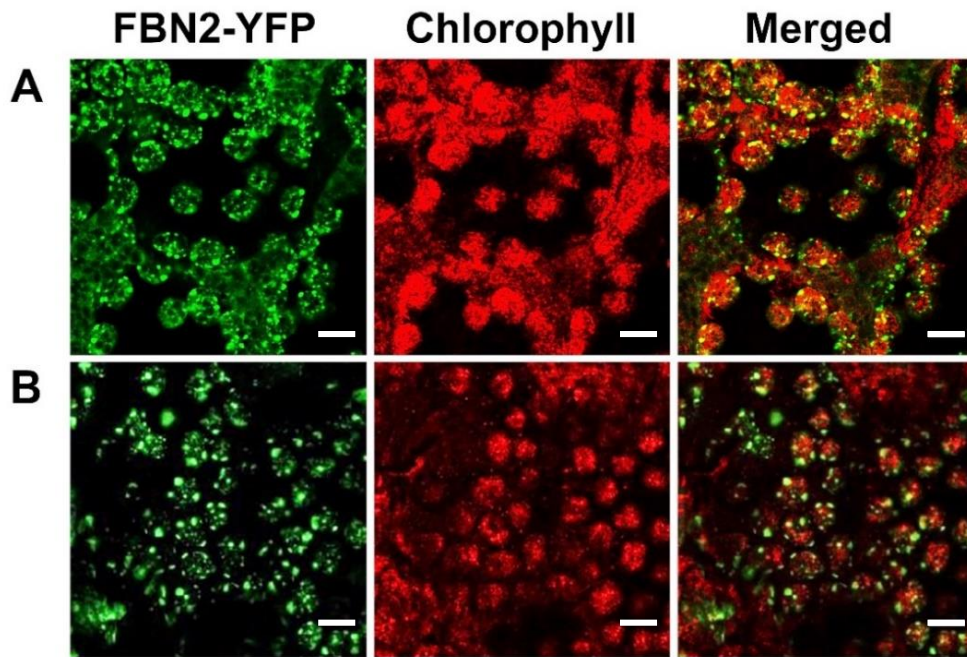
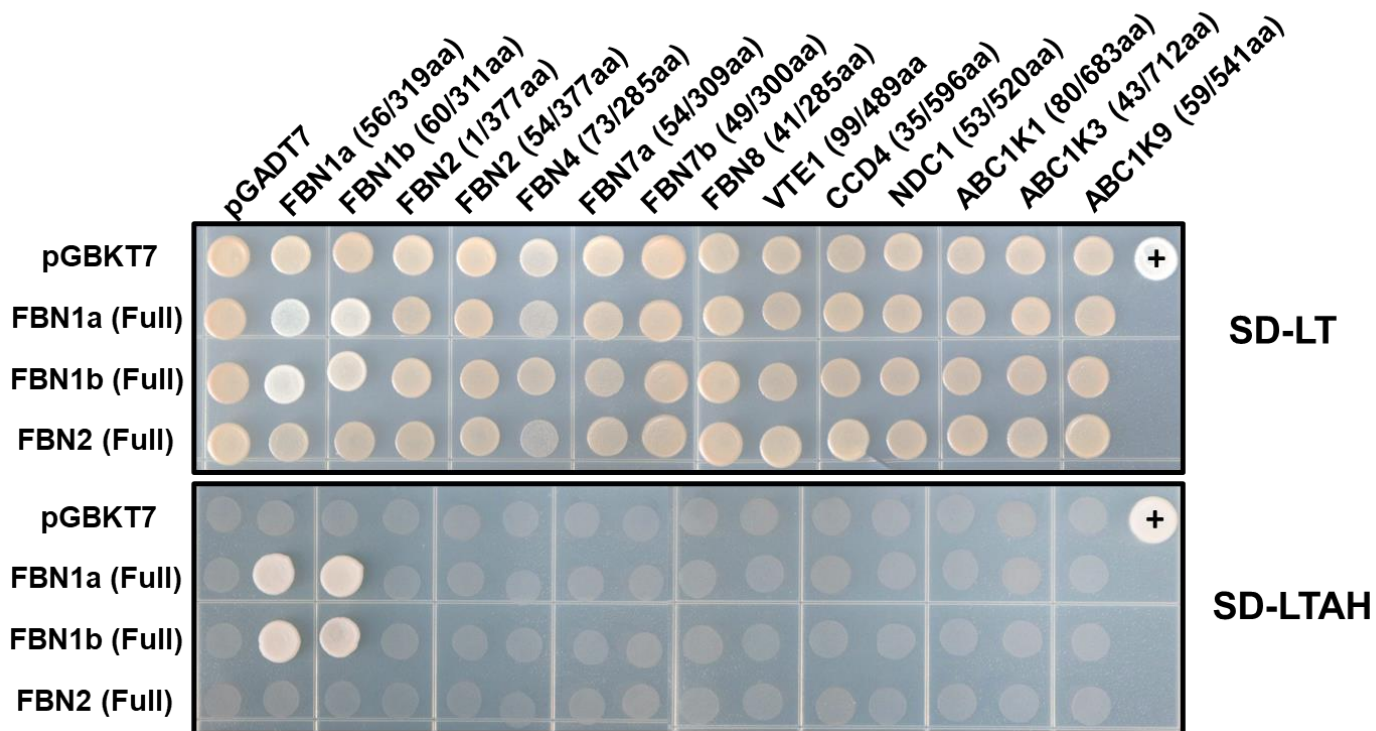


Supplemental Figure S1. Comparison of protein sequences and expression patterns of *FBN1a*, *FBN1b*, and *FBN2*. (A) Comparison of amino acid sequence of *FBN1a*, *1b*, and *2*, Orange (lipocalin motif), Green (start region of mature protein). (B) Phylogenetic tree of *FBN* gene family in Arabidopsis. The scale bar refer to evolutionary distances of the number of base substitutions per site. (C) GUS expression patterns for *FBN1a*, *FBN1b*, and *FBN2* promoters in vegetative and reproductive tissues. Scale bars = 5 mm for leaf, 20 μ m for anther and pollen.

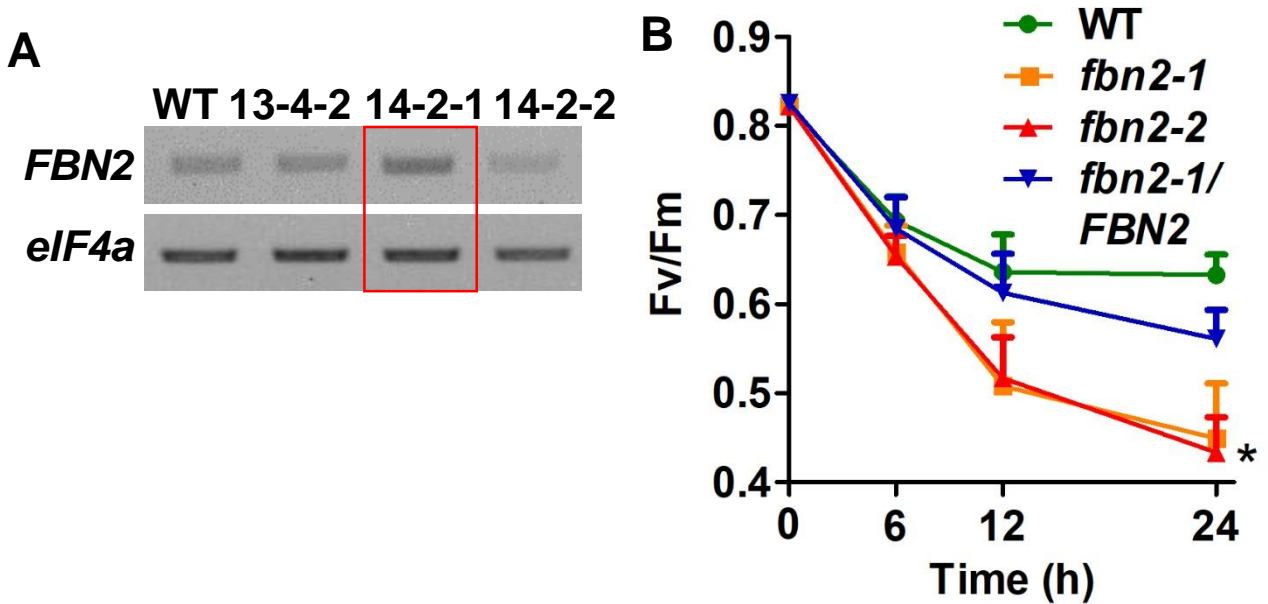


Supplemental Figure S2. Subcellular localization of FBN2 in *Arabidopsis* and *N.benthamiana* cells.

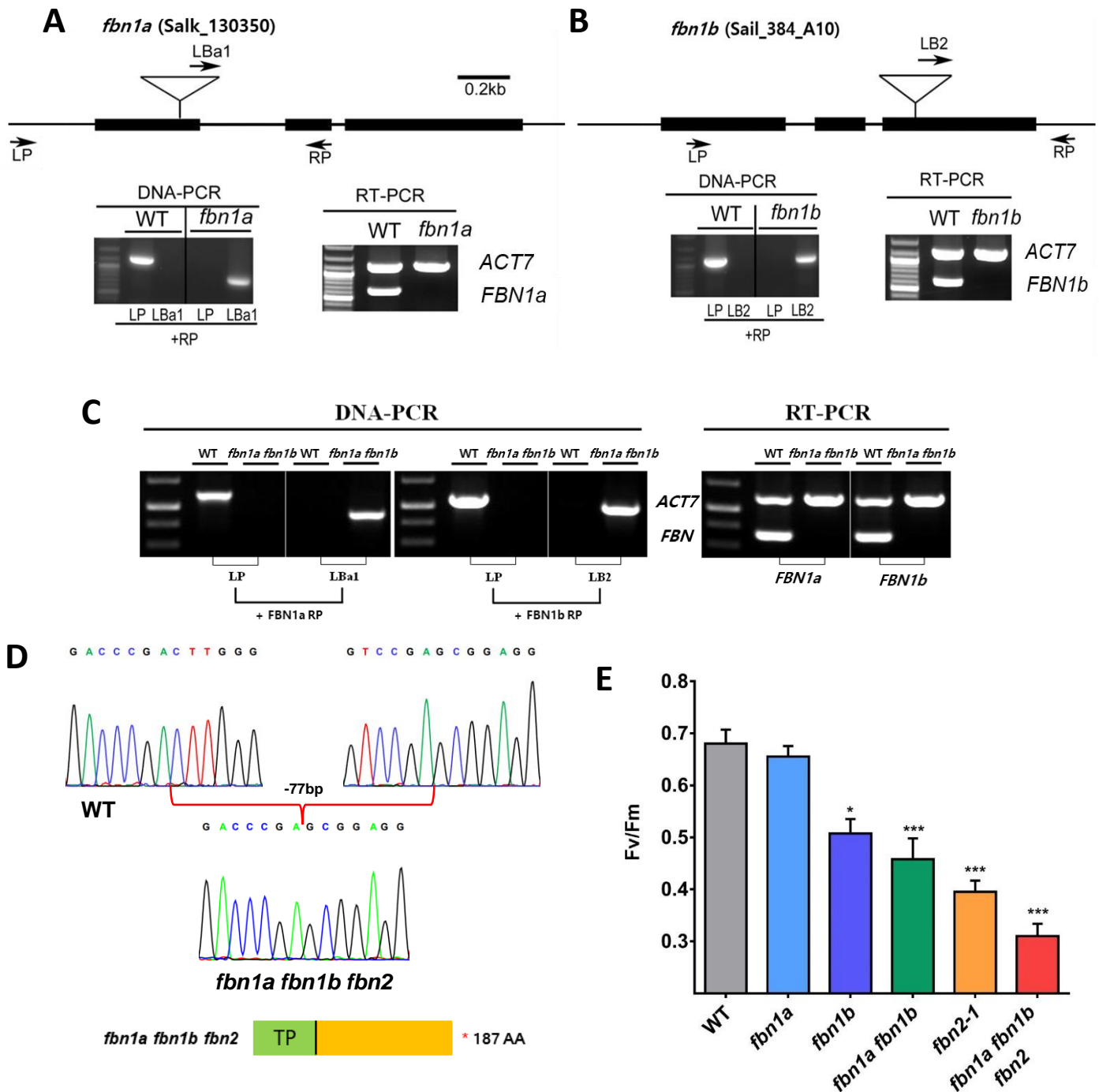
(A) YFP image of a leaf from *Arabidopsis* plant stably transformed with the 35S:FBN2-YFP construct. (B) YFP image of a leaf from *Nicotiana benthamiana* plant transiently transformed with the 35S: FBN2-YFP construct. Scale bar = 10 μ m.



Supplemental Figure S3. Yeast two-hybrid analysis of the interaction between FBN2 and PG proteins. Yeast strain AH109 was co-transformed with pGBKT7-FBN1a, 1b, and 2 bait vector and pGADT7 prey vectors. Protein-protein interactions were grown on the SD/-Leu/Trp (non selective medium) and on the SD/-Leu/-Trp/-Ade/-His (selective medium). p53/tag protein interaction was used as positive control, and the pGBKT7 and pGADT7 empty vectors were used as negative control.

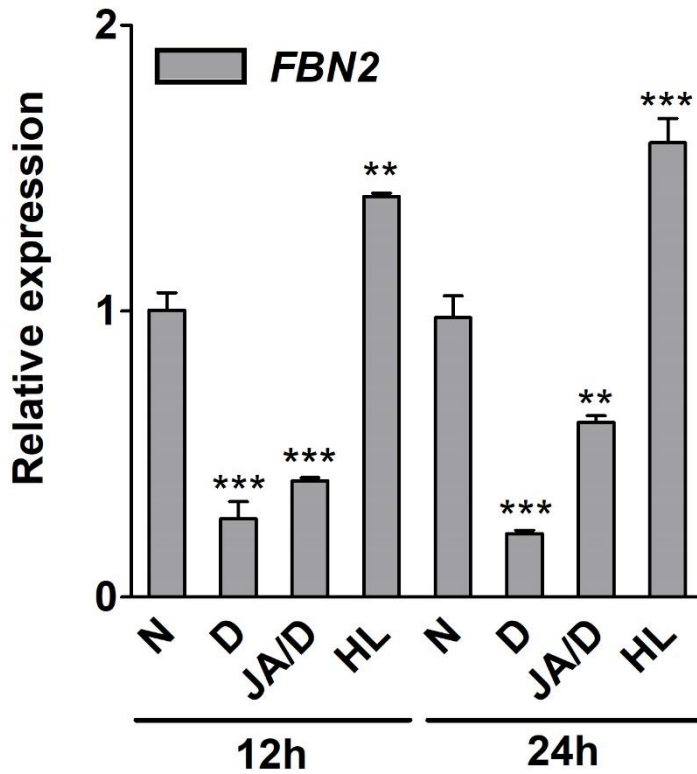


Supplemental Figure S4. Complementation of *fbn2-1* mutant in Arabidopsis. (A) *FBN2* expression in wild type and three *fbn2-1+35S:FBN2* complementation plants by RT-PCR. 14-2-1 line was used for *fbn2-1/FBN2* of (B). (B) Maximum quantum yield of PSII (Fv/Fm) in the wild type and *fbn2* mutants, complementation lines under high-light/cold stress ($850 \mu\text{mol m}^{-2} \text{s}^{-1}$ light/ 15°C). Data represent means with SEM from independent samples ($n = 3$). Statistically significant differences from wild type are indicated by one-way ANOVA with Tukey's post test ($*p < 0.05$)



Supplemental Figure S5. Comparison of *fbn* mutants in Arabidopsis.

Confirmation of (A) *fbn1a*, (B) *fbn1b*, and (C) *fbn1a fbn1b* T-DNA insertion mutants by DNA- and RT-PCR. (D) The *fbn1a fbn1b fbn2* triple mutant was confirmed a 77 bp deletion in the *FBN2* gene by sanger sequencing. This shows an early stop in predicted *FBN2* protein. TP, transit peptide (E) Maximum quantum yield of PSII (Fv/Fm) are measured in wild type, *fbn1a*, *fbn1b*, *fbn1a fbn1b*, *fbn2-1*, *fbn1a fbn1b*, *fbn2* at 24 h under high-light/cold stress ($850 \mu\text{mol m}^{-2} \text{s}^{-1}$ light/ 15°C). Data represent means with SEM from independent samples ($n = 4$). Statistically significant differences from wild type are indicated by one-way ANOVA with Tukey's post test (* $p < 0.05$, *** $p < 0.001$)



Supplemental Figure S6. Expression of *FBN2* under dark and JA treatments.

Expression of *FBN2* under normal (N), dark (D), MeJA/dark (JA/D), and high-light (HL) conditions in wild type plants. Data represent means with SEM from independent samples ($n = 3$). Statistically significant differences from wild type are indicated by one-way ANOVA with Tukey's post test (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$). WT, wild type.

Supplemental Table S1. Top 20 coexpressed genes with *FBN2*

Rank	Locus	Alias	Function	Supportability*	MR**
0	At2g35490	fibrillin2	Plastid-lipid associated protein PAP / fibrillin family protein	3	0
1	At4g38225	unknown	glycerol kinase	3	4.4
2	At1g10830	Z-ISO	15-cis-zeta-carotene isomerase	3	7.9
3	At5g06130	chaperonin	chaperone protein dnaJ-related	3	8
4	At5g44000	transferase	Glutathione S-transferase family protein	3	8
5	At2g01110	UNE3	Sec-independent periplasmic protein translocase	3	8
6	At1g09130	crotonase	ATP-dependent caseinolytic (Clp) protease/crotonase family protein	3	8.4
7	At2g27680	oxidoreductase	NAD(P)-linked oxidoreductase superfamily protein	3	8.4
8	At5g03880	Thioredoxin	Thioredoxin family protein	3	10.8
9	At3g27925	DEGP1	DegP protease 1	3	12.6
10	At4g25130	PMSR4	peptide met sulfoxide reductase 4	3	16.2
11	At4g14910	HISN5B	HISTIDINE BIOSYNTHESIS 5B	3	23.2
12	At3g10670	NAP7	non-intrinsic ABC protein 7	3	25.5
13	At1g73060	LPA3	Low PSII Accumulation 3	3	27.2
14	At1g03680	TRX-M1	thioredoxin M-type 1	3	28.9
15	At2g24820	TIC55-II	translocon at the inner envelope membrane of chloroplasts 55-II	3	28.9
16	At4g25650	TIC55-IV	ACD1-like	3	29
17	At5g11840	DUF1230	Protein of unknown function (DUF1230)	3	29.5
18	At2g30950	VAR2	FtsH extracellular protease family	3	29.8
19	At1g49970	SVR2	CLP protease proteolytic subunit 1	3	34.2
20	At2g20860	LIP1	lipoic acid synthase 1	3	35

*Reproducibility of a coexpressed gene; Threshold E-03

**Coexpressed degree is represented as Mutural Rank (MR) value

Supplemental Table S2. Oligonucleotides used in this study

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
RT-qPCR		
<i>eIF4a</i>	TGACCACACAGTCTCTGCAA	ACCAGGGAGACTTGTTGGAC
<i>FBN1a</i>	ACCAATCGAAATCTCCGATCC	TCCATCTTGACCCCATTCGT
<i>FBN1b</i>	AGCTGCCAAACCAGAGTTTCA	AGATCATCGGGCGGTGAATA
<i>FBN2</i>	CCCCGGTGATCAAATCAAGT	CCAGAGAGTGCCCGTGAAAT
<i>PAP1</i>	AGATAAGAAGAAAGACCAACTAGTGA	CCAAGGTGTCCCCCTTTTC
<i>DFR</i>	TGGTGGTCCGGTCCATTCAT	GAGAGAGCGCGGTGATAAGG
<i>LDOX</i>	CGTGTCAAGAAAGCCGGAGA	GTCCACTCGCGTTGTTAGCC
<i>LOX3</i>	CACCTCCAGTCGATGCAACC	CCAAGCATGCATGTGTCCGT
<i>LOX4</i>	CCATCGAGCTAAGCCTCCCT	CTTGGCTAGCTGCCACATCC
<i>PES1</i>	CAATGCTCCCCTTCTCTCTG	AGCATGGATGCGGGAATTGG
<i>PES2</i>	CCCGATGGTCTTCCAACGC	GCCCATTGCTGGACAGAAA
<i>PGM48</i>	AAGTGTGATCACGGCGTGTG	CAGCTCTGCTGAACGTAGCC
<i>PPH</i>	CCGTGGGCTGATCAACTTGT	GAGGATGGGTTGCTGCAAAG
<i>CCD4</i>	ACGTCTCCGTCGTTTCTCCA	CAACCGGAGAACCACCTTCG
<i>PG SAG</i>	AAGGCACCGAAGAGGAACCA	GGCTCCACGGAGCTCAAGAA
<i>SAG12</i>	GAGCAAGCACTGATGAAGGC	GCACTCTCCAGTGAACACACC
DNA-PCR		
<i>FBN1a-LP,RP</i>	TTCTCCCCACACAAATAATG	TGAAGCTATCGGAATCAATGG
<i>FBN1b-LP,RP</i>	AGAGTTTTCAAAGTCCGAGCC	GGCCATAGACGAGATGTTCTG
<i>Lba1</i>	TGGTTCACGTAGTGGGCCATCG	
<i>LB2</i>	GCTTCCTATTATATCTTCCCAAATTACCAATACA	
RT-PCR		
<i>FBN1a</i>	GAGTATTTGCCTCATCTTCAACCG	AGCCACGACTGCGTGTGTCACTA
<i>FBN1b</i>	ATACGGGAGAGATAGGATCAGCTC	AGCCAAGACTGCGCATTGTCCGCC
<i>FBN2</i>	GGGGTGAGAAACCTGGAGAT	TGTCGAACCCGCAGCTAGTAG
<i>ACT7</i>	TCCATTTCTCTATCTTCTCTCTCGCTG	CAAACCTACCACCACGAACCAGATAA
Vector construction		
<i>FBN1aPro-GUS</i>	GAAGTTCCTATGAACAGGTTTAC	TTTTGTGTTTGTCTTTCAGAGAAACCTCAC
<i>FBN1bPro-GUS</i>	CATTATTCACAGTTTGTGACTTACTT	TTTTTTTTGTTTCTTCGACTAAAATTTCAAG
<i>FBN2Pro-GUS</i>	ATATTTACTCTTTTGGTGAAACTAGTCT	GGCCGATCTTTGTGTTTCGAGCTTGGTGA
<i>FBN2 sgRNA1</i>	TGTGGTCTCAAATTGGAATCCGGGACCCG	
<i>For</i>	G	
	TTTAGTTTTAGAGCTAGAAATAGCAAG	
<i>FBN2 sgRNA2</i>	TGTGGTCTCAAATTGTGCGGTGTCTGACC	
<i>For</i>	C	
	GACTGTTTTAGAGCTAGAAATAGCAAG	
<i>CRISPR</i>		TGTGGTCTCAAGCGTAATGCCAACTTTGTAC
<i>universal Rev</i>		
<i>CR_PICH61</i>	TCCTGTCAAACACTGATAG	TAATGTACTGGGGTGGATGCAG
<i>CR_PAGM4723</i>	ATAAGCCCATCAGGGAGCAG	CGGATAAACCTTTTCACGCC
<i>CR FBN2</i>	GGGGTGAGAAACCTGGAGAT	TACTCCGGCTCCGTTAGAGA

VTE1-
Xba1/BamH1

GGTCTAGAATGGAGATACGGA

TGGATCCACAGACCCGGT

Yeast two hybrid (Gateway system)

<i>FBN1a</i>	AAAAAGCAGGCTGTGCGACGGACATCGA	AGAAAGCTGGGTGTTAAGGGTTTAAGAGAGAGC
<i>FBN1b</i>	AAAAAGCAGGCTGTGCCACAGATACGGG	AGAAAGCTGGGTGTCAAGGATTCAAGAGAG
<i>FBN2</i>	AAAAAGCAGGCTGTTCTTCTCTGCCCTC	AGAAAGCTGGGTGTCAGAGCTCAAGCAGA
<i>FBN4</i>	AAAAAGCAGGCTGTTCATCATCTGGATCA G	AGAAAGCTGGGTGTTAAGCAATGACGAATAC
<i>FBN7a</i>	AAAAAGCAGGCTGTGCTATGGTTCAAGA CT	AGAAAGCTGGGTGTTAACTGTTGTATTCAAGATT
<i>FBN7b</i>	AAAAAGCAGGCTGTGCAATGGTGCAGGA A	AGAAAGCTGGGTGCTAGTGCAGATTTGAGCG
<i>FBN8</i>	AAAAAGCAGGCTGTGTAGCTGTAGCTTCT GG	AGAAAGCTGGGTGTCACAGCTCGAGGGG
<i>VTE1</i>	AAAAAGCAGGCTGTGTTTCCATCCCAGAG A	AGAAAGCTGGGTGTTACAGACCCGGTGG
<i>CCD4</i>	AAAAAGCAGGCTGTCCGCCGTCGTCGA A	AGAAAGCTGGGTGTTAAAGCTTATTAAGGTCACTT TC
<i>NDC1</i>	AAAAAGCAGGCTGTGCAGTGACAAACAA CA	AGAAAGCTGGGTGTCAAGAACCAGACAAAA
<i>ABC1K1</i>	AAAAAGCAGGCTGTGCGATGAGCGGGGT G	AGAAAGCTGGGTGTCATCTGTCCGATAATACTG
<i>ABC1K3</i>	AAAAAGCAGGCTGTGCGGCCCTGGTACA A	AGAAAGCTGGGTGCTATGGGGATGGTGCA
<i>ABC1K9</i>	AAAAAGCAGGCTGTCAAAGCCAGATAGA GA	AGAAAGCTGGGTGTTAGTTGAAGCTGTCC
