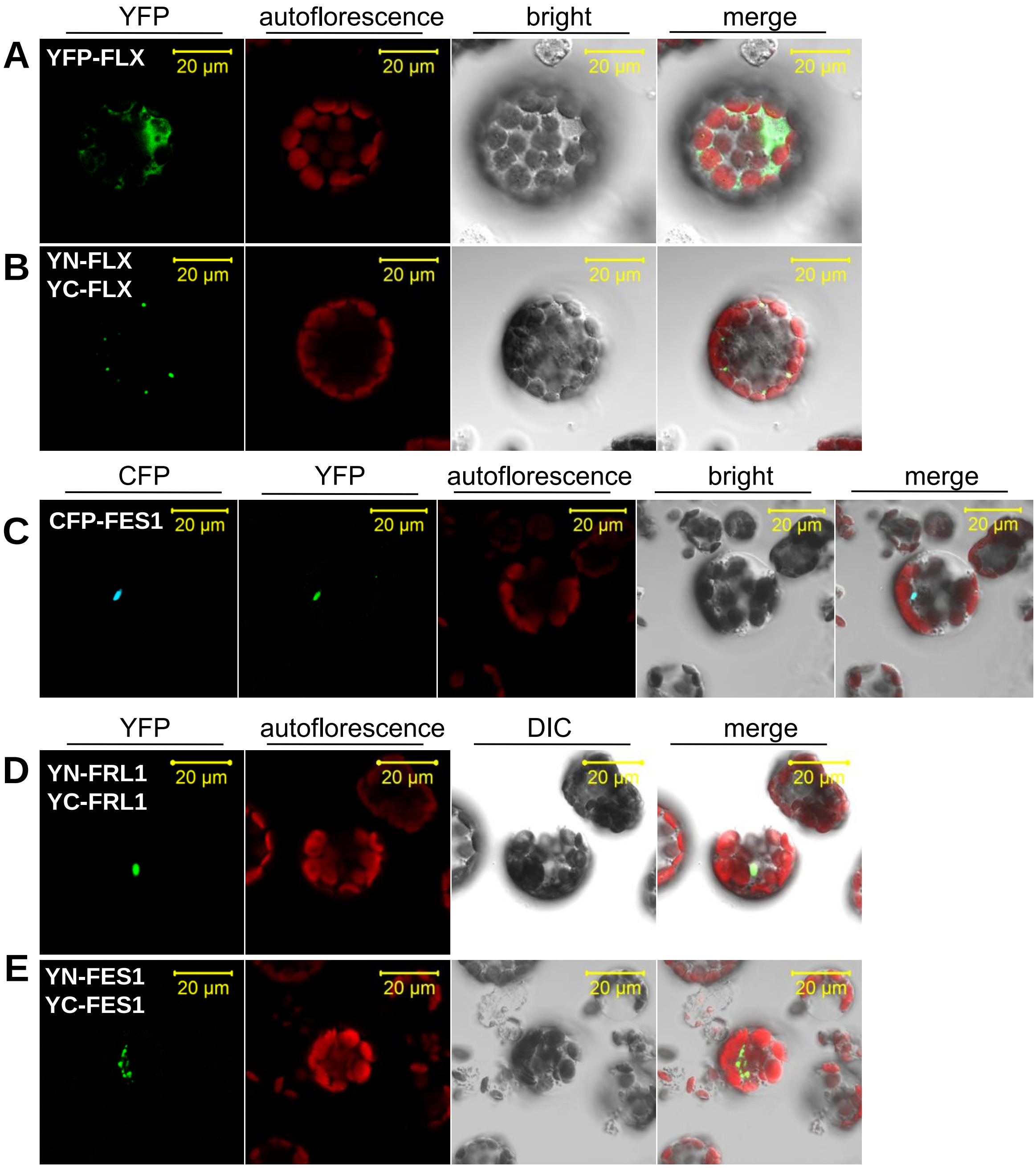


Supplemental Figure 5. Characteristics of the C-terminal 150 amino acids of FRI

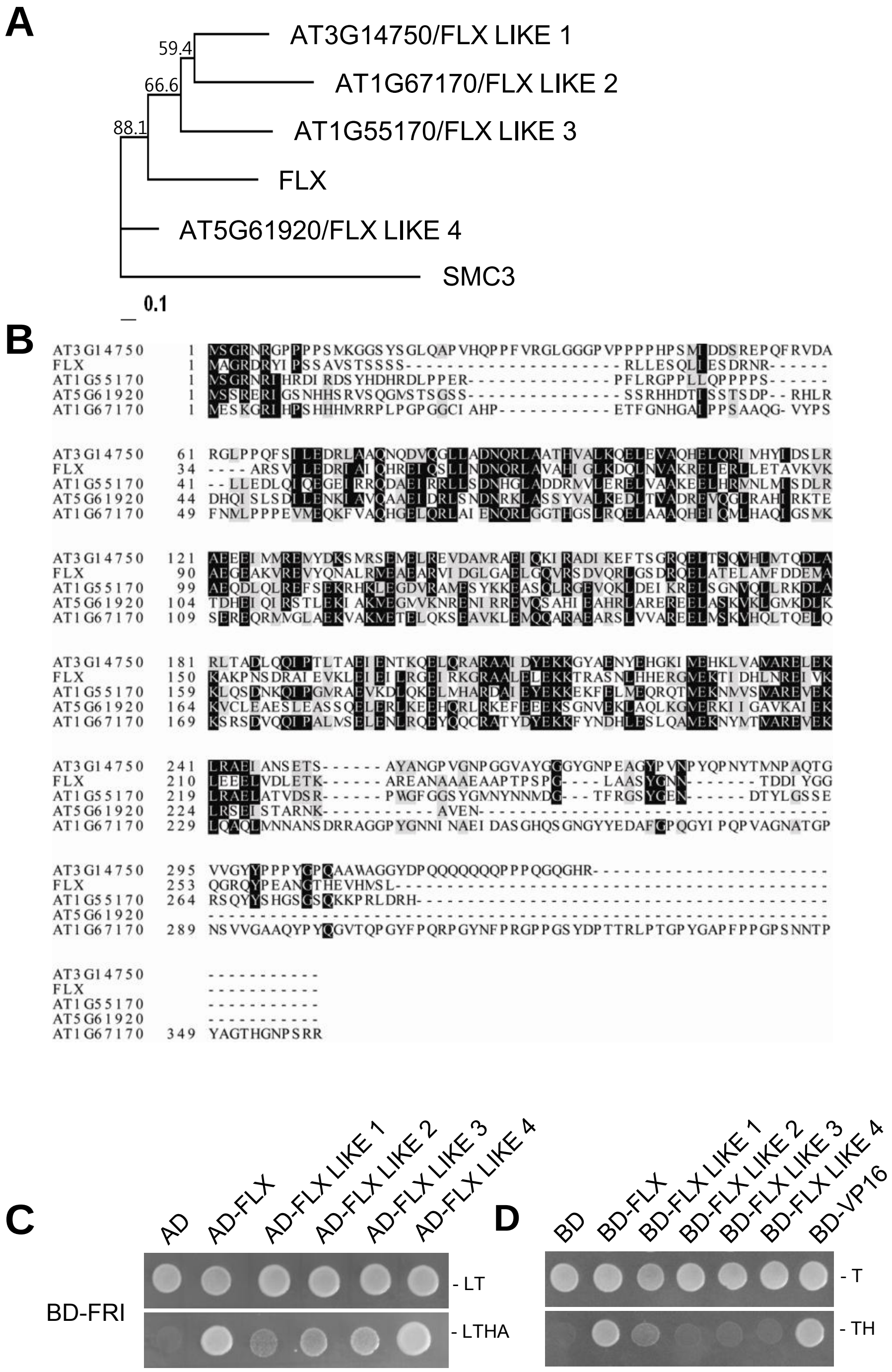
(A) The amino acid composition and the abundant prolines of FRI-CTR (aa 459-609). Green indicates hydrophilic, basic (+charge) amino acids (24 aa); blue, hydrophilic, polar (OH-) (53 aa); red, hydrophilic, acid (- charge) (12 aa); black, hydrophobic (61 aa). FRI-CTR includes 19 of the total 42 prolines of FRI (aa 1-609).

(B) Predicted phosphorylation sites in FRI-CTR. FRI-CTR contains 14 or 15 putative phospho-serines and 3 putative phospho-tyrosines which were predicted using NetPhos 2.0 (http://www.cbs.dtu.dk/services/NetPhos/).

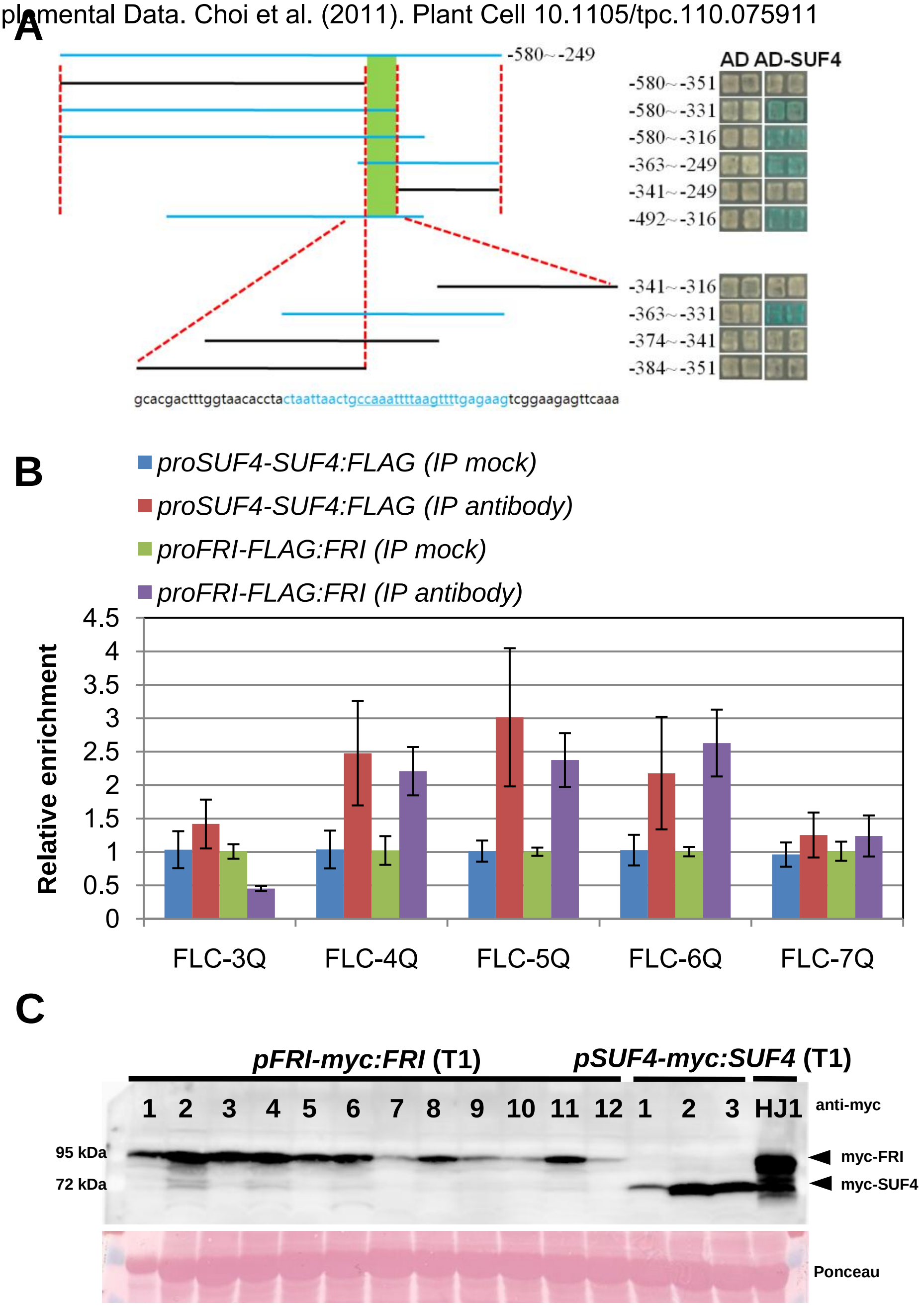
(C) The alignment of the C-terminal regions of the FRI homologs in different plant species. GenBank accession numbers are as follows: ABY51872, AAZ92551, and AAY90142 for *Arabidopsis lyrata, Arabidopsis arenosa,* and *T.halophial,* respectively; EEF51656 for castorbean (*Ricinus communis*); XP_002283789 for grape (*Vitis vinifera*); NP_001060162 for rice (*Oryza sativa);* and NP_001141761 for maize (*Zea mays*). The C-terminal region (aa 381-609) of *Arabidopsis thaliana* FRI was aligned with the corresponding C-terminal regions of homologs of different species by CLUSTALW (http://seqtool.sdsc.edu/CGI/BW.cgi)) and then the alignment was illustrated using BOXSHADE 3.21 (http://www.ch.embnet.org/software/BOX_form.html). Dots indicate the predicted phosphorylated sites of FRI in Arabidopsis thaliana shown in (B)



Supplemental Figure 6. Localization of FLX, FRL1, and FES1
(A) Localization of YFP-FLX proteins in the protoplast transient assays.
(B) BiFC analysis showing the FLX homodimer in protoplasts expressing both YN-FLX and YC-FLX.
(C) Colocalization analysis of protoplasts expressing CFP-FES1, YN-FLX, and YC-FLX.
(D, E) BiFC analysis displaying the FRL1 and FES1 homodimer in protoplasts expressing YN-FRL1/YC-FRL1 (D) and YN-FES1/YC-FES1 (E).



Supplemental Figure 7. *FLX* like genes in Arabidopsis thaliana
(A) Phylogentic tree of four FLX like proteins with a SMC3 homolog in Arabidopsis drawn by PHYLIP program. Bootstrap values from 1000 trials are shown and the scale bar for branch length are shown in lower panel. The SMC3 is used as outgroup.
(B) Alignment of the deduced amino acid sequences of four FLX like proteins and FLX. The conserved middle region is similar to the N terminal portion of the SMC domain identified in the SMC proteins.
(C) Yeast two hybrid analysis used to determine the interactions between FRI and FLX-like proteins. FLX like proteins also bind to FRI.
(D) Yeast one hybrid analysis used to monitor the transcriptional activity of FLX like proteins. FLX alone has a strong transcriptional activity in yeast.

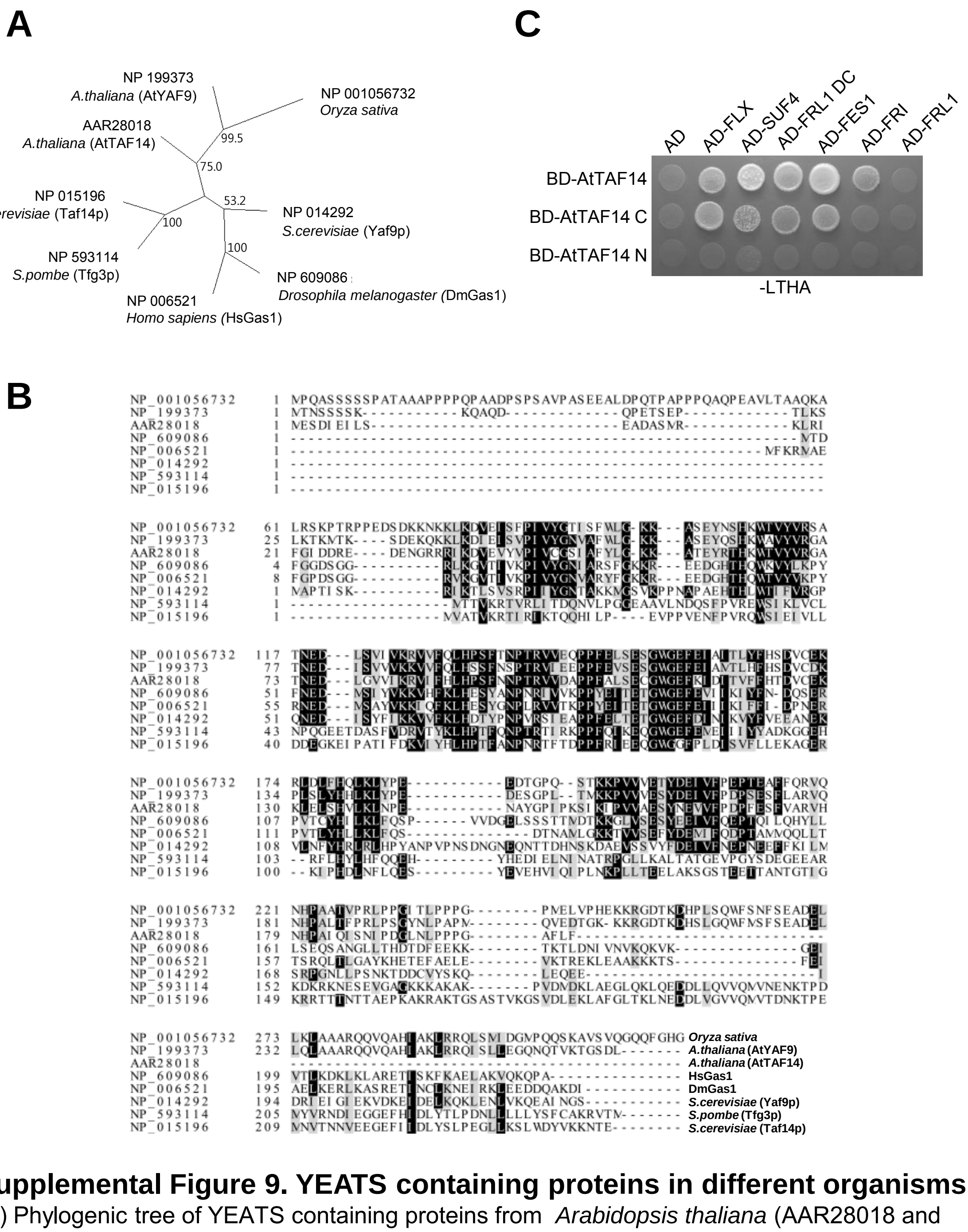


Supplemental Figure 8. SUF4 binding to the *FLC* promoter *in vitro* and *in vivo*

(A) Diagrams for the search for the *FLC* promoter *cis*-element that binds SUF4 by yeast one hybrid analysis. Blue lines indicate the promoter regions that provided blue colonies on Y1H plates. The green box indicates the minimal region required for SUF4 binding to the *FLC* promoter. The numbers indicate the distance from the transcriptional start site. The *FLC* promoter sequence from -384 to -316 is represented below.

(B) ChIP-quantitative PCR analysis with epitope tagged transgenic plants of *proSUF4-SUF4:FLAG suf4* and *proFRI-FLAG:FRI fri*. Mock indicates immunoprecipitation without the FLAG antibody. FLC-3Q~7Q indicates the primer sequences from the *FLC* promoter, as shown in Figure 5C. The *TUB2* promoter region was used for the normalization of the qPCR. Error bars indicate the SDs of triplicate experiments.

(C) Western blot data for *pFRI-myc:FRI* transgenic plant.s The protein was extracted from the adult leaves of individual transgenic lines. HJ1 (*35S-myc:FRI*) transgenic plants were used as a positive control. The protein from *pSUF4-myc:SUF4*, which was used for the ChIP experiment in B is also presented.

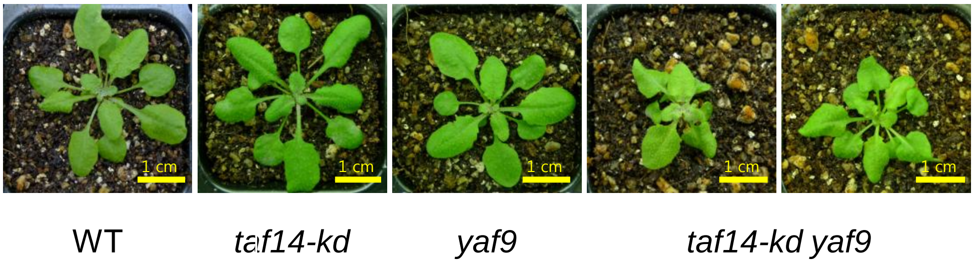


Supplemental Figure 9. YEATS containing proteins in different organisms

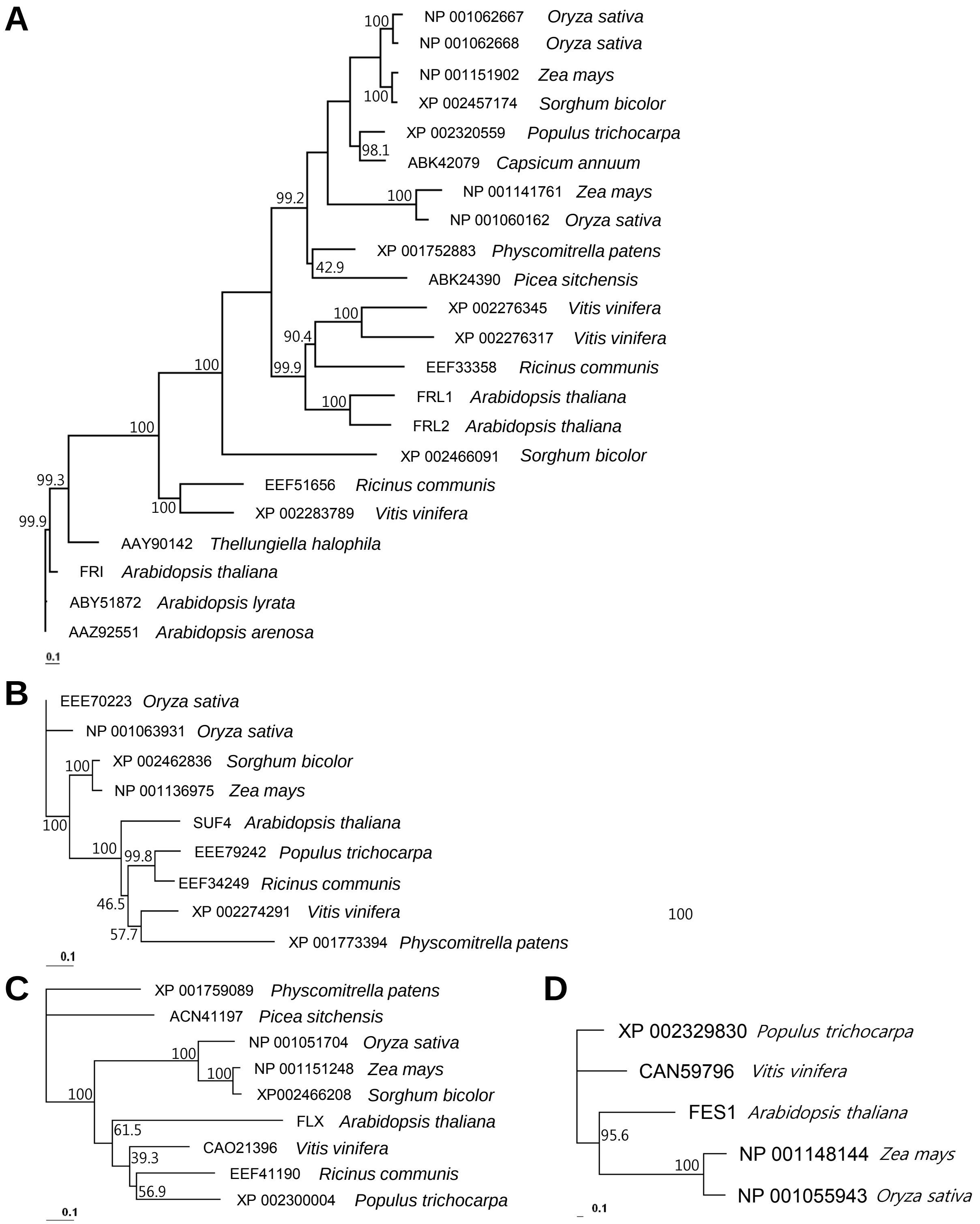
(A) Phylogenic tree of YEATS containing proteins from *Arabidopsis thaliana* (AAR28018 and NP199373), *Saccharomyces cerevisiae* (Yaf9p, NP 014292 and Taf14p, NP 015196), *Saccharomyces pombe* (Tfg3p, NP 593114), *Oryza sativa* (NP 001056732), *Drosophila melanogaster* (DmGas1, NP609086) and *Homo sapiens* (HsGas1, NP006521). The phylogenetic tree is drawn using PHYLIP program. The bootstrap values from 1000 trials are shown.

(B) The alignment of the deduced amino acid sequences of the YEATS containing proteins from Arabidopsis, yeast, rice, fruit fly, and human that is shown in (A). The highly conserved region indicates the YEATS domain.

(C) The Y2H analysis between AtTAF14 and FRI-C, FLX, SUF4, FES1, and FRL1 shows interaction with the C-terminal region (aa 114-202) of AtTAF14, while FRI requires the entire AtTAF14 protein for the interaction. AtTAF14 can bind to the N terminal fragment of FRL1, which supports the BiFC result (Figure 7A).

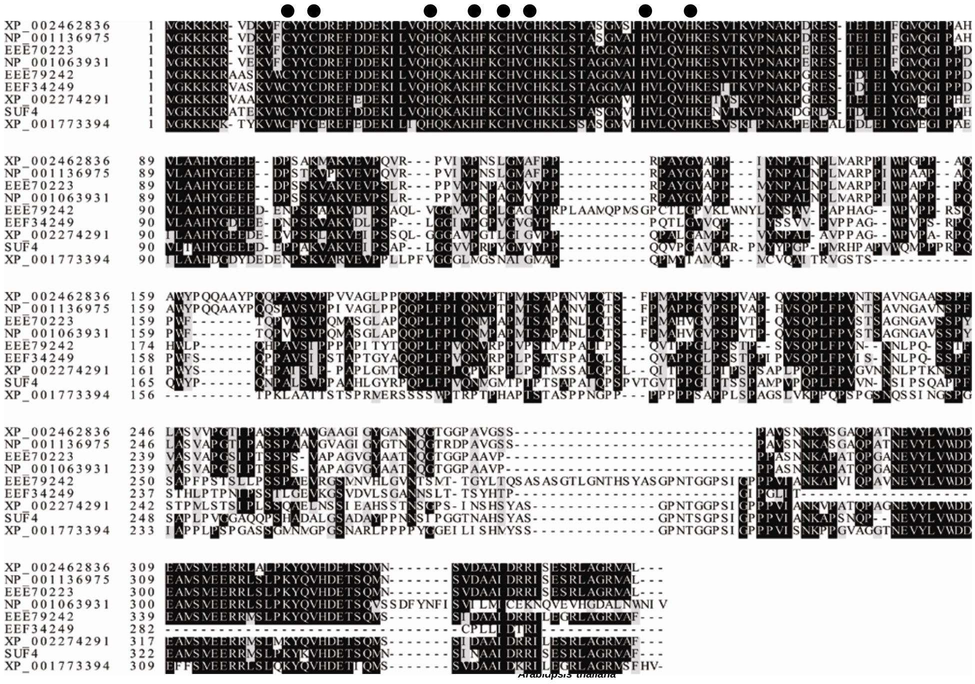


Supplemental Figure 10. Phenotype of *atyaf9* and *attaf14-kd* plants
Morphology of 3-weeks-old mutant lines, *taf14 knock-down* (kd), *yaf9* (salk_075203), and *taf14-kd yaf9*, respectively. The *taf14-kd* and *yaf9* show the same phenotype as the wild type, but *taf14-kd yaf9* double mutants show an ectopic phenotype of growth retardation and a wrinkled-leaf morphology.

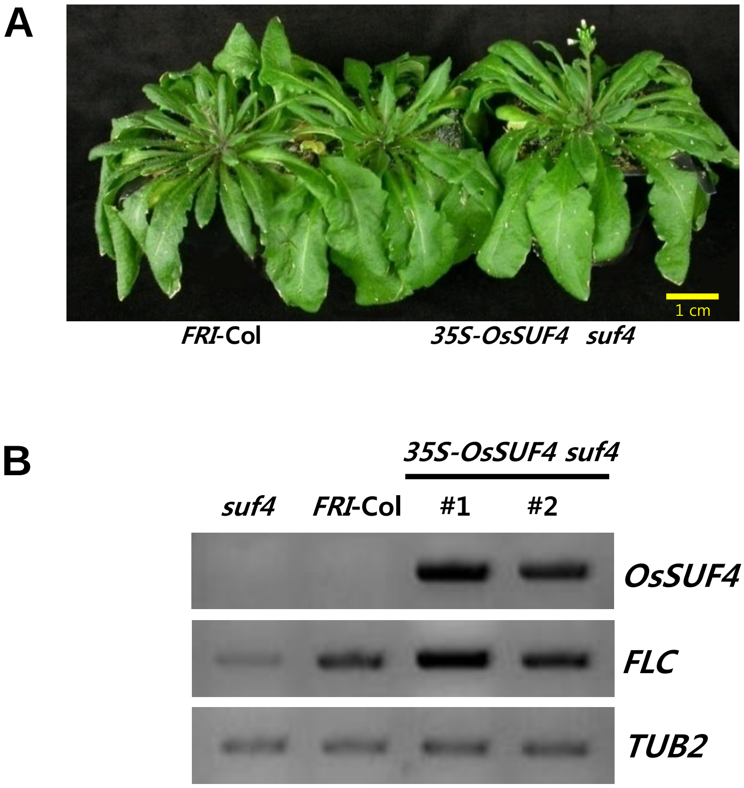


Supplemental Figure 11. Phylogenetic trees of FRI-C components

Phylogentic tree s of FRI and FRL1 (A), SUF4 (B), FLX (C), and FES1 (D) homologs from different species including Arabidopsis, grape (*Vitis vinifera*), castorbean (*Ricinus communis*), rice (*Oryza sativa*), maize (*Zea mays*), sorghum (*Sorghum bicolor*), popular (*Populus trichocarpa*), spruce (*Picea sitchensis)* and moss (*Physcomitrella patens).* The phylogenic analysis was performed using the PHYLIP program. The bootstrap values from 1000 trials are shown and the scale bars for branch length are shown in lower panel.



Supplemental Figure 12. Alignment of SUF4 homologs from different plant species
GenBank accession numbers are as follows: NP_111063931 and EEE70223 for rice (*Oryza sativa*), NP_001136975 for maize (*Zea mays*), XP_002462836 for sorghum (*Sorghum bicolor*), EEF34249 for castorbean (*Ricinus communis*), EEE79242 for popular (*Populus trichocarpa*), XP_002274291 for grape (*Vitis vinifera*), and XP_001773394 for moss (*Physcomitrella patens).* Dots indicate the C2H2 type zinc finger motifs conserved between SUF4 homologs.



Supplemental Figure 13. The over-expression of *OsSUF4* rescued *suf4* mutant phenotype

(A) Morphology of two 6-week-old *35S-OsSUF4 suf4* and *FRI*-Col plants.

(B) RT-PCR analysis of the expression of *OsSUF4* and *FLC* in *suf4*, wild type (*FRI*-Col) and *35S-OsSUF4* plants. The b-*tublin* 2 gene (*TUB2*) was amplified as a quantitative control.

Supplemental Table 1. These tables contain all of the LC-MS/MS results for the myc-FRI IP and the control sample. The FRI associated proteins reported in the text are shown in green colored boxes. These data were processed by SEQUEST program.

(A) Identified protein and their peptide sequence list with myc-FRI IP

	Gene	Peptide Sequence	Score	Accession	Peptides (Hits)
#1	RBL_ARATH RecName: Full=Ribulose bisphosphate carbo		520.28	3914541.0	52 (52 0 0 0 0)
		K.SQAETGEIK.G			
		R.LSGGDHIHAGTVVGK.L			
		R.LSGGDHIHAGTVVGK.L			
		K.LGLSAKNYGR.A			
		K.TFQGPPHGIQVER.D			
		K.TFQGPPHGIQVER.D			
		K.TFQGPPHGIQVER.D			
		K.TFQGPPHGIQVER.D			
		K.TFQGPPHGIQVER.D			
		K.TFQGPPHGIQVER.D			
		R.VALEACVQAR.N			
		R.LSGGDHIHAGTVVGKLEGDR.E			
		R.LSGGDHIHAGTVVGKLEGDR.E			
		K.LTYYTPEYETK.D			
		R.DNGLLLHIHR.A			
		R.NEGRDLAVEGNEIIR.E			
		K.LTYYTPEYETK.D			
		K.LTYYTPEYETK.D			
		R.NEGRDLAVEGNEIIR.E			
		R.NEGRDLAVEGNEIIR.E			
		R.NEGRDLAVEGNEIIR.E			
		R.LEDLRIPPAYTK.T			
		R.LEDLRIPPAYTK.T			
		R.LEDLRIPPAYTK.T			
		R.DLAVEGNEIIR.E			
		R.DLAVEGNEIIR.E			
		R.LEDLRIPPAYTK.T			
		R.DLAVEGNEIIR.E			
		R.DLAVEGNEIIR.E			
		R.VALEACVQAR.N			
		R.GGLDFTKDDENVNSQPFMR.W			
		R.GGLDFTKDDENVNSQPFMR.W			
		R.GGLDFTKDDENVNSQPFMR.W			
		K.DTDILAAFR.V			
		K.DTDILAAFR.V			
		K.DTDILAAFR.V			
		K.DTDILAAFR.V			
		K.DTDILAAFR.V			
		K.DTDILAAFR.V			
		K.DTDILAAFR.V			
		K.LEGDRESTLGFVDLLR.D			
		K.LEGDRESTLGFVDLLR.D			
		K.LEGDRESTLGFVDLLR.D			
		K.LEGDRESTLGFVDLLR.D			
		K.LTYYTPEYETKDTDILAAFR.V			
		K.LTYYTPEYETKDTDILAAFR.V			
		K.EYKLTYYTPEYETKDTDILAAFR.V			

		K.EYKLTYYTPEYETKDTDILAAFR.V R.ESTLGFVDLLRDDYVEKDR.S K.LEGDRESTLGFVDLLRDDYVEK.D K.EITFNFPTIDKLDGQE.- K.EITFNFPTIDKLDGQE.-			
#2	RCA_ARATH RecName: Full=Ribulose bisphosphate carb	R.GLAYDTSDDQQDITR.G R.GLAYDTSDDQQDITR.G R.GLAYDTSDDQQDITR.G R.GLAYDTSDDQQDITR.G R.EGPPVFEQPEMTYEK.L R.EGPPVFEQPEMTYEK.L R.EGPPVFEQPEMTYEK.L R.EGPPVFEQPEMTYEK.L K.LMEYGNMLVMEQENVKR.V K.LMEYGNMLVMEQENVKR.V R.VQLAETYLSQAALGDANADAIGR.G R.VQLAETYLSQAALGDANADAIGR.G K.RVQLAETYLSQAALGDANADAIGR.G R.VQLAETYLSQAALGDANADAIGR.G R.VQLAETYLSQAALGDANADAIGR.G R.VQLAETYLSQAALGDANADAIGR.G R.VQLAETYLSQAALGDANADAIGR.G K.MGINPIMMSAGELESGNAGEPAK.L R.VYDDEVRKFVESLGVEK.I K.MGINPIMMSAGELESGNAGEPAK.L R.VYDDEVRKFVESLGVEK.I R.VYDDEVRKFVESLGVEK.I R.TDKIKDEDIVTLVDQFPGQSIDFFGALR.A K.IKDEDIVTLVDQFPGQSIDFFGALR.A K.IKDEDIVTLVDQFPGQSIDFFGALR.A	250.35	12643259.0	25 (25 0 0 0 0)
#3	ATPB_ARATH RecName: Full=ATP synthase subunit beta,	R.IVGEEHYETAQQVK.Q R.IVGEEHYETAQQVK.Q K.ESGVINEQNLAESK.V K.ESGVINEQNLAESK.V K.VALVYGQMNEPPGAR.M K.VALVYGQMNEPPGAR.M K.VALVYGQMNEPPGAR.M K.VALVYGQMNEPPGAR.M R.FVQAGSEVSALLGR.M R.FVQAGSEVSALLGR.M R.FVQAGSEVSALLGR.M R.IFNVLGEPVDNLGPVDTR.T R.GMDVVDMGNPLSVPVGGATLGR.I R.GMDVVDMGNPLSVPVGGATLGR.I K.GIYPAVDPLDSTSTMLQPR.I R.IFNVLGEPVDNLGPVDTR.T R.IFNVLGEPVDNLGPVDTR.T R.IFNVLGEPVDNLGPVDTR.T R.IFNVLGEPVDNLGPVDTR.T R.GMDVVDMGNPLSVPVGGATLGR.I R.GMDVVDMGNPLSVPVGGATLGR.I	220.34	6686269.0	22 (22 0 0 0 0)

		K.TVLIMELINNIAK.A			
#4	CATA3_ARATH RecName: Full=Catalase-3	R.IFAYGDTQR.H R.IFAYGDTQR.H R.APGVQTPVIVR.F R.APGVQTPVIVR.F R.APGVQTPVIVR.F R.APGVQTPVIVR.F R.WVEILSEPR.L K.DLHDAIASGNYPEWK.L K.DLHDAIASGNYPEWK.L R.WVEILSEPR.L R.WVEILSEPR.L R.EGNFDLVGNNTPVFFIR.D R.EGNFDLVGNNTPVFFIR.D K.LFIQTMDPADEDKFDFDPLDVTK.I	140.31	21903384.0	14 (14 0 0 0 0)
#5	PGKH_ARATH RecName: Full=Phosphoglycerate kinase,	K.GVTTIIGGGDSVAAVEK.V K.GVTTIIGGGDSVAAVEK.V K.KLASLADLYVNDAFGTAHR.A K.AKGVSLLLPTDVVVADKFAPDANSK.I K.KLASLADLYVNDAFGTAHR.A K.AKGVSLLLPTDVVVADKFAPDANSK.I K.KLASLADLYVNDAFGTAHR.A K.LASLADLYVNDAFGTAHR.A K.AKGVSLLLPTDVVVADKFAPDANSK.I K.LASLADLYVNDAFGTAHR.A K.AKGVSLLLPTDVVVADKFAPDANSK.I K.IVPASGIEDGWMGLDIGPDSIK.T K.IVPASGIEDGWMGLDIGPDSIK.T	130.29	12644295.0	13 (13 0 0 0 0)
#6	FRIGI_ARATH RecName: Full=Protein FRIGIDA	K.EMEEK.A R.LMTEGGLAAAEK.M R.LMTEGGLAAAEK.M K.DTLQLDK.E K.LMEEIPSALK.L K.YIYANISDQAK.L R.QFDDLQKHIESIENAIDSK.L K.GLRKYIYANISDQAK.L K.FVLDCIGKFYLQGR.R K.ELPGWQIKEQIVSLEK.D K.RSQFLVPMVSGIVESSIKR.G K.EMEEKARSLSLMEEAALAK.R	120.09	17432946.0	12 (12 0 0 0 0)
#7	GDL19_ARATH RecName: Full=GDSL esterase/lipase At1	R.ELVVYPADEPMR.E K.IGPMLNELAR.T K.IGPMLNELAR.T K.SRDDPNGKFSDGLIAPDFLAK.F K.TLLPQTFWPYGK.S K.TLLPQTFWPYGK.S R.GASFAVADATLLGAPVESLTLNQQVR.K R.GASFAVADATLLGAPVESLTLNQQVR.K R.GASFAVADATLLGAPVESLTLNQQVR.K	110.29	75162477.0	11 (11 0 0 0 0)

		R.TAPASAPFQFTVFDFYNAILTR.T R.TAPASAPFQFTVFDFYNAILTR.T			
#8	TBB4_ARATH RecName: Full=Tubulin beta-4 chain; Alt	R.RVSEQFTAMFRR.K R.AVLMDLEPGTMDSLR.S R.AVLMDLEPGTMDSLR.S K.NSSYFVEWIPNNVK.S K.NSSYFVEWIPNNVK.S K.LAVNLIPFPR.L R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G K.GHYTEGAELIDSVLDVVRK.E	90.70	27735260.0	9 (9 0 0 0 0)
#9	HSP83_ARATH RecName: Full=Heat shock protein 81-3;	R.KPEEINKEEYAAFYK.S R.KPEEINKEEYAAFYK.S K.ADLVNNLGTIAR.S K.ADLVNNLGTIAR.S K.SGDELTSLKDYVTR.M K.SGDELTSLKDYVTR.M K.SGDELTSLKDYVTR.M K.GIVDSEDLPLNISR.E K.GIVDSEDLPLNISR.E	90.43	26454636.0	9 (9 0 0 0 0)
#10	ACT1 (ACTIN 1); structural constituent of cyt	R.AVFPSIVGRPR.H R.AVFPSIVGRPR.H R.AVFPSIVGRPR.H R.AVFPSIVGRPR.H K.EITALAPSSMK.I R.VAPEEHPILLTEAPLNPK.A R.VAPEEHPILLTEAPLNPK.A R.VAPEEHPILLTEAPLNPK.A	81.12	30687201.0	8 (8 0 0 0 0)
#11	RUBA_ARATH RecName: Full=RuBisCO large subunit-bind	R.NVVLDEFGSPKVVNDGVTIAR.A R.NVVLDEFGSPKVVNDGVTIAR.A R.AIELPNAMENAGAALIR.E R.AIELPNAMENAGAALIR.E R.GIDKTVQGLIEELQK.K R.GIDKTVQGLIEELQK.K R.VLITDQKITAIKDIIPILEK.T R.VLITDQKITAIKDIIPILEK.T	80.32	2506276.0	8 (8 0 0 0 0)
#12	BGL23_ARATH RecName: Full=Beta-glucosidase 23; Sho	K.IGIAHSPAWFEAHDLADSQDGASIDR.A K.IGIAHSPAWFEAHDLADSQDGASIDR.A R.WMQDSLITWESK.N R.WMQDSLITWESK.N K.ASTDFVGLNYYTSVFSNHLEKPDPSKPR.W R.SGYEAYLVTHNLLISHAEAVEAYR.K R.IVKDFREYADFVFQEYGGK.V R.IVKDFREYADFVFQEYGGK.V	80.28	75313794.0	8 (8 0 0 0 0)
#13	CATA2_ARATH RecName: Full=Catalase-2	R.GPILLEDYHLVEK.L R.GPILLEDYHLVEK.L R.VGGTNHSHATQDLYDSIAAGNYPEWK.L	80.26	17865693.0	8 (8 0 0 0 0)

		K.TWPEDILPLQPVGR.M K.LFIQIIDPADEDKFDFDPLDVTK.T K.LFIQIIDPADEDKFDFDPLDVTK.T R.EGNFDLVGNNFPVFFIR.D R.EGNFDLVGNNFPVFFIR.D			
#14	ATPA_ARATH RecName: Full=ATP synthase subunit alpha	R.ELIIGDRQTGK.T R.LIESPAPGIISR.R R.EAYPGDVFYLHSR.L K.ASSVAQVVTSLQER.G K.TLTAEAESFLKEGIQEQLER.F K.TLTAEAESFLKEGIQEQLER.F K.TLTAEAESFLKEGIQEQLER.F K.TLTAEAESFLKEGIQEQLER.F	80.24	6685244.0	8 (8 0 0 0 0)
#15	GAPA-2 (GLYCERALDEHYDE 3-PHOSPHATE DEHYDR	R.AAALNIVPTSTGAAK.A R.AAALNIVPTSTGAAK.A R.AAALNIVPTSTGAAK.A R.AAALNIVPTSTGAAK.A R.VVDLADIVANNWK.- R.VVDLADIVANNWK.- R.VVDLADIVANNWK.- R.VPTPNVSVVDLVVQVSK.K	80.22	186478427.0	8 (8 0 0 0 0)
#16	RUBB_ARATH RecName: Full=RuBisCO large subunit-bin	R.IVNDGVTVAR.E R.IVNDGVTVAR.E K.VVAAGANPVLITR.G K.VVAAGANPVLITR.G R.EVELEDPVENIGAK.L R.IVNDGVTVAREVELEDPVENIGAK.L R.IVNDGVTVAREVELEDPVENIGAK.L	70.50	27735252.0	7 (7 0 0 0 0)
#17	EFTU_ARATH RecName: Full=Elongation factor Tu, chlor	K.VGETVDLVGLRETR.S K.VGETVDLVGLRETR.S K.VGETVDLVGLR.E K.VGETVDLVGLR.E R.EGGKTVGAGVIGTILE.- K.ILDEALAGDNVGLLLR.G K.ILDEALAGDNVGLLLR.G	70.23	119194.0	7 (7 0 0 0 0)
#18	FES1; nucleic acid binding / zinc ion binding	K.SDEIDGEVR.S K.SDEIDGEVR.S K.SDEIDGEVR.S R.EDISFMNPQR.V R.EDISFMNPQR.V K.EISSATAAENRVVLK.R	60.94	30685865.0	6 (6 0 0 0 0)
#19	HSP74_ARATH RecName: Full=Heat shock cognate 70 kD	R.TTPSYVAFTDSER.L K.NALENYAYNMR.N K.NALENYAYNMR.N K.NAVVTVPAYFNDSQR.Q R.IINEPTAAAIAYGLDK.K R.IINEPTAAAIAYGLDK.K	60.62	75311168.0	6 (6 0 0 0 0)

#20	ACT8_ARATH RecName: Full=Actin-8	K.AGFAGDDAPR.A K.AGFAGDDAPR.A R.AVFPSVVGRPR.H R.IAPEEHPVLLTEAPLNPK.A K.NYELPDGQVITIGAER.F K.LSFVAVDYEQEMETSK.T	60.39	25452791.0	6 (6 0 0 0 0)
#21	METE_ARATH RecName: Full=5-methyltetrahydropteroylt	K.NMVDAAK.L R.SDEKLLSVFR.E K.ALAGQKDEALFSANAAALASRR.S K.ALAGQKDEALFSANAAALASRR.S R.SDEKLLSVFR.E K.KLNLPILPTTTIGSFPQTVELRR.V	60.20	8134566.0	6 (6 0 0 0 0)
#22	CATA1_ARATH RecName: Full=Catalase-1	R.LGPNYLQLPVNAPK.C R.LGPNYLQLPVNAPK.C R.LGPNYLQLPVNAPK.C K.IWPEDILPLQPVGR.L K.IWPEDILPLQPVGR.L K.IWPEDILPLQPVGR.L	58.20	21903389.0	6 (5 1 0 0 0)
#23	GOX1_ARATH RecName: Full=Probable peroxisomal (S)-	R.IAIQAGAAGIIVSNHGAR.Q R.ESDIKNRFTLPPNLTLK.N R.ESDIKNRFTLPPNLTLK.N R.QLDYVPATISALEEVVK.A R.QLDYVPATISALEEVVK.A	50.37	13124263.0	5 (5 0 0 0 0)
#24	transketolase, putative [Arabidopsis thaliana]	K.ALPTYTPESPGDATR.N K.ALPTYTPESPGDATR.N K.TPSILALSR.Q K.VVPGFLGGSADLASSNMTLLK.A K.KYPEEASELKSIITGELPAGWEK.A	50.30	18411711.0	5 (5 0 0 0 0)
#25	GAS41; protein binding [Arabidopsis thaliana]	R.QISLLEGQNQTVKTGSDL.- K.SDEKQKK.L K.SDEKQKK.L K.WAVYVRGATNEDISVVVKK.V	41.01	15242448.0	4 (4 0 0 0 0)
#26	EFS (EARLY FLOWERING IN SHORT DAYS); histone	K.LPER.E K.LPER.E K.SQEMSNEEINEELGIGQDEADAYDCDAAK.R K.TANSPIPGNLTLEKK.L	40.92	240254387.0	4 (4 0 0 0 0)
#27	EF1A_ARATH RecName: Full=Elongation factor 1-alpha;	R.DMRQTVAVGVIK.S R.DMRQTVAVGVIK.S K.MTPTKPMVVETFSEYPPLGR.F R.YDEIIKEVSSYLKK.V	40.41	119143.0	4 (4 0 0 0 0)
#28	IF4A3_ARATH RecName: Full=Eukaryotic initiation fa	R.VLITTDLLAR.G R.VLITTDLLAR.G K.MFVLDEADEMLSR.G K.MFVLDEADEMLSR.G	40.38	75333652.0	4 (4 0 0 0 0)

#29	VATA_ARATH RecName: Full=V-type proton ATPase catal	R.TTLVANTSNMPVAAR.E R.TTLVANTSNMPVAAR.E K.LAADTPLLTGQR.V R.LAEMPADSGYPAYLAAR.L	40.25	3334404.0	4 (4 0 0 0 0)
#30	ATPBO_ARATH RecName: Full=ATP synthase subunit bet	K.VLNTGAPITVPVGR.A K.VLNTGAPITVPVGR.A K.VLNTGAPITVPVGR.A R.DAPALVDLATGQEILATGIK.V	40.23	75333362.0	4 (4 0 0 0 0)
#31	GLNA2_ARATH RecName: Full=Glutamine synthetase, ch	R.AKAAEIFSNKK.V R.AKAAEIFSNKK.V R.TIEKPVEDPSELPK.W R.TIEKPVEDPSELPK.W	40.17	11386828.0	4 (4 0 0 0 0)
#32	FRL1 (FRIGIDA LIKE 1) [Arabidopsis thaliana]	R.VEELEKNKALR.K R.IWDDETPLNQEVSAAIR.Y K.LAYHWKSKVGVK.P K.EVSALKPLIKIIK.D	40.13	15237325.0	4 (4 0 0 0 0)
#33	unnamed protein product [Arabidopsis thaliana]	K.TAIAEGLAQR.I K.LAEEGKLDPVVGRQPQIER.M R.VLENLGADPSNIR.T R.VLENLGADPSNIR.T	38.20	296529804.0	4 (3 1 0 0 0)
#34	putative hsp 70 protein [Arabidopsis thaliana]	R.KMNEVDEESKQVSYR.V R.IINEPTAASLAYGFDR.K R.IINEPTAASLAYGFDR.K	30.51	25054945.0	3 (3 0 0 0 0)
#35	jasmonate inducible protein isolog [Arabidopsis	K.SGFQISAPEATGK.Q K.SGFQISAPEATGK.Q K.VSVGGQAQDGIGAVSFVYDK.A	30.24	2062157.0	3 (3 0 0 0 0)
#36	EF1G2_ARATH RecName: Full=Probable elongation fact	K.MNPIGKVPVLETPEGPIFESNAIAR.Y K.AKNPLDLLPPSPMVLDDWKR.L K.AKNPLDLLPPSPMVLDDWKR.L	30.22	13626393.0	3 (3 0 0 0 0)
#37	unnamed protein product [Arabidopsis thaliana]	R.ADLNVPLDDNQTITDDTR.I R.LSELLGIEVTK.A R.LSELLGIEVTK.A	30.20	298541613.0	3 (3 0 0 0 0)
#38	LOS1; copper ion binding / translation elonga	R.RVIYASQITAKPR.L K.AYLPVVESFGFSSQLR.A K.AYLPVVESFGFSSQLR.A	30.19	30696056.0	3 (3 0 0 0 0)
#39	ATPAM_ARATH RecName: Full=ATP synthase subunit alp	R.AAELTNLFESR.I R.EVAAFAQFGSDLDAATQALLNR.G R.EVAAFAQFGSDLDAATQALLNR.G	30.19	14916970.0	3 (3 0 0 0 0)
#40	GCST_ARATH RecName: Full=Aminomethyltransferase, m	R.VGFFSSGPPAR.S R.RAEGGFLGADVILQQLK.D R.AEGGFLGADVILQQLKDGPTIR.R	30.16	18206365.0	3 (3 0 0 0 0)

#41	myb family transcription factor [Arabidopsis	K.YNKSVDILK.Y K.DRYYSVNR.A K.DRYYSVNR.A	30.11	30690620.0	3 (3 0 0 0 0)
#42	SWC2; DNA binding / transcription factor [Ara	K.KAIVHKAVYK.G R.NLERVLAREEEVK.K K.EENEAQEDMEGEK.V	30.10	79568513.0	3 (3 0 0 0 0)
#43	FLX	K.PNSDR.A R.MEAEARVIDGLGAELGQVR.S	20.49	238479397.0	2 (2 0 0 0 0)
#44	unnamed protein product [Arabidopsis thaliana]	R.AKHYLSLTSGGLGAYSDSR.G R.AKHYLSLTSGGLGAYSDSR.G	20.48	300649192.0	2 (2 0 0 0 0)
#45	ALFC1_ARATH RecName: Full=Probable fructose-bispho	K.MVDVLVEQNIVPGIKVDK.G K.MVDVLVEQNIVPGIKVDK.G	20.41	75313518.0	2 (2 0 0 0 0)
#46	transketolase, putative [Arabidopsis thaliana]	R.FLAIDAVEKAK.S R.FLAIDAVEKAK.S	20.38	30689983.0	2 (2 0 0 0 0)
#47	CAHC_ARATH RecName: Full=Carbonic anhydrase, chlor	R.NIANMVPPFDKVK.Y R.NIANMVPPFDKVK.Y	20.38	38503395.0	2 (2 0 0 0 0)
#48	PRS7A_ARATH RecName: Full=26S protease regulatory	R.KVEFGLPDLESR.T R.KVEFGLPDLESR.T	20.38	28558169.0	2 (2 0 0 0 0)
#49	G3PB_ARATH RecName: Full=Glyceraldehyde-3-phosphat	R.VVDLAHLVASK.W R.VPTPNVSVVDLVINVEK.K	20.23	20455491.0	2 (2 0 0 0 0)
#50	TBA1_ARATH RecName: Full=Tubulin alpha-1 chain	R.QLFHPEQLISGKEDAANNFAR.G R.QLFHPEQLISGKEDAANNFAR.G	20.21	135391.0	2 (2 0 0 0 0)
#51	ATPG1_ARATH RecName: Full=ATP synthase gamma chain 1	R.RPYIPVDKYLEAGTLPTAK.E R.RPYIPVDKYLEAGTLPTAK.E	20.18	461550.0	2 (2 0 0 0 0)
#52	DHE2_ARATH RecName: Full=Glutamate dehydrogenase 2	K.FIVEAANHPTDPDADEILSK.K K.FIVEAANHPTDPDADEILSK.K	20.18	12229806.0	2 (2 0 0 0 0)
#53	At3g42170 [Arabidopsis thaliana]	R.AIAGEDPFVTGIAK.T R.AIAGEDPFVTGIAK.T	20.18	27808618.0	2 (2 0 0 0 0)
#54	METK3_ARATH RecName: Full=S-adenosylmethionine syn	R.FVIGGPHGDAGLTGR.K R.FVIGGPHGDAGLTGR.K	20.17	75313514.0	2 (2 0 0 0 0)
#55	DHE1_ARATH RecName: Full=Glutamate dehydrogenase 1	K.GGIRYHPEVDPDEVNALAQLMTWK.T R.YHPEVDPDEVNALAQLMTWK.T	20.17	12229807.0	2 (2 0 0 0 0)
#56	ESM1_ARATH RecName: Full=GDSL esterase/lipase ESM1	K.IGPMLNEFAK.I K.DLPQTYWPYGK.S	20.14	75273556.0	2 (2 0 0 0 0)
#57	TBA6_ARATH RecName: Full=Tubulin alpha-6 chain	R.AVFVDLEPTVIDEVR.T	20.14	267070.0	2 (2 0 0 0 0)

		R.AVFVDLEPTVIDEVR.T			
#58	TBB5_ARATH RecName: Full=Tubulin beta-5 chain; AltNa	R.AVLMDLEPGTMDSIR.S R.AVLMDLEPGTMDSIR.S	20.13	267077.0	2 (2 0 0 0 0)
#59	MB31_ARATH RecName: Full=Myrosinase-binding protei	K.LGVNVAPIAK.- K.LGVNVAPIAK.-	20.13	12230212.0	2 (2 0 0 0 0)
#60	C71BQ_ARATH RecName: Full=Cytochrome P450 71B26	R.FNDSNIDAK.G R.FNDSNIDAK.G	16.45	13878380.0	2 (0 2 0 0 0)
#61	AT5g11760/T22P22_150 [Arabidopsis thaliana]	R.SQRTPEVQNPESR.D R.SQRTPEVQNPESR.D	16.18	16974389.0	2 (0 2 0 0 0)
#62	TAF14 (TBP-associated factor 14) [Arabidopsis	K.LNPENAYGPIPK.S	10.76	15227942.0	1 (1 0 0 0 0)
#63	SUF4 (suppressor of FRIGIDA4); DNA binding /	K.ENVTKVPNAKDGR.D	10.73	18397747.0	1 (1 0 0 0 0)
#64	P5CS2_ARATH RecName: Full=Delta-1-pyrroline-5-carbo	R.GPVGVEGLLTTR.W	10.48	1709535.0	1 (1 0 0 0 0)
#65	Clp amino terminal domain-containing protein	R.VLEILGADPSNIR.T	10.42	15230702.0	1 (1 0 0 0 0)
#66	METK4_ARATH RecName: Full=S-adenosylmethionine syn	K.YLDEKTIFHLNPSGR.F	10.34	75311602.0	1 (1 0 0 0 0)
#67	hypothetical protein At5g54062 [Arabidopsis tha	K.MFPLNPLFPPLLK.D K.MFPLNPLFPPLLK.D	10.31	67906738.0	2 (0 0 1 1 0)
#68	putative rab geranylgeranyl transferase [Arabid	K.AFLHKVTSSSESLSR.H	10.30	21436465.0	1 (1 0 0 0 0)
#69	BIP1_ARATH RecName: Full=Luminal-binding protein 1	R.ITPSWVGFTDSER.L	10.29	18206379.0	1 (1 0 0 0 0)
#70	putative Poly-A Binding Protein [Arabidopsis th	R.GSGFVAFSTPEEATR.A	10.27	17978685.0	1 (1 0 0 0 0)
#71	MFP1_ARATH RecName: Full=MAR-binding filament-like	K.KLEEDLGSAKGEILR.M	10.25	83304464.0	1 (1 0 0 0 0)
#72	G3PA_ARATH RecName: Full=Glyceraldehyde-3-phosphat	K.YDSTLGIFDADVKPSGETAISVDGK.I	10.25	20455490.0	1 (1 0 0 0 0)
#73	FTSH1_ARATH RecName: Full=Cell division protease f	R.SYLENQMAVALGGR.V	10.23	17865766.0	1 (1 0 0 0 0)
#74	PP437_ARATH RecName: Full=Putative pentatricopepti	R.NEMLRQGLIPNNK.T R.NEMLRQGLIPNNK.T	10.22	75171023.0	2 (0 0 1 1 0)
#75	CADH9_ARATH RecName: Full=Probable cinnamyl alcoh	K.SGVLSPFHFSR.R	10.19	148887169.0	1 (1 0 0 0 0)
#76	PRS6B_ARATH RecName: Full=26S protease regulatory	R.LAKENAPAIIFIDEVDAIATAR.F	10.19	28558168.0	1 (1 0 0 0 0)
#77	GDL18_ARATH RecName: Full=GDSL esterase/lipase At	K.TLVAQGFWPYGK.S	10.18	122178777.0	1 (1 0 0 0 0)
#78	BGL24_ARATH RecName: Full=Beta-glucosidase 24; Sh	R.YKEDIQLMK.N	10.18	269969442.0	1 (1 0 0 0 0)
#79	AC012563_16 hydroxypyruvate reductase (HPR); 509	R.VGLDVFEEEPFMKPGLADTK.N	10.17	12324078.0	1 (1 0 0 0 0)
#80	ACCC_ARATH RecName: Full=Biotin carboxylase,		10.17	75317871.0	1 (1 0 0 0 0)

	chlor	R.ALNDTIITGVPTTINYHK.L			
#81	unknown protein [Arabidopsis thaliana]	K.REMPAELLRASLR.H	10.17	14334732.0	1 (1 0 0 0 0)
#82	G3PC_ARATH RecName: Full=Glyceraldehyde-3-phosphat	K.VINDRFGIVEGLMTTVHSITATQK.T	10.17	20455492.0	1 (1 0 0 0 0)
#83	HSP73_ARATH RecName: Full=Heat shock cognate 70 kD	R.FTDSSVQSDIKLWPFTLK.S	10.17	18206367.0	1 (1 0 0 0 0)
#84	SAHH1_ARATH RecName: Full=Adenosylhomocysteinase 1;	K.TGQVPDPTSTDNPEFQIVLSIIKEGLQVDPK.K	10.16	6174970.0	1 (1 0 0 0 0)
#85	AL2B4_ARATH RecName: Full=Aldehyde dehydrogenase f	R.TGEVIAHVAEGDAEDINR.A	10.16	75313899.0	1 (1 0 0 0 0)
#86	F16P1_ARATH RecName: Full=Fructose-1,6-bisphosphat	R.VLDIQPTEIHQR.V	10.16	21431766.0	1 (1 0 0 0 0)
#87	AT4G35090 [Arabidopsis thaliana]	K.LFIQIIDPTDEDKFDFDPLDVTK.T	10.16	222423086.0	1 (1 0 0 0 0)
#88	RH36_ARATH RecName: Full=DEAD-box ATP-dependent RN	K.FLVLDEADRVLDVGFQDELR.T	10.16	75336890.0	1 (1 0 0 0 0)
#89	CAH2_ARATH RecName: Full=Carbonic anhydrase 2, chl	K.LLIEKDDLKDVAAAK.V	10.16	21903379.0	1 (1 0 0 0 0)
#90	ARGI2_ARATH RecName: Full=Probable arginase	R.VLSDVGDIPVQEIR.E	10.15	11131457.0	1 (1 0 0 0 0)
#91	ribulose-bisphosphate carboxylase [Arabid	R.AVYECLRGGLYFTKDDENVNSQPFMR.W	10.15	238479213.0	1 (1 0 0 0 0)
#92	NDUS1_ARATH RecName: Full=NADH-ubiquinone oxidored	R.ALSEVSGVKLPYNSIEGVR.S	10.15	55977290.0	1 (1 0 0 0 0)
#93	Y1934_ARATH RecName: Full=Uncharacterized protein	K.DLATAFLNVLGNEK.A	10.15	75313128.0	1 (1 0 0 0 0)
#94	hypothetical protein [Arabidopsis thaliana]	R.ELLIGDRQTGK.T	10.15	20198280.0	1 (1 0 0 0 0)
#95	unknown protein [Arabidopsis thaliana]	K.IMLEAIEREFEAATK.G	10.15	24899759.0	1 (1 0 0 0 0)
#96	unnamed protein product [Arabidopsis thaliana]	K.GVPLTQLNLASSVK.N	10.14	300540337.0	1 (1 0 0 0 0)
#97	DWA1_ARATH RecName: Full=WD repeat-containing prot	K.GQDVMVAEPER.V	10.14	75329665.0	1 (1 0 0 0 0)
#98	beta-glucosidase 1 [Arabidopsis thaliana]	R.YKEDIQXMK.D	10.14	166715126.0	1 (1 0 0 0 0)
#99	mRNA cleavage factor subunit-like protein [Arab	K.HPHVLLLQYRNSIFK.L	10.13	21554114.0	1 (1 0 0 0 0)
#100	MPPB_ARATH RecName: Full=Probable mitochondrial-pr	R.RIPTAELFAR.I	10.13	85700445.0	1 (1 0 0 0 0)
#101	BGL20_ARATH RecName: Full=Beta-glucosidase 20; Sho	R.YKEDIKLMK.N	10.13	75298266.0	1 (1 0 0 0 0)
#102	unknown protein [Arabidopsis thaliana]	R.SIAEEGVSGVRK.G	10.13	28973069.0	1 (1 0 0 0 0)
#103	putative aldehyde oxidase [Arabidopsis thaliana]	K.SVKSMPVATACALAANK.L	10.13	2792304.0	1 (1 0 0 0 0)
#104	DEAD/DEAH box helicase, putative [Arabido	R.ILVATDLVGR.G	10.13	238481240.0	1 (1 0 0 0 0)
#105	GAPC2 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDRO	K.AGIALSDKFVK.L	10.13	145323882.0	1 (1 0 0 0 0)
#106	unknown protein [Arabidopsis thaliana]		10.07	145334569.0	1 (1 0 0 0 0)

		K.KQKLSVLDK.T			

(B) Identified protein and their peptide sequence list with control IP

	Reference	Sequence	Score	Accession	Peptides (Hits)
#1	GDL19_ARATH RecName: Full=GDSL esterase/lipase At1		330.35	75162477.0	33 (33 0 0 0 0)
		K.AANWNDDFVKK.S			
		K.AANWNDDFVKK.S			
		K.NNPNADASTQQAFVTSVTNK.L			
		K.NNPNADASTQQAFVTSVTNK.L			
		K.QHNEKIGPMLNELAR.T			
		R.ELVVYPADEPMR.E			
		R.ELVVYPADEPMR.E			
		K.LKNDISLLYSSGASK.F			
		K.LKNDISLLYSSGASK.F			
		K.IGPMLNELAR.T			
		K.IGPMLNELAR.T			
		K.IGPMLNELAR.T			
		K.IGPMLNELAR.T			
		K.SRDDPNGKFSDGLIAPDFLAK.F			
		K.SRDDPNGKFSDGLIAPDFLAK.F			
		K.SRDDPNGKFSDGLIAPDFLAK.F			
		K.SRDDPNGKFSDGLIAPDFLAK.F			
		R.DDPNGKFSDGLIAPDFLAK.F			
		R.DDPNGKFSDGLIAPDFLAK.F			
		R.DDPNGKFSDGLIAPDFLAK.F			
		R.DDPNGKFSDGLIAPDFLAK.F			
		K.SRDDPNGKFSDGLIAPDFLAK.F			
		K.FSDGLIAPDFLAK.F			
		K.FSDGLIAPDFLAK.F			
		K.TLLPQTFWPYGK.S			
		K.TLLPQTFWPYGK.S			
		K.TLLPQTFWPYGK.S			
		R.GASFAVADATLLGAPVESLTLNQQVRK.F			
		R.GASFAVADATLLGAPVESLTLNQQVRK.F			
		R.GASFAVADATLLGAPVESLTLNQQVRK.F			
		R.GASFAVADATLLGAPVESLTLNQQVR.K			
		R.GASFAVADATLLGAPVESLTLNQQVR.K			
		R.GASFAVADATLLGAPVESLTLNQQVR.K			
#2	jasmonate inducible protein isolog [Arabidopsis		284.31	2062157.0	29 (26 3 0 0 0)
		K.DGQKIVGFHGR.A			
		K.DGQKIVGFHGR.A			
		K.VYVGQGQDGVAAVK.F			
		K.LTAEGGETGAVWDDGSHDDVKK.V			
		K.FGVHVAPITK.-			
		K.SGFQISAPEATGK.Q			
		K.SGFQISAPEATGK.Q			
		K.FEYKNGSQVVFGDER.G			
		K.IYASYGGEGIQYVK.F			
		R.AGDLLHKFGVHVAPITK.-			
		R.KVSVGQAQDGIGAVSFVYDK.A			
		R.KVSVGQAQDGIGAVSFVYDK.A			
		K.LEGAGSEAGTLWDDGAFDGVRK.V			
		K.LEGAGSEAGTLWDDGAFDGVRK.V			

		K.LEGAGSEAGTLWDDGAFDGVRK.V K.VSVGQAQDGIGAVSFVYDK.A K.VSVGQAQDGIGAVSFVYDK.A K.LEGAGSEAGTLWDDGAFDGVR.K K.LEGAGSEAGTLWDDGAFDGVR.K K.LEGAGSEAGTLWDDGAFDGVR.K K.LEGAGSEAGTLWDDGAFDGVR.K R.VSIPFGIGAGTAFEFKK.D R.VSIPFGIGAGTAFEFKK.D K.VSVGQAQDGIGAVSFVYDKAGQVVEGK.E K.VSVGQAQDGIGAVSFVYDKAGQVVEGK.E K.SLSTQEVITALTFTTNKTSYGPYGTK.S K.SLSTQEVITALTFTTNKTSYGPYGTK.S K.SAEFTLAPDEYITALSAYGK.S K.SAEFTLAPDEYITALSAYGK.S			
#3	BGL23_ARATH RecName: Full=Beta-glucosidase 23; Sho	K.NLNTDAFR.M K.NLNTDAFR.M K.NLNTDAFR.M K.NLNTDAFR.M K.NLNTDAFR.M K.DIVGHRLPKFTTEQK.A R.SLLKYIK.D R.MSIAWPR.I R.MSIAWPR.I R.MSIAWPR.I R.YKEDIQLMKNLNTDAFR.M K.IGIAHSPAWFEAHDLADSQDGASIDR.A R.YKEDIQLMKNLNTDAFR.M K.IGIAHSPAWFEAHDLADSQDGASIDR.A K.NAQNYAIGSKPLTAALNVYSR.G K.NAQNYAIGSKPLTAALNVYSR.G K.NAQNYAIGSKPLTAALNVYSR.G K.NAQNYAIGSKPLTAALNVYSR.G K.NAQNYAIGSKPLTAALNVYSR.G R.WMQDSLITWESK.N R.WMQDSLITWESK.N R.FGLYYVDFK.N K.ASTDFVGLNYYTSVFSNHLEKPDPSKPR.W K.ASTDFVGLNYYTSVFSNHLEKPDPSKPR.W	234.38	75313794.0	24 (23 0 0 1 0)
#4	MB31_ARATH RecName: Full=Myrosinase-binding protei	K.ASKPVLGSDHGKK.T K.ASKPVLGSDHGKK.T R.GGEEWDDGGAYENVKK.V K.LGVNVAPIAK.- K.LEAQGGRGGDVWDDGGAYDNVKK.V K.LGVNVAPIAK.- K.GKTSQPFGLTSGEEAELGGGK.I K.TSQPFGLTSGEEAELGGGK.I K.TSQPFGLTSGEEAELGGGK.I K.IYVGQGDSCVTYFK.A K.IVGFYGQAGEYLYK.L	110.31	12230212.0	11 (11 0 0 0 0)
#5	ESM1_ARATH RecName: Full=GDSL esterase/lipase		100.27	75273556.0	10 (10 0 0 0 0)

	ESM1	R.KDLPQTYWPYGK.S R.KDLPQTYWPYGK.S R.ELIVYPTGETMR.E K.DLPQTYWPYGK.S K.DLPQTYWPYGK.S K.DLPQTYWPYGK.S K.DLPQTYWPYGK.S K.AQEEMAHLLYGADPDVVQPMTVR.E K.AQEEMAHLLYGADPDVVQPMTVR.E R.GVSFAVADASILGAPVESMTLNQQVVK.F			
#6	CATA3_ARATH RecName: Full=Catalase-3	R.LNVRPSI.- R.LNVRPSI.- R.LNVRPSI.- R.LNVRPSI.- R.LNVRPSI.- R.APGVQTPVIVR.F R.APGVQTPVIVR.F	70.14	21903384.0	7 (7 0 0 0 0)
#7	AC008051_11 Identical to gene ZW9 from Arabidopsi	R.VIDQIQSNNFEK.K R.VIDQIQSNNFEK.K K.LRVIDQIQSNNFEKK.V K.LRVIDQIQSNNFEKK.V R.FLDSYTSDSFSSGGR.N	50.46	8979946.0	5 (5 0 0 0 0)
#8	GDL18_ARATH RecName: Full=GDSL esterase/lipase At	K.IGPMLNEMAR.N K.TLVAQGFWPYGK.S K.TLVAQGFWPYGK.S K.TLVAQGFWPYGK.S K.SRDDPNGKFSDGLITPDFLAK.F	48.24	122178777.0	5 (4 1 0 0 0)
#9	unknown protein [Arabidopsis thaliana]	R.YNYDHDLSLGELKFLARR.G R.YNYDHDLSLGELKFLARR.G R.YNYDHDLSLGELKFLARR.G R.YNYDHDLSLGELKFLARR.G	40.16	240254445.0	4 (4 0 0 0 0)
#10	BGL18_ARATH RecName: Full=Beta-glucosidase 18; Sh	K.DLNTDAFR.L K.DLNTDAFR.L R.YKEDIQLMKDLNTDAFR.L R.YKEDIQLMKDLNTDAFR.L	32.21	166897681.0	4 (0 4 0 0 0)
#11	BGL20_ARATH RecName: Full=Beta-glucosidase 20; Sho	R.YKEDIKLMK.N R.YKEDIKLMK.N R.FSIAWPR.I	30.18	75298266.0	3 (3 0 0 0 0)
#12	BGL24_ARATH RecName: Full=Beta-glucosidase 24; Sh	K.DIVGHRLPK.F R.YKEDIQLMK.N R.YKEDIQLMK.N	30.14	269969442.0	3 (3 0 0 0 0)
#13	RH48_ARATH RecName: Full=Probable DEAD-box ATP-dep	R.SGSITGSLWNRISSR.N R.SGSITGSLWNRISSR.N R.SGSITGSLWNRISSR.N	30.11	75333533.0	3 (3 0 0 0 0)
#14	RCA_ARATH RecName: Full=Ribulose bisphosphate		20.42	12643259.0	2 (2 0 0 0 0)

	carb	R.GLAYDTSDDQQDITR.G R.GLAYDTSDDQQDITR.G			
#15	binding / calmodulin binding [Arabidopsis th	R.GQIVRSRLQGASTLYSK.L R.GQIVRSRLQGASTLYSK.L	20.29	240256033.0	2 (2 0 0 0 0)
#16	BGL22_ARATH RecName: Full=Beta-glucosidase 22; Sho	K.NVDHSAIGSQPLTAALPVYAK.G K.NVDHSAIGSQPLTAALPVYAK.G	20.17	75308894.0	2 (2 0 0 0 0)
#17	RBL_ARATH RecName: Full=Ribulose bisphosphate carbo	R.DLAVEGNEIIR.E K.DTDILAAFR.V	20.16	3914541.0	2 (2 0 0 0 0)
#18	beta-glucosidase 1 [Arabidopsis thaliana]	R.YKEDIQXMK.D R.YKEDIQXMK.D	20.14	166715126.0	2 (2 0 0 0 0)
#19	At2g19385 [Arabidopsis thaliana]	K.GQSKSANGTPAK.P K.AELELKVNLSSR.F	20.13	87116626.0	2 (2 0 0 0 0)
#20	EF1A_ARATH RecName: Full=Elongation factor 1-alpha;	K.IGGIGTVPVGR.V K.IGGIGTVPVGR.V	20.13	119143.0	2 (2 0 0 0 0)
#21	DIN9 (DARK INDUCIBLE 9); mannose-6-phosphate	R.GKSTVFPAVPGPSVYLVIEGKGQLR.T R.GKSTVFPAVPGPSVYLVIEGKGQLR.T	20.13	15219821.0	2 (2 0 0 0 0)
#22	AC026237_3 Similar to protein kinases [Arabidopsi	K.GTRNGSVAIAIDK.D K.GTRNGSVAIAIDK.D	20.12	9954729.0	2 (2 0 0 0 0)
#23	unknown protein [Arabidopsis thaliana]	K.MTVNDVVLGVSQAGLSQYLDR.R K.MTVNDVVLGVSQAGLSQYLDR.R	20.11	15229104.0	2 (2 0 0 0 0)
#24	AC010795_8 RNA polymerase IIA largest subunit, p	K.KLVGFEGNTLELSSR.V K.KLVGFEGNTLELSSR.V	18.22	12323252.0	2 (1 1 0 0 0)
#25	putative protein [Arabidopsis thaliana]	K.PHSDNNLVELGDVAEKDDDK.A K.PHSDNNLVELGDVAEKDDDK.A K.PHSDNNLVELGDVAEKDDDK.A	18.21	22531002.0	3 (0 1 1 1 0)
#26	FBK37_ARATH RecName: Full=Putative F-box/kelch-rep	R.AVAEVINGKIYVIGGCEK.R R.AVAEVINGKIYVIGGCEK.R	18.18	75100655.0	2 (1 1 0 0 0)
#27	hypothetical protein At2g20805 [Arabidopsis tha	R.KYENNLVKAK.N R.KYENNLVKAK.N	18.13	91805453.0	2 (1 1 0 0 0)
#28	unknown protein [Arabidopsis thaliana]	K.QFVDLLTEELKLQEAVADEHSR.H K.QFVDLLTEELKLQEAVADEHSR.H	16.63	21281115.0	2 (0 2 0 0 0)
#29	UDP-glucose 6-dehydrogenase, putative [Arabid	K.KLDFQRIFENMQK.P K.KLDFQRIFENMQK.P	16.56	15242316.0	2 (0 2 0 0 0)
#30	AGL5_ARATH RecName: Full=Agamous-like MADS-box prote	-.MEGGASNEVAESSKK.I -.MEGGASNEVAESSKK.I	16.54	113515.0	2 (0 2 0 0 0)
#31	4325351 T25H8.2 TNP2 pr	K.QNIVLIICNFEK.I	16.49	6272381.0	2 (0 2 0 0 0)

		K.QNIVLIICNFEK.I			
#32	PUB50_ARATH RecName: Full=Putative U-box domain-co	R.KYEDQKIDK.L R.KYEDQKIDK.L	16.39	75333799.0	2 (0 2 0 0 0)
#33	CPSF1_ARATH RecName: Full=Cleavage and polyadenyl	K.RGGVMDGVYGVSLELVCHYR.L K.RGGVMDGVYGVSLELVCHYR.L	16.38	290457637.0	2 (0 2 0 0 0)
#34	ALA8_ARATH RecName: Full=Putative phospholipid-tra	R.WYLRPDHTTVFYDPRR.A R.WYLRPDHTTVFYDPRR.A	16.28	12229655.0	2 (0 2 0 0 0)
#35	RH33_ARATH RecName: Full=Putative DEAD-box ATP-dep	K.KQSVDNVMEEK.Q K.KQSVDNVMEEK.Q	16.25	75318697.0	2 (0 2 0 0 0)
#36	AC012680_8 putative mitochondrial carrier protei	K.QLLKIAGNQEATNFER.F K.QLLKIAGNQEATNFER.F	16.15	12324250.0	2 (0 2 0 0 0)
#37	putative protein kinase [Arabidopsis thaliana]	R.ENLVAREVLLVLK.T R.ENLVAREVLLVLK.T	16.12	3980410.0	2 (0 2 0 0 0)
#38	FK125_ARATH RecName: Full=F-box/kelch-repeat prot	R.PKLRIDPSLTLIPGLSNDVGR.L R.PKLRIDPSLTLIPGLSNDVGR.L	16.11	122223580.0	2 (1 0 1 0 0)
#39	BIM1; DNA binding / protein binding / tra	R.DKASFLLEVIEYIQFLQEKADK.Y R.DKASFLLEVIEYIQFLQEKADK.Y	14.67	238481217.0	2 (0 1 1 0 0)
#40	glycosyl hydrolase family 10 protein [Arabido	K.LGFPFGCEVEKNILGNK.A K.LGFPFGCEVEKNILGNK.A	14.57	42567365.0	2 (0 1 1 0 0)
#41	AC011661_23 T23J18.16 [Arabidopsis thaliana]	R.TTVELICNTGYSHKLGK.M R.TTVELICNTGYSHKLGK.M	14.54	6554199.0	2 (0 1 1 0 0)
#42	PP334_ARATH RecName: Full=Pentatricopeptide repeat	K.AEAMLEDLAR.R K.AEAMLEDLAR.R	14.13	75146702.0	2 (0 1 1 0 0)
#43	NAD+ dependent isocitrate dehydrogenase subunit	K.CRTKDLGGTSTTQEVVDAGIAK.L K.CRTKDLGGTSTTQEVVDAGIAK.L	12.71	1766046.0	2 (0 0 2 0 0)
#44	galactinol synthase, putative [Arabidopsis th	-.MAPTEMNIERKVEADVAVIPNDGK.R -.MAPTEMNIERKVEADVAVIPNDGK.R	12.69	30692339.0	2 (0 1 0 1 0)
#45	Unknown protein [Arabidopsis thaliana]	K.SVNWHSTPFEARLEKALNNIDK.- K.SVNWHSTPFEARLEKALNNIDK.-	12.65	4204286.0	2 (0 0 2 0 0)
#46	downy mildew resistance protein RPP5 [Arabidopsi	R.NEIVVEDCFWNK.N R.NEIVVEDCFWNK.N	12.59	6449046.0	2 (0 0 2 0 0)
#47	ANP1_ARATH RecName: Full=Mitogen-activated protein	K.PSFSPPPPANTVDMAPPISWR.K K.PSFSPPPPANTVDMAPPISWR.K	12.14	46576858.0	2 (0 1 0 1 0)
#48	ATP binding / protein binding / transmembran	R.FLWDPTEIHYVLDSNTGTR.R R.FLWDPTEIHYVLDSNTGTR.R	12.12	145337463.0	2 (0 0 2 0 0)
#49	CADH6_ARATH RecName: Full=Probable cinnamyl		10.62	75318586.0	2 (0 0 1 1 0)

	alcoho	K.AFGTKVTVVSSTTGKSK.D K.AFGTKVTVVSSTTGKSK.D			
#50	AF339713_1 unknown protein [Arabidopsis thaliana]	K.ALLGEGATVVLEGQKVLPVR.A	10.41	12642906.0	1 (1 0 0 0 0)
#51	RQL5_ARATH RecName: Full=ATP-dependent DNA helica	K.SDGVDFVPEPPLVEVIAPPK.S	10.38	298289257.0	1 (1 0 0 0 0)
#52	zinc finger protein-related [Arabidopsis thal	R.YNILLAQPPRASVPLVAAAR.D	10.36	30697493.0	1 (1 0 0 0 0)
#53	At3g29035 [Arabidopsis thaliana]	K.FAIDNLSKTAK.N	10.33	30984532.0	1 (1 0 0 0 0)
#54	P2A01_ARATH RecName: Full=Protein PHLOEM PROTEIN 2	K.MFRNQDSKYLIPVQK.E	10.31	75100453.0	1 (1 0 0 0 0)
#55	At1g19690 [Arabidopsis thaliana]	-.MAVFQLPSLSPEIPFR.F	10.31	109946403.0	1 (1 0 0 0 0)
#56	CATA1_ARATH RecName: Full=Catalase-1	R.LGPNYLQLPVNAPK.C	10.31	21903389.0	1 (1 0 0 0 0)
#57	TBB4_ARATH RecName: Full=Tubulin beta-4 chain; Alt	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	10.30	27735260.0	1 (1 0 0 0 0)
#58	FER4_ARATH RecName: Full=Probable ferredoxin-4, ch	R.ISPSQAQLTTR.L	10.29	75309110.0	1 (1 0 0 0 0)
#59	catalytic/ transferase [Arabidopsis thaliana]	R.ACSFLSNSYILEEGK.V	10.29	240256302.0	1 (1 0 0 0 0)
#60	serine/threonine protein kinase, putative [Ar	K.FGDEISREDK.E	10.29	15240865.0	1 (1 0 0 0 0)
#61	unknown protein [Arabidopsis thaliana]	R.VFLLQDIIR.V	10.27	30793793.0	1 (1 0 0 0 0)
#62	SCL26_ARATH RecName: Full=Scarecrow-like protein 2	R.FSHQTPSSVISFLSEAK.T	10.26	75208411.0	1 (1 0 0 0 0)
#63	suppressor of ABI3-5 [Arabidopsis thaliana]	R.TLLHKKALAR.F	10.23	293339650.0	1 (1 0 0 0 0)
#64	AC068602_19 F14D16.28 [Arabidopsis thaliana]	K.LMGLLRSFDQFGTCLSLLHRK.S	10.22	8778287.0	1 (1 0 0 0 0)
#65	PROL_ARATH RecName: Full=Protein PROLIFERA	K.GFLENFADANGRSK.Y	10.22	20141757.0	1 (1 0 0 0 0)
#66	antiporter/ drug transporter/ transporter [A	K.LRECVGCVSEETSK.A	10.20	186512202.0	1 (1 0 0 0 0)
#67	CX32_ARATH RecName: Full=Probable serine/threonine	-.MGACISFFSSSSPSK.T	10.17	49066036.0	1 (1 0 0 0 0)
#68	unknown protein [Arabidopsis thaliana]	R.LIVTNLGEQVIEAQIVTGTHAGKMVSIPR.F	10.15	15241916.0	1 (1 0 0 0 0)
#69	EFTU_ARATH RecName: Full=Elongation factor Tu, chlor	K.ILDEALAGDNVGLLLR.G	10.15	119194.0	1 (1 0 0 0 0)
#70	AC018363_34 unknown protein [Arabidopsis thaliana]	-.MDLVWLLSVLLVGAALGYYISTLR.Q	10.14	6728991.0	1 (1 0 0 0 0)
#71	hypothetical protein At3g02410 [Arabidopsis tha	R.RSIVYGGHPRNR.L	10.14	91806373.0	1 (1 0 0 0 0)
#72	unknown protein [Arabidopsis thaliana]	R.EAVTFGVTGAALGAVSTAAFAWKYSR.S	10.14	18390902.0	1 (1 0 0 0 0)
#73	PP276_ARATH RecName: Full=Pentatricopeptide repeat	K.ALCLTESLSAIAENSTTLLNLNRR.L	10.14	75183390.0	1 (1 0 0 0 0)
#74	DRL18_ARATH RecName: Full=Probable disease resista	K.ENFVVQASAGLHEIPEVKDWGAVR.R	10.14	46395618.0	1 (1 0 0 0 0)

#75	unknown protein [Arabidopsis thaliana]	R.IPESLTNIYR.L	10.13	21436417.0	1 (1 0 0 0 0)
#76	AF332462_1 unknown protein [Arabidopsis thaliana]	K.TVSDGFVGGFFPVSTTKIAWKSR.K	10.13	12083332.0	1 (1 0 0 0 0)
#77	FAR1_ARATH RecName: Full=Protein FAR-RED IMPAIRED	R.QSGGYKNIGSLLQTDVSSQVDK.G	10.13	75213095.0	1 (1 0 0 0 0)
#78	AC079284_3 hypothetical protein [Arabidopsis tha	K.CCSEAEKEDADGGISDK.V	10.13	12321786.0	1 (1 0 0 0 0)
#79	DEGP3_ARATH RecName: Full=Putative protease Do-lik	R.LFQPWQITMQSESTGSGFVISGKK.I	10.13	75265871.0	1 (1 0 0 0 0)
#80	unknown protein [Arabidopsis thaliana]	-.MVFYFKARPDAGDYTIFMGLDK.F	10.13	23297161.0	1 (1 0 0 0 0)
#81	GGPP1_ARATH RecName: Full=Geranylgeranyl pyrophosp	K.IHEAMRYSLLAGGKR.V	10.13	13432144.0	1 (1 0 0 0 0)
#82	RBCMT_ARATH RecName: Full=Probable ribulose-1,5 bi	K.EYVENEFLK.L	10.13	17369870.0	1 (1 0 0 0 0)
#83	SBP_ARATH RecName: Full=Putative selenium-binding p	R.QFYPEIMEK.G	10.13	6094242.0	1 (1 0 0 0 0)
#84	AT4g27860/T27E11_100 [Arabidopsis thaliana]	R.YTTTATTASGFSQFVGYLVSQWLEK.S	10.13	17063191.0	1 (1 0 0 0 0)
#85	putative rab geranylgeranyl transferase [Arabid	K.AFLHKVTSSSESLSR.H	10.13	21436465.0	1 (1 0 0 0 0)
#86	PHD finger family protein [Arabidopsis thaliana]	R.VHVQGVPGGDLGLFECVSSVFSR.Q	10.13	15235176.0	1 (1 0 0 0 0)
#87	NUD24_ARATH RecName: Full=Nudix hydrolase 24, chlo	K.DSCSLVIIDFLFRHGLIRPESPGYLDLYR.R	10.13	68565860.0	1 (1 0 0 0 0)
#88	MYB transcription factor [Arabidopsis thaliana]	R.LMNFILNNGIHCWR.I	10.12	41619392.0	1 (1 0 0 0 0)
#89	ATP binding / kinase [Arabidopsis thaliana]	R.EAIYKLK.C	10.12	240254425.0	1 (1 0 0 0 0)
#90	unknown protein [Arabidopsis thaliana]	R.DSSVFALDSDTGNMIGTNMIK.P	10.12	145353594.0	1 (1 0 0 0 0)
#91	AB5A_ARATH RecName: Full=ABC transporter A family	K.VYPCRDGNPQKMAVR.G	10.11	257050992.0	1 (1 0 0 0 0)
#92	At3g55910 [Arabidopsis thaliana]	R.HPPIDVYCICREVTEVMEK.L	10.11	119360115.0	1 (1 0 0 0 0)
#93	MRS23_ARATH RecName: Full=Magnesium transporter MR	R.TWLVLNSSGQSEPK.E	10.11	75273604.0	1 (1 0 0 0 0)
#94	BG5 (beta-1,3-glucanase 5); glucan 1,3-beta-g	K.VITLYKSIDITKIR.I	10.11	15241326.0	1 (1 0 0 0 0)
#95	WPP3_ARATH RecName: Full=WPP domain-containing pr	K.NLEVYGIETSER.M	10.11	122175407.0	1 (1 0 0 0 0)
#96	unnamed protein product [Arabidopsis thaliana]	R.GCTSLKSLPEIQLISLK.T	10.11	257729095.0	1 (1 0 0 0 0)
#97	SYK_ARATH RecName: Full=Lysyl-tRNA synthetase; Alt	R.KADNVNAK.K	10.11	55583786.0	1 (1 0 0 0 0)
#98	MYRS2_ARATH RecName: Full=Myrcene/ocimene synthase	R.FVETAMNLAR.M	10.11	75273871.0	1 (1 0 0 0 0)
#99	unnamed protein product [Arabidopsis thaliana]	R.ESLVTRLFTSAENKR.M	10.11	9758394.0	1 (1 0 0 0 0)
#100	AF454354_1 sulfolipid synthase [Arabidopsis thal	R.AGGIPDIIPEDQEGK.T	10.11	20302857.0	1 (1 0 0 0 0)

#101	unknown protein [Arabidopsis thaliana]	R.KIVAQGSR.L	10.11	3341696.0	1 (1 0 0 0 0)
#102	anthranilate N-hydroxycinnamoyl/benzoyltransfer	R.IPLPETETPNR.V	10.10	21536885.0	1 (1 0 0 0 0)
#103	AC025294_6 NADP-specific glutatamate dehydrogena	K.TVMSKSAGSIVEGALK.R	10.10	12321666.0	1 (1 0 0 0 0)
#104	AC022456_5 Tam1 transposon protein TNP2, putativ	K.FLKDFVRNPAR.P	10.10	12324112.0	1 (1 0 0 0 0)
#105	AC012562_29 hypothetical protein; 78804-81924 [A	K.PEDKLFGDLVELSKFK.K	10.10	12322744.0	1 (1 0 0 0 0)
#106	ALFC1_ARATH RecName: Full=Probable fructose-bispho	K.MVDVLVEQNIVPGIKVDK.G	10.10	75313518.0	1 (1 0 0 0 0)
#107	SYP73_ARATH RecName: Full=Syntaxin-73; Short=AtSYP73	K.GLSKEELDAR.N	10.10	28380157.0	1 (1 0 0 0 0)
#108	putative pre-mRNA splicing factor [Arabidopsis t	K.GVKLIPNSVKLWLEAAK.L	10.10	4206197.0	1 (1 0 0 0 0)
#109	AC022456_2 hypothetical protein; 33648-34648 [Ar	K.ISVARAKFK.P	10.10	12324109.0	1 (1 0 0 0 0)
#110	ATP binding / nucleoside-triphosphatase/	K.RNASAASDISSISSR.S	10.10	145334803.0	1 (1 0 0 0 0)
#111	unknown protein [Arabidopsis thaliana]	R.MSNKQKK.E	10.10	14532606.0	1 (1 0 0 0 0)
#112	hypothetical protein [Arabidopsis thaliana]	-.MFGSLVYPKK.V	10.10	3643596.0	1 (1 0 0 0 0)
#113	NUA_ARATH RecName: Full=Nuclear-pore anchor; AltN	K.EDALLSASAEIASLR.E	10.10	302425121.0	1 (1 0 0 0 0)
#114	unknown protein [Arabidopsis thaliana]	K.ELQILEYGESDDEVKR.L	10.10	238478373.0	1 (1 0 0 0 0)
#115	AC011622_2 unknown protein; 58777-61253 [Arabido	K.SQLDLLKKLHEK.C	10.10	12324935.0	1 (1 0 0 0 0)
#116	At4g21500 [Arabidopsis thaliana]	R.ESDLMGGFVEWNLR.A	10.10	45752754.0	1 (1 0 0 0 0)
#117	FPP7_ARATH RecName: Full=Filament-like plant prote	K.ASQEYER.R	10.10	75206690.0	1 (1 0 0 0 0)

Supplemental Table 2. Primers for plasmid construction and PCR

primer			**sequence**
For transgenic line			
HJ1	*35S-myc:FRI*	F	5'-aaaaggatccaaATGTCCAATTATCCACCGAC
		R	5'-ttttggatccCTATTTGGGGTCTAATGATG
KH160	*35S-myc:FLX*	F	5'-ggatccgtATGGCCGGACGAGATCGTTA
		R	5'-ggatccCTATAGACTCATGTGTAC
KH169	*proFLX-FLX:GUS*	F	5'-ctgcagGACTAGCTTGTGACCATCGC
		R	5'-ggatccttAACTGTGTAAAGCAAAAAGC
SIRI169	*proSUF4-SUF4-FLAG*	F	5'-ctgcagATCTTTAACTTTTTTGTTGTTGC
		R	5'-tctagaCACTAAATCTTTCTCCTATTTG
		F	5'-ggatccATGGGTAAGAAGAAGAAGAG
		R	5'-ggatccCTAAAACGCCATCCGCC
SIRI172	*proFRI-FLAG-FRI*	F	5'-ctgcagTATAAGAAAGTTACGAAAATGCC
		R	5'-tctagaGAGATTGCGGCGAAGAAAA
		F	5'-gtcgacATGTCCAATTATCCACC
		R	5'-gtcgacCTATTTGGGGTCTAATGATG
	35S-OsSUF4	F	5'-aaaaggatccaaATGGGGAAGAAGAAG
		R	5'-ccggatccTTACACAATATTCCAG

For yeast two hybrid assay			
KH185	AD/BD-FLX	F	5'-ggatccgtATGGCCGGACGAGATCGTTA
KH184		R	5'-ggatccCTATAGACTCATGTGTAC
KH211	AD/BD-FES1	F	5'-agatctgtATGTCTGATTCCGACATG
KH210		R	5'-agatctGGGTTTACCATACTTTTC
KH344	AD/BD-FLX-D1	F	5'-gtagcccggggATCCTCGAGGATCGAATCGC
KH342		R	5'-ggatccCTATAGACTCATGTGTAC
KH345	AD/BD-FLX-D2	F	5'-gtagcccggggATGGCTAAGGCTAAACCGAA
KH343		R	5'-ggatccCTATAGACTCATGTGTAC
KH331	AD/BD-SUF4-D1	F	5'-ggatccgtATGGGTAAGAAGAAGAAGAGA
KH330		R	5'-ggatccATCCTCTTCTTCTCCATAATG
KH333	AD/BD-SUF4-D2	F	5'-ggatccgtATGGGTAAGAAGAAGAAGAGA
KH332		R	5'-ggatccTGGAGTTGGAGTCATCCCCAT
KH335	AD/BD-SUF4-D3	F	5'-ggatccgtAATGTTACAAAAGTTCCTAAT
KH334		R	5'-ggatccCTAAAACGCCATCCGCCCAGC
KH271	AD/BD-FRI-D1	F	5'-ggatccgtATGTCCAATTATCCACCGAC
KH270		R	5'-ggatccCCATCCTGGTAGTTCTTTCGC
KH273	AD/BD-FRI-D2	F	5'-ggatccgtAAGCAGCCTCAATTTTTGAAATCC
KH272		R	5'-ggatccTTGGTTATACATTCTCTTGGC
KH275	AD/BD-FRI-D3	F	5'-ggatccgtGGCGTTGTCCTCGCCGCG
KH274		R	5'-ggatccCTATTTGGGGTCTAATGATG
KH341	AD/BD-FRI-D4	F	5'-ggatccccATGGAAATGCCACCAGTAACT
KH340		R	5'-ggatccCTATTTGGGGTCTAATGATG
SIRI134	BD-PIE1	F	5'-atgcggatccatATGGCGTCTAAAGGTGGTAAATC

		R	5'-atgcggatccCTACTCTATTTCTGAGATATC
SIRI73	BD-RVB1	F	5'-atgcgaattcATGGAGAAAGTAAAGATTGAAG
		R	5'-atgcgaattcTCATGAGATGTATTTTTCTTG
SIRI72	BD-YAF9	F	5'-atgcggatccatATGACGAACAGCTCGTCA
		R	5'-atgcggatccTCACAGGTCTGATCCTGT
SIRI71	BD-SWC5	F	5'-atgcggatccatATGGGATCTCATGAGCAATC
		R	5'-atgcggatccTCATACATCATCGTGTCTTCT
SIRI70	BD-ACT1	F	5'-atgcggatccatATGGCTGATGGTGAAGAC
		R	5'-atgcggatccTCAGAAGCACTTCCTGTG
SIRI69	BD-ARP4	F	5'-atgcggatccatATGTACGGCGGAGATGAA
		R	5'-atgcggatccTTAAGGGCATTTTCTCTGAATG
KH364	AD/BD-FLX LIKE1	F	5'-gtagcccggggATGTCTGGAAGAAACCGGAT
KH350		R	5'-gtacggatccTCAATGACGATCCAAACGAG
KH363	AD/BD-FLX LIKE2	F	5'-gtagcccggggATGGAAAGCAAAGGAAGAAT
KH349		R	5'-gtacggatccTCATCTGCGACTAGGGTTTC
KH362	AD/BD-FLX LIKE3	F	5'-gtagcccggggATGTCTGGAAGAAATCGTGG
KH348		R	5'-gtacggatccTCATCGATGTCCTTGTCCTT
KH365	AD/BD-FLX LIKE4	F	5'-gtaggaattcATGTCTTCAAGGGAGAGGAT
KH351		R	5'-gtagcccgggTCAATTCTCGACAGCTTTGT
SIRI186	AD/BD-TAF14	F	5'-ggatccgtATGGAGTCGGATATCGAGATTTTG
SIRI183		R	5'-ggatccTCAGAACAAGAATGCACCTGG
SIRI180	BD-FES1-D3	F	5'-agatctgtATGTCTGATTCCGACATG
		R	5'-agatctAACAAAAACGTGCAGCTCTTC
SIRI182	BD-FES1-D4	F	5'-agatctAACAAAAACGTGCAGCTCTTC
		R	5'-agatctGGGTTTACCATACTTTTC

For bimolecular flourescence complementation

KH518	nYFP-FLX	F	5'-ggatccgtATGGCCGGACGAGATCGTTA
		R	5'-ggatccCTATAGACTCATGTGTAC
KH523	cYFP-FLX	F	5'-ggatccATGGCCGGACGAGATCGTTA
		R	5'-ggatccCTATAGACTCATGTGTAC
KH519	nYFP-SUF4	F	5'-ggatccgtATGGGTAAGAAGAAGAAGAGA
		R	5'-ggatccCTAAAACGCCATCCGCCCAGC
KH524	cYFP-SUF4	F	5'-ggatccATGGGTAAGAAGAAGAAG
		R	5'-ggatccCTAAAACGCCATCCGCCCAGC
KH520	nYFP-FRL1	F	5'-ggatccgtATGACGGCGAGTGAGACTATC
		R	5'-ggatccCTACTGAGAATAATAAGGCGG
KH525	cYFP-FRL1	F	5'-ggatccATGACGGCGAGTGAGACT
		R	5'-ggatccCTACTGAGAATAATAAGGCGG
KH521	nYFP-FES1	F	5'-agatctgtATGTCTGATTCCGACATG
		R	5'-agatctGGGTTTACCATACTTTTC
KH526	cYFP-FES1	F	5'-agatctATGTCTGATTCCGACATG
		R	5'-agatctGGGTTTACCATACTTTTC
KH522	nYFP-FRI	F	5'-ggatccgtATGTCCAATTATCCACCGAC
		R	5'-ggatccCTATTTGGGGTCTAATGATG

KH527	cYFP-FRI	F	5'-ggatccATGTCCAATTATCCACCGAC
		R	5'-ggatccCTATTTGGGGTCTAATGATG
KH614	nYFP-SUF3	F	5'-ggatccatATATGTCAAACATCGTTGTTC
		R	5'-ggatccTCAATGAAAGAATCGTCTACG
KH615	cYFP-SUF3	F	5'-ggatccATATGTCAAACATCGTTGTTC
		R	5'-ggatccTCAATGAAAGAATCGTCTACG
KH595	nYFP-SWC6	F	5'-ggatccgtATGGAGGAAGAGATGTCGAAC
		R	5'-ggatccCTATGCAACAAATTTCTGACA
KH596	cYFP-SWC6	F	5'-ggatccATGGAGGAAGAGATGTCGAAC
		R	5'-ggatccCTATGCAACAAATTTCTGACA
KH597	nYFP-YAF9	F	5'-ccccggatccgtATGACGAACAGCTCGTCATCGAAG
		R	5'-ccccggatccACAGGTCTGATCCTGTTTTAACGGT
KH598	cYFP-YAF9	F	5'-ccccggatccATGACGAACAGCTCGTCATCGAAG
		R	5'-ccccggatccACAGGTCTGATCCTGTTTTAACGGT
KH599	nYFP-TAF14	F	5'-ggatccgtATGGAGTCGGATATCGAGATTTTG
		R	5'-ggatccTCAGAACAAGAATGCACCTGG
KH600	cYFP-TAF14	F	5'-ggatccATGGAGTCGGATATCGAGATTTTG
		R	5'-ggatccTCAGAACAAGAATGCACCTGG
KH610	nYFP-EFS-N	F	5'-ccccggatccgtATGGACTGTAAGGAAAACG
		R	5'-ccccggatccGATTACCAAGCAAGACCACT
KH611	cYFP-EFS-N	F	5'-ccccggatccATGGACTGTAAGGAAAACGGTGTT
		R	5'-ccccggatccGATTACCAAGCAAGACCACT

For protein localization

KH455	CFP-FES1	F	5'-ggattagatctATGTCTGATTCCGACATGGA
		R	5'-ggattaggcctGGGTTTACCATACTTTTCGA

For yeast one hybrid & EMSA

KH185	AD/BD-FLX	F	5'-ggatccgtATGGCCGGACGAGATCGTTA
KH184		R	5'-ggatccCTATAGACTCATGTGTAC
KH211	AD/BD-FES1	F	5'-agatctgtATGTCTGATTCCGACATG
KH210		R	5'-agatctGGGTTTACCATACTTTTC
KH376	BD-VP16	F	5'-ggatccttGCCCCCCCGACCGATGTCAG
		R	5'-gggagatctTTACCCACCGTACTCGTCAA
KH344	AD/BD-FLX-D1	F	5'-gtagcccggggATCCTCGAGGATCGAATCGC
KH342		R	5'-ggatccCTATAGACTCATGTGTAC
KH345	AD/BD-FLX-D2	F	5'-gtagcccggggATGGCTAAGGCTAAACCGAA
KH343		R	5'-ggatccCTATAGACTCATGTGTAC
KH398	proFLC 2kb-LacZi	F	5'-ggggagtcgacAGAAATAATTTCATATGGAG
		R	5'-ggggactcgagGGCTTCTCTCCGAGAGGGC
KH419	FLC 1st exon & intron-LacZi	F	5'-ggggccATGGGAAGAAAAAAACTA
		R	5'-ccccggatccttATCAAGGATCTTGACCAGGCT
KH542	proFLC (-1916~ -546)-LacZi	F	5'-gggggatccAGAAATAATTTCATATGGAG
		R	5'-CAAGAAATCTTAAATGTCCACACA
KH543	proFLC (-1546~ -367)-	F	5'-TTGAAAGTCTTTGTAGGTTTGGTT

	LacZi	R	5'-GTGTTACCAAAGTCGTGCCTAC
KH544	proFLC (-1443~ -249)-LacZi	F	5'-GGTAGCCAAAGATTTGGG
		R	5'-ATTGCAGAAAGAACCTCCAC
KH545	proFLC (-1172~ -129)-LacZi	F	5'-AAATGTTTGTGTGGCTCCAA
		R	5'-AAGACAAGATTGCCACGTGTA
KH546	proFLC(-1172~ -367)-LacZi	F	5'-AAATGTTTGTGTGGCTCCAA
		R	5'-GTGTTACCAAAGTCGTGCCTAC
KH547	proFLC(-648~ -129)-LacZi	F	5'-GCTGATACAAGCATTTCACCA
		R	5'-AAGACAAGATTGCCACGTGTA
KH552	proFLC(-2347~ -1426)-LacZi	F	5'-TGCCTTGAAGAAATGATAATTGA
		R	5'-CCCAAATCTTTGGCTACCAT
KH548	proFLC(-580~ -249)-LacZi	F	5'-CTATTGCCATATGTGTGGAC
		R	5'-ATTGCAGAAAGAACCTCCAC
KH549	proFLC(-849~ -547)-LacZi	F	5'-TCGTTTATTGTGTTACCATTC
		R	5'-AAGAAATCTTAAATGTCC
KH580	proFLC(-580~ -351)-LacZi	F	5'-CTATTGCCATATGTGTGGAC
		R	5'-GGCAGTTAATTAGTAGGTGTTACCAAAGTCGTGC
KH578	proFLC(-580~ -331)-LacZi	F	5'-CTATTGCCATATGTGTGGAC
		R	5'-CTTCTCAAAACTTAAAATTTGGCAGTTAATTAG
KH569	proFLC(-580~ -316)-LacZi	F	5'-CTATTGCCATATGTGTGGAC
		R	5'-TTTGAACTCTTCCGACTTCTCAAAAC
KH575	proFLC(-363~ -249)-LacZi	F	5'-CTAATTAACTGCCAAATTTTAAGTTTTGAGAAG
		R	5'-ATTGCAGAAAGAACCTCCAC
KH553	proFLC(-319~ -249)-LacZi	F	5'-GTTTTGAGAAGTCGGAAGAGTTCAAA
		R	5'-ATTGCAGAAAGAACCTCCAC
KH571	proFLC(-492~ -316)-LacZi	F	5'-TTTGTGTTAATCTCCCGAACA
		R	5'-TTTGAACTCTTCCGACTTCTCAAAAC
KH556	proFLC(-341~ -316)-LacZi	S	5'-GTTTTGAGAAGTCGGAAGAGTTCAAA
		A	5'-TTTGAACTCTTCCGACTTCTCAAAAC
KH572	proFLC(-363~ -331)-LacZi / WT	S	5'-CTAATTAACTGCCAAATTTTAAGTTTTGAGAAG
		A	5'-CTTCTCAAAACTTAAAATTTGGCAGTTAATTAG
KH573	proFLC(-374~ -341)-LacZi	S	5'-GGTAACACCTACTAATTAACTGCCAAATTTTAAG
		A	5'-CTTAAAATTTGGCAGTTAATTAGTAGGTGTTACC
KH574	proFLC(-384~ -351)-LacZi	S	5'-GCACGACTTTGGTAACACCTACTAATTAACTGCC
		A	5'-GGCAGTTAATTAGTAGGTGTTACCAAAGTCGTGC
KH589	proFLCm1-LacZi	S	5'-CTAATTAACTGCCA***ggg***TTTAAGTTTTGAGAAG
		A	5'-CTTCTCAAAACTTAAA***ccc***TGGCAGTTAATTAG
KH590	proFLCm2-LacZi	S	5'-CTAATTAACTGCCAAAT***ggg***AAGTTTTGAGAAG
		A	5'-CTTCTCAAAACTT***ccc***ATTTGGCAGTTAATTAG
KH591	proFLCm3-LacZi	S	5'-CTAATTAACTGCCAAATTTT***gga***TTTTGAGAAG
		A	5'-CTTCTCAAAA***tcc***AAAATTTGGCAGTTAATTAG
KH592	proFLCm4-LacZi	S	5'-CTAATTAACTGCCAAATTTTAAG***ggg***TGAGAAG
		A	5'-CTTCTCA***ccc***CTTAAAATTTGGCAGTTAATTAG
KH593	proFLCm5-LacZi	S	5'-CTAATTAACTGCCAAATTTTAAGTTT***gag***GAAG
		A	5'-CTTC***ctc***AAACTTAAAATTTGGCAGTTAATTAG

KH594	proFLCm6-LacZi	S	5'-CTAATTAACTGCCAAATTTTAAGTTTTGA***acc***G
		A	5'-C***ggt***TCAAAACTTAAAATTTGGCAGTTAATTAG
KH618	proFLCm7-LacZi	S	5'-CTAATTAACTG***aag***AATTTTAAGTTTTGAGAAG
		A	5'-CTTCTCAAAACTTAAAATT***ctt***CAGTTAATTAG
KH619	proFLCm8-LacZi	S	5'-CTAATTAA***aga***CCAAATTTTAAGTTTTGAGAAG
		A	5'-CTTCTCAAAACTTAAAATTTGG***tct***TTAATTAG
KH620	proFLCm9-LacZi	S	5'-CTAAT***cgg***CTGCCAAATTTTAAGTTTTGAGAAG
		A	5'-CTTCTCAAAACTTAAAATTTGGCAG***ccg***ATTAG

For quantitative-PCR

	FLC-1Q	F	5'-TGCCTTGAAGAAATGATAATTGA
		R	5'-GGTGAATGTACGGCATGATT
	FLC-2Q	F	5'-TTGAAAGTCTTTGTAGGTTTGGTT
		R	5'-CCCAAATCTTTGGCTACCAT
	FLC-3Q	F	5'-AAATGTTTGTGTGGCTCCAA
		R	5'-CGATATTGGTGATTGGTATTAACTTT
	FLC-4Q	F	5'-GCTGATACAAGCATTTCACCA
		R	5'-CAAGAAATCTTAAATGTCCACACA
	FLC-5Q	F	5'-TTTGTGTTAATCTCCCGAACA
		R	5'-GTGTTACCAAAGTCGTGCCTAC
	FLC-6Q	F	5'-GAGTGGAGGTTCTTTCTGCAA
		R	5'-AAGACAAGATTGCCACGTGTA
	FLC-7Q	F	5'-TGCATGTCATTCACGATTTG
		R	5'-AGATGGCTTGAAACTTCACTCA
	FLC-8Q	F	5'-AGTAGTTTGGCCATGTTGGTC
		R	5'-GTCTCGACAATTCCAAGGCT
	FLC-1	F	5'-CTTCGTCGGGCCAGATATT
		R	5'-CGAAAGTGAAAACTAAGGCAATG
	FLC-2	F	5'-GGATGCGTCACAGAGAACAG
		R	5'-GAACCCAAACCTGAGGATCA
	FLC-3	F	5'-TCCCGTAAGTGCATTGCATA
		R	5'-CGTGCTCGATGTTGTTGAGT
	Ta3	F	5'-TGGAATCTCAGGGTCAAGG
		R	5'-CCTTCTGAGGTGAGGGACA
	ACTIN	F	5'-AGTGTGTCTTGTCTTATCTGGTTCG
		R	5'-AATAGCTGCATTGTCACCCGATACT
	TUB2p	F	5'-ACAAACACAGAGAGGAGTGAGCA
		R	5'-ACGCATCTTCGGTTGGATGAGTGA

For reverse transcription-PCR

	FLX / AT2G30120	F	5'-ATGGCCGGACGAGATCGTTA
		R	5'-TCACCTTCCTTTACGAATCT
	AT5G04830	F	5'-TGCGAATTGAAATCGAACAA
		R	5'-CTCCATTACCCGTCCGACTA
	AT3G18490	F	5'-AAGCGGCGAGTATTTCTCAA

	R	5'-CAAGATCACTCCTCCGCTTC
AT5G26040	F	5'-CTTTACCCATTCCGAAAGCA
	R	5'-ACTTCATGTACCCGCCTGAG
AT5G04840	F	5'-ACCTGCTTGGCTTGATGAGT
	R	5'-AGTATCGCCATCTGCTGCTT
AT3G18500	F	5'-TCTTTCGTGTGTTGCTCCTC
	R	5'-CCAGCTTCACATCTCCTTGA

Supplemental Dataset 1:

Sequences used for phylogenetic analysis in Supplemental Figure 7A (FASTA format)

```
>At-FLX
MAGRDRYIPSSAVSTSSSSRLLESQLIESDRNRARSVILEDRIAIQHREIQSLLNDNQRLAVAHIGLKDQLNVAKRELER
LLETAVKVKAEGEAKVREVYQNALRMEAEARVIDGLGAELGQVRSDVQRLGSDRQELATELAMFDDEMAKAKPNSDRAIE
VKLEIEILRGEIRKGRAALELEKKTRASNLHHERGMEKTIDHLNREIVKLEEELVDLETKAREANAAAEAAPTPSPGLAA
SYGNNTDDIYGGQGRQYPEANGTHEVHMSL

>At-AT3G14750
MSGRNRGPPPPSMKGGSYSGLQAPVHQPPFVRGLGGGPVPPPPHPSMIDDSREPQFRVDARGLPPQFSILEDRLAAQNQD
VQGLLADNQRLAATHVALKQELEVAQHELQRIMHYIDSLRAEEEIMMREMYDKSMRSEMELREVDAMRAEIQKIRADIKE
FTSGRQELTSQVHLMTQDLARLTADLQQIPTLTAEIENTKQELQRARAAIDYEKKGYAENYEHGKIMEHKLVAMARELEK
LRAEIANSETSAYANGPVGNPGGVAYGGGYGNPEAGYPVNPYQPNYTMNPAQTGVVGYYPPPYGPQAAWAGGYDPQQQQQ
QQPPPQGQGHR

>At-AT1G55170
MSGRNRIHRDIRDSYHDHRDLPPERPFLRGPPLLQPPPPSLLEDLQIQEGEIRRQDAEIRRLLSDNHGLADDRMVLEREL
VAAKEELHRMNLMISDLRAEQDLQLREFSEKRHKLEGDVRAMESYKKEASQLRGEVQKLDEIKRELSGNVQLLRKDLAKL
QSDNKQIPGMRAEVKDLQKELMHARDAIEYEKKEKFELMEQRQTMEKNMVSMAREVEKLRAELATVDSRPWGFGGSYGMN
YNNMDGTFRGSYGENDTYLGSSERSQYYSHGSGSQKKPRLDRH

>At-AT5G61920
MSSRERIGSNHHSRVSQGMSTSGSSSSRHHDTISSTSDPRHLRDHQISLSDILENKIAVQAAEIDRLSNDNRKLASSYVA
LKEDLTVADREVQGLRAHIRKTETDHEIQIRSTLEKIAKMEGMVKNRENIRREVQSAHIEAHRLAREREELASKVKLGMK
DLKKVCLEAESLEASSQELERLKEEHQRLRKEFEEEKSGNVEKLAQLKGMERKIIGAVKAIEKLRSEISTARNKAVEN

>At-AT1G67170
MESKGRIHPSHHHMRRPLPGPGGCIAHPETFGNHGAIPPSAAQGVYPSFNMLPPPEVMEQKFVAQHGELQRLAIENQRLG
GTHGSLRQELAAAQHEIQMLHAQIGSMKSEREQRMMGLAEKVAKMETELQKSEAVKLEMQQARAEARSLVVAREELMSKV
HQLTQELQKSRSDVQQIPALMSELENLRQEYQQCRATYDYEKKFYNDHLESLQAMEKNYMTMAREVEKLQAQLMNNANSD
RRAGGPYGNNINAEIDASGHQSGNGYYEDAFGPQGYIPQPVAGNATGPNSVVGAAQYPYQGVTQPGYFPQRPGYNFPRGP
PGSYDPTTRLPTGPYGAPFPPGPSNNTPYAGTHGNPSRR

>At-SMC3
MEEDEPMGGGESEPEQRKSGTPRLYIKELVMRNFKSYAGEQRVGPFHKSFSAVVGPNGSGKSNVIDAMLFVFGKRAKQMR
LNKVSELIHNSTNHQNLDSAGVSVQFEEIIDLENGLYETVPGSDFMITRVAFRDNSSKYYINERSSNFTEVTKKLKGKGV
DLDNNRFLILQGEVEQISLMKPKAQGPHDEGFLEYLEDIIGTNKYVEKIDELNKQLETLNESRSGVVQMVKLAEKERDNL
EGLKDEAETYMLKELSHLKWQEKATKMAYEDTVAKITEQRDSLQNLENSLKDERVKMDESNEELKKFESVHEKHKKRQEV
LDNELRACKEKFKEFERQDVKHREDLKHVKQKIKKLEDKLEKDSSKIGDMTKESEDSSNLIPKLQENIPKLQKVLLDEEK
KLEEIKAIAKVETEGYRSELTKIRAELEPWEKDLIVHRGKLDVASSESELLSKKHEAALKAFTDAQKQLSDISTRKKEKA
AATTSWKADIKKKKQEAIEARKVEEESLKEQETLVPQEQAAREKVAELKSAMNSEKSQNEVLKAVLRAKENNQIEGIYGR
MGDLGAIDAKYDVAISTACAGLDYIVVETTSSAQACVELLRKGNLGFATFMILEKQTDHIHKLKEKVKTPEDVPRLFDLV
RVKDERMKLAFYAALGNTVVAKDLDQATRIAYGGNREFRRVVALDGALFEKSGTMSGGGGKARGGRMGTSIRATGVSGEA
VANAENELSKIVDMLNNIREKVGNAVRQYRAAENEVSGLEMELAKSQREIESLNSEHNYLEKQLASLEAASQPKTDEIDR
LKELKKIISKEEKEIENLEKGSKQLKDKALELQTNIENAGGEKLKGQKAKVEKIQTDIDKNNTEINRCNVQIETNQKLIK
KLTKGIEEATREKERLEGEKENLHVTFKDITQKAFEIQETYKKTQQLIDEHKDVLTGAKSDYENLKKSVDELKASRVDAE
FKVQDMKKKYNELEMREKGYKKKLNDLQIAFTKHMEQIQKDLVDPDKLQATLMDNNLNEACDLKRALEMVALLEAQLKEL
NPNLDSIAEYRSKVELYNGRVDELNSVTQERDDTRKQYDELRKRRLDEFMAGFNTISLKLKEMYQMITLGGDAELELVDS
LDPFSEGVVFSVRPPKKSWKNIANLSGGEKTLSSLALVFALHHYKPTPLYVMDEIDAALDFKNVSIVGHYVKDRTKDAQF
IIISLRNNMFELADRLVGIYKTDNCTKSITINPGSFAVCQKTPA
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Alignment used for phylogenetic analysis in Supplemental Figure 7A

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AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            MEEDEPMGGGESEPEQRKSGTPRLYIKELVMRNFKSYAGEQRVGPFHKSFSAVVGPNGSG

AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            KSNVIDAMLFVFGKRAKQMRLNKVSELIHNSTNHQNLDSAGVSVQFEEIIDLENGLYETV

AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            PGSDFMITRVAFRDNSSKYYINERSSNFTEVTKKLKGKGVDLDNNRFLILQGEVEQISLM

AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            KPKAQGPHDEGFLEYLEDIIGTNKYVEKIDELNKQLETLNESRSGVVQMVKLAEKERDNL

AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            EGLKDEAETYMLKELSHLKWQEKATKMAYEDTVAKITEQRDSLQNLENSLKDERVKMDES

AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            NEELKKFESVHEKHKKRQEVLDNELRACKEKFKEFERQDVKHREDLKHVKQKIKKLEDKL

AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            EKDSSKIGDMTKESEDSSNLIPKLQENIPKLQKVLLDEEKKLEEIKAIAKVETEGYRSEL
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AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            TKIRAELEPWEKDLIVHRGKLDVASSESELLSKKHEAALKAFTDAQKQLSDISTRKKEKA


AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            AATTSWKADIKKKKQEAIEARKVEEESLKEQETLVPQEQAAREKVAELKSAMNSEKSQNE


AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            VLKAVLRAKENNQIEGIYGRMGDLGAIDAKYDVAISTACAGLDYIVVETTSSAQACVELL


AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            RKGNLGFATFMILEKQTDHIHKLKEKVKTPEDVPRLFDLVRVKDERMKLAFYAALGNTVV


AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            AKDLDQATRIAYGGNREFRRVVALDGALFEKSGTMSGGGGKARGGRMGTSIRATGVSGEA


AT3G14750       -----------MSGRNRGPPPPSMKGGSYSGLQAPVHQPPFVRGLGGGPVPPPPHPSMID
AT1G67170       -----------MESKGRIHPSHHHMRRPLPGPGGCIAHPETFG--NHGAIPPSAAQGVY-
AT1G55170       -----------MSGRNRIHR---DIRDSYHDHRDLPPERPFLR--GPPLLQPPPPS----
AT5G61920       -----------MSSRERIGSNHHSRVSQGMSTSGSSSSR------HHDTISSTSDPRHLR
FLX             -----------MAGRDRYIPSSAVSTSSSSRLLES------------QLIESDRNR----
SMC3            VANAENELSKIVDMLNNIREKVGNAVRQYRAAENEVSGLEMELAKSQREIESLNSEHNYL
                           :    .                                : .

AT3G14750       DSREPQFRVDA---RGLPPQFSILEDRLAAQNQDVQGLLADNQRLAATHVALKQELE-VA
AT1G67170       ----PSFN--------MLPPPEVMEQKFVAQHGELQRLAIENQRLGGTHGSLRQELA-AA
AT1G55170       ----------------LLEDLQIQEGEIRRQDAEIRRLLSDNHGLADDRMVLERELV-AA
AT5G61920       --------------DHQISLSDILENKIAVQAAEIDRLSNDNRKLASSYVALKEDLT-VA
FLX             ------------------ARSVILEDRIAIQHREIQSLLNDNQRLAVAHIGLKDQLN-VA
SMC3            EKQLASLEAASQPKTDEIDRLKELKKIISKEEKEIENLEKGSKQLKDKALELQTNIENAG
                                        :  :  :  ::  *   .: *      *. ::  ..
```

```
AT3G14750       QHELQRIMHYIDSLRAEEEIMMREMYDKSMRSEMELREVDAMRAEIQKIRADIKEFTSGR
AT1G67170       QHEIQMLHAQIGSMKSEREQRMMGLAEKVAKMETELQKSEAVKLEMQQARAEARSLVVAR
AT1G55170       KEELHRMNLMISDLRAEQDLQLREFSEKRHKLEGDVRAMESYKKEASQLRGEVQKLDEIK
AT5G61920       DREVQGLRAHIRKTETDHEIQIRSTLEKIAKMEGMVKNRENIRREVQSAHIEAHRLARER
FLX             KRELERLLETAVKVKAEGEAKVREVYQNALRMEAEARVIDGLGAELGQVRSDVQRLGSDR
SMC3            GEKLKGQKAKVEKIQTDIDKNNTEINRCNVQIETNQKLIKKLTKGIEEATREKERLEGEK
                 .::.       . .:: :           : *   :  .       .   : . :   :

AT3G14750       QELTSQVHLMTQDLARLTADLQQIPTLTAE----IENTKQELQRARAAIDYEKKGYAENY
AT1G67170       EELMSKVHQLTQELQKSRSDVQQIPALMSE----LENLRQEYQQCRATYDYEKKFYNDHL
AT1G55170       RELSGNVQLLRKDLAKLQSDNKQIPGMRAE----VKDLQKELMHARDAIEYEKKEKFELM
AT5G61920       EELASKVKLGMKDLKKVCLEAESLEASSQE----LERLKEEHQRLRKEFEEEKSGNVEKL
FLX             QELATELAMFDDEMAKAKPNSDRAIEVKLE----IEILRGEIRKGRAALELEKKTRASNL
SMC3            ENLHVTFKDITQKAFEIQETYKKTQQLIDEHKDVLTGAKSDYENLKKSVDELKASRVDAE
                .:*   .    ..  .     .       *    :   : :  . :   :  *    .

AT3G14750       EHGKIMEHKL------------------VAMARELEKLRAEIAN-SETSAYANGPVGNPG
AT1G67170       ESLQAMEKNY------------------MTMAREVEKLQAQLMNNANSDRRAGGPYGNNI
AT1G55170       EQRQTMEKNM------------------VSMAREVEKLRAELATVDSRPWGFGGSYGMNY
AT5G61920       AQLKGMERKI------------------IGAVKAIEKLRSEISTARNKAVEN--------
FLX             HHERGMEKTI------------------DHLNREIVKLEEELVDLETKAREANAAAEAAP
SMC3            FKVQDMKKKYNELEMREKGYKKKLNDLQIAFTKHMEQIQKDLVDPDKLQATLMDNNLNEA
                   : *::.                       : : ::. ::

AT3G14750       GVAYGGGYGNPEAGYPVNPYQPN-YTMNPAQTGVVG-------------------YYP--
AT1G67170       NAEIDASGHQSGNGYYEDAFGPQGYIPQPVAGNATGPNSVVGAAQYPYQGVTQPGYFPQR
AT1G55170       NNMDGTFRG---------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             TPSPGLAAS---------------------------------------------------
SMC3            CDLKRALEMVALLEAQLKELNPNLDSIAEYRSKVELYNGRVDELNSVTQERDDTRKQYDE


AT3G14750       PPYGPQAAWAGGYDPQQQQQQ----QPPPQGQGHR-------------------------
AT1G67170       PGYNFPRGPPGSYDPTTRLPTGPYGAPFPPGPSNNTPYAGTHGNPSRR------------
AT1G55170       -SYGENDTYLGSSERSQYYSHGSGSQKKPRLDRH--------------------------
AT5G61920       ------------------------------------------------------------
FLX             --YGNNTDDIYGGQGRQYPEANGTHEVHMSL-----------------------------
SMC3            LRKRRLDEFMAGFNTISLKLKEMYQMITLGGDAELELVDSLDPFSEGVVFSVRPPKKSWK


AT3G14750       ------------------------------------------------------------
AT1G67170       ------------------------------------------------------------
AT1G55170       ------------------------------------------------------------
AT5G61920       ------------------------------------------------------------
FLX             ------------------------------------------------------------
SMC3            NIANLSGGEKTLSSLALVFALHHYKPTPLYVMDEIDAALDFKNVSIVGHYVKDRTKDAQF


AT3G14750       --------------------------------------------
AT1G67170       --------------------------------------------
AT1G55170       --------------------------------------------
AT5G61920       --------------------------------------------
FLX             --------------------------------------------
SMC3            IIISLRNNMFELADRLVGIYKTDNCTKSITINPGSFAVCQKTPA
```

Supplemental Dataset 2:

Sequences used for phylogenetic analysis in Supplemental Figure 9B (FASTA format)

```
>At-AAR28018
MESDIEILSEADASMRKLRIFGIDDREDENGRRRIKDVEVYVPIVCGSIAFYLGKKATEYRTHKWTVYVRGATNEDLGVV
IKRVIFHLHPSFNNPTRVVDAPPFALSECGWGEFKIDITVFFHTDVCEKKLELSHVLKLNPENAYGPIPKSIKIPVVAES
YNEVVFPDPFESFVARVHNHPAIQISNIPDGLNLPPPGAFLF

>At-NP199373
MTNSSSSKKQAQDQPETSEPTLKSLKTKMTKSDEKQKKLKDIEISVPIVYGNVAFWLGKKASEYQSHKWAVYVRGATNED
ISVVVKKVVFQLHSSFNSPTRVIEEPPFEVSESGWGEFEIAMTLHFHSDVCDKPLSLYHHLKLYPEDESGPLTMKKPVVV
ESYDEIVFPDPSESFLARVQNHPALTFPRLPSGYNLPAPMQVEDTGKKKRGDTKDHSLGQWFMSFSEADELLQLAAARQQ
VQAHIAKLRRQISLLEGQNQTVKTGSDL

>Sc-NP015196
MVATVKRTIRIKTQQHILPEVPPVENFPVRQWSIEIVLLDDEGKEIPATIFDKVIYHLHPTFANPNRTFTDPPFRIEEQG
WGGFPLDISVFLLEKAGERKIPHDLNFLQESYEVEHVIQIPLNKPLLTEELAKSGSTEETTANTGTIGKRRTTTNTTAEP
KAKRAKTGSASTVKGSVDLEKLAFGLTKLNEDDLVGVVQMVTDNKTPEMNVTNNVEEGEFIIDLYSLPEGLLKSLWDYVK
KNTE

>Sc-NP014292
MAPTISKRIKTLSVSRPIIYGNTAKKMGSVKPPNAPAEHTHLWTIFVRGPQNEDISYFIKKVVFKLHDTYPNPVRSIEAP
PFELTETGWGEFDINIKVYFVEEANEKVLNFYHRLRLHPYANPVPNSDNGNEQNTTDHNSKDAEVSSVYFDEIVFNEPNE
EFFKILMSRPGNLLPSNKTDDCVYSKQLEQEEIDRIEIGIEKVDKEIDELKQKLENLVKQEAINGS

>Sp-NP593114
MTTVKRTVRLITDQNVLPGGEAAVLNDQSFPVREWSIKLVCLNPQGEETDASFVDRVTYKLHPTFQNPTRTIRKPPFQIK
EQGWGEFEMEIIIYYADKGGEHRFLHYLHFQQEHYHEDIELNINATRPGLLKALTATGEVPGYSDEGEEARKDKRKNESE
VGAGKKKAKAKPVDMDKLAEGLQKLQEDDLLQVVQMVNENKTPDMYVRNDIEGGEFHIDLYTLPDNLLLLLYSFCAKRVT
M

>Os-NP001056732
MPQASSSSSPATAAAPPPPQPAADPSPSAVPASEEALDPQTPAPPPQAQPEAVLTAAQKALRSKPTRPPEDSDKKNKKLK
DVEISFPIVYGTISFWLGKKASEYNSHKWTVYVRSATNEDLSVIVKRVVFQLHPSFTNPTRVVEQPPFELSESGWGEFEI
AITLYFHSDVCEKRLDLFHQLKLYPEEDTGPQSTKKPVVVETYDEIVFPEPTEAFFQRVQNHPAATVPRLPPGITLPPPG
PMELVPHEKKRGDTKDHPLSQWFSNFSEADELLKLAAARQQVQAHIAKLRRQLSMIDGMPQQSKAVSVQGQQFGHG

>Dm-NP609086
MTDFGGDSGGRLKGVTIVKPIVYGNIARSFGKKREEDGHTHQWKVYLKPYFNEDMSIYVKKVHFKLHESYANPNRIVVKP
PYEITETGWGEFEVIIKIYFNDQSERPVTCYHILKLFQSPVVDGELSSSTTMDTKKGLVSESYEEIVFQEPTQILQHYLL
LSEQSANGLLTHDTDFEEKKTKTLDNIVNVKQKVKGEIVTLKDKLKLARETISKFKAELAKVQKQPA

>Hs-NP006521
MFKRMAEFGPDSGGRVKGVTIVKPIVYGNVARYFGKKREEDGHTHQWTVYVKPYRNEDMSAYVKKIQFKLHESYGNPLRV
VTKPPYEITETGWGEFEIIIKIFFIDPNERPVTLYHLLKLFQSDTNAMLGKKTVVSEFYDEMIFQDPTAMMQQLLTTSRQ
LTLGAYKHETEFAELEVKTREKLEAAKKKTSFEIAELKERLKASRETINCLKNEIRKLEEDDQAKDI
```

Alignment used for phylogenetic analysis in Supplemental Figure 9B

```
Os-NP001056732      MPQASSSSSPATAAAPPPPQPAADPSPSAVPASEEALDPQTPAPPPQAQPEAVLTAAQKA
At-NP199373         MTNSSSSK-----------KQAQD-------------QPETSEP------------TLKS
At-AAR28018         MESDIEILS----------------------------EADASMR------------KLRI
Dm-NP609086         ---------------------------------------------------------MTD
Hs-NP006521         ---------------------------------------------------------MTD
Sc-NP014292         ------------------------------------------------------------
Sp-NP593114         ------------------------------------------------------------
Sc-NP015196         ------------------------------------------------------------

Os-NP001056732      LRSKPTRPPEDSDKKNKKLKDVEISFPIVYGTISFWLG-KKASEY---NSHKWTVYVRSA
At-NP199373         LKTKMTK----SDEKQKKLKDIEISVPIVYGNVAFWLG-KKASEY---QSHKWAVYVRGA
At-AAR28018         FGIDDRE----DENGRRRIKDVEVYVPIVCGSIAFYLG-KKATEY---RTHKWTVYVRGA
Dm-NP609086         FGGDSGG----------RLKGVTIVKPIVYGNIARSFGKKREEDG---HTHQWKVYLKPY
Hs-NP006521         FGGDSGG----------RLKGVTIVKPIVYGNIARSFGKKREEDG---HTHQWKVYLKPY
Sc-NP014292         MAPTISK----------RIKTLSVSRPIIYGNTAKKMGSVKPPNAPAEHTHLWTIFVRGP
Sp-NP593114         -MTTVKR-----------TVRLITDQNVLPGGEAAVLNDQSFPVR---EWSIKLVCLNPQ
Sc-NP015196         MVATVKR-----------TIRIKTQQHILP----EVPPVENFPVR---QWSIEIVLLDDE
                                         :     ::                   .     : :

Os-NP001056732      TNEDLSVIVKRVVFQLHPSFTNPTRVVEQPPFELSESGWGEFEIAITLYFHSDVCEKRLD
At-NP199373         TNEDISVVVKKVVFQLHSSFNSPTRVIEEPPFEVSESGWGEFEIAMTLHFHSDVCDKPLS
At-AAR28018         TNEDLGVVIKRVIFHLHPSFNNPTRVVDAPPFALSECGWGEFKIDITVFFHTDVCEKKLE
Dm-NP609086         FNEDMSIYVKKVHFKLHESYANPNRIVVKPPYEITETGWGEFEVIIKIYFN-DQSERPVT
Hs-NP006521         FNEDMSIYVKKVHFKLHESYANPNRIVVKPPYEITETGWGEFEVIIKIYFN-DQSERPVT
Sc-NP014292         QNEDISYFIKKVVFKLHDTYPNPVRSIEAPPFELTETGWGEFDINIKVYFVEEANEKVLN
Sp-NP593114         GEETDASFVDRVTYKLHPTFQNPTRTIRKPPFQIKEQGWGEFEMEIIIYYADKGGEH--R
Sc-NP015196         GKEIPATIFDKVIYHLHPTFANPNRTFTDPPFRIEEQGWGGFPLDISVFLLEKAGER--K
                     :*  .  ..:* ::** :: .* * .  **: : * *** * : : :.   .  ::

Os-NP001056732      LFHQLKLYPE-----------EDTGPQ--STKKPVVVETYDEIVFPEPTEAFFQRVQNHP
At-NP199373         LYHHLKLYPE-----------DESGPL--TMKKPVVVESYDEIVFPDPSESFLARVQNHP
At-AAR28018         LSHVLKLNPE-----------NAYGPIPKSIKIPVVAESYNEVVFPDPFESFVARVHNHP
Dm-NP609086         CYHILKLFQSP------VVDGELSSSTTMDTKKGLVSESYEEIVFQEPTQILQHYLLLSE
Hs-NP006521         CYHILKLFQSP------VVDGELSSSTTMDTKKGLVSESYEEIVFQEPTQILQHYLLLSE
Sc-NP014292         FYHRLRLHPYANPVPNSDNGNEQNTTDHNSKDAEVSSVYFDEIVFNEPNEEFFKILMSRP
Sp-NP593114         FLHYLHFQQEH---------YHEDIELNINATRPGLLKALTATGEVPGYSDEGEEARKDK
Sc-NP015196         IPHDLNFLQES---------YEVEHVIQIPLNKPLLTEELAKSGSTEETTANTGTIGKRR
                      * *.:              .

Os-NP001056732      AATVPRLPPGITLPPPG-------PMELVPHEKKRGDTKDHPLSQWFSNFSEA-DELLKL
At-NP199373         ALTFPRLPSGYNLPAPM-------QVEDTGK-KKRGDTKDHSLGQWFMSFSEA-DELLQL
At-AAR28018         AIQISNIPDGLNLPPPG-------AFLF--------------------------------
Dm-NP609086         QSANGLLTHDTDFEEKK-------TKTLDNIVNVKQKVKG---------------EIVTL
Hs-NP006521         QSANGLLTHDTDFEEKK-------TKTLDNIVNVKQKVKG---------------EIVTL
Sc-NP014292         G---NLLPSNKTDDCVY-------SKQLEQE------------------------EIDRI
Sp-NP593114         RKNESEVGAGKKKAKAK-------PVDMDKLAEGLQKLQEDDLLQVVQMVNENKTPDMYV
Sc-NP015196         TTTNTTAEPKAKRAKTGSASTVKGSVDLEKLAFGLTKLNEDDLVGVVQMVTDNKTPEMNV


Os-NP001056732      AAARQQVQAHIAKLRRQLSMIDGMPQQSKAVSVQGQQFGHG
At-NP199373         AAARQQVQAHIAKLRRQISLLEGQNQTVKTGSDL-------
At-AAR28018         -----------------------------------------
Dm-NP609086         KDKLKLARETISKFKAELAKVQKQPA---------------
```

```
Hs-NP006521         KDKLKLARETISKFKAELAKVQKQPA---------------
Sc-NP014292         EIGIEKVDKEIDELKQKLENLVKQEAINGS-----------
Sp-NP593114         RNDIEGGEFHIDLYTLPDNLLLLLYSFCAKRVTM-------
Sc-NP015196         TNNVEEGEFIIDLYSLPEGLLKSLWDYVKKNTE--------
```

Supplemental Dataset 3:

Sequences used for phylogenetic analysis in Supplemental Figure 11A (FASTA format)

```
>At-FRIGIDA
MSNYPPTVAAQPTTTANPLLQRHQSEQRRRELPKIVETESTSMDITIGQSKQPQFLKSIDELAAFSVAVETFKRQFDDLQ
KHIESIENAIDSKLESNGVVLAARNNNFHQPMLSPPRNNVSVETTVTVSQPSQEIVPETSNKPEGGRMCELMCSKGLRKY
IYANISDQAKLMEEIPSALKLAKEPAKFVLDCIGKFYLQGRRAFTKESPMSSARQVSLLILESFLLMPDRGKGKVKIESW
IKDEAETAAVAWRKRLMTEGGLAAAEKMDARGLLLLVACFGVPSNFRSTDLLDLIRMSGSNEIAGALKRSQFLVPMVSGI
VESSIKRGMHIEALEMVYTFGMEDKFSAALVLTSFLKMSKESFERAKRKAQSPLAFKEAATKQLAVLSSVMQCMETHKLD
PAKELPGWQIKEQIVSLEKDTLQLDKEMEEKARSLSLMEEAALAKRMYNQQIKRPRLSPMEMPPVTSSSYSPIYRDRSFP
SQRDDDQDEISALVSSYLGPSTSFPHRSRRSPEYMVPLPHGGLGRSVYAYEHLAPNSYSPGHGHRLHRQYSPSLVHGQRH
PLQYSPPIHGQQQLPYGIQRVYRHSPSEERYLGLSNQRSPRSNSSLDPK

>At-FRL1
MTASETIATAINQIDEKKEKLKKAFDDLQAHRSLLSPSFSLSWSEIDSHFSSLQSSLASRFRLLHSTSPLEHDSYRIDAS
DAGKSSSSEEVSEQPVVEPELRALCEKIDGIGLIKYLIRIWDDETPLNQEVSAAIRYSPDTASMVLDAIEGSNYTPSSSG
RSFDVRRVFVLLMEVLIEINANITVDTRNRAKKLAYHWKSKVGVKPFEALVFLHLVAAFELGSEFDTEELSDYVFMIAKY
KQATLVCNKIGVDRKRVGKLIKTLLDSGKPILAVKFMYECGMTDEFEPIPVLKSYIKDCREAALRVCVEDNYSLKSQNEA
SDKEVSALKPLIKIIKDQNLESEFTQEKVEERVEELEKNKALRKRNTTNPPKQEPQQKGKKRTRDCKNGSQVPVPSQQLL
SRPEALLMPEHSHHGLQLNPYGLMTSAFSGVVVNPLTGLFGSGATPQSLYYAQQTGYVLPPQYHPPYYSQ

>At-FRL2
MTAAESIAASINQIDEKKQKLKKAFDDLQAHRSLLSPSFNLSWSEIDSHFSSLQSSLFNRLQSAVTSSNSGNIETPTAVT
TETPVLWPELRKFCEKNDGKGLGNYMIENSRKRLSINEELPNAIRCSENPAPLVLDAIEGSYHCSSPSSSSSARAIDVKR
IFVLLLEALIEINANLTNDLRERARTIAYDWKPNIGNKPSEALGFLHLVAAFELGSLFSTEEICDYIFLISKYKQATTIC
KKIGLDRNRIGVLVQKFLDTGRLLVAIRFIYENEMVGEFEPVSILKTSLKNSREAAKRVCAEGNYSLKVQNEATDKELSA
LRAVIKVVKEKNIESEFMEEKLEECVKELEDQKAQRKRATKFNSPANPQQPQEQKVDNKRPRVANGSSMEYNLTIPPLRP
QQQPPLLPTPSQILQVNPYGLLSSILPGVAVPYGNPRALFGSVPAPASRPVFYVQQTGYGMPPPQYRPPYYPQ

>Aa-AAZ92551
MANYPPTVAAQSSTAAIPLLHQSERRRGELPAVVETESTAMEISIGQSKQPQFLKSIDELAAFSVAVEAFKRQFDDLQKH
IDSIENAIESKLKSNGADLAASSNFHQPLLSPPRNNASVETTVSVSQSSQEPAETVPETSNKTEGERLCELMCSKGLRKY
IYANISDRAKLMEEIPSALKLAKEPAKFVLECIGKFYLQGRRAFTKESPMVSARQVSLLILESFLLMPDRGKGKVKIESC
IKDEAETAAVAWRKRLMSEGGLAAAEKMDARGLLLLVACFGVPSNFRSMDLLDLIRMSGSNEIAGALKRSPFLVPMISGI
VESSIKRGMHIEALEMVYTFGMEDKFSASSVLTSFLRMSKESFERAKRKAQSPLAFKEAAAKQLAALSSVMQCMETHKLD
PVKELPGWQIKEQIVNLEKDTLQLDKEMEEKARSISLMEEAVLAKRMYNQQMKRPRLSPMEMPPVASSSYSPLYLDRSFP
SQRDEDRDEISALVSSYLGPSSSFPHRSSLRRSPEYMVPLPPGGLGRSVYAYEHLPPNSYSPGHGQRLPRQYSPSPVHGQ
RHPRQYSPPIHGQQQIPFGLQRVYRHSPSEERYLGLSNHRSPRSNSSLDPK

>Al-ABY51872
MANYPPTVAAQSSTAAIPLLHQRHQSERRRGELPAVVETESTAMEISIGQSKQPQFLKSIDELAAFSVAVEAFKRQFDDL
QKHIESIENAIDSKLKSNGAYLAASSNFHQPLLSPPRNNASVETTVSLSQSSQEPAETVPETSNKTEGERLCELMCSKGL
RKYIYANISDRAKLMEEIPSALKLAKEPAKFVLDCIGKFYLQGRRAFTKESPMVSARQVSLLILESFLLMPDRGKGKVKI
ESCIKDEAETAAVAWRKRLMSEGGLAAAEKMDARGLLLLVACFGVPSNFRSMDLLDLIRMSGSNEIAGALKRSPFLVPMI
SGIVESSIKRGMHIEALEMVYTFGMEDKFSASSVLTSFLRMSKESFERTKRKAQSPLAFKEAAAKQLAALSSVMRCMETH
KLDPAKELPGWQIKEQIVNLEKDTLQLDKEMEEKARSISLMEEAVLAKRIYNQQMKRPRLSPMEMPPVASSSYSSIYLDR
SFHSQRDEDRDEISALVSSYLGPSSSFPHRSSLRRSPEYIVPLPPGGLGRSVYAYEHLPPNSYSPGHGQRLPRQYSPSPV
HGQRHPRQYSPPIHGQQQIPFGLQRVYRHSPSEERYLGLSNHRSPRSNSSLDPK

>Th-AAY90142
MIPARGYSHHYPSTTEEKPSSPATIPRLHQRDQSERRGDFPAINRTEPTNKEITSGDSKHPQFMKSIDDLAKFSAAFDAF
KRHYDDLQKHMDDIENAIESKFKSNGVDDSSSHSPEHDASREIATAIVCPPPPEEAETAPEMITSNDKAEGQRLCESMCS
KGLRKYIYANISERAKLMEEIPAGLKLAKEPAKFVLECIGKFYLQGRKAFSHDSHMIPARQVSLLILECFLLMIEPGEEK
VKSMIESSVKEEAEAAAFAWKRRIMNEGKLATAEAIDARGLLLLIACFGVPSSFRSMDLLDLIRQSGTSEIAGALKRSPF
LVPIVSGIVDSCLKRGTNIEALEIVFTFGMEDKISPSSLLTPFLRKSKESFELAKRKAHSPTAFKEAIEKQLAALLSVTK
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```
CLEAHKLDPAKEIPGWPIKEQIVKLEKDTLQIDKQMEEQARSISLMEEAVLTKRLYNQQMKRPRLSEMEMPPAASSSYSP
IYRDRNFSSHIDGDRDEISALVSSYLGPSSSFPHRSSLRRSPEYMVPPGGLGRSVSAYEHLLPSSYSPVHGQRLPREYSP
PVHGQQQIPYGLQRVYRHSPSVERLLTLPHHRSPRNSSQDHIGGM

>Vv-XP002283789
MAKTSMTLTVKEGQPPPPLCAAAVSGESGGGDPMRSVNELRNLSTVLHAFRRRWDELQKHLDFIQDAIASRSRELDASPQ
HHQALASNTLETSSPESADLHSEPMPAQTSVSELGFLCGMMRSRGLRKYIISHLSDVAKLREEVPAALKGAPKPAKLVLE
CIGRFFLQGSKAFGKATHMVPSRQASLLILEFFLLSDCTEMEPSVKEEADLAAVTWRKRLINEGGVSNASDIDARGLLLL
VASFGIPALFRNEDLRNLIRLSCPKEISDALRRSRFLLARVPDVIQGMIKNQMNVEAVDFAYTFGLEEKFPIWKILTSFL
REHKEEWKRTREEDSPIRLKKANENYLSAMKSVTRCLEDHRVDPSKLLSGWHIDEKIIQLEKEMADLDKKMEGKVMLKRK
ADEIDSLKKMKTREIKHSPIAAPSSVIGLQEQRVADNMASRSFYDSTMPINFLDSGFPGHISTYPAASAMLHGSGGGSLP
ENITGTMSGSGSGTRVHGTGTGPGMAGTGGVPSMASFSGAHGEMLFDRTGQMMKNNGPPYAGRRDMGFNDRVIGQSFIAH
PASMGVDSIFGPSTSMESFPGMPNAPSINAANGSSASDLYQFADAVFGR

>Vv-XP002276345
MAELKTISAALKLIDAKKESLRKAFEDLEAHSSSLSSFTLTWSAIDAHFSSIQSSLSRQFEILESRTDSVPQNDTLPTNN
AVSLPAQSNAVSLPPQNNAVSLPPQNNAVSLPPQESAISRPTQNSAVSRPPQNNANPSHPQLRLLCSAMDAEALRRYIMD
HPNDRETLRSELLDAFQVARDPAKMVLDALTGFFPSNANEDGSSELHTMRRSCVFMLEQLMLFSPEIGEDVRQRAKSLAQ
EWKGKVKVGDNTLKPMGFLHLLAAYGLGSDYDSTELLELLIDVVRYREVFGLCRGLNLVDKVPDLIQNLIGSGKPNLAVK
FVLEFKLTHKFPLIAILKDIVESSRDVARKVRKDGKHSLQSQNEATSKEISALKLVTKYIKDYDLNNEYPGAPLEERIQK
LESQMAARTAAKKRPALAPAPRPKQQKKQKSKQAQTTATASPSVPSGAAGTSSTAAPFQQPHLQAPGLVPDGPVPFMNPS
AGLYGFAGVPMGFPGNLGPPMPHLHPMEPQLPMPFAHGGYGLQSLYPPAYFHQ

>Vv-XP002276317
MATVKTIALGLTLIDEKKEELRIAFEDLQAHSSSPSSFTLTWSDIDSHFSSIQSSLTRQFDLIQCQNDVVPEILQKYVPP
SHPRLKLLCSNMDANGLTRYIIDHSKDRQEIASELPDAFRVAPVPAKLVLDALQEFFPPNEVDNEGNKLGSLMQTRLLLL
EQLTAVLPEIKADVMQRAKYLAQEWKGKINRGAVTSNGFLGFLYLLAAYGMGSDFDSSEYVEFLANVVVQNRQQGFTLCC
RLNCVDKVPGVYLRKLCSVSSAMWACVAKEALYLCQIGLTDKCPLAPILKAHVKKFENLAQNVYDSRNQSLQYLNGATGA
EITILKQIISCLEEYKLEAEYPREHLEMRIKMLEREMKDRKRSAAALVPRHQQQQELGSKHPWTKPAGAAVPSVAGFLPD
RSVPYLSSSVELQGLAGPTLSTARYTAPSAGLYCSAGVPMSFPGNLSPARPHVQALDSQMPIPSGYFDRPSGLGGYNLQP
HYHWTYYPSSS

>Rc-EEF51656
MATPPLFSVKQEPDHQSPLPLIPLPQPYVKGEPVEELPIVTIQQQEPQFLQSIEELNTLSSAINEFYRRFSELQNHLDFI
HTSIKQHEEQQQIQDAPTPTITTPTIVTDNQTTITDAKKETVINSAPPPAKSSSSSELISLCEMMCGRGLRKYLTSNLTN
IPKLRNEVPTALKYAPKPAKLVFDCFGGFYLQGSRAYTKDSPMVPGRKASILVLELFLLILDDGIQFDSDLRQEAQQAAA
AWRKRLIAEGGVSKACEIDARGLLLFVGCFGIPKVFTSGDIWDLIRSSNLQQISDALKRSHVLVTKVSDILERMMNNGMK
IEAIDVAYTFGIEDKFPPQKLLTSFLRDSKEALKRRRREANNSPVLLKEASQKHLSTLKSAMKFLEGRKLDPKKLLPGWQ
VTEKIDKLEKEIADLNRKIDDKVAPKRKADENEFSINLKSQEVKRLRFTGSPLISSPSFGLHEQRVPSHLDGNGSYNAST
RINMVDGGFSCLISNPPVAGSMLYGSGSYSAAYGVPSTSSFAGVYRETLADRTGNITGSNVSAFGWHGVGDASIIDGTRG
QSLVHQSGSGLFGPSIEGFAGLPNSSPAGAANQSSASDLYRFADAVK

>Rc-EEF33358
MSSSNSTQMTTLKTIESALNLIDIKKQTLKRAYDDLQSHSSLLSSFSLSWSDLDSHFTSVQTALTRRFLRLQSTRPGPET
VQPEPVQDNPTRKALVPFCEKMDGRGLRDYISEHSREREAIRAELVGLMGLVSDPGEMILDAMEGFYLSKSKGDRDVDLY
RLRKSCLDLLEVLSEIKPKPKFSDEVKIKAKNLAFEWKEKVSLNGDSPSEALGFLNLIVAFELKDMFDDVNELLNYFVVI
ARFKQATVLARDIGLGDKINDLVQKLIDSGKQLLAVKFIFEFGLTDKFQPAPLLRDHLKESKEFTDKVCKEEKNSVKAQN
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>Pt-XP002320559
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KHNALEVQRKSCILLMEAIAPALGMKEPGGDDPWSSEIKEQAKEIAEEWKSKLAEIDLDASNGYSLEAQAFLQLLTTFNV
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Alignment used for phylogenetic analysis in Supplemental Figure 11A

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Zm-NP001141761      ------------------MSTEATLNNSGGSESALLLLEQLAEVFGKLKTHT---ETFLH
Pp-XP001752883      --------------------------------------------MADLEIQR---AAIVN
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At-FRL2             --------------------MTAAESIAASINQIDEKKQKLKKAFDDLQAHRSLLSPSFN
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Vv-XP002276317      --------------------MATVKTIALGLTLIDEKKEELRIAFEDLQAHSSSPS-SFT
Sb-XP002466091      -------MPPPPPPASTAASRAAMLHSVNTLASFSDTLADFLDQWDSVVLDVASIAATFA


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Th-AAY90142         HPQFMKSIDDLAKFSAAFDAFKRHYDDLQKHMDDIENAIESKFKSNGVDDSSSHS-----
Vv-XP002283789      DP--MRSVNELRNLSTVLHAFRRRWDELQKHLDFIQDAIASRSRELDASPQHHQA-----
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At-FRL2             LS----WSEIDSHFSSLQSSLFNRLQSAVTSS----------------------------
Rc-EEF33358         LS----WSDLDSHFTSVQTALTRRFLRLQSTR----------------------------
Vv-XP002276345      LT----WSAIDAHFSSIQSSLSRQFEILESRTDSVPQNDTLPTNNAVSLPAQSNAVSLPP
Vv-XP002276317      LT----WSDIDSHFSSIQSSLTRQFDLIQCQNDVVP------------------------
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At-FRIGIDA          MLSPPRNNVSVETTVTVS---------------------------------------QPS
Th-AAY90142         ---PEHDASREIATAIVC---------------------------------------PPP
Vv-XP002283789      --LASNTLETS----------------------------------------------SPE
Rc-EEF51656         --ITTPTIVTDNQTTITD---------------------------------------AKK
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Os-NP001062668      LERLQQKRDAALAMIFGK-SKLNLSMPVINPISKSVSNNAVLNGNIAS----LWPKP-AT
Os-NP001060162      LNQFQELRDTAVSALSEVRQKYKVELAGILDANGSKDKKVRTSTNDMNALCASEENTTAS
Zm-NP001141761      LNQLQELRDAAVSSLAEVRQKYKVELAEILEASGSKDKKVSTSINDNNASRASEENTPAS
Pp-XP001752883      LSRVQEQKDSAIASLFEE--KRNTTTAALLTSNTVSPS-----------PTTTSPTSNGL
Ps-ABK24390         PKNTSEKKSVAEKSIGNP------------------------------------------
At-FRL1             ----------------------------------------------------YRIDASDA
At-FRL2             ---------------------------------------------------------NSG
Rc-EEF33358         -----------------------------------------------------------P
Vv-XP002276345      QNNAVSLPPQNNAVSLPP--------------------------------QESAISRPTQ
Vv-XP002276317      ------------------------------------------------------------
Sb-XP002466091      PQWEREPSPLPEPQSSPLPEPAPALQPRPAPESAPAPQ------------------PEPA


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At-FRIGIDA          QE---IVPETSN---KPEGGRMCELMCSKGLRKYIYANISD--QAKLMEEIPSALKLAKE
Th-AAY90142         PEEAETAPEMITSNDKAEGQRLCESMCSKGLRKYIYANISE--RAKLMEEIPAGLKLAKE
Vv-XP002283789      SADLHSEPMPAQTSVS-ELGFLCGMMRSRGLRKYIISHLSD--VAKLREEVPAALKGAPK
Rc-EEF51656         ETVINSAPPPAKSSSSSELISLCEMMCGRGLRKYLTSNLTN--IPKLRNEVPTALKYAPK
Pt-XP002320559      G--EIIDPSENGNLEYPQLVELCEQMDSEGLHKFISDNRKN--LAVLKEEIPLALKAAAN
Ca-ABK42079         DNMKSFKNDVVEVKLYPELIKLCQDMDSEGLHKFISDNRKN--LAAVREEIPSALRTAVD
Sb-XP002457174      EESVHLQDGNAAVRPRSELASLCEEMNVKGLHKFISDNRKN--LAAIREEIPSALKKTSD
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Os-NP001060162      GLGEPSEASPVDVKPRPVLKQLCEQMDTAGLLKFLSENWKK--LSSLRDELSAALRCATD
Zm-NP001141761      GSGEASEALPVETKPRPVLKQLCEQMDTKGLLKFLSENCRK--LASFRDELSVALKCATD
Pp-XP001752883      TPTPAPTALGAEVRVRPELKVLCEIMDGDGLRKYIVNHKKD--VGALRNELPSALQCAID
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At-FRL2             NIETPTAVTTETPVLWPELRKFCEKNDGKGLGNYMIENSRK--RLSINEELPNAIRCSEN
Rc-EEF33358         GPETVQPEPVQDNPTRKALVPFCEKMDGRGLRDYISEHSRE--REAIRAELVGLMGLVSD
Vv-XP002276345      NSAVSRPPQNNANPSHPQLRLLCSAMDAEALRRYIMDHPND--RETLRSELLDAFQVARD
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At-FRIGIDA          PAKFVLDCIGKFYLQ--GRRAFTKESPMSSARQVSLLILESFLLMPDRGKGKVK-----I
Th-AAY90142         PAKFVLECIGKFYLQ--GRKAFSHDSHMIPARQVSLLILECFLLMIEPGEEKVKS---MI
Vv-XP002283789      PAKLVLECIGRFFLQ--GSKAFGKATHMVPSRQASLLILEFFLLS--DCTEMEP------
Rc-EEF51656         PAKLVFDCFGGFYLQ--GSRAYTKDSPMVPGRKASILVLELFLLILDDGIQFDS------
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Ca-ABK42079         PADLVLDSLKGFYPSEVLISDAKKDANLLGLRRTCIMLMECLSVLLTT--LELDSISSLI
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Zm-NP001151902      PYGLVLDSLEDFYSGDNLVLDGKKDGDLLGVRRTCLMLLESLGQLHTAGITCFSLEGHML
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Os-NP001060162      PARFVLGSLEGFFPSDHTSSPGNKQIILQGQRRSCIILMEAITPALATK---EPGDNHPW
Zm-NP001141761      PARFVLNSLEGFFPPDQTNSPGSKHNALEVQRKSCILLMEAIAPALGMK---EPGGDDPW
Pp-XP001752883      PARMVLGTLEGYHLPEPTSVAKDKESGASANRRACILLLECLAVVLADP--VLGADHPVV
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Vv-XP002276345      PAKMVLDALTGFFP--SNA-NEDGSSELHTMRRSCVFMLEQLMLFSPE-----------I
Vv-XP002276317      PAKLVLDALQEFFP--PNE-VDNEGNKLGSLMQTRLLLLEQLTAVLPE-----------I
Sb-XP002466091      PAALVLRAIGRYYIR----------AESPDVEAACTLLLELYVRAGCPRLPWGQG--RDA
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Al-ABY51872         ESCIKDEAETAAVAWRKR-LMSEGGLAAAE--KMDARGLLLLVACFGVPSNFR-SMDLLD
At-FRIGIDA          ESWIKDEAETAAVAWRKR-LMTEGGLAAAE--KMDARGLLLLVACFGVPSNFR-STDLLD
Th-AAY90142         ESSVKEEAEAAAFAWKRR-IMNEGKLATAE--AIDARGLLLLIACFGVPSSFR-SMDLLD
Vv-XP002283789      --SVKEEADLAAVTWRKR-LINEGGVSNAS--DIDARGLLLLVASFGIPALFR-NEDLRN
Rc-EEF51656         --DLRQEAQQAAAAWRKR-LIAEGGVSKAC--EIDARGLLLFVGCFGIPKVFT-SGDIWD
Pt-XP002320559      SEDVKDQAKAIAEEWKPRLDSLDVDANNGN--SLEAHAFLQLLATFGIASDFD-EEELSR
Ca-ABK42079         SESVKGRAKAIAKEWKPKLDELEIDANNGN--SLEAHAFLQLLATFSINSNFN-QEKLYK
Sb-XP002457174      TTNIVERAKKIAFEWKSKLDNLDIDASNGN--CLEAHAFLQLLATFGISAEYN-EDDLCK
Zm-NP001151902      TTNIIERAKKIAFEWKSKLDNLEIDASNGN--CLEAHAFLQLLATFGISAEYN-EDDLCK
Os-NP001062667      TASIKERAKKIALEWKSKLDSLDFDASNGN--CLEAHAFLQLLATFGIFAEFA-QDELCK
Os-NP001062668      TASIKERAKKIALEWKSKLDSLDFDASNGN--CLEAHAFLQLLATFAIFSEFA-EDELCK
Os-NP001060162      SSEIRELAKAIAEEWKSKLAEVDLDASDGY--SLEAQAFLQLLTTFNVDSVLD-EDELCK
Zm-NP001141761      SSEIKEQAKEIAEEWKSKLAEIDLDASNGY--SLEAQAFLQLLTTFNVDSVLD-EDELCK
Pp-XP001752883      PSNVKESAKQVADQWKSRMN-LQGDT-AGN--SLDAQAFLQLVATFGIATEYN-DDELCK
Ps-ABK24390         SSEAKKDAQKIAASWKSKLN--LDAESRIK--FVEAHAFLQLLASYGISKEFK-DDDLCE
At-FRL1             TVDTRNRAKKLAYHWK-----SKVGVK-----PFEALVFLHLVAAFELGSEFD-TEELSD
At-FRL2             TNDLRERARTIAYDWK-----PNIGNK-----PSEALGFLHLVAAFELGSLFS-TEEICD
Rc-EEF33358         SDEVKIKAKNLAFEWK-----EKVSLNGDS--PSEALGFLNLIVAFELKDMFDDVNELLN
Vv-XP002276345      GEDVRQRAKSLAQEWK-----GKVKVGDNT--LK-PMGFLHLLAAYGLGSDYDSTELLEL
Vv-XP002276317      KADVMQRAKYLAQEWK-----GKINRGAVT--SNGFLGFLYLLAAYGMGSDFDSSEYVEF
Sb-XP002466091      ELLLRQEAREVALTWRSRLLRGSGGGVGNAPGAAGARGLAFFMAAFGVPVEFP-AQELCD
                           *   *  *:                      :  ::  : :         :

Aa-AAZ92551         LIRMSGSNEIAGALKRSPFLV-PMISGIVESSIKRGM------HIEALEMVYTFGMEDKF
Al-ABY51872         LIRMSGSNEIAGALKRSPFLV-PMISGIVESSIKRGM------HIEALEMVYTFGMEDKF
At-FRIGIDA          LIRMSGSNEIAGALKRSQFLV-PMVSGIVESSIKRGM------HIEALEMVYTFGMEDKF
Th-AAY90142         LIRQSGTSEIAGALKRSPFLV-PIVSGIVDSCLKRGT------NIEALEIVFTFGMEDKI
Vv-XP002283789      LIRLSCPKEISDALRRSRFLL-ARVPDVIQGMIKNQM------NVEAVDFAYTFGLEEKF
Rc-EEF51656         LIRSSNLQQISDALKRSHVLV-TKVSDILERMMNNGM------KIEAIDVAYTFGIEDKF
Pt-XP002320559      LIPMVSRRRQAAELCRFLGLS-EKMPGVIEVLVNSGR------QIDAVNLAFAFDLTEQF
Ca-ABK42079         LIPMVSRRRQTADLCRSLGLS-DSMPGVIDVLISNGR------HIDAVNLAFAFELTEQF
Sb-XP002457174      LLPYVSRRRQTPELCRLLGLS-QKMPGVIEVLVESGR------PIDAINLAYVFELTEQF
Zm-NP001151902      LLPYVSRRRQTPELCRLLGLS-QKMPGVIEVLVKSGR------TIDAINLAYVFELTEQF
Os-NP001062667      LLPSVSRRRQTPELCRILGLS-QNMPGVIGVLVENGR------TIDAINLAYAFELTNQF
Os-NP001062668      LLPSVSRRRQTPELCRILGLS-QNMPGVIGVLIENGR------TIDAINLAYAFELTDQF
Os-NP001060162      LVVAVSRRKQTAELCRSLCLN-ERIPDIIKELVNRHR------QIDAVQFIHAFGLSESF
Zm-NP001141761      IVVAVSRRKQTAVSCRSLGLN-EKVPGIIEELVKRHR------QIDAVHFIQAFGLSETF
Pp-XP001752883      LVTAVARRRQTPALCRSLGLT-AKIPDVVDRLAKEGK------QIEALSFAHSFGIMDRV
Ps-ABK24390         LVPSIYRHPETPELCRALQIS-HKIPDVVEKLSSSGK------QIGAIQFIYAFGLVEKF
At-FRL1             YVFMIAKYKQATLVCNKIGVDRKRVGKLIKTLLDSGK------PILAVKFMYECGMTDEF
At-FRL2             YIFLISKYKQATTICKKIGLDRNRIGVLVQKFLDTGR------LLVAIRFIYENEMVGEF
Rc-EEF33358         YFVVIARFKQATVLARDIGLG-DKINDLVQKLIDSGK------QLLAVKFIFEFGLTDKF
Vv-XP002276345      LIDVVR--YREVFGLCRGLNLVDKVPDLIQNLIGSGK------PNLAVKFVLEFKLTHKF
Vv-XP002276317      LANVVVQNRQQGFTLCCRLNCVDKVPGVYLRKLCSVSSAMWACVAKEALYLCQIGLTDKC
Sb-XP002466091      LVNAADVAACVEVLKASKLFV-RKMRDVVIEMINKAM------YLQAMRIILAFEFQEAF
                                            :  :                           :

Aa-AAZ92551         SASSVLTSFLRMSKESFERAKRKAQ-SPLAFKEAAAKQLAALSSVMQCMETHKLDPVKEL
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Al-ABY51872         SASSVLTSFLRMSKESFERTKRKAQ-SPLAFKEAAAKQLAALSSVMRCMETHKLDPAKEL
At-FRIGIDA          SAALVLTSFLKMSKESFERAKRKAQ-SPLAFKEAATKQLAVLSSVMQCMETHKLDPAKEL
Th-AAY90142         SPSSLLTPFLRKSKESFELAKRKAH-SPTAFKEAIEKQLAALLSVTKCLEAHKLDPAKEI
Vv-XP002283789      PIWKILTSFLREHKEEWKRTREED--SPIRLKKANENYLSAMKSVTRCLEDHRVDPSKLL
Rc-EEF51656         PPQKLLTSFLRDSKEALKRRRREANNSPVLLKEASQKHLSTLKSAMKFLEGRKLDPKKLL
Pt-XP002320559      SPVTLLKSYLKEARKVSSSFKPGNASPITGQNEVNERELAALKAVIKCIEEHKLEEQYPG
Ca-ABK42079         PPVSLLKSYLNDASKASTPLNSGNASP-TVQNEVNEKELSALKAVLKCIEDHKLEEQYPV
Sb-XP002457174      EPVQLLKAYLRDVKKVS-HARNVKGSP-GAQNEMNERELSALKSVIKCIEEHKLEEQYPV
Zm-NP001151902      EPVQLLKAYLRDVKKLS-HARNVKISP-GAQNEMNERELCALKSVIKCIEDHKLEEQYPV
Os-NP001062667      EPVELLKAYLQEVKSVP-HFKTGKISL-QVQNEMNERELSALKAAIKCIEEHKLDEKYPI
Os-NP001062668      EPVELLKAYLKEVKSMS-HVKTGKMSP-GVQNEINERELSALKAVIKCIEEHKLDEKYPI
Os-NP001060162      PPAPLLKTYVEELKDSLGNNGDGNAAS--LKDDPKTRELLALRAVIKCIEEYKLQKDYPL
Zm-NP001141761      PPAPLLKTYVEEQKDTIENNGDATAIS--LTDDPKSRELIALRAVIKCIEEHKLQKECSL
Pp-XP001752883      LPIPLLKAYLKEARRTAQSILKSGSSSAAAQNDATMKELAALKAVLKCIEEYQLESQYPS
Ps-ABK24390         PPVPLLKAYLEDEKRVSQELAQQGGYPVNAQNYAAKREIASLNTVIKCIEDYKLESQMSI
At-FRL1             EPIPVLKSYIKDCREAALRVCVEDNYSLKSQNEASDKEVSALKPLIKIIKDQNLESEFTQ
At-FRL2             EPVSILKTSLKNSREAAKRVCAEGNYSLKVQNEATDKELSALRAVIKVVKEKNIESEFME
Rc-EEF33358         QPAPLLRDHLKESKEFTDKVCKEEKNSVKAQNEARSREVNALKSVLRYIDEHNLEFDYPH
Vv-XP002276345      PLIAILKDIVESSRDVARKVRKDGKHSLQSQNEATSKEISALKLVTKYIKDYDLNNEYPG
Vv-XP002276317      PLAPILKAHVKKFENLAQNVYDSRNQSLQYLNGATGAEITILKQIISCLEEYKLEAEYPR
Sb-XP002466091      PLAPTLALIIEKLEHDTKDENEGQ------ASERDEEDLALLSSISKCMEDHKLSPSEFT
                         *   :.                    .      :  :      :.   :.

Aa-AAZ92551         PGWQIKEQIVNLEKDTLQLDKEMEEKARSISLMEEAVLAKRMYNQQMKRPRLSPMEMPPV
Al-ABY51872         PGWQIKEQIVNLEKDTLQLDKEMEEKARSISLMEEAVLAKRIYNQQMKRPRLSPMEMPPV
At-FRIGIDA          PGWQIKEQIVSLEKDTLQLDKEMEEKARSLSLMEEAALAKRMYNQQIKRPRLSPMEMPPV
Th-AAY90142         PGWPIKEQIVKLEKDTLQIDKQMEEQARSISLMEEAVLTKRLYNQQMKRPRLSEMEMPPA
Vv-XP002283789      SGWHIDEKIIQLEKEMADLDKKMEGKVMLKRKADEIDSLKKMKTREIKHSPIAAP----S
Rc-EEF51656         PGWQVTEKIDKLEKEIADLNRKIDDKVAPKRKADENEFSINLKSQEVKRLRFTGSPLISS
Pt-XP002320559      D--PLQKRLLQLEKAKAEKKRATEAAKPQPKRPRASGVGCGPRVTSSVPERTFYP----R
Ca-ABK42079         D--PLQKRVLQLEKAKADKKKANEVAKPQSKRPRPNGVGNGPRVNNVVAEKNF-------
Sb-XP002457174      D--PLQKRVLQLEKAKADKRRAVEAAKPQSKRPRANGSAFAHRA-TGFADKSFYPA--AA
Zm-NP001151902      D--PLQKRVLQLEKAKADKRRAVEAAKPQSKRPRANGSTFAPRA-TGFADKSFYP----A
Os-NP001062667      D--LLQKRVIQLEKAKADKRRAVEAAKPQSKRPRANGSVYAPH--TSFPDKSFYQ---AA
Os-NP001062668      D--PLQRRVIQLEKAKADKRRAVEAGKPQSKRPRANGSVYAPHI-TSFSDKSFYQ---AA
Os-NP001060162      G--PLQKRVAELK-SKGEKRP-LEAGRHNAKKPRTFGNSAARRPPNPVGSAGRRPSGPAG
Zm-NP001141761      G--PLQKRVSELK-PKGEKRPSSDAGRTYAKKPRGPGISFPRRPAGSVGSAARRPPFPGY
Pp-XP001752883      M--PLQKRVLHLEKAKSDRKRAAVAVKAQTKRPRAS------------------------
Ps-ABK24390         K--DLQKRVGEVQKSMSKRKRNAKSIKFLTKQARLYSGAGVVAGAGAASVAGAGVASVAG
At-FRL1             E--KVEERVEELEKNKALRKR----NTTNPPKQEPQQKGKKR------------TRDCKN
At-FRL2             E--KLEECVKELEDQKAQRKRATKFNSPANPQQPQEQKVDNK------------RPRVAN
Rc-EEF33358         L--DLEKRIEMLEKQKADRKVAAPSPDNRPRQQPKKQQLSKKQ------QQHQGKQQAKK
Vv-XP002276345      A--PLEERIQKLESQMAARTAAKKRPALAPAPRPKQQKKQKSKQAQTTATASPSVPSGAA
Vv-XP002276317      E--HLEMRIKMLEREMKDR----KRSAAALVPRHQQQQELGSKHPWTKP-AGAAVPSVAG
Sb-XP002466091      S---FAAKIALLEERVGKPKQACTGVKRKRAEECVG------------------------
                        .   :  ::

Aa-AAZ92551         ASSSYSPLYLDRSFPSQ---------RDEDRDEISALVSSYLGPSSSFPHRSSLRRSPEY
Al-ABY51872         ASSSYSSIYLDRSFHSQ---------RDEDRDEISALVSSYLGPSSSFPHRSSLRRSPEY
At-FRIGIDA          TSSSYSPIYRDRSFPSQ---------RDDDQDEISALVSSYLGPSTSFPHRS--RRSPEY
Th-AAY90142         ASSSYSPIYRDRNFSSH---------IDGDRDEISALVSSYLGPSSSFPHRSSLRRSPEY
Vv-XP002283789      SVIGLQEQRVADNMASRS--------FYDSTMPINFLDSGFPGHISTYPAASAMLHGSGG
Rc-EEF51656         PSFGLHEQRVPSHLDGNG--------SYNASTRINMVDGGFSCLISNPPVAGSMLYGSGS
Pt-XP002320559      VPERYP-----------------------QYVYDRPYIYTGPADNHVPQLMSSAAT----
Ca-ABK42079         ------------------------------------------------------------
Sb-XP002457174      TPERHP-----------------------SNPYERQFVYG--AEAHLPP-MVSSAS----
Zm-NP001151902      TPERHP-----------------------SNPYERQFVYG--AEAHLPP-MMSSAS----
```

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Os-NP001062667      PPQRH------------------------SYPYERQYVYG--AEAHHHPTMISSAP----
Os-NP001062668      APQRH------------------------SYPYERQYVYG--AEAHHHPTMISSAP----
Os-NP001060162      TWQRPPPPMPS---------------YPDRYGHADRYHYTAPSATYDPPAYASYSEPYSA
Zm-NP001141761      TWQRAPAPMPSRGPAPVPSRAPLPAPLPDRYGAADRYHYTPPAPAYDSGAFSSYSEPFSA
Pp-XP001752883      ------------------------------------------------------------
Ps-ABK24390         AASVAGAVG-----------------LLPKPSPPSAFALFNSSALLPKPTPPSAFALSNS
At-FRL1             GS--QVPVPSQ-----------------QLLSRPEAL--LMPEHSHHGLQLNPYGLMTS-
At-FRL2             GSSMEYNLTIP-----------------PLRPQQQPP--LLPTPSQI-LQVNPYGLLSS-
Rc-EEF33358         QQLKGNKRPRM-----------------AMLPGPAAVPISIAGPSSAGASAGPYGLAGAG
Vv-XP002276345      GTSSTAAPFQQ-----------------PHLQAPGLVPD--GPVPFMNPSAGLYGFAGVP
Vv-XP002276317      FLPDRSVPYLS-----------------SSVELQGLAGPTLSTARYTAPSAGLYCSAGVP
Sb-XP002466091      ------------------------------------------------------------


Aa-AAZ92551         -------------------------MVPLPPGGLGRSVYAYEHLPPNSYSPGHGQRLPRQ
Al-ABY51872         -------------------------IVPLPPGGLGRSVYAYEHLPPNSYSPGHGQRLPRQ
At-FRIGIDA          -------------------------MVPLPHGGLGRSVYAYEHLAPNSYSPGHGHRLHRQ
Th-AAY90142         -------------------------MVP--PGGLGRSVSAYEHLLPSSYSP---------
Vv-XP002283789      GSLPENITGTMSGSGSGTRVHGTGTGPGMAGTGGVPSMASFSGAHGEMLFDRTGQMMKNN
Rc-EEF51656         ----------------------------YSAAYGVPSTSSFAGVYRETLADRTGNITGSN
Pt-XP002320559      ------------------------------YNFSP---SHGNYFGNGY--QYQTPYHH--
Ca-ABK42079         ------------------------------------------------------------
Sb-XP002457174      ------------------------------YTMQP---AHGPYYGNGYPVQYQVPYIH--
Zm-NP001151902      ------------------------------YPMQP---AHGPYYGNGYPVQYQVPYIH--
Os-NP001062667      ------------------------------YGISP---AHTTYYEKDGEPNRG-------
Os-NP001062668      ------------------------------YGMSP---AHTTYYGNGYQVQYQVPYIH--
Os-NP001060162      ---------------------------SKPYQYTPGSVAPASYNSNQFKVAYGGPGAPPT
Zm-NP001141761      ---------------------------PKPFQYTPGSVA-ASYNSSPYKVAYGGPGAPVR
Pp-XP001752883      ------------------------------------------------------------
Ps-ABK24390         ---------------------------SDLYRPAPVASIPSYNLPGQGVYDRGSQSIYRS
At-FRL1             ----------------------------AFSGVVVNP---LTGLFGSGATPQS--LYYAQ
At-FRL2             ----------------------------ILPGVAVPYGN-PRALFGSVPAPASRPVFYVQ
Rc-EEF33358         ---------------------------MCFPGNPSPVR--AHPYSSNSHMSSSYYDRSAA
Vv-XP002276345      ---------------------------MGFPGNLGPPMPHLHPMEPQLPMP-------FA
Vv-XP002276317      ---------------------------MSFPGNLSPARPHVQALDSQMPIPSGYFDRPSG
Sb-XP002466091      ------------------------------------------------------------


Aa-AAZ92551         YSPSPVHGQRHPRQYSPPIHGQQQIPFGLQR----VYRHSPSEERYLGLSNHRSPRSNSS
Al-ABY51872         YSPSPVHGQRHPRQYSPPIHGQQQIPFGLQR----VYRHSPSEERYLGLSNHRSPRSNSS
At-FRIGIDA          YSPSLVHGQRHPLQYSPPIHGQQQLPYGIQR----VYRHSPSEERYLGLSNQRSPRSNSS
Th-AAY90142         -----VHGQRLPREYSPPVHGQQQIPYGLQR----VYRHSPSVERLLTLPHHRSPR-NSS
Vv-XP002283789      GPPY--AGRRD-MGFNDRVIGQSFIAHPASMGVDSIFGPSTSMESFPGMPNAPSINAANG
Rc-EEF51656         VSAFGWHGVGD-ASIIDGTRGQSLVHQSGSG----LFGP--SIEGFAGLPNSSPAGAANQ
Pt-XP002320559      ------------------------------------------------------------
Ca-ABK42079         ------------------------------------------------------------
Sb-XP002457174      ------------------------------------------------------------
Zm-NP001151902      ------------------------------------------------------------
Os-NP001062667      ------------------------------------------------------------
Os-NP001062668      ------------------------------------------------------------
Os-NP001060162      AGGYGSYNDAAGQSTSSSYSGYSGYHPSLPRL----------------------------
Zm-NP001141761      S-TYPGYASASGPAASSSYANYMGSVYRPPQQP---------------------------
Pp-XP001752883      ------------------------------------------------------------
Ps-ABK24390         ACDVGSNPSFLSRSHLYPSDSVQ-------------------------------------
At-FRL1             QTGYVLPP-QYHPPYYSQ------------------------------------------
At-FRL2             QTGYGMPPPQYRPPYYPQ------------------------------------------
Rc-EEF33358         FGGYGFPP-QYCPGYYPQ------------------------------------------
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Vv-XP002276345      HGGYGLQS-LYPPAYFHQ------------------------------------------
Vv-XP002276317      LGGYNLQP-HYHWTYYPSSS----------------------------------------
Sb-XP002466091      ------------------------------------------------------------


Aa-AAZ92551         LDPK------------
Al-ABY51872         LDPK------------
At-FRIGIDA          LDPK------------
Th-AAY90142         QDHIGGM---------
Vv-XP002283789      SSASDLYQFADAVFGR
Rc-EEF51656         SSASDLYRFADAVK--
Pt-XP002320559      ----------------
Ca-ABK42079         ----------------
Sb-XP002457174      ----------------
Zm-NP001151902      ----------------
Os-NP001062667      ----------------
Os-NP001062668      ----------------
Os-NP001060162      ----------------
Zm-NP001141761      ----------------
Pp-XP001752883      ----------------
Ps-ABK24390         ----------------
At-FRL1             ----------------
At-FRL2             ----------------
Rc-EEF33358         ----------------
Vv-XP002276345      ----------------
Vv-XP002276317      ----------------
Sb-XP002466091      ----------------
```

Sequences used for phylogenetic analysis in Supplemental Figure 11B (FASTA format)

```
>At-SUF4
MGKKKKRATEKVWCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTASGMVIHVLQVHKENVTKVPNAKDGRDSTDIEI
YGMQGIPPHVLTAHYGEEEDEPPAKVAKVEIPSAPLGGVVPRPYGMVYPPQQVPGAVPARPMYYPGPPMRHPAPVWQMPP
PRPQQWYPQNPALSVPPAAHLGYRPQPLFPVQNMGMTPTPTSAPAIQPSPVTGVTPPGIPTSSPAMPVPQPLFPVVNNSI
PSQAPPFSAPLPVGGAQQPSHADALGSADAYPPNNSIPGGTNAHSYASGPNTSGPSIGPPPVIANKAPSNQPNEVYLVWD
DEAMSMEERRMSLPKYKVHDETSQMNSINAAIDRRISESRLAGRMAF

>Vv-XP002274291
MGKKKKRVAAKVWCYYCDREFEDEKILVQHQKAKHFKCHVCHKKLSTAGGMVIHVLQVHKETVSKVPNAKPGRESTEIEI
YGMEGIPHEILAAHYGEEDEDVPSKLAKVEIPSSQLGGGAVPGTLGIGVPPQPALGAMPPVYNPALAVPPAGWPVPARPQ
PWYSQHPAISIPPAPLGMTQQPLFPIQPVKPPLPSTMSSALQPSLQITPPGLPIPSPSAPLPQPLFPVGVNNNLPTKNSP
FSTPMLSTSIPLSSQAELNSSIEAHSSTNSGPSINSHSYASGPNTGGPSIGPPPVIANKVPATQPAGNEVYLVWDDEAMS
MEERRMSLMKYQVHDETSQMSSIDAAIDRRILESRLAGRMAF

>Rc-EEF34249
MGKKKKRVASKVWCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTAGGMAIHVLQVHKESITKVPNAKPGRESTDIEI
YGMQGIPPDVLAAHYGDEEEDNPSKVAKVDLPSPLGGIMPGPVGVGYPPQTLGVVQPIYSSVVPVPPAGWPVPSRPQPWF
SQPPAVSIPSTAPTGYAQQPLFPVQNVRPPLPSATSPALQLSQVAPPGLPSSTPPIPVSQPLFPVISNNLPQSSPFSTHL
PTPNIPSSTLGEVKGSVDVLSGANNSLTTSYHTPGIPGLITCPLLIDTRI

>Pt-EEE79242
MGKKKKRAASKVWCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTAGGMAIHVLQVHKESVTKVPNAKPGRESTDIEI
YGMQGIPPDVLAAHYGEEEDENPSKAAKVDIPSAQLVGGMVPGPLGAGYPRPLAAMQPMSGPCTLGPVKLWNYLYNSAVP
APHAGWPVPPRSQHWLPQHPAVSIPPPAPITYTQQPLFPVQNVRPPVPSTMTPALIPSQVTPPGLPSSTPSVSQPLFPVN
NNLPQSSTFSAPFPSTSLLPSSPAEVRGSMNVHLGVNTSMTTGYLTQSASASGTLGNTHSYASGPNTGGPSIGPPPVIAN
KAPVIQPAVNEVYLVWDDEAMSMEERRMSLPKYQVHDETSQMSSIDAAIDRRILEGRLAGRMAF

>Sb-XP002462836
mgkkkkrvdkvfcyycdrefddekilvqhqkakhfkchvchkklstasgmsihvlqvhkesvtkvpnakpdresteieif
gmqgipahvlaahygeeedpsakmakvevpqvrpvimpnslgmafpprpaygvappiynpalnplmarppiwpgppaqaw
ypqqaaypqqpavsvppvvaglppqqplfpiqnvptpmtsapanvlqtsfpmappgvpspvapqvsqplfpvntsavnga
asspflasvvpgtipasspaavgaagigygannqgtggpavgsspavsnnkasgaqpatnevylvwddeamsmeerrlal
pkyqvhdetsqmnsvdaaidrrisesrlagrmal

>Os-EEE70223
MGKKKKRVEKVFCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTAGGMAIHVLQVHKESVTKVPNAKPERESTEIEIF
GMQGIPPDVLAAHYGEEEDPSSKVAKVEVPSLRPPVMPNPAGMVYPPRPAYGVAPPMYNPALNPLMARPPIWPAPPPQPW
FTQPVVSVPQMASGLAPQQPLFPIQNMPAPMTSAPANLLQTSFPMAHVGVPSPVTPQVSQPLFPVSTSAGNGAVSSPYVA
SVAPGSIPTSSPSVAPAGVGYAATNQGTGGPAAVPPPASNNKAPATQPGANEVYLVWDDEAMSMEERRLSLPKYQVHDET
SQMNSVDAAIDRRISESRLAGRMAL

>Os-NP001063931
MGKKKKRVEKVFCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTAGGMAIHVLQVHKESVTKVPNAKPERESTEIEIF
GMQGIPPDVLAAHYGEEEDPSSKVAKVEVPSLRPPVMPNPAGMVYPPRPAYGVAPPMYNPALNPLMARPPIWPAPPPQPW
FTQPVVSVPQMASGLAPQQPLFPIQNMPAPMTSAPANLLQTSFPMAHVGVPSPVTPQVSQPLFPVSTSAGNGAVSSPYVA
SVAPGSIPTSSPSVAPAGVGYAATNQGTGGPAAVPPPASNNKAPATQPGANEVYLVWDDEAMSMEERRLSLPKYQVHDET
SQVSSDFYNFISVILMICEKNQVEVHGDALNWNIV

>Zm-NP001136975
mgkkkkrvdkvfcyycdrefddekilvqhqkakhfkchvchkklstasgmaihvlqvhkesvtkvpnakpdresteieif
gmqgipahvlaahygeeedpstkvpkvevpqvrpvimpnslgmafpprpaygvappiynpalnplmarppiwpaapaqaw
ypqqaaypqqsavsvppivaglppqqplfpiqnvptpmtsaaanvlqtsfpmappgvpspvaphvsqplfpvntsavnga
vnspflasvapgtipasspaavgvagigygtnnqgtrdpavgsspavsnnkasgaqpatnevylvwddeamsmeerrlsl
pkyqvhdetsqmnsvdaaidrrisesrlagrmal
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>Pp-XP001773394
MGKKKKKTYKVWCFYCEREFEDEKILIQHQKAKHFKCHVCHKKLSSASGMVIHVLQVHKESVSKIPNAKPEREALTDLEI
YGMEGIPAEILAAHDGDYDEDENPSKVARVEVPPLLPFVGGGLMGSNAIGMAPQPMYTAMQPMCVQAITRVGSTSTPKLA
ATTSTSPRMERSSSSWPTRPTPHAPTSTASPPNGPPPPPPPSAPPLSPAGSLVKPPQPSPGSNQSSINGSPGIAPPLPSP
GASSGMNMGPGSNARLPPPPYGGEILISHMYSSGPNTGGPSIGPPPVISNKPPGVAGGTNEVYLVWDDEFFSMEERRLSL
QKYQVHDETIQMSSVDAAIDKRILEGRLAGRMSFHV
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Alignment used for phylogenetic analysis in Supplemental Figure 11B

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Sb-XP002462836      MGKKKKR-VDKVFCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTASGMSIHVLQVHK
Zm-NP001136975      MGKKKKR-VDKVFCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTASGMAIHVLQVHK
Os-EEE70223         MGKKKKR-VEKVFCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTAGGMAIHVLQVHK
Os-NP001063931      MGKKKKR-VEKVFCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTAGGMAIHVLQVHK
Rc-EEF34249         MGKKKKRVASKVWCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTAGGMAIHVLQVHK
Pt-EEE79242         MGKKKKRAASKVWCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTAGGMAIHVLQVHK
Vv-XP002274291      MGKKKKRVAAKVWCYYCDREFEDEKILVQHQKAKHFKCHVCHKKLSTAGGMVIHVLQVHK
At-SUF4             MGKKKKRATEKVWCYYCDREFDDEKILVQHQKAKHFKCHVCHKKLSTASGMVIHVLQVHK
Pp-XP001773394      MGKKKKK-TYKVWCFYCEREFEDEKILIQHQKAKHFKCHVCHKKLSSASGMVIHVLQVHK
                    ******: . **:*:**:***:*****:******************:*.** ********

Sb-XP002462836      ESVTKVPNAKPDRES-TEIEIFGMQGIPAHVLAAHYGEEE--DPSAKMAKVEVPQVR---
Zm-NP001136975      ESVTKVPNAKPDRES-TEIEIFGMQGIPAHVLAAHYGEEE--DPSTKVPKVEVPQVR---
Os-EEE70223         ESVTKVPNAKPERES-TEIEIFGMQGIPPDVLAAHYGEEE--DPSSKVAKVEVPSLR---
Os-NP001063931      ESVTKVPNAKPERES-TEIEIFGMQGIPPDVLAAHYGEEE--DPSSKVAKVEVPSLR---
Rc-EEF34249         ESITKVPNAKPGRES-TDIEIYGMQGIPPDVLAAHYGDEEE-DNPSKVAKVDLPSP---L
Pt-EEE79242         ESVTKVPNAKPGRES-TDIEIYGMQGIPPDVLAAHYGEEED-ENPSKAAKVDIPSAQL-V
Vv-XP002274291      ETVSKVPNAKPGRES-TEIEIYGMEGIPHEILAAHYGEEDE-DVPSKLAKVEIPSSQL-G
At-SUF4             ENVTKVPNAKDGRDS-TDIEIYGMQGIPPHVLTAHYGEEED-EPPAKVAKVEIPSAP--L
Pp-XP001773394      ESVSKIPNAKPEREALTDLEIYGMEGIPAEILAAHDGDYDEDENPSKVARVEVPPLLPFV
                    *.::*:****  *:: *::**:**:*** .:*:** *: :  : .:* .:*::*

Sb-XP002462836      PVIMPNSLGMAFPP----------RPAYGVAPP---IYNPALNPLMARPPIWPGPP--AQ
Zm-NP001136975      PVIMPNSLGMAFPP----------RPAYGVAPP---IYNPALNPLMARPPIWPAAP--AQ
Os-EEE70223         PPVMPNPAGMVYPP----------RPAYGVAPP---MYNPALNPLMARPPIWPAPP--PQ
Os-NP001063931      PPVMPNPAGMVYPP----------RPAYGVAPP---MYNPALNPLMARPPIWPAPP--PQ
Rc-EEF34249         GGIMPGPVGVGYP-----------PQTLGVVQP---IYSSVV-PVPPAG--WPVPS-RPQ
Pt-EEE79242         GGMVPGPLGAGYPRPLAAMQPMSGPCTLGPVKLWNYLYNSAV-PAPHAG--WPVPP-RSQ
Vv-XP002274291      GGAVPGTLGIGVPP----------QPALGAMPP---VYNPAL-AVPPAG--WPVPA-RPQ
At-SUF4             GGVVPRPYGMVYPP----------QQVPGAVPAR-PMYYPGP-PMRHPAPVWQMPPPRPQ
Pp-XP001773394      GGGLMGSNAIGMAP----------QPMYTAMQP---MCVQAITRVGSTS-----------
                       :  . .   .                       :

Sb-XP002462836      AWYPQQAAYPQQPAVSVPPVVAGLPPQQPLFPIQNVPTPMTSAPANVLQTS--FPMAPPG
Zm-NP001136975      AWYPQQAAYPQQSAVSVPPIVAGLPPQQPLFPIQNVPTPMTSAAANVLQTS--FPMAPPG
Os-EEE70223         PWF-------TQPVVSVPQMASGLAPQQPLFPIQNMPAPMTSAPANLLQTS--FPMAHVG
Os-NP001063931      PWF-------TQPVVSVPQMASGLAPQQPLFPIQNMPAPMTSAPANLLQTS--FPMAHVG
Rc-EEF34249         PWFS------QPPAVSIPSTAPTGYAQQPLFPVQNVRPPLPSATSPALQLS---QVAPPG
Pt-EEE79242         HWLP------QHPAVSIPPPAPITYTQQPLFPVQNVRPPVPSTMTPALIPS---QVTPPG
Vv-XP002274291      PWYS------QHPAISIP-PAPLGMTQQPLFPIQPVKPPLPSTMSSALQPSL--QITPPG
At-SUF4             QWYP------QNPALSVPPAAHLGYRPQPLFPVQNMGMTPTPTSAPAIQPSPVTGVTPPG
Pp-XP001773394      ----------TPKLAATTSTSPRMERSSSSWPTRPTPHAPTSTASPPNGPP---PPPPPS
                                   : .         .. :* :    . ..: :     .     .  .

Sb-XP002462836      VPSPVAP-QVSQPLFPVNTSAVNGAASSPFLASVVPGTIPASSPAAVGAAGIGYGANNQG
Zm-NP001136975      VPSPVAP-HVSQPLFPVNTSAVNGAVNSPFLASVAPGTIPASSPAAVGVAGIGYGTNNQG
Os-EEE70223         VPSPVTP-QVSQPLFPVSTSAGNGAVSSPYVASVAPGSIPTSSPS-VAPAGVGYAATNQG
Os-NP001063931      VPSPVTP-QVSQPLFPVSTSAGNGAVSSPYVASVAPGSIPTSSPS-VAPAGVGYAATNQG
Rc-EEF34249         LPSSTPPIPVSQPLFPVIS-NNLPQ-SSPFSTHLPTPNIPSSTLGEVKGSVDVLSGANNS
Pt-EEE79242         LPSSTP--SVSQPLFPVN--NNLPQ-SSTFSAPFPSTSLLPSSPAEVRGSMNVHLGVNTS
Vv-XP002274291      LPIPSPSAPLPQPLFPVGVNNNLPTKNSPFSTPMLSTSIPLSSQAELNSSIEAHSSTNSG
At-SUF4             IPTSSPAMPVPQPLFPVVN-NSIPSQAPPFSAPLPVGGAQQPSHADALGSADAYPPNNSI
Pp-XP001773394      APPLSPAGSLVKPPQPSPGSNQSSINGSPGIAPPLPSPGASSGMNMGPGSNARLPPPPYG
                     *   .   : :*  *           ..  :         .       :
```

```
Sb-XP002462836      TGGPAVGSS---------------------------PAVSNNKASGAQPATNEVYLVWDD
Zm-NP001136975      TRDPAVGSS---------------------------PAVSNNKASGAQPATNEVYLVWDD
Os-EEE70223         TGGPAAVP----------------------------PPASNNKAPATQPGANEVYLVWDD
Os-NP001063931      TGGPAAVP----------------------------PPASNNKAPATQPGANEVYLVWDD
Rc-EEF34249         LT-TSYHTP-------------------------GIPGLIT-------------------
Pt-EEE79242         MT-TGYLTQSASASGTLGNTHSYASGPNTGGPSIGPPPVIANKAPVIQPAVNEVYLVWDD
Vv-XP002274291      PS-INSHSYAS--------------GPNTGGPSIGPPPVIANKVPATQPAGNEVYLVWDD
At-SUF4             PGGTNAHSYAS--------------GPNTSGPSIGPPPVIANKAPSNQP--NEVYLVWDD
Pp-XP001773394      GEILISHMYSS--------------GPNTGGPSIGPPPVISNKPPGVAGGTNEVYLVWDD
                                                        *

Sb-XP002462836      EAMSMEERRLALPKYQVHDETSQMN-------SVDAAIDRRISESRLAGRMAL---
Zm-NP001136975      EAMSMEERRLSLPKYQVHDETSQMN-------SVDAAIDRRISESRLAGRMAL---
Os-EEE70223         EAMSMEERRLSLPKYQVHDETSQMN-------SVDAAIDRRISESRLAGRMAL---
Os-NP001063931      EAMSMEERRLSLPKYQVHDETSQVSSDFYNFISVILMICEKNQVEVHGDALNWNIV
Rc-EEF34249         ---------------------------------CPLLIDTRI--------------
Pt-EEE79242         EAMSMEERRMSLPKYQVHDETSQMS-------SIDAAIDRRILEGRLAGRMAF---
Vv-XP002274291      EAMSMEERRMSLMKYQVHDETSQMS-------SIDAAIDRRILESRLAGRMAF---
At-SUF4             EAMSMEERRMSLPKYKVHDETSQMN-------SINAAIDRRISESRLAGRMAF---
Pp-XP001773394      EFFSMEERRLSLQKYQVHDETIQMS-------SVDAAIDKRILEGRLAGRMSFHV-
                                                     *  :
```

Sequences used for phylogenetic analysis in Supplemental Figure 11C (FASTA format)

```
>At-FLX
MAGRDRYIPSSAVSTSSSSRLLESQLIESDRNRARSVILEDRIAIQHREIQSLLNDNQRLAVAHIGLKDQLNVAKRELER
LLETAVKVKAEGEAKVREVYQNALRMEAEARVIDGLGAELGQVRSDVQRLGSDRQELATELAMFDDEMAKAKPNSDRAIE
VKLEIEILRGEIRKGRAALELEKKTRASNLHHERGMEKTIDHLNREIVKLEEELVDLETKAREANAAAEAAPTPSPGLAA
SYGNNTDDIYGGQGRQYPEANGTHEVHMSL

>Vv-CAO21396
MAGRNHLPPPNALKIREVSSTRAPYPSHHNHHALIEEDRYRHRSGPIPVSAGRYHPAVIDERIVIQHREIQTLLGDNQRL
AATHVALKQELAAAQQEISHLSAAAASVKAERDAQVREVYERSLKMEAEVRSIDALNAELAQVRADVQKLSASRQELAAQ
LQTINTDLSVSRSELKEVQAVKDGIENMRKELQRGRAAIEYEKKTHSNNLEQSEAMGKNMMAMAHEVEKLRAELANAEKR
ARAAAAAAAANPSMSS

>Rc-EEF41190
MAGRNNLPPNTLKHRQVPVDDPRLHNRVPRLHHPSTILEDRIAIQHREIQTLLLDNQQLTATHLALKQDLALVDDELRHL
SAAAADVKAQRDDQVREVYERSLKLDAEVRSIDALRAELVQVTADVEKLSVHRQELTAELRAINSDVAKARTEAQQVAAI
EADIQTMQKEIQRGRAAIENEKKLYASNLEHGQTMEQNMIAVAREIEKLHAELANLEKRERAEAAAAIAANPSPGYAGSY
SNPEVSYGGNLGPDLYAIHQVQGGTDAGPQFVPG

>Pt-XP002300004
MAGRNHLQLREIPLSRAALLPHPTTDPHRLHARPHHLLLEDRITIQHREIQSLLLENERLAAAHFALKQELSLSQQDLRH
LSTLAADVKAERDNQVREVYERSLKSDAELRSIDAMSAELVQVRTNVQKLTAQRQDMTAQLKGMNNEIVKAKTETQQVGV
LKAEIETVQQEIQRGRAAIAYEKKTRAINLEQEKVLEKNMNLVIREIEKLRGEFANAEKRARAAAAAANPSPGYGGNYGS
AEVGCGGSSYPDPYGLQQVQVGSDSGPTFASGVMSNGPYDTAHG

>Sb-XP002466208
MAARRGPHVIKLHDPNPPLLGRAPGPAAAAVSAPSRDEGILAQHPRAAPSSASAAHPAFALIEERLVARDQDIQELLVDN
QRFAATHVALQQQLIAAQHELRAVSVAATRARAEREGEVRALADQAAHIEAEARAVAAARAEVDQVHADVQVLAAARTDL
VNRLQGLREKLAHKKAEASKTDSVRAQIETMRREIQKGRAAVDFEKKAHSDNLEQSKAMEKNMISVASEIERLRGELANA
EKGATAVNPVAAVGNSGYAAAYGNSEPTYTGMYGNPDATYTAQAYPDAYSTNQAHMHTGANSHYMSQPVSYGQYEGQHTN
VQR

>Ps-ACN41197
MAGRNRLPAHALKGGLQAMPSMHEGPYAMGAGPLPPHPAFVDEMRNGPHGRGPGPMLPHPGFLEERLSAQHQEIQGLLLE
NQRLAATHVALRQELASTHQELQHLSHVATNMQADKDHQLRGLYDNSKKLEAEMRAMEPMKAELMQLQADNQKMGAVRQE
LTSQVQSLTQELTRAWNDMQQSVPLRTEIESLHGEFERARTAIEYEKKARAGRQEQGQAMEKNFISMSREVEKLRAELAK
VDKRERGAANPGGAYAGNYGSAEKGYSSGAYGGDGYGMHPVQGAEESAGQYGAGAAPWGAYEMQRSHVRR

>Os-NP001051704
MAARRGPHVIKLHDSAPALLGRAPMPPPPGPRDELPPPSAVLVHHPRGGLAPHPAVAALEDRLAVRDRDIQELLVDNQRF
AATHVALQQQLIAAQHELRVVSIAATRARAEREDEVRALAEQAARIEAEARAAVAARAEVDQVHADVQVLAGARTELVDR
LQDLRGQLARFQAEAGKTESVRAQVETMRREIQKGRAAVEFEKKAHADNLEQSKAMEKNMIAVASEIEKLRGDLANAEKR
ATAVTATAPVANPGFPTTYGNSEATYPAPAAYGNSETTYAPTYGNTEAAYASTYGSSEAAYAAAYGNSDAYSTNQAHTRT
DGNPHYMAPPVHYAQYDSQHTNVQR

>Zm-NP001151248
MAARRGPHVIKLHDPNPPLLGRAPGAAPAAVPASSRDEGLLAQHLRASAAHPAFALIEERLAARDQDIQELLVDNQRFAA
THVALQQQLIAAQHELRAVSVAATRARAEREGEVRSLADQAAHMEAEARAIAAARAEIDQVHADVQVLAAARTDLVNRLQ
VLREKLAHKKAEASKTDSVRPQIETMRREIQNGRAAVDFEKKAHSDNLEQSKAMEKNMIAVASEIERLRGELANAEKGAT
AVNPAAAVGNSGYAAPYGNSASTYTGMYGNPDATYTAQAYPDAYSTNQGHMHTVANPHYMSQPVPYGQYESQHTNVQR

>Pp-XP001759089
MGGGPMPAILEQKIQSQHMEIQSLLSENQRLAATHVALRQELASAQQEMARLTAMLTGVQSEKEAQIRSLIEKSAKLESE
LRSTENVRQDLVQARADCQKLHLHSQDLTQQVRTTTQELQRARTDVQQIPILRGEMDNIRAELQRARTAFELEKKVNAEQ
MEHRQAMEQNLSAMARDLEKLRTEAVNAEKRARANSGKHNCDALI
```

Alignment used for phylogenetic analysis in Supplemental Figure 11C

```
Rc-EEF41190         MAGRNNLP----------PNTLKHR---QVPVDDPRLHNRVP-----RLHHPS-------
Pt-XP002300004      MAGRNHLQ----------LREIPLSRAALLPHPTTDPHRLHA-----RPHH---------
Vv-CAO21396         MAGRNHLPP---------PNALKIREVSSTRAPYPSHHNHHALIEEDRYRHRSGPIPVSA
Ps-ACN41197         MAGRNRLPAHALKGGLQAMPSMHEGPYAMGAGPLPPHPAFVD-----EMRNGPHGRGPGP
Pp-XP001759089      ----------------------------MGGGPMP-------------------------
At-FLX              MAGRDRYIP-------SSAVSTSSSSRLLESQLIESDRNRAR------------------
Sb-XP002466208      MAARRGPHVIKLHD--PNPPLLGRAPG-PAAAAVSAPSRDEG---ILAQHPRAAPSSASA
Zm-NP001151248      MAARRGPHVIKLHD--PNPPLLGRAPG-AAPAAVPASSRDEG---LLAQHLR-----ASA
Os-NP001051704      MAARRGPHVIKLHD--SAPALLGRAPMPPPPGPRDELPPPSA---VLVHHPRG----GLA


Rc-EEF41190         -----TILEDRIAIQHREIQTLLLDNQQLTATHLALKQDLALVDDELRHLSAAAADVKAQ
Pt-XP002300004      -----LLLEDRITIQHREIQSLLLENERLAAAHFALKQELSLSQQDLRHLSTLAADVKAE
Vv-CAO21396         GRYHPAVIDERIVIQHREIQTLLGDNQRLAATHVALKQELAAAQQEISHLSAAAASVKAE
Ps-ACN41197         MLPHPGFLEERLSAQHQEIQGLLLENQRLAATHVALRQELASTHQELQHLSHVATNMQAD
Pp-XP001759089      -----AILEQKIQSQHMEIQSLLSENQRLAATHVALRQELASAQQEMARLTAMLTGVQSE
At-FLX              ----SVILEDRIAIQHREIQSLLNDNQRLAVAHIGLKDQLNVAKRELERLLETAVKVKAE
Sb-XP002466208      AHPAFALIEERLVARDQDIQELLVDNQRFAATHVALQQQLIAAQHELRAVSVAATRARAE
Zm-NP001151248      AHPAFALIEERLAARDQDIQELLVDNQRFAATHVALQQQLIAAQHELRAVSVAATRARAE
Os-NP001051704      PHPAVAALEDRLAVRDRDIQELLVDNQRFAATHVALQQQLIAAQHELRVVSIAATRARAE
                           :::::  :. :** ** :*::::.:*..*:::*   . ::  :    .  :::

Rc-EEF41190         RDDQVREVYERSLKLDAEVRSIDALRAELVQVTADVEKLSVHRQELTAELRAINSDVAKA
Pt-XP002300004      RDNQVREVYERSLKSDAELRSIDAMSAELVQVRTNVQKLTAQRQDMTAQLKGMNNEIVKA
Vv-CAO21396         RDAQVREVYERSLKMEAEVRSIDALNAELAQVRADVQKLSASRQELAAQLQTINTDLSVS
Ps-ACN41197         KDHQLRGLYDNSKKLEAEMRAMEPMKAELMQLQADNQKMGAVRQELTSQVQSLTQELTRA
Pp-XP001759089      KEAQIRSLIEKSAKLESELRSTENVRQDLVQARADCQKLHLHSQDLTQQVRTTTQELQRA
At-FLX              GEAKVREVYQNALRMEAEARVIDGLGAELGQVRSDVQRLGSDRQELATELAMFDDEMAKA
Sb-XP002466208      REGEVRALADQAAHIEAEARAVAAARAEVDQVHADVQVLAAARTDLVNRLQGLREKLAHK
Zm-NP001151248      REGEVRSLADQAAHMEAEARAIAAARAEIDQVHADVQVLAAARTDLVNRLQVLREKLAHK
Os-NP001051704      REDEVRALAEQAARIEAEARAAVAARAEVDQVHADVQVLAGARTELVDRLQDLRGQLARF
                     : ::* : :.: : ::* *       :: *  :: : :     ::. .:     .:

Rc-EEF41190         RTEAQQVAAIEADIQTMQKEIQRGRAAIENEKKLYASNLEHGQTMEQNMIAVAREIEKLH
Pt-XP002300004      KTETQQVGVLKAEIETVQQEIQRGRAAIAYEKKTRAINLEQEKVLEKNMNLVIREIEKLR
Vv-CAO21396         RSELKEVQAVKDGIENMRKELQRGRAAIEYEKKTHSNNLEQSEAMGKNMMAMAHEVEKLR
Ps-ACN41197         WNDMQQSVPLRTEIESLHGEFERARTAIEYEKKARAGRQEQGQAMEKNFISMSREVEKLR
Pp-XP001759089      RTDVQQIPILRGEMDNIRAELQRARTAFELEKKVNAEQMEHRQAMEQNLSAMARDLEKLR
At-FLX              KPNSDRAIEVKLEIEILRGEIRKGRAALELEKKTRASNLHHERGMEKTIDHLNREIVKLE
Sb-XP002466208      KAEASKTDSVRAQIETMRREIQKGRAAVDFEKKAHSDNLEQSKAMEKNMISVASEIERLR
Zm-NP001151248      KAEASKTDSVRPQIETMRREIQNGRAAVDFEKKAHSDNLEQSKAMEKNMIAVASEIERLR
Os-NP001051704      QAEAGKTESVRAQVETMRREIQKGRAAVEFEKKAHADNLEQSKAMEKNMIAVASEIEKLR
                      :  .   :.  :: :: *:...*:*.  ***  : . .: . : :.:  :  :: :*.

Rc-EEF41190         AELANLEKRERAE-AAAAIA---------------------ANPSPGYAGSYSNPEVS-Y
Pt-XP002300004      GEFANAEKRAR----AAAAA---------------------ANPSPGYGGNYGSAEVG-C
Vv-CAO21396         AELANAEKRARAA-AAAAAA---------------------ANPSMSS------------
Ps-ACN41197         AELAKVDKRERG-------A---------------------ANPGGAYAGNYGSAEKGYS
Pp-XP001759089      TEAVNAEKRAR------------------------------AN-----------------
At-FLX              EELVDLETKAREANAAAEAA---------------------PTPSPGLAASYGNNTDDIY
Sb-XP002466208      GELANAEKGATAVNPVAAVGNSGY-------------AAAYGNSEPTYTGMYGNPDATYT
Zm-NP001151248      GELANAEKGATAVNPAAAVGNSGY-------------AAPYGNSASTYTGMYGNPDATYT
Os-NP001051704      GDLANAEKRATAVTATAPVANPGFPTTYGNSEATYPAPAAYGNSETTYAPTYGNTEAAYA
                     : .. :.                                  .
```

```
Rc-EEF41190        ---------GGNLG--PDLYAIHQVQGGTDAGPQFVPG----------------
Pt-XP002300004     ---------GGSSY--PDPYGLQQVQVGSDSGPTFASGVMSNGPYDTAHG----
Vv-CAO21396        ------------------------------------------------------
Ps-ACN41197        ---------SGAYG--GDGYGMHPVQGAEESAGQYGAGAAPWGAYEMQRSHVRR
Pp-XP001759089     ---------SGKHN--CDALI---------------------------------
At-FLX             ---------GGQGRQYPEANGTHEVHMSL-------------------------
Sb-XP002466208     ----------AQAY--PDAYSTNQAHMHTGANSHYMSQPVSYGQYEGQHTNVQR
Zm-NP001151248     ----------AQAY--PDAYSTNQGHMHTVANPHYMSQPVPYGQYESQHTNVQR
Os-NP001051704     STYGSSEAAYAAAYGNSDAYSTNQAHTRTDGNPHYMAPPVHYAQYDSQHTNVQR
```

Sequences used for phylogenetic analysis in Supplemental Figure 11D (FASTA format)

```
>At-FES1
MSDSDMDIDDDEVEQKVQVHTIVRESELFDKPPIQASNSHNDVKRHSVTTPLDEQSKIIKEQAFAQDNGTLPRFPAPGIP
PRSFFTGGGGNEPEQKRAALPCKFFAKGWCFNGVSCKFLHVKENSNCTSQQLAENSMAGNGGIRSDLERRILDSREGVRV
SQLSENGVTSLPTREDISFMNPQRVFSSMSFVNPPGSQRVFPFNNEMRFMPSFENIRRESLKQTYGADFTDNRSLVINNA
NSFALRSSFVHEHRPSISSYLKTDMGSAGPAWTGSLSSSVPMNDRASTVGDFENGNSLSGSGSLPTLQGVAVSSDKGAEA
NTTSTKKKVSSDDWEPSEPFKASFTIPPYILPSSDALYDPFTDIENLGDRPLNDSLSSKGEHARKSSCQQKDGDSASGPQ
ARDCKNDDKSSSCSQNQHQETVARSLEAHGVVEGVATSVVDQNDTATPSKEISSATAAENRVVLKRIKPAGHDSWHRSDG
SSYKKTKKSDEIDGEVRSDAGMKVMRLFRTAVVETIKEMLKPLWREGRLTKDVHNMIVKKAAEKVVGAAVQFHQVPTDTE
SVDQYLGLSGTRIVKLVEGYVEKYGKP

>Vv-CAN59796
MPSPPSDGGTHPPPPWTDHSNDAVLRGGGGRGGGDGRGLPDSAIGAAGDRRGEVNFWFLVAVGDVSRDKESKGHVKHLLS
GSSTLGKFEAGLQSDTLAVEDGSSSFKISGLSKEQTKSCVNDDHSKYPKLGYHFFPYEENRNTKSAVDGKYTEAMPEKKS
EIMDARNTKPFSVPGKGAAVVIPMRDVFGEEANIVQCSNKEIKQIDFQSPEEMNQRASRLAASLLRRRSLSPTDSKDENK
RPAIICQYFSQGWCVNGPNCKFMHNIDSMDNTNQQIGGDVAIATRRYESQADKGLSEIPERTTLFCFPGRVRQWENEESL
TWHQYNGKHRFSSLQRDDLSYGFPADSQRFPMYKDGPRNYVSPNTEGSYPILGNRLFPEYGSFSVGSSTLAISSKTYQTS
RTLSSKATSLEGLAGKQNEFTLNDYASPVLSHQPNPRVDTTLQTTNLLPSHXSSAWGGYSFSQNAGPCVQKCVDSDTKTK
FSSDDWEPSIPFRPSYFSAFTDMSSARSVHDTVGDTCEEHPLGDRPYKVSCPTQGASILGSSHQRVYHDPVLPGTLGPEY
NADIESIHIHDKFDQSTLDKGVYGHQRDFFTNETEPAGSSVAELQDSQLKEGKPDGHTRVEDVSDQNPRNYSDGASHEEE
LKMEWGKQSNAKCDDHKIDEDVQKESKALRHFRFVLIDFIKDLVRPTWHRGQLSKDAHNSIVKRSVDKVLSTLEPHQIPS
TEEAIHHYLSVSQPKIAKLVQIPVLMDDICMLFSSSCSHPSTNGDIWGMLEAGLYDGSK

>Pt-XP002329830
MGSHSTHEMSELREDSVSNFKCSGPLDGPLTLQKEKSCVNYLDSWSPKLSKHLVIAQKNGPLEHAINKTDAFRNSKTHLS
NSSEAIAVETTEPFVITGIEVDVVLSKRNCLGQEANVVLDSKEELKPVDVKSEDSKEQTESRISRLVASGTRARSLSPST
ELRDGNKRAAVICDFFAKGWCIRGSSCRFLHTTNKADNTGQQLGVDEVATREDQFDEGVRNILETPKFPHFPDPVAASTG
KEATFSSHFSSERLPPLEHKENERLHQLDDKHKLSLRQRVGIPLNAKQFSSSKDDPGFSSSFKDVGIENFRQQWPATDYG
SYTSLINRGSSFSFSSSFDTSLLGSQKLLDSDRASRSSSLLQSASAFSGSEPESLSLASVPGDQLRHAEHKTKISSNDWE
PSVPFRPSFFITPEMISSAGSKYDPLRDSFVLPNVGDKSFKFSFFSLGASISNTSQQPIYGDSLSNRNFGTEFNGDKSTI
SSHDKPHGSLSDKNCSTPGKDSFTTATVTGGAGTADGENGSALKEESASGIGYDKVNRVTNKIDRDARPQTDGSRHKKDL
KADSVRQNNDMEVDQKIGGDTQKESKVLRHFRSALIDFVKDLLKPTWREGHLSKDAHNTIVKKTVEKVLSTLQPHQIPAT
VESIKQYLSSSQPKMAKLVEGYISKYGKS

>Os-NP001055943
MAGGGRGAGLPAAGEAAKAGRVGVGTTKRARDPSPNSKDPNGFVGVIAAEKKPALQLHGDEKYQKKAGNDPVPPTIDDTS
KTGGLHLHGGHVSQSPPDSNALSSQRFGSSSPGGDMKNKTRKRTCTFYAQGRCKNGKSCTFLHEGEVSGSDNQVYGNHGG
TGEGSEIQHPSSSKEHQFKNSAGSSQHEIYRTLVHAYGEDNRGLTHPVVKHSCHMLKASHGFKIGGSLTANPTNEVVQLP
VVQEKNHEPYFMGHQISLGTNNCLNDMGAYSRLRLDGGKLQFEVAKGDSPRDSHLSRSYLEKNPLKPDYRYQPFDSTISL
DPHQYSKKLSAYGGATENLPHKHQEEKSSSHVSYSLNSYTGFRKQGHDSSDFFLVNQSLRATSHHGTLPLHQLTPDKDAS
HHKGADFDKGGTSRSTLHVSSSSQPVVASAGKLSPIKDEVWITSVPFVPSFNFPDFPGSTSPSKSQYDPLVDSIDPPKVE
SLNNLKTSNISCSISSQHVDTNVIRGGSLEKPLTFADKLARNVSAKGSNDFGLISYDRGHSSSLDGDNRVKTCERKNDAS
LNNEKSDFRFHLVEHVKELVKPIWKEGNLSKEAHKLIVKKSVDKIFASLEPNQMPETEKAITTYITASAPKIEKLVKAYV
DRYRTS

>Zm-NP001148144
MMQSRDVDKYLNKADNINHVLMNSGDISKIGGHCLHGTHGLGTRLDSDAQSSSPGENMNNKIRRPIEICTFDAQGRCKKG
KSCISLHEREGFGSAKTGLLAPAGSGNHRGSEGGSQVQHISDLKVHQFKDSEGLSKDEMCRNLIYAFGKDNQMSVHLAGK
HSSPIPGVSQRMPVSIGHSLAQNPLVHEKNNKRFMGHHIDVAAENYLDAGGTYPRLDGGIFQFDIDKESSVSDSHVSRTY
LSDYPYKSFGLSISSDPLQLSEKLSAYGGVTNTIPNIHQKEHHSCHASYSSHSLTGSRNPCFATSEHTFGSPSLLATSHL
GIQSHHLFTSDIEKADLHRCLDVGKGYGTSSSGPALLVSSKPEPSMTPVGPHSPIKNEVWETSVPFVPSFSFPDSTTASE
SQYDPFVDYVEPPKVGNTNNLKPSTISCNITSQHTDQYAVTDKSLNCNDKLTRNITAKGSNEPAYFIAPDRGCSSSLDDT
IKVKACDRKKDAVDYNEKTRDFRFHLAEHIKELVKPIWKKGNLSKDAHKLVVRKSVEKVVDSIEPNQVPTTEELITKYIA
TCGPKIEKLVKAYVDRHSTCHPTIKYSSSEMGA
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Alignment used for phylogenetic analysis in Supplemental Figure 11D

Vv-CAN59796         MPSPPSDGGTHPPPPWTDHSNDAVLRGGGGRGGGDGRGLPDSAIGAAGDRRGEVNFWFLV
Pt-XP002329830      -------MGSHSTHEMSELREDSVSN-----------------FKCSGPLDG--------
Os-NP001055943      ------------------------------------------------------------
Zm-NP001148144      ------------------------------------------------------------
At-FES1             ------------------------------------------------------------


Vv-CAN59796         AVGDVSRDKESKGHVKHLLSGSSTLGKFEAGLQSDTLAVEDGSSSFKISGLSKEQTKSCV
Pt-XP002329830      ---PLTLQKE-KSCVNYLDSWSPKLSKHLV------IAQKNGPLEHAIN-----------
Os-NP001055943      -----------------MAGGGRGAGLPAAG-----EAAKAGRVGVGTT-----------
Zm-NP001148144      ------------------------------------------------------------
At-FES1             ----------------------------------------MSDSDMDID-----------


Vv-CAN59796         NDDHSKYPKLGYHFFPYEENRNTKSAVDGKYTEAMPEKKSEIMDARNTKPFSVPGKGAAV
Pt-XP002329830      ---------------KTDAFRNSKTHLS---------NSSEAIAVETTEPFVITGIEVDV
Os-NP001055943      ---------------KRARDPSPNSKDPNGFVGVIAAEKKPALQLHGDEKYQKKAGN-DP
Zm-NP001148144      -----------------------------------------MMQSRDVDKYLNKADNINH
At-FES1             -----------------DDEVEQKVQVHTIVRESELFDKPPIQASNSHN--DVKRHSVTT
                                                                 .  .

Vv-CAN59796         VIPMRDVFGEEANIVQCSNKEIKQIDFQSP---EEMNQRASRLAASLLRRRSLSP-TDSK
Pt-XP002329830      VLSKRNCLGQEANVVLDSKEELKPVDVKSEDSKEQTESRISRLVASGTRARSLSPSTELR
Os-NP001055943      VPPTIDDTSKTGGLHLHGG--------------HVSQSPPDSNALSSQRFGSSSPGGDMK
Zm-NP001148144      VLMNSGDISKIGGHCLHGT--------------HGLGTRLDSDAQSS------SPGENMN
At-FES1             PLDEQSKIIKEQAFAQDNG------------------TLPRFPAPGIPPRSFFTGGGGNE
                         .   :       .                         . .       :     .

Vv-CAN59796         DENKRPAIICQYFSQGWCVNGPNCKFMHNID--------------SMDNTNQQIGGDVAI
Pt-XP002329830      DGNKRAAVICDFFAKGWCIRGSSCRFLHTTN--------------KADNTGQQLGVD-EV
Os-NP001055943      NKTRK--RTCTFYAQGRCKNGKSCTFLHEGEVSGSDNQ------VYGNHGGTGEGSEIQH
Zm-NP001148144      NKIRRPIEICTFDAQGRCKKGKSCISLHEREGFGSAKTGLLAPAGSGNHRGSEGGSQVQH
At-FES1             PEQKRAALPCKFFAKGWCFNGVSCKFLHVKE--------------NSNCTSQQLAENSMA
                       ::    * : ::* * .* .*  :*  :                :  .   . :

Vv-CAN59796         ATRRYESQADKGLSEIPERTTLFCFPGRVRQWENEESLTWHQYNGKHRFSSLQRDDLSYG
Pt-XP002329830      ATR--EDQFDEGVRNILETPKFPHFPDPVAASTGKEATFSSHFS-SERLPPLEHK-----
Os-NP001055943      PSSSKEHQFKNSAGSSQHEIYRTLVHAYGEDNRGLTHPVVKHSCHMLKASHGFKIGGSLT
Zm-NP001148144      ISDLKVHQFKDSEGLSKDEMCRNLIYAFGKDNQMSVHLAGKHSSPIPGVSQRMPVS----
At-FES1             GNGGIRSDLERRILDSREGVRVSQLSENGVTSLPTREDISFMNPQRVFSSMSFVNP----
                     .     : .       .      .                        .

Vv-CAN59796         FPADSQRFPMYKDGPRNYVSPNTEGSYPILGNR--LFPEYGSFSVGSSTLAISSKTYQTS
Pt-XP002329830      ---ENERLHQLDD--KHKLSLRQRVGIPLNAKQ--FSSSKDDPGFSSSFKDVGIENFRQQ
Os-NP001055943      ANPTNEVVQLPVVQEKNHEPYFMGHQISLGTNN--CLNDMGAYSRLRLDGGKLQFEVAKG
Zm-NP001148144      --IGHSLAQNPLVHEKNNK-RFMGHHIDVAAEN--YLDAGGTYP--RLDGGIFQFDIDKE
At-FES1             --PGSQRVFPFNNEMRFMPSFENIRRESLKQTYGADFTDNRSLVINNANSFALRSSFVHE
                         .         :            :

Vv-CAN59796         RTLSSKATSLEGLAG-------KQNEFTLN-DYASPVLSHQPNPRVDTTLQTTNLLPSHX
Pt-XP002329830      WPATDYG-SYTSLIN-------RGSSFSFSSSFDTSLLGSQKLLDSDRASRSSSLLQSAS
Os-NP001055943      DSPRDSHLSRSYLEKNPLKPDYRYQPFDSTISLDPHQYSKKLSAYGGATENLPHKHQEEK
Zm-NP001148144      SSVSDSHVSRTYLS------DYPYKSFGLSISSDPLQLSEKLSAYGGVTNTIPNIHQKEH
At-FES1             HRPSISSYLKTDMGS---------AGPAWTGSLSSSVPMNDRASTVGDFENGNSLGSGS
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                                :                .  .  .     .     .          .

Vv-CAN59796         SSAWGGYSFSQNAGPCVQKCVDSDTKTKFSSDDWEPSIPFRPSYFSAFTDMSSARSVHDT
Pt-XP002329830      AFSGSEPESLSLASVPGDQLRHAEHKTKISSNDWEPSVPFRPSFFITPEMISSAGSKYDP
Os-NP001055943      SSSHVSYSLNSYTGFRKQGHDSSDFFLVNQSLRATSHHGTLPLHQLTPDKD-ASHHKGAD
Zm-NP001148144      HSCHASYSSHSLTGSRNPCFATSEHTFGSPSLLATSHLGIQSHHLFTSDIEKADLHRCLD
At-FES1             LPTLQGVAVSSDKGAEAN---TTSTKKKVSSDDWEPSEPFKASFTIPPYILPSSDALYDP
                              .  .        :.      *    .     . .  .     :

Vv-CAN59796         VGDTCEEHPLGDRPYKVSCPTQGASILGSSHQRVYHDPVLPGTLGPEYNADIESIHIHDK
Pt-XP002329830      LRDSFVLPNVGDKSFKFSFFSLGASISNTSQQPIYGDSLSNRNFGTEFNGDKSTISSHDK
Os-NP001055943      FDKG-GTSRS--TLHVSSSSQPVVASAGKLSPIKDEVWITSVPFVPSFN--FPDFPGSTS
Zm-NP001148144      VGKGYGTSSSGPALLVSSKPEPSMTPVGPHSPIKNEVWETSVPFVPSFS--FPD---STT
At-FES1             FTDI---ENLGDRPLNDSLSSKGEHARKSSCQQKDGDSASGPQARDCKN--------DDK
                    . .              *                              .          .

Vv-CAN59796         FDQSTLDKGVYGHQRDFFTNETEPAGSSVAELQD-SQLKEGKPD--GHTRVEDVS---DQ
Pt-XP002329830      PHGSLSDKNCSTPGKDSFTTATVTGGAGTADGENGSALKEESASGIGYDKVNRVTNKIDR
Os-NP001055943      PSKSQYDPLVDSIDPPKVESLNNLKTSNISCSISSQHVDTNVIRGGSLEKPLTFADKLAR
Zm-NP001148144      ASESQYDPFVDYVEPPKVGNTNNLKPSTISCNITSQHTDQYAVT----DKSLNCNDKLTR
At-FES1             SSSCSQNQHQETVARSLEAHGVVEGVATSVVDQNDTATPSKEIS----SATAAENRVVLK
                       .  :                   :                                :

Vv-CAN59796         NPRNYSD---GASHEEELKMEWGKQSNAKCDDHKIDEDVQKESKALRHFRFVLIDFIKDL
Pt-XP002329830      DARPQTD---GSRHKKDLKADSVRQNNDMEVDQKIGGDTQKESKVLRHFRSALIDFVKDL
Os-NP001055943      NVSAKGSNDFG-LISYDRGHSSSLDGDNRVKTCERKNDASLNNEKS-DFRFHLVEHVKEL
Zm-NP001148144      NITAKGSNEPAYFIAPDRGCSSSLDDTIKVKACDRKKDAVDYNEKTRDFRFHLAEHIKEL
At-FES1             RIKPAGH------DSWHRSDGSSYKKTKKSDEIDGEVRSDAGMKVMRLFRTAVVETIKEM
                                    .       .        .         :    **  : : :*::

Vv-CAN59796         VRPTWHRGQLSKDAHNSIVKRSVDKVL-STLEPHQIPSTEEAIHHYLSVSQPKIAKLVQI
Pt-XP002329830      LKPTWREGHLSKDAHNTIVKKTVEKVL-STLQPHQIPATVESIKQYLSSSQPKMAKLVEG
Os-NP001055943      VKPIWKEGNLSKEAHKLIVKKSVDKIF-ASLEPNQMPETEKAITTYITASAPKIEKLVKA
Zm-NP001148144      VKPIWKKGNLSKDAHKLVVRKSVEKVV-DSIEPNQVPTTEELITKYIATCGPKIEKLVKA
At-FES1             LKPLWREGRLTKDVHNMIVKKAAEKVVGAAVQFHQVPTDTESVDQYLGLSGTRIVKLVEG
                    ::* *:.*.*:*:.*: :*:::.:*:.  ::: :*:*   : :  *:  . .:: ***:

Vv-CAN59796         PVLMDDICMLFSSSCSHPSTNGDIWGMLEAGLYDGSK
Pt-XP002329830      ----------------YISKYGKS-------------
Os-NP001055943      ----------------YVDRYRTS-------------
Zm-NP001148144      ----------------YVDRHSTCHPTIKYSSSEMGA
At-FES1             ----------------YVEKYGKP-------------
                                    : .
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