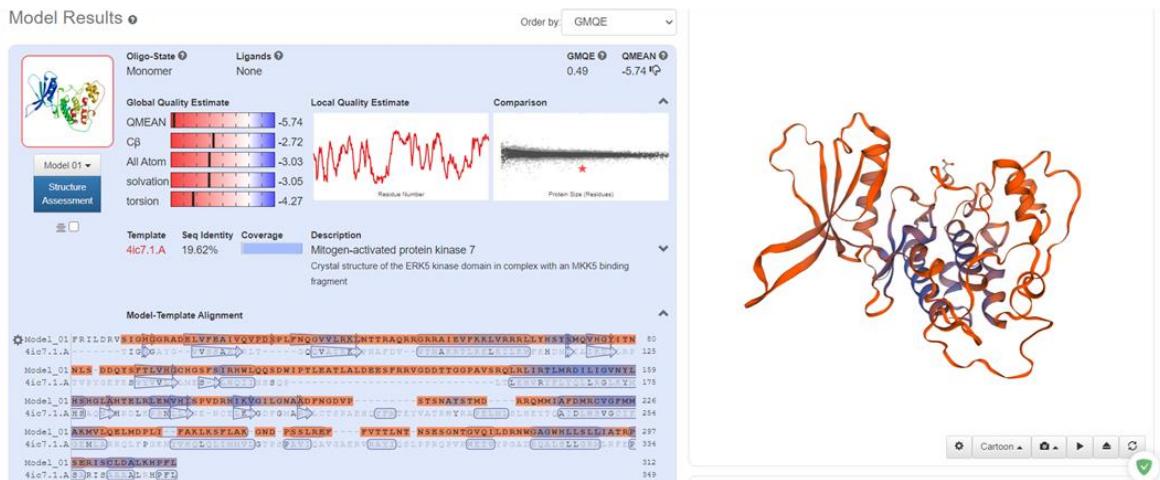


## Supplementary Data

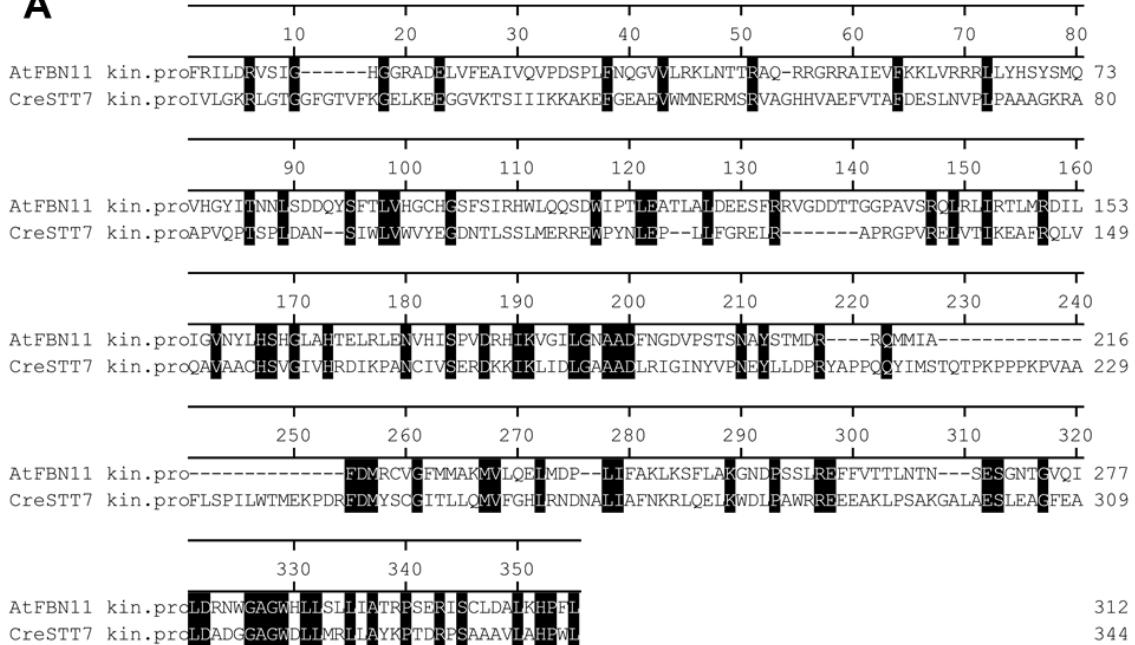
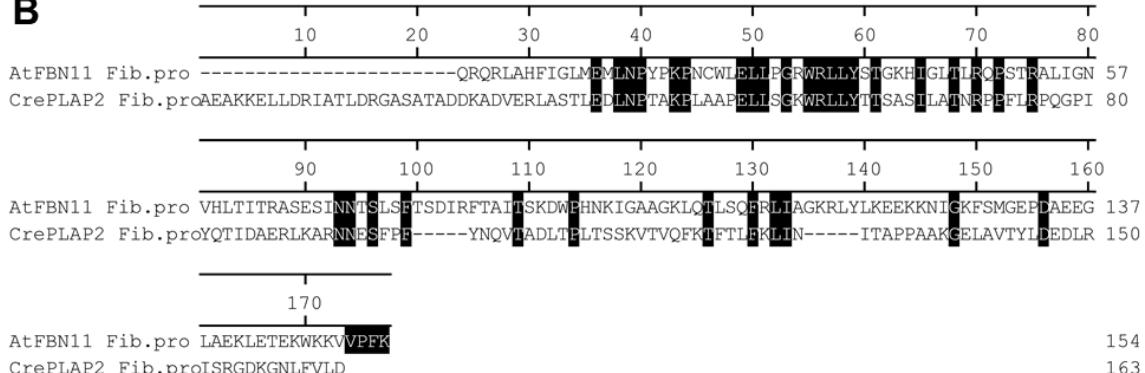
**A**

	Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/> <input checked="" type="checkbox"/> 4ic7.1.A	Mitogen-activated protein kinase 7 Crystal structure of the ERK5 kinase domain in complex with an MKK5 binding fragment	0.53	-	19.62	X-ray, 2.6Å	hetero-dimer ▲	1 x ANP ⚡	
<input type="checkbox"/> 4ic7.2.A	Mitogen-activated protein kinase 7 Crystal structure of the ERK5 kinase domain in complex with an MKK5 binding fragment	0.52	-	19.62	X-ray, 2.6Å	hetero-dimer ▲	1 x ANP ⚡	
<input type="checkbox"/> 3hko.1.A	Calcium/calmodulin-dependent protein kinase with a kinase domain and 2 calmodulin-like EF hands Crystal structure of a cdpk kinase domain from cryptosporidium Parvum, cgd7_40	0.51	-	18.08	X-ray, 1.8Å	monomer ✓	1 x ZN ⚡, 1 x ANP ⚡, 1 x MG ⚡	
<input type="checkbox"/> 2no3.3.C	Mitogen-activated protein kinase 8 Novel 4-anilinopyrimidines as potent JNK1 Inhibitors	0.51	0.03	20.53	X-ray, 3.2Å	hetero-tetramer ▲	2 x 859 ⚡	
<input type="checkbox"/> 2h96.2.A	Mitogen-activated protein kinase 8 Discovery of Potent, Highly Selective, and Orally Bioavailable Pyridine Carboxamide C-jun NH2-terminal Kinase Inhibitors	0.51	-	20.53	X-ray, 3.0Å	hetero-dimer ▲	1 x 893 ⚡	

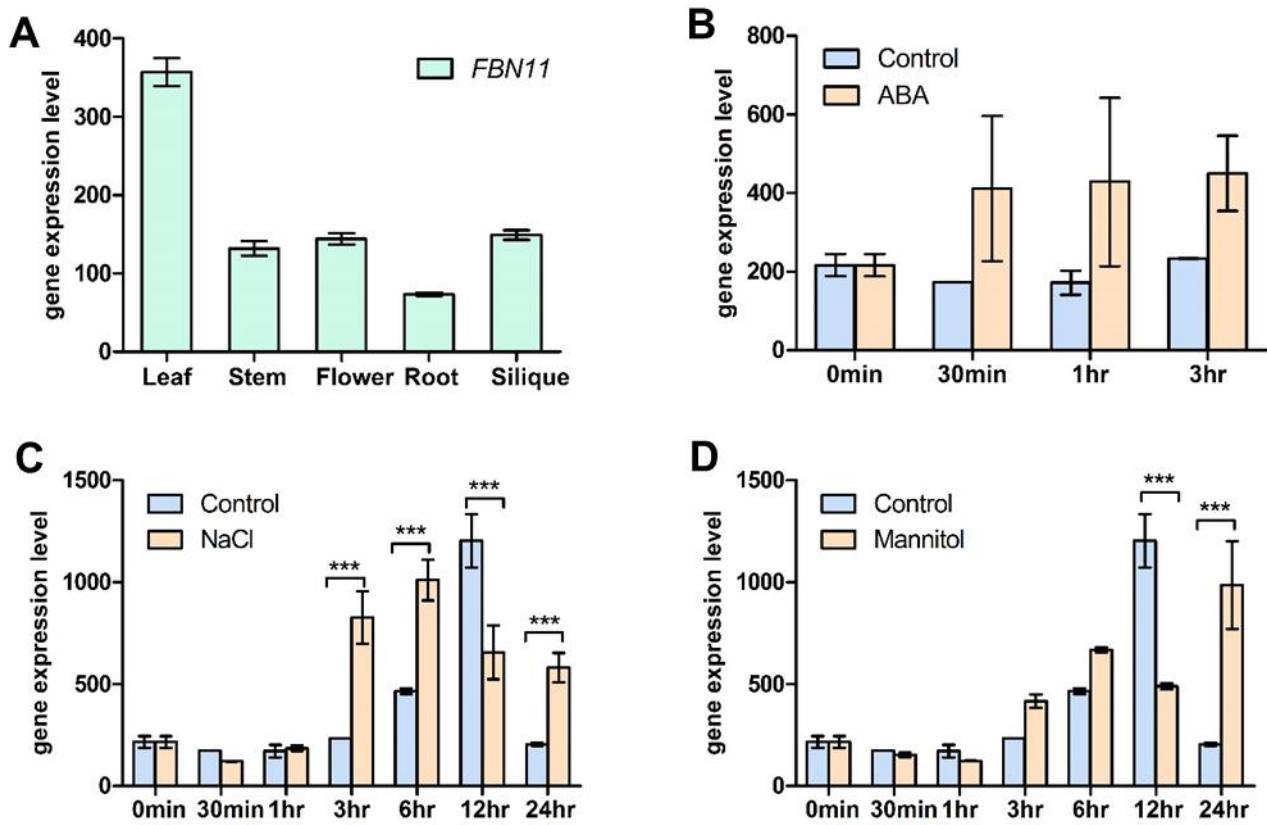
**B**



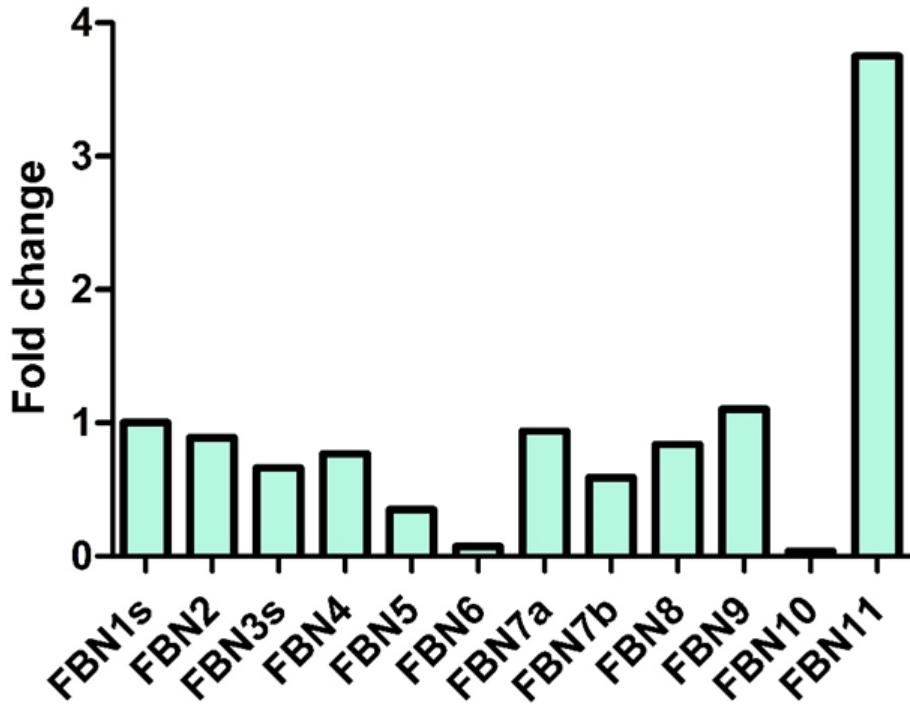
**Figure S1.** Tertiary structure analyses of the FBN11 kinase domain using SWISS-MODEL (A) List of Top 5 proteins with structures most similar to the FBN11 kinase domain (B) Tertiary structure model of the kinase domain of FBN11 based on the tertiary structure of mitogen-activated protein kinase 7

**A****B**

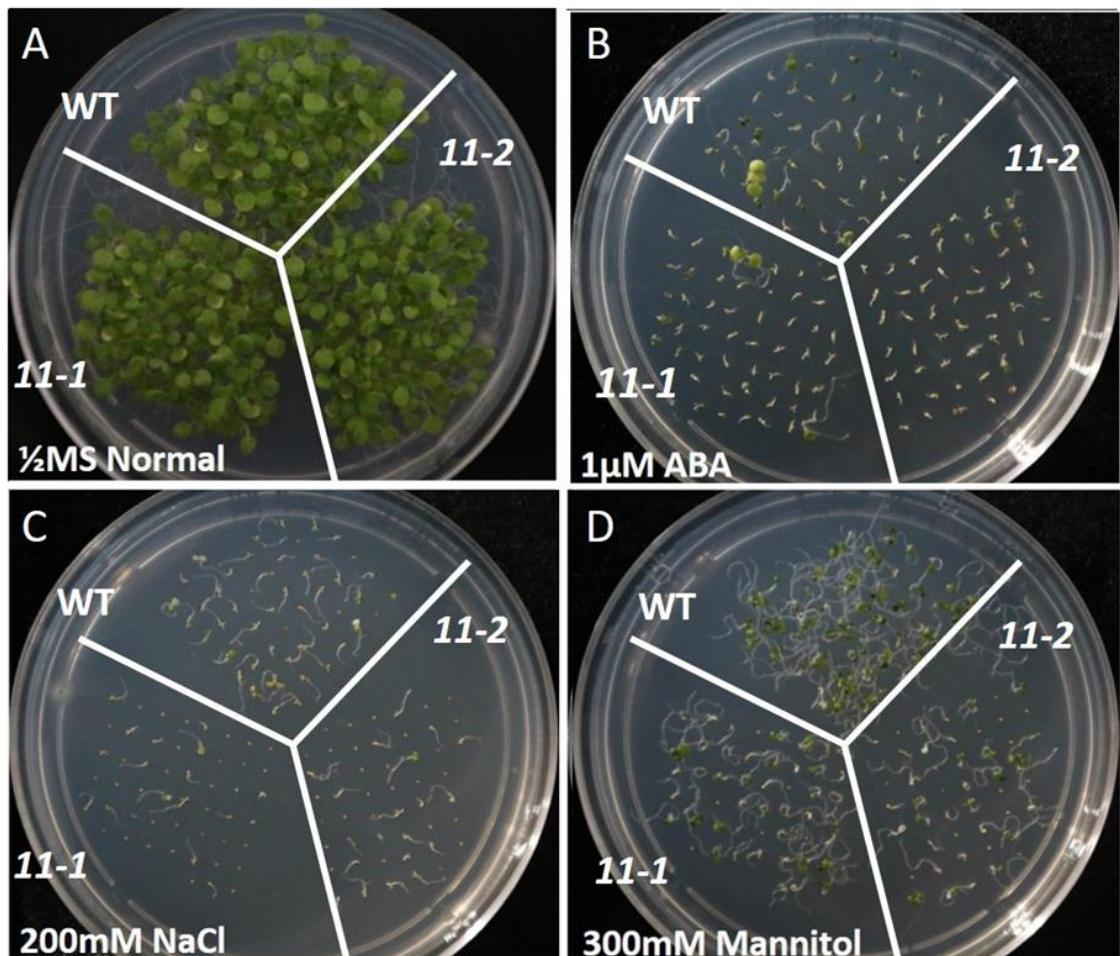
**Figure S2.** (A) Amino acid alignment between the kinase domain of *Arabidopsis* FBN11 and CreSTT7 of Chlamydomonas. (B) Amino acid alignment between FBN11 and the CrePLAP2 FBN domain of Chlamydomonas.



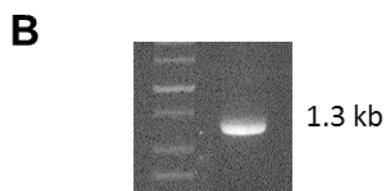
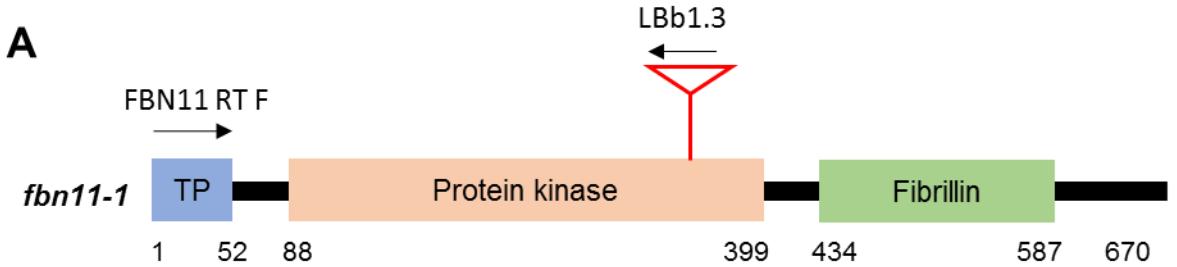
**Figure S3.** *FBN11* gene expression profiles in various tissues under various abiotic stresses. (A) *FBN11* gene expression levels in leaves, stems, flowers, roots, and siliques of wild-type Arabidopsis. (B) Effect of 10 µM ABA treatment on *FBN11* gene expression levels in 7-day-old Arabidopsis seedlings. (C) Effects of 150 mM NaCl (C) and 300 mM mannitol (D) on *FBN11* gene expression levels in 18-day-old Arabidopsis seedlings. Statistical analysis is done by two-way ANOVA with Bonferroni post-test (\*\*P<0.001).



**Figure S4.** Expression profiles of *FBN* family genes in stage 10 seeds without siliques. This analysis was performed with data from the TAIR eFP browser ([http://bar.utoronto.ca/efp2/Arabidopsis/Arabidopsis\\_eFPBrowser2.html](http://bar.utoronto.ca/efp2/Arabidopsis/Arabidopsis_eFPBrowser2.html)). The expression value of each gene is a fold change based on *FBN1a*. *FBN1s* represents *FBN1a* and *1b*. *FBN3s* stands for *FBN3a* and *3b*. These duplicated genes are indistinguishable because of their high sequence homology.

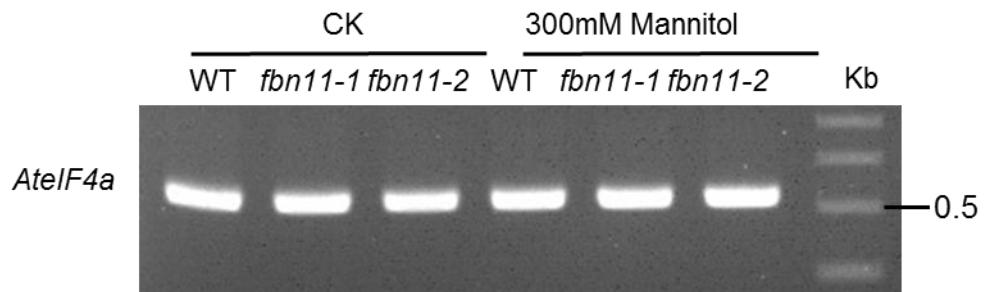


**Figure S5.** Seed germination phenotypes of wild type and *fbn11* homozygous mutants under stress. Unsupplemented growth media (A), or media supplemented with 1  $\mu$ M ABA (B), 200 mM NaCl (C), or 300 mM mannitol (D). Representative photographs of 7- day old plants.



MQFKWSDFRILDRVSIGHGGRADELVFEAIVQVPDSPLFNQGVVLRKLNNTTRAQRRGRRRAIE  
 VFKKLVRRRLLYHSYSMQVHGYITNNLSDDQYSFTLVHGCHGSFSIRHWLQQSDWIPTLEATLA  
 LDEESFRRVGDDTTGGPAVSRLRLIRTLMRDILIGVNYLHSHGLAHTELRLENVHISPVDRHIK  
 VGILGNAADFNGDVSTSNAYSTMDRRQMMIAFDMRCVGFMMAKMVLQELMDPLIFAKL  
 KSFLAKGNDPSSLREFFVTLNTNSESGNTGVQILDWNWGAGWH**Q**

**Figure S6.** *fbn11-1* truncated transcript and deduced protein sequences. (A) The T-DNA insertion site of *fbn11-1* and primers position for truncated transcript detection (B) Transcript detected by RT-PCR from RNA of *fbn11-1* seedlings using FBN11 RT F and LBb1.3 primer (Table S1) (C) Protein sequence (295AA) encoded by *fbn11-1* truncated transcript. The black box represents the wild-type FBN11 amino acid sequences, and the red box represents the amino acid sequence generated by T-DNA fusion.



**Figure S7.** RT-PCR expression analysis of *AteIF4* during seed germination of wild type and *fbn11* mutants non-treated (CK) and treated with 300 mM mannitol. PCR with 30 cycle amplification was performed using primers (forward: 5'-CGTGGTTCAAGGACCAGAT-3' and reverse: 5'-ATTGATCGAACACCCTTCT-3') that detect 0.5 kb of *AteIF4* transcript.

**Table S1.** Primers used in this study.

Primer name			Sequence
Relative expression for ABA pathway gene			
qRT-ABF2	F	5'-ACATACCAGCAATCGCAACA-3'	
	R	5'-CCACAAGACCACCACCTCTT-3'	
qRT-ABF4	F	5'-TGGTCAGCAAATCAAAACA-3'	
	R	5'-GTTGTTGTTGCTGCTGCATT-3'	
qRT-ABF1	F	5'-GCCTGGAGAAGGTTGTTGAG-3'	
	R	5'-TCAGCTTCCAGTTCCAAGGT-3'	
qRT-ABF3	F	5'-CTGGAAGGAGCTGATGAAGG-3'	
	R	5'-AGCCCTGACCAAAAAACTCCT-3'	
qRT-DREB2A	F	5'-GGGTAAATGGGTTGCTGAGA-3'	
	R	5'-CGAGCCAAAGGACCATAACAT-3'	
qRT-CBF3	F	5'-ACAGAGGAGTCGTCGGAGA-3'	
	R	5'-CCATCTCAGCGGTTGAAAT-3'	
qRT-CBF1	F	5'-CTACGAATCCCGGAGTCAAC-3'	
	R	5'-ATCGTCTCCTCCATGTCCAG-3'	
qRT-CBF2	F	5'-AACAGAGCCAAGATGCGTTT-3'	
	R	5'-ACGTACATCATCTCCCTCGAC-3'	
Identification for T-DNA insertion mutants			
<i>fbn11-1</i>	LP	5'-TATTAAGGCACGTGTGGAAGG-3'	
	RP	5'-GCAACGCTTACAGTACCATGG-3'	
<i>fbn11-2</i>	LP	5'-CGAATTTCAAACCTAAATCG-3'	
	RP	5'-TTGTAAATTGGCAGATTGG-3'	
LBb1.3	genotyping	5'-ATTTGCCGATTCGGAAC-3'	
FBN11 RT	F	5'-ATGGCACTTGTGGTGT-3'	
	R	5'-CTACATAGACTTATGGTCCAAG-3'	
Generation of complementary plant			
pDONR-FBN11	F	5'-AAAAAGCAGGCTGTATGGCACTTGTTGTTG-3'	
	R	5'-AGAAAGCTGGGTGCATAGACTTATGGTCCAAGCTG-3'	
qRT-FBN11	F	5'-AGCCAAACTGTTGGTGGAG-3'	
	R	5'-ATTAAGGCACGTGTGGAAGG-3'	
GFP	R	5'-TGAACTTGTGGCCGTTACG-3'	
	R(full)	5'-TTACTTGTACAGCTCGTCC-3'	

**Table S2.** Amino acid composition and secondary structure of FBN11.

Amino acid composition	
Ala (A)	5.1%
Arg (R)	7.8%
Asn (N)	4.5%
Asp (D)	4.8%
Cys (C)	1.5%
Gln (Q)	3.1%
Glu (E)	5.1%
Gly (G)	6.4%
His (H)	3.3%
Ile (I)	6.0%
Leu (L)	11.3%
Lys (K)	4.8%
Met (M)	3.1%
Phe (F)	4.2%
Pro (P)	4.5%
Ser (S)	9.9%
Thr (T)	4.9%
Trp (W)	1.8%
Tyr (Y)	1.9%
Val (V)	6.1%

SOPMA secondary structure prediction	
Alpha helix (Hh)	32.09%
Extended strand (Ee)	19.25%
Random coil (Cc)	44.33%

**Table S3.** FBN11 physical parameters.

Number of amino acids	670 aa
Molecular weight	75,766. Da
Theoretical pI	9.43
Instability index	49.17
Aliphatic index	90.34
Grand average of hydropathicity (GRAVY)	-0.242
Number of predicted TMHs	0
Number of AAs in TMHs	0.03

**Table S4.** FBN11 orthologs analysis of plant evolution

Green plants	species	common name	FBN11 ortholog (Locus)	AA identity (%)
Dicots*	<i>Arabidopsis thaliana</i>	Thale Cress	AT5G53450	100
	<i>Brassica rapa</i>	Mustard	Bra003055	88
	<i>Carica papaya</i>	Papaya	evm.model.supercontig_3.70	69
	<i>Cucumis sativus</i>	Cucumber	Cucs.a.040680.2	65
	<i>Glycine max</i>	Soybean	Glyma04g41510.1	70
			Glyma06g13320.1	68
	<i>Lotus japonicus</i>	Lotus	Lj1g0007393.1	70
	<i>Manihot esculenta</i>	Cassava	cassava4.1_003020m	68
	<i>Mimulus guttatus</i>	Mimulus	mgv11b005497m	64
	<i>Medicago truncatula</i>	Barrel medic	Medtr3g091290.1	68
	<i>Ricinus communis</i>	Ricinus	30169.m006496	69
	<i>Prunus persica</i>	Peach	ppa002468m	67
Monocots*	<i>Populus trichocarpa</i>	Poplar	POPTR_0015s01910.1	69
	<i>Solanum tuberosum</i>	Potato	POPTR_0492s00210.1	63
			PGSC0003DMP400016058	64
			PGSC0003DMP400016057	62
	<i>Vitis vinifera</i>	Wine Grape	GSVIVG01038710001	67
Lycophytes*	<i>Brachypodium distachyon</i>	Brachypodium	Bradi2g45450.1	59
	<i>Oryza sativa</i>	Rice	LOC_Os01g46720.1	58
	<i>Sorghum bicolor</i>	Sorghum	Sb03g029870.1	59
	<i>Setaria italica</i>	Foxtail millet	Si000637m	60
	<i>Zea mays</i>	Maize	GRMZM2G150952_T01	60
Lycophytes*	<i>Selaginella moellendorffii</i>	Spike Moss	g105971	48
Bryophytes**	<i>Physcomitrella patens</i>	earthmoss	Pp1s110_47V6.1	24
	<i>Marchantia polymorpha</i>	umbrella liverwort	Pp1s159_111V6.1	23
			Mapoly0022s0163.1.p	47
Charophytes**	<i>Chara braunii</i>	charophyte green algae	CBR_g39728	36
Chlorophyta**	<i>Chlamydomonas reinhardtii</i>	Chlamydomonas	Cre02.g120250.t1.1 (STT7)	26

\* The protein sequence of *Arabidopsis* FBN11 was analyzed by BLAST in the Plant Genome Database, and the ortholog was found based on E-value 1x10<sup>-4</sup>.

\*\*The genome database of lower plants was analyzed using Ensembl Plants.

**Table S5.** *FBN* gene family comparison between Arabidopsis and *Chlamydomonas reinhardtii*.

<i>Arabidopsis</i> <i>thaliana</i>	<i>Chlamydomonas</i> <i>reinhardtii</i>
AtFBN1a	
AtFBN1b	CrePLAP7, 8, 10
AtFBN2	
AtFBN3a	
AtFBN3b	CrePLAP2
AtFBN4	CrePLAP9
AtFBN5	CrePLAP6
AtFBN6	CrePLAP4
AtFBN7a	x
AtFBN7b	
AtFBN8	CrePLAP1
AtFBN9	CrePLAP3
AtFBN10	CrePLAP5
AtFBN11	STT7