**Supplementary Table S1**. Oligonucleotides used in this work

| Name | Gene | Sequence | Use |
|---|---|---|---|
| FBN1a_F | FBN1a (At4g04020) | CTATCCAGGCCCATTTAGTCC | Oligos used to amplify the WT allele in the T-DNA mutant line SALK_024528 |
| FBN1a_R | | TCACCGGGAAATTAAACTTCC | |
| FBN1b_F | FBN1b (At4g22240) | AAGAACCCTACTCCAGCTCCGA | Oligos used to amplify the WT allele in the T-DNA mutant line Sail_384_a10 |
| FBN1b_R | | TCAAGGATTCAAGAGAGGGCTT | |
| FBN2_SALK_LP | FBN2 (At2g35490 | TGTAATCAGCAATCCATTCCG | Oligos used to amplify the WT allele in the T-DNA mutant line SALK_124590 |
| FBN2_SALK_RP | | TTCAGTTCCGTACACCGAATC | |
| LBb1.3 | T-DNA insert | ATTTTGCCGATTTCGGAAC | To identify mutant alleles in the T-DNA SALK lines together with FBN1a_R (*fbn1a* mutant) and FBN2_SALK_RP (*fbn2* mutant) |
| SynLB3 | | TAGCATCTGAATTTCATAACCAATCTCGAT | To identify mutant alleles in the T-DNA Syngenta line (*fbn1b* mutant) together with FBN1b_R |
| FBN1a_attB1 | FBN1a (At4g04020) | GGGGACAAGTTTGTACAAAAAAGCAGGCTTC ATGGCGACGGTACCATTGTTCACC | Cloning of FBN1a full-length cDNA into pDONR207 (without the stop codon) |
| FBN1a_attB2 | | GGGGACCACTTTGTACAAGAAAGCTGGGTCAAC AGGGTTTAAGAGAGAGCTTCCTTC | |

| | | | |
|---|---|---|---|
| FBN1b_attB1 | FBN1b (At4g22240) | GGGGACAAGTTTGTACAAAAAAGCAGGCTTC ATGGCGACGGTACAATTGTCC | Cloning of FBN1b full-length cDNA into pDONR207 (without the stop codon) |
| FBN1b_attB2 | | GGGGACCACTTTGTACAAGAAAGCTGGGTCA GGATTCAAGAGAGGGCTTCC | |
| FBN2_attB1 | FBN2 (At2g35490) | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCAT GGCTACGCTCTTCACCGTC | Cloning of FBN2 full-length cDNA into pDONR207 (without the stop codon) |
| FBN2_attB2 | | GGGGACCACTTTGTACAAGAAAGCTGGGTAGA GCTCAAGCAGAGAGCTTCC | |
| FBN4_attB1 | FBN4 (At3g23400) | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCAT GGCGACTTCTTCTACTTTC | Cloning of FBN4 full-length cDNA into pDONR207 (without the stop codon) |
| FBN4_attB2 | | GGGGACCACTTTGTACAAGAAAGCTGGGTAAGC AATGACGAATACCCTAAG | |
| AOS_attB1 | AOS (At5g42650) | GGGGACAAGTTTGTACAAAAAAGCAGGCTTCA TGGCTTCTATTTCAACCCCT | Cloning of AOS full-length cDNA into pDONR207 (without the stop codon) |
| AOS_attB2 | AOS (At5g42650) | GGGGACCACTTTGTACAAGAAAGCTGGCGAAA AGCTAGCTTTCCTTAA | |
| OCSterm_F | Octopine synthase | GGATCCTCTAGAGTCCTGCTTTAA | Cloning of OCS terminator in pPZP211 |
| OCSterm_R | | GTCGAGGCTCAGCAGGACCTGCAG | |
| FBN2g_F | FBN2 (At2g35490) | GAATTCCCACTTCAATTCCCCATCCACCTTCB | Cloning of the genomic DNA fragment containing FBN2 and its promoter in pZPZ211 |
| FBN2g_R | | GGTACCTCAGAGCTCAAGCAGAGAGCTTCC | |

**Supplementary Fig. S1**

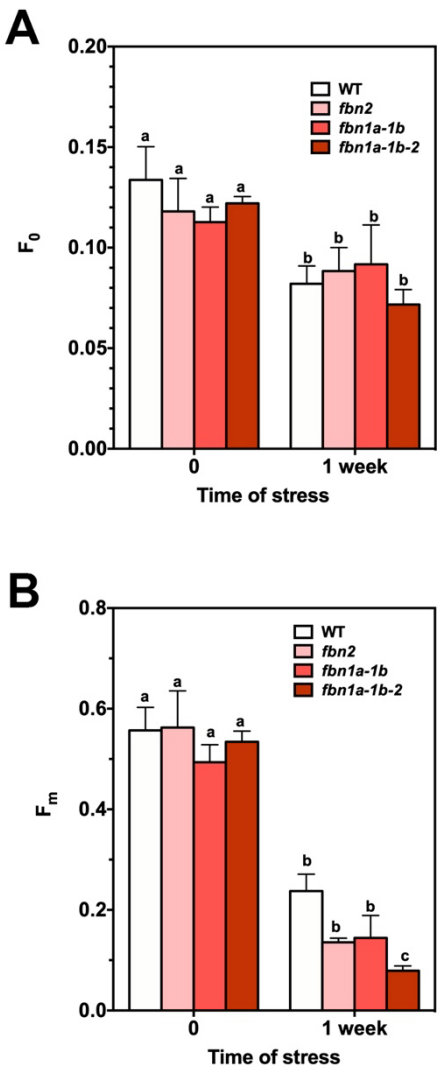


**Figure S1. $F_0$ and Fm values of WT, *fbn2*, *fbn1a-1b*, and *fbn1a-1b-2* mutant plants.** These values were obtained from the same experiment indicated in Figure 4. The values represent the mean ± SD. PRISM software (version 6.0) was used to carry out a two-way ANOVA with Tukey's *post hoc* test analysis. Significance is denoted if $p<0.01$, and mean values varying significantly at the 1% level are marked with different letters.

**Supplementary Fig. S2**

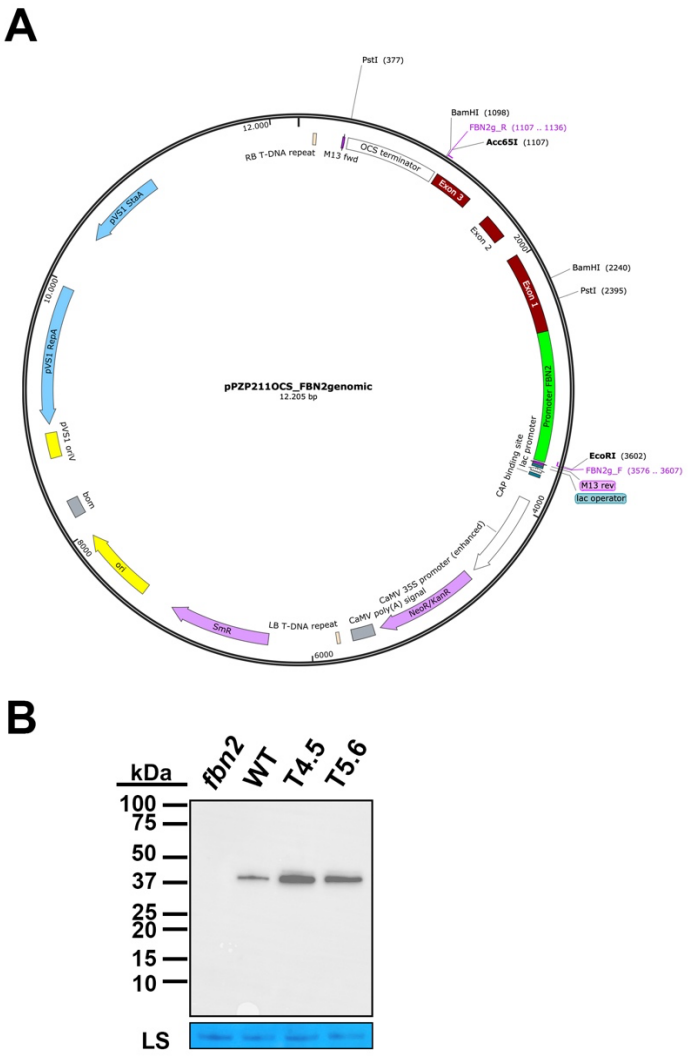


**Figure S2. Complementation of *fbn2* mutation**. **A**. Map of the binary plasmid used to transform to *fbn2* mutant plants. The three exons of FBN2 are indicated in red. The promoter region of FBN2 (1 kbp) is indicated in green. Restriction sites used to clone the OCS terminator (PstI/BamHI) and the FBN2 genomic DNA (Acc65I/EcoRI) in pPZP211 are indicated. **B**. Immunoblot analysis of *fbn2*, WT, transgenic T4.5 and transgenic T5.6 plants. Leaves crude extracts of these plants (15 µg) were loaded into a SDS-PAGE, blotted onto a PVDF membrane and hybridized with specific antibody against FBN2. After the chemiluminescence detection, the filter was stained with Coomassie-blue and the large subunit (LS) of Rubisco is shown as loading control

**Supplementary Fig. S3**

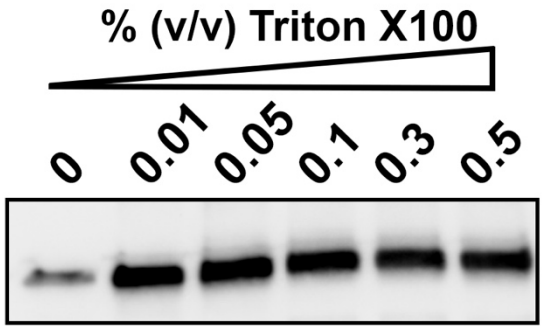


**Figure S3. Solubilization of FBN2 by Triton X-100 treatment**. Chloroplasts isolated from *Arabidopsis* rosette leaves were disrupted and the resulting extract treated with increasing amounts (v/v) of Triton X100 and incubated at 4ºC for 30 min. After the incubation, samples were ultracentrifuged at 100,000 x g for 1 hour at 4ºC. The pellet was discarded and 20 µl of each soluble fraction run in SDS-PAGE. Proteins were blotted on a PVDF filter and hybridized with specific antibodies against FBN2

**Supplementary Fig. S4**

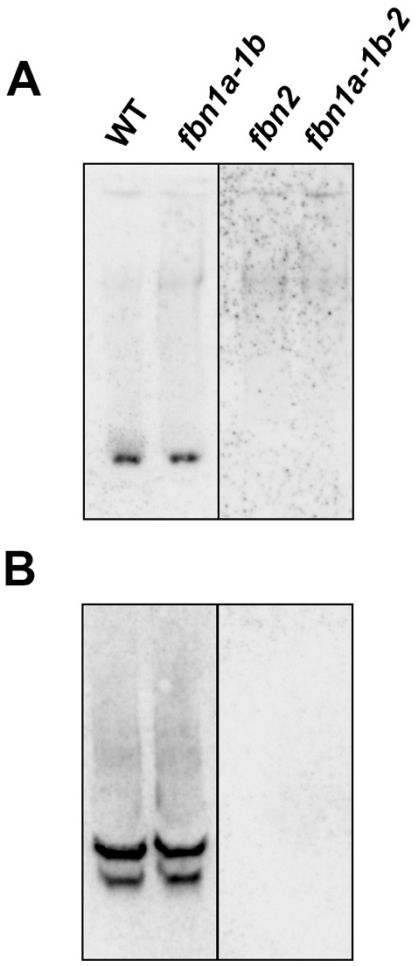


**Figure S4. Specificity of anti-FBN2 antibody**. Rosette leaves from *Arabidopsis* plants cultured under normal growth conditions were disrupted with a Tissue Tearor (Biospec Products Inc., Bartlesville, OK, USA) in 50 mM Hepes (pH 7.5) buffer, and 25 µg of protein from the whole crude extracts were loaded into a native (**A**) or SDS (**B**) polyacrylamide electrophoresis gel. Proteins were transferred to a PVDF filter and hybridized with anti-FBN2