

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.

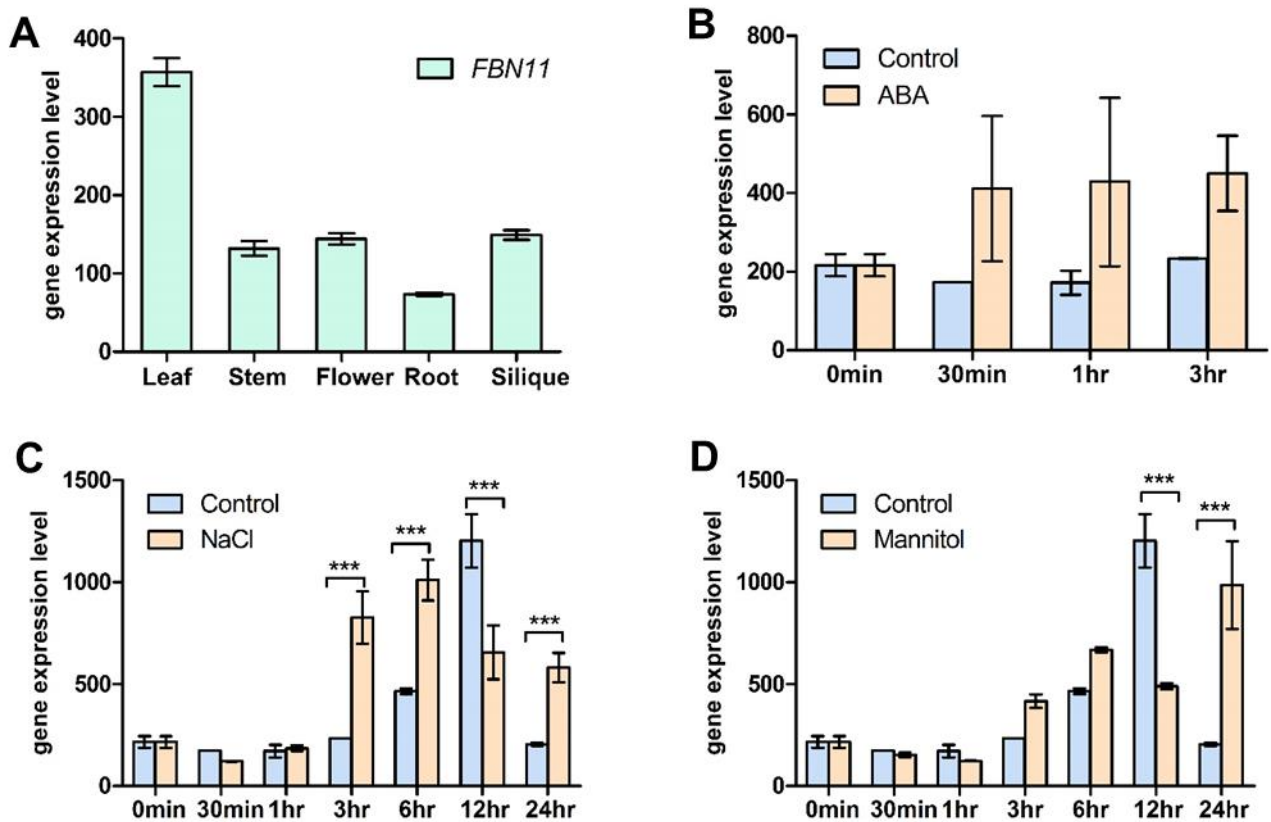


Figure S3. *FBN11* gene expression profiles in various tissues under various abiotic stresses. (A) *FBN11* gene expression levels in leaves, stems, flowers, roots, and silique of wild-type Arabidopsis. (B) Effect of 10 μ M ABA treatment on *FBN11* gene expression levels in 7-day-old Arabidopsis seedlings. (D) 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 (***) $P < 0.001$.

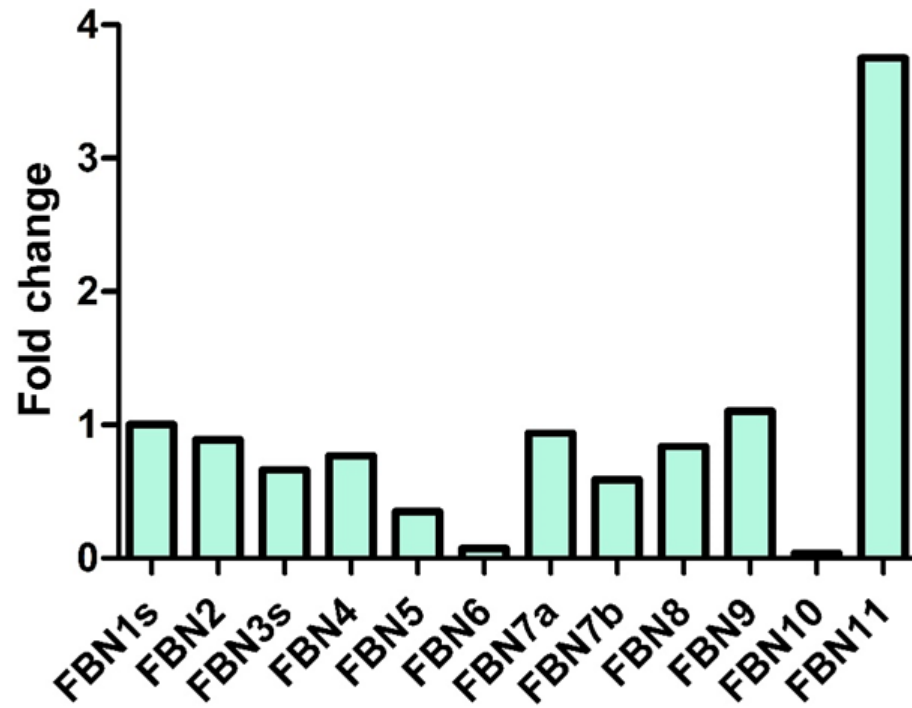


Figure S4. Expression profiles of *FBN* family genes in stage 10 seeds without siliques. This analysis was performed with data from the TAIR eFP browser (http://bar.utoronto.ca/efp2/Arabidopsis/Arabidopsis_eFPBrowser2.html). The expression value of each gene is a fold change based on *FBN1a*. *FBN1s*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

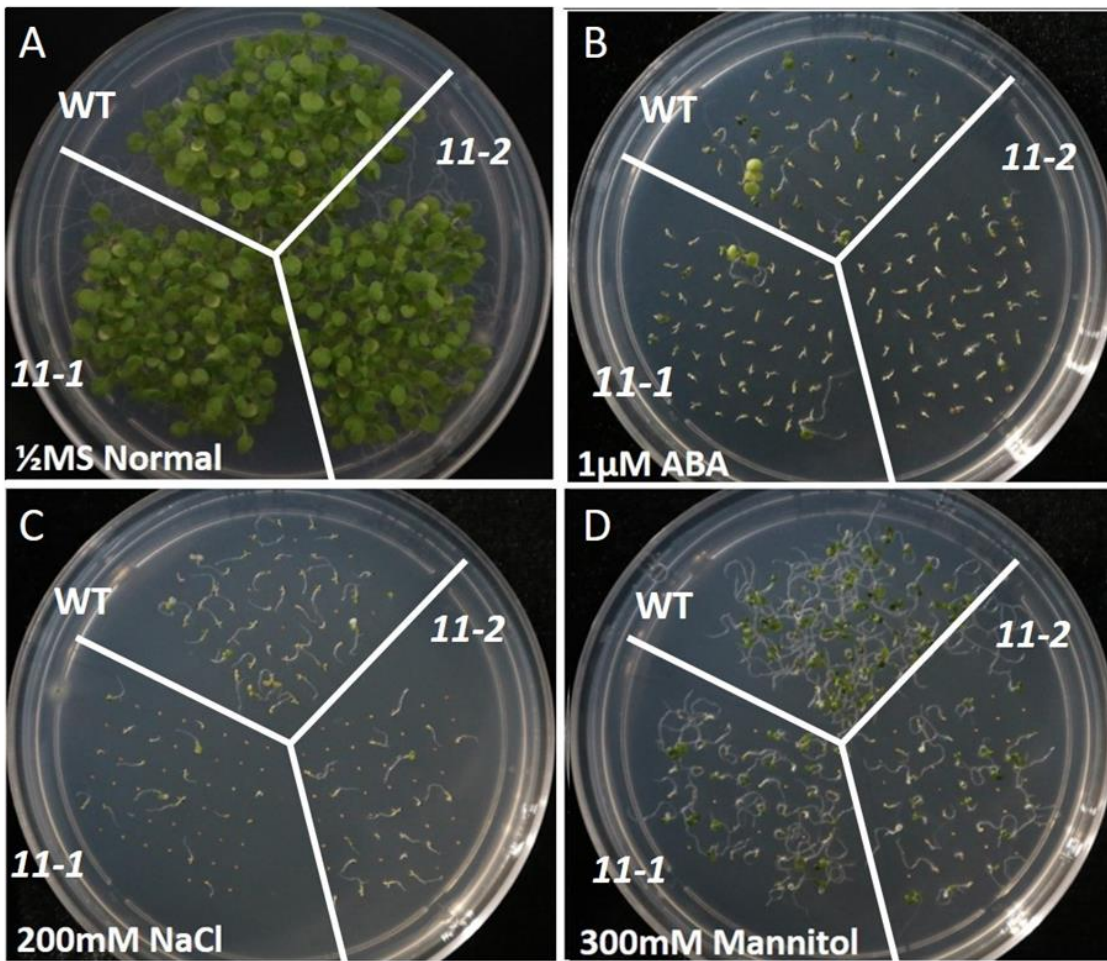


Figure S5. Seed germination phenotypes of wild type and *fbn11* homozygous mutants under stress. Unsupplemented growth media (A), or media supplemented with 1 μ M ABA (B), 200 mM NaCl (C), or 300 mM mannitol (D). Representative photographs of 7- day old plants.

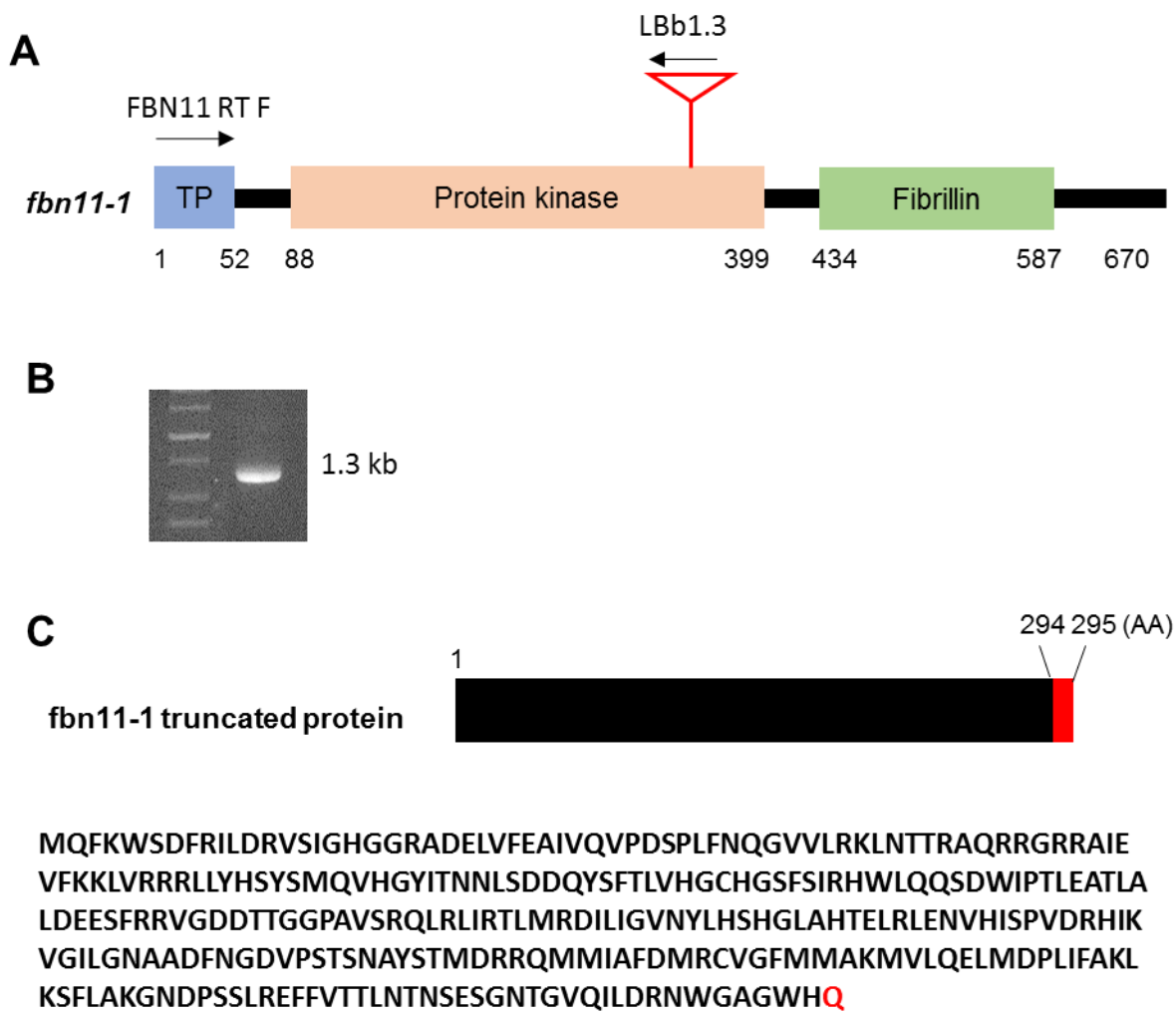


Figure S6. *fbn11-1* truncated transcript and deduced protein sequences. (A) The T-DNA insertion site of *fbn11-1* and primers position for truncated transcript detection (B) Transcript detected by RT-PCR from RNA of *fbn11-1* seedlings using FBN11 RT F and LBb1.3 primer (Table S1) (C) Protein sequence (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.

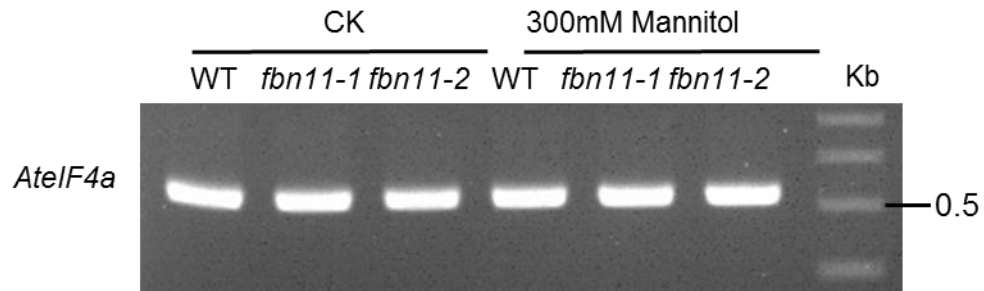


Figure S7. RT-PCR expression analysis of *AteIF4* during seed germination of wild type and *fbn11* mutants non-treated (CK) and treated with 300 mM mannitol. PCR with 30 cycle amplification was performed using primers (forward: 5'-CGTGGTTTCAAGGACCAGAT-3' and reverse: 5'-ATTGATCGCAACACCCTTCT-3') that 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'-TGGTCAGCCAAATCAAAACA-3'
	R	5'-GTTGTTGTTGCTGCTGCATT-3'
qRT-ABF1	F	5'-GCCTGGAGAAGGTTGTTGAG-3'
	R	5'-TCAGCTTCCAGTTCCAAGGT-3'
qRT-ABF3	F	5'-CTGGAAGGAGCTGATGAAGG-3'
	R	5'-AGCCCTGACCAAAACTCCT-3'
qRT-DREB2A	F	5'-GGGTAAATGGGTGCTGAGA-3'
	R	5'-CGAGCCAAAGGACCATACAT-3'
qRT-CBF3	F	5'-ACAGAGGAGTTCGTCGGAGA-3'
	R	5'-CCATCTCAGCGTTTGAAAT-3'
qRT-CBF1	F	5'-CTACGAATCCCGGAGTCAAC-3'
	R	5'-ATCGTCTCCTCCATGTCCAG-3'
qRT-CBF2	F	5'-AACAGAGCCAAGATGCGTTT-3'
	R	5'-ACGTCATCATCTCCCTCGAC-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'-CGAATTTTCAAACCCTAAATCG-3'
	RP	5'-TTGTAAATTTCGGCAGATTTGG-3'
LBb1.3	genotyping	5'-ATTTTGCCGATTTTCGGAAC-3'
FBN11 RT	F	5'-ATGGCACTTTGTGGTGTTC-3'
	R	5'-CTACATAGACTTATGGTCCAAG-3'
Generation of complementary plant		
pDONR-FBN11	F	5'-AAAAAGCAGGCTGTATGGCACTTTGTGGTGTTC-3'
	R	5'-AGAAAGCTGGGTGCATAGACTTATGGTCCAAGCTG-3'
qRT-FBN11	F	5'-AGCCAAACTGTTGGTTGGAG-3'
	R	5'-ATTAAGGCACGTGTGGAAGG-3'
GFP	R	5'-TGAACCTGTGGCCGTTTACG-3'
	R(full)	5'-TACTTGTACAGCTCGTCC-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	Cucsa.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
	<i>Populus trichocarpa</i>	Poplar	POPTR_0015s01910.1	69
			POPTR_0492s00210.1	63
	<i>Solanum tuberosum</i>	Potato	PGSC0003DMP400016058	64
			PGSC0003DMP400016057	62
	<i>Vitis vinifera</i>	Wine Grape	GSVIVG01038710001	67
Monocots*	<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
			Pp1s159_111V6.1	23
	<i>Marchantia polymorpha</i>	umbrella liverwort	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 1×10^{-4} .

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

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

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