Table 1 Suppl. Forward (F) and reverse (R) primers used for cloning, quantitative real-time PCR, and reverse transcription PCR in this study. In some primers restriction sites are underlined.

Primer name	Primer sequences (5′ to 3′)
p-004385-F	GATGATATGGAGAATAGGCAG
p-004385-R	GAGTCGTCTTAGCTATCTGTG
p-Lba1	TGGTTCACGTAGTGGGCCATCG
p-*AtHsfA4a*- T-DNA-R	ATAATAACGCTGCGGACATCTACATTTT
p-*AtHsfA4a*-F	CTTCTTCACACACAAGAGAGCATC
p-*AtHsfA4a*-R	TTGGCTTTCTGCTTTCTGTAAAAT
p-*AtHsfA4a -Bam*HI-F	CGGGATCCATGGATGAGAATAATCATGGAG
p-*AtHsfA4a-Pst*I-R	AACTGCAGACTTCTCTCTGAAGAAGTCAGATG
p-*AtHsfA4aΔNES-Pst*I-R	AACTGCAGAATTGCATTAACATTTCTCGAATTC
p-p*AtHsfA4a-Xho*I-F	CCGCTCGAGTCTCAGATCACCGGAATTTGGAA
p-p*AtHsfA4a -Pst*I-F	AACTGCAGTCTCAGATCACCGGAATTTGGAA
p-p*AtHsfA4a -Sma*I-R	TCCCCCGGGCTCTGAAAACACTTTTAACAACTC
p-p*AtHsfA5 -Xho*I-F	CCGCTCGAGTCCTCAATATTCCTCATAGTAGT
p-p*AtHsfA5-Sal*I-F	ACGCGTCGACTCCTCAATATTCCTCATAGTAGT
p-p*AtHsfA5-Sma*I-R	TCCCCCGGGTGTTGAATCTAATCAGAAACGGT
p-*AtHsfA5-Bam*HI-F	CGGGATCCATGAACGGCGCATTAGGTAAC
p-*AtHsfA5-Pst*I-R	AACTGCAGTAAGGTCAGCTGCTCGAT
p-*AtHsfA5ΔNES-Pst*I-R	CGGGATCCGATATTCTTTGTATTACGTAACATC
p-*hit2*-EcoRI-dCAPS-F	CATATTCGAGTCCTAGAATCAACGCC
p-*hit2*-EcoRI-dCAPS-R	GCATCAAATAGCTCCAACACCAACGAATT
p-*AtHsfA4a*-511 -F	CAACACATGGAGAAGCGTCA
p-*AtHsfA5*-600-F	GGTAAGAAAGTCGAGCAGTT
p-*UBC28*q-F	TCCAGAAGGATCCTCCAACTTCCTGCAGT
p-*UBC28*q -R	ATGGTTACGAGAAAGACACCGCCTGAATA

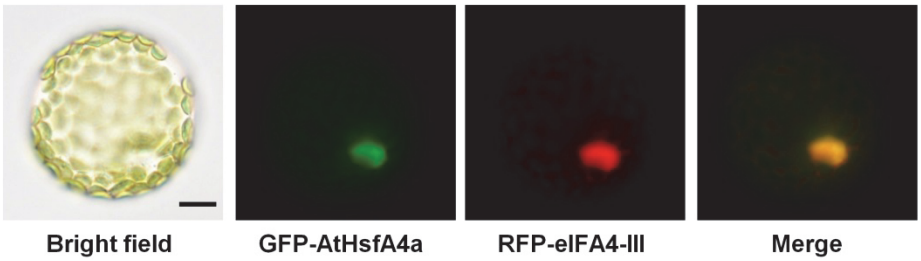

Fig. 1 Suppl. AtHsfA4a was localized in the nucleus of the *hit2* protoplast. Protoplasts from the *Arabidopsis hit2* leaf tissue were co-transformed with expression vectors for the *AtHsfA4a* promoter driven GFP-AtHsfA4a and the cauliflower mosaic virus 35S promoter driven nuclear marker RFP-eIF4A-III. *Bar* = 10μm.

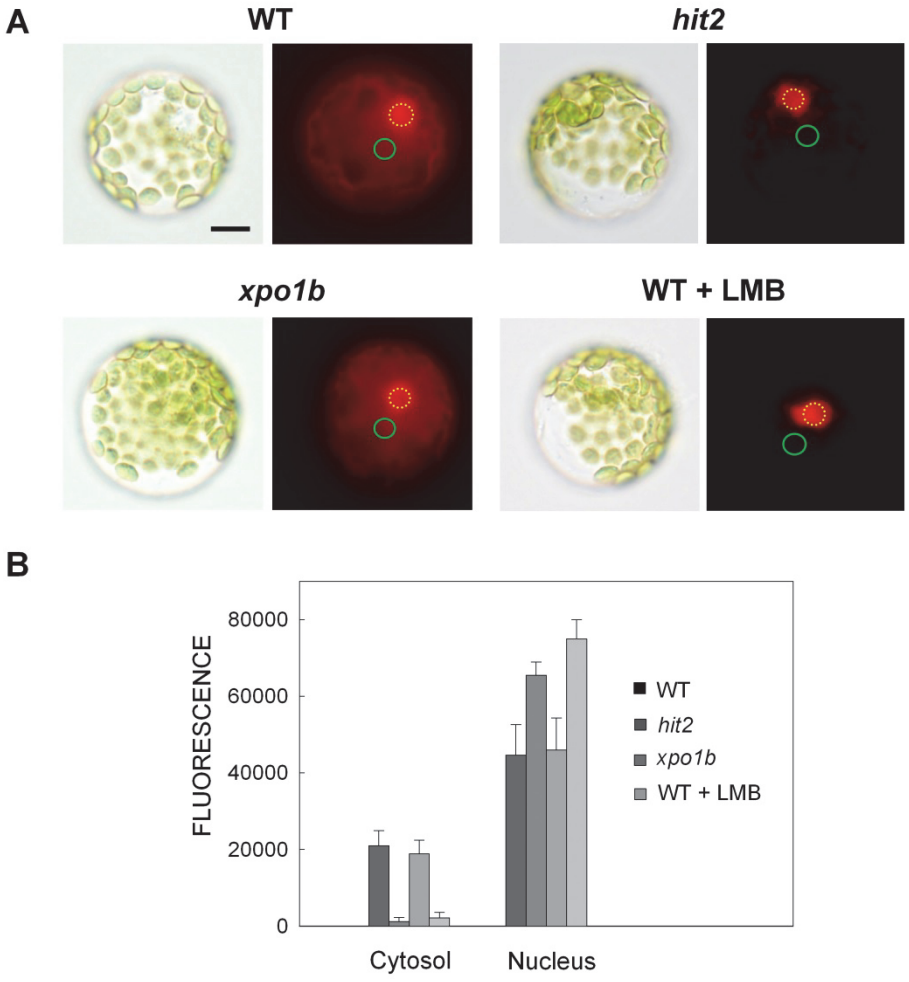

Fig. 2 Suppl. Fluorescence (arbitrary units) of mCherry-AtHsfA5 in wild-type, *hit2*, *xpo1b,* and LMB treated wild-type (WT+LMB) protoplasts. AtHsfA5 was present in both cytoplasm and nuclei in wild-type and *xpo1b*cells, but confined in the nuclei in *hit2* and LMB treated WT cells. Fluorescence was measured by the publicly available image analysis software *Image J* (Schneider *et al*. 2012). *A* - The integrated density of the area delineated by the yellow dashed line represents the fluorescence of mCherry-AtHsfA5 in the nucleus, and the green solid line represents the fluorescence of mCherry-AtHsfA5 in the cytoplasm. *B* - Data obtained from *A* indicate that the cytoplasmic fluorescence intensity of mCherry-AtHsfA5 in *hit2* is much less than the intensity in wild-type and *xpo1b* protoplasts, and is similar to that in LMB treated wild-type protoplasts. Values are reported as average ± SD of four biological repeat measurements. *Bar* = 10μm.

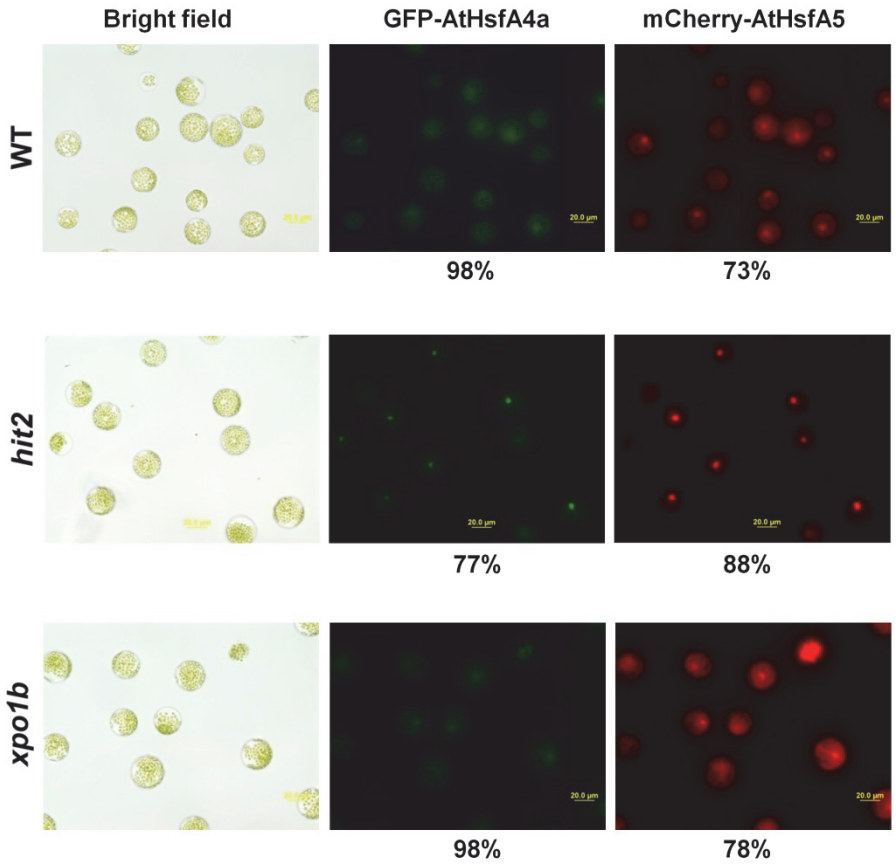

Fig. 3 Suppl. Representative images supporting quantitative data in the Fig. 2*A*. These fluorescence microscopic images mirror the images presented in Fig. 2*A*, but show a larger field with more cells. Percentages of cells showing nuclear/cytoplasmic fluorescence partition (identical to Fig. 2*A*) were calculated from 100 cells examined and shown under each fluorescent image panel.

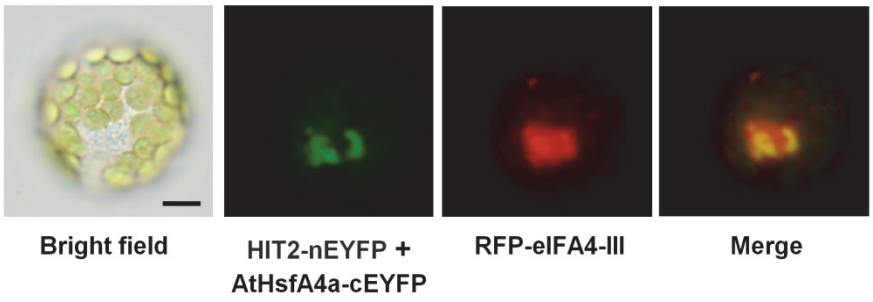

Fig. 4 Suppl. Interaction of AtHsfA4a with HIT2 as examined by bimolecular fluorescent complementation (BiFC) assay in *Arabidopsis* protoplasts. Protoplasts from *Arabidopsis* leaf tissue were co-transformed with HIT2-nEYFP, AtHsfA4a-cEYFP and RFP-eIFA4-III. *Bar* = 10µm.

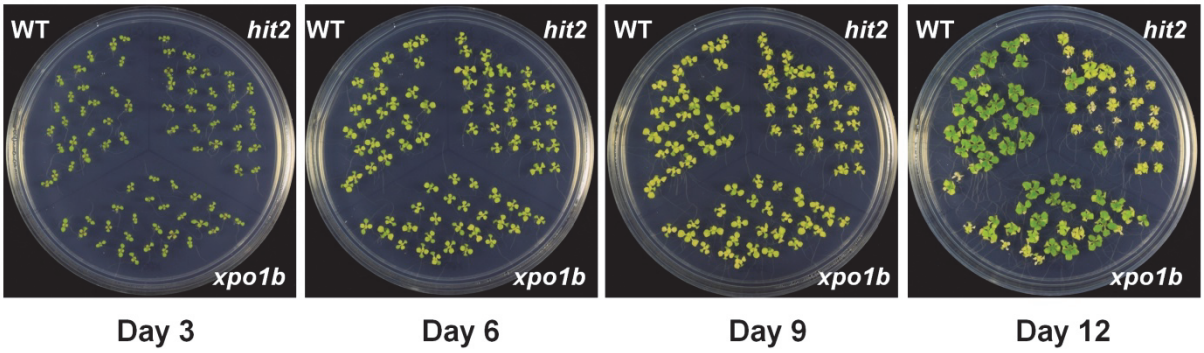

Fig. 5 Suppl. Wild-type and *xpo1b* leaves which gradually reverted from yellowish to a green colour under high irradiance whereas *hit2* leaves remained yellow throughout the treatments. Seedlings were grown under a irradiance of 100 µmol m^{-2} s^{-1} for 4 d and then transferred to irradiance of 500 µmol m^{-2} s^{-1} and cultured for an additional 12 d. Plants were photographed on days 3, 6, 9, and 12.