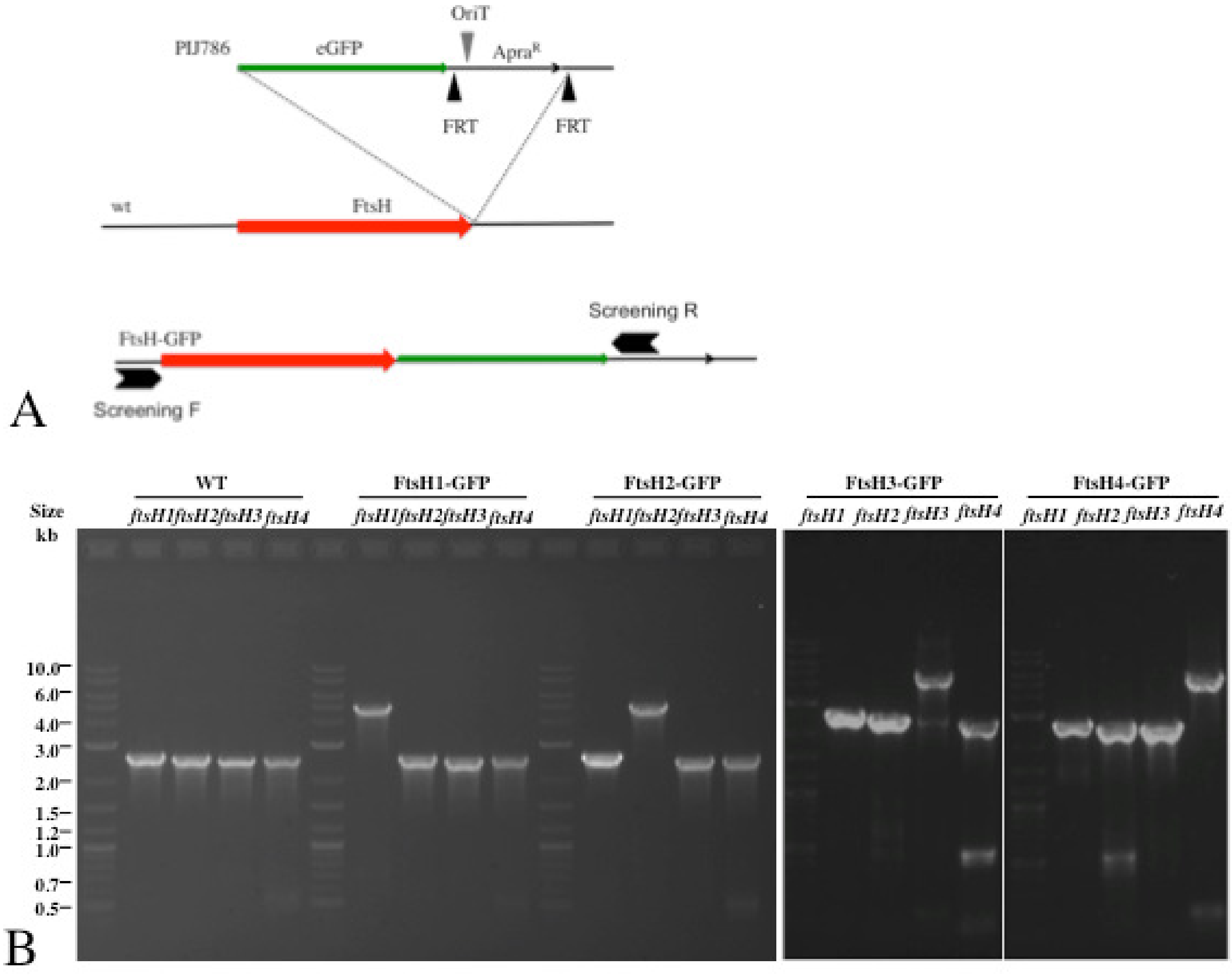
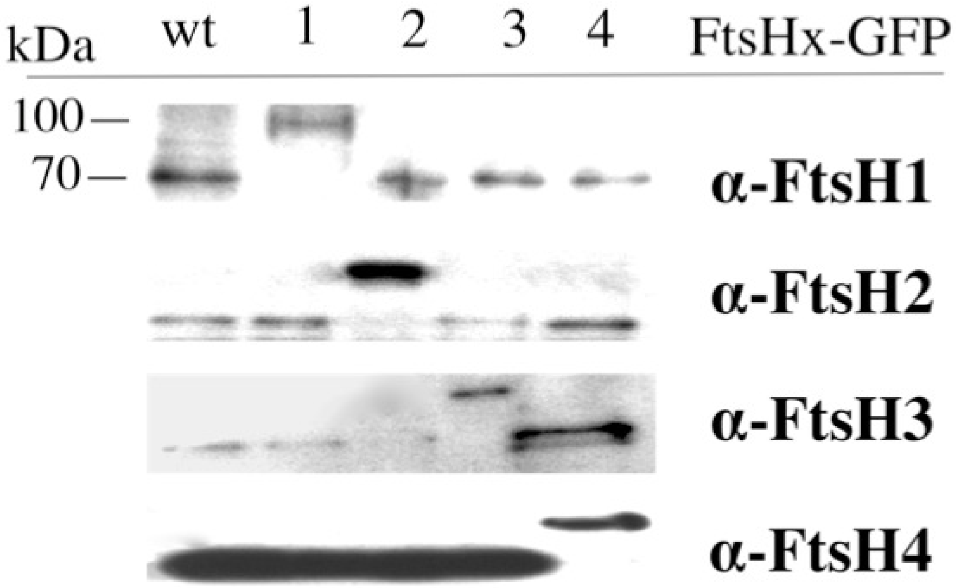
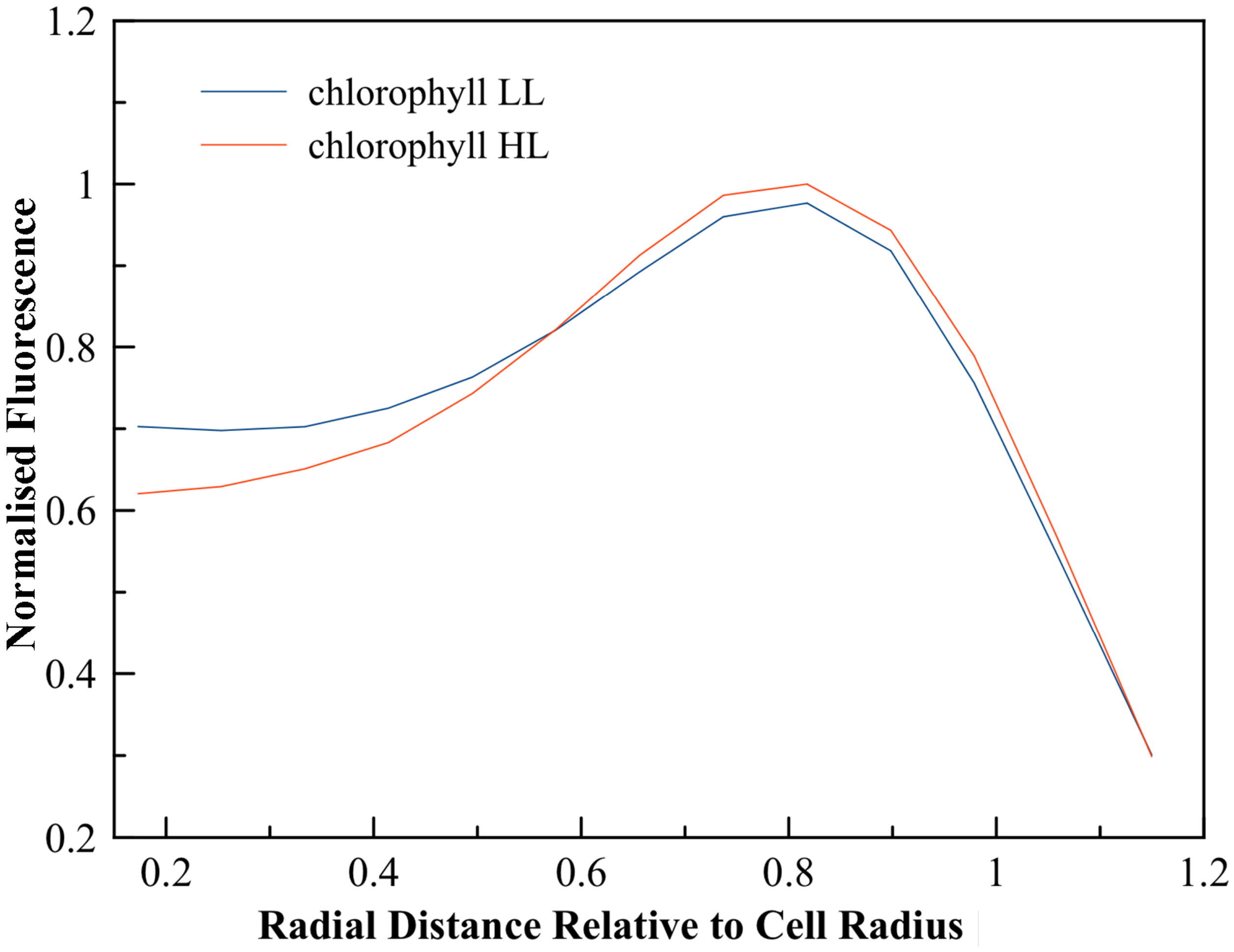


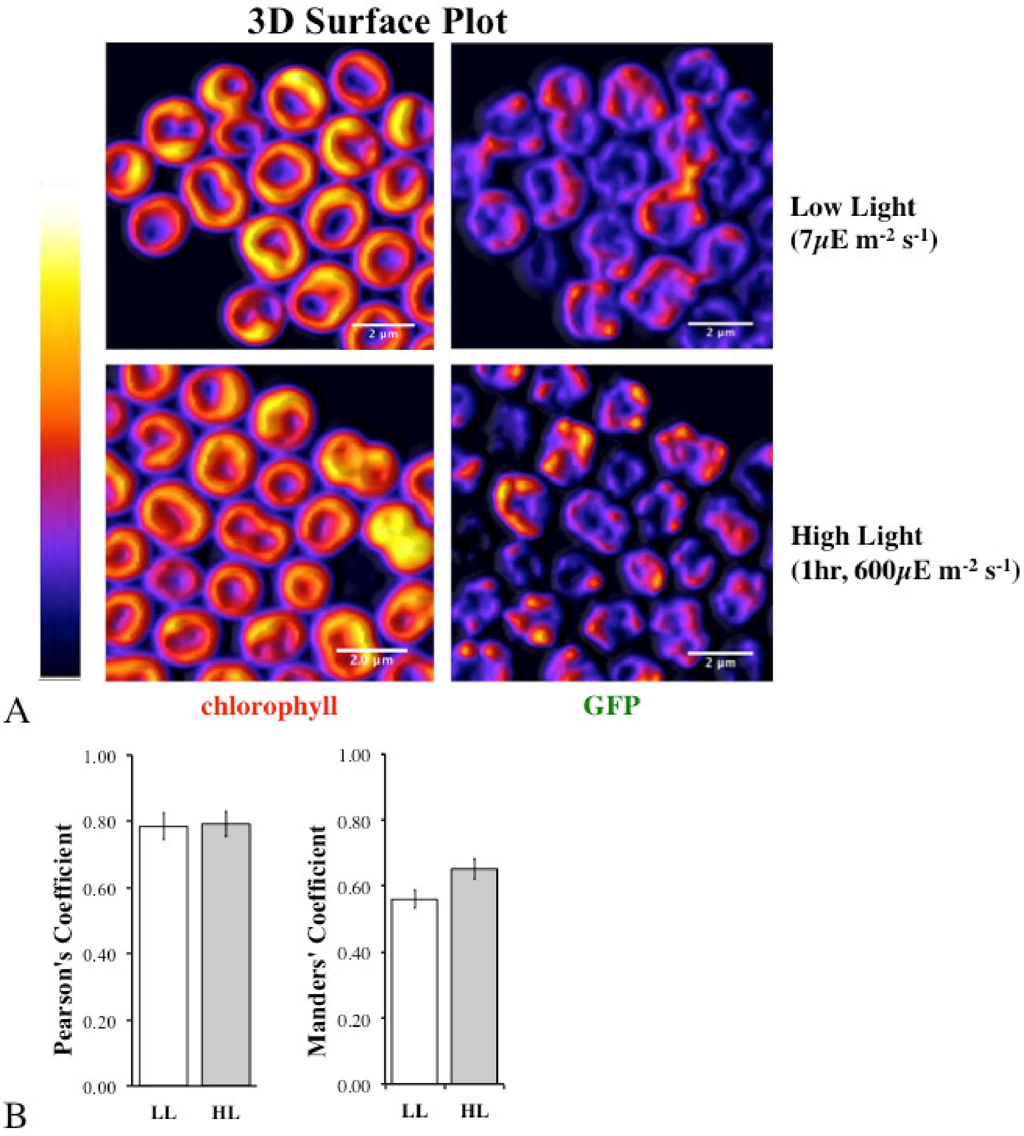
Supporting Figure 1 (A) Construction of genes encoding GFP fusions to the C-terminal end of each FtsH protease by amplification of wild-type gene and *gfp-Apramycin*^{R} cassette from plasmid PIJ786. (B) segregation test and screening for *gfp* fusion with PCR. Primers chosen to amplify the entire *ftsH* ORF and 650bp downstream sequence. Expected sizes of PCR products ~2.5kb for wild-type and ~4.5kb for *ftsH+gfp+Apra*^{R}.



Supporting Figure 2 Immunoblots with crude membrane fractions isolated from wild-type and each of the GFP-tagged strains (1 = *ftsH1-gfp*; 2 = *ftsH2-gfp*; 3 = *ftsH3-gfp*; 4 = *ftsH4-gfp*). Immunoblots performed with anti-FtsH antibodies specific for each FtsH protein. GFP-tagged FtsH proteins are ~100 kDa; native FtsH proteins ~70 kDa. Lanes loaded according to chlorophyll concentration (0.1 nmol chlorophyll per lane).



Supporting Figure 3 High light exposure has little effect on the radial distribution of chlorophyll fluorescence in *Synechocystis* cells. Wild-type cells were grown in low light (LL) or exposed to high light (HL) at 600 μE m^{-2} s^{-1} for 45-60 min. Averaged fluorescence radial distributions (n = 30, for 3 biological replicates), standardised to cell radius.



Supporting Figure 4 Effect of high-light exposure on the relative distributions of chlorophyll and FtsH2-GFP in *Synechocystis* cells (A) False-colour 3D surface plots (with linear colour scale) of GFP and chlorophyll fluorescence in low-light and high light-exposed *Synechocystis* cells (B) Co-localisation of GFP and chlorophyll fluorescence assessed by Pearson's and Manders' coefficients. There are no significant differences between HL and LL (n = 30, p = 0.30 for Pearson's coefficient and 0.26 for Manders' coefficient, error bars show standard deviation, tested and averaged for 3 biological replicates).

Supporting Table 1. Mass spectrometric analysis of proteins from anti-GFP pull-downs from *Synechocystis ftsh2-gfp* cells, showing recognised peptide sequences and ion scores, based on the calculated probability, P, Ion score cut off = 1. Sequences and ion scores are from low-light samples, except for proteins detected exclusively after high-light treatment (see Table 1). Data from 2 biological replicates for each condition.

ORF	**Protein ID**	**Sequence**	**Ion score**
slr0335	**ApcE**	**FVELGQVSAIR**	**31**
		AYSQSISYLESQVR	**36**
		RFPTLPAANFPNTER	**6**
		EIQQYNQILASQGLK	**31**
		EYSDAFGEDTVPYER	**31**
slr1311	**CcmM**	**Carbon dioxide concentrating mechanism protein**	**✓**
slr0012	**RBL_SYN3**	**FLFVQEAIEK**	**51**
		WSPELAAACELWK	**17**
slr1834	**psaA**	**WGKPGHFDR**	**56**
		LVPDKGQLGFR	**41**

		DYDPAKNVNNLLDR	**53**
slr1835	**psaB**	**FSQDLAQDPTTR**	**28**
		DFGYSFPCDGPGR	**27**
		VYLGAETTR	**28**
ssl0563	**psaC**	**CETACPTDFLSIR**	**72**
		IYDTCIGCTQCVR	**78**
		ACPLDVLEMVPWDGCK	**16**
slr0737	**psaD**	**IGQNPEPVTIK**	**51**
		KEQCLALGTQLR	**26**
		VYPSGEVQYLHPADGVF PEKVNEGR	**64**
smr0004	**psaI**	**Photosystem I reaction center subunit II**	
ssr2831	**psaE**	**SGILYPVIVR**	**50**
slr1655	**psaL**	**TFIGNLPAYR**	**70**
		TFIGNPAYRK	**23**
		AESNQVVQAYNGDPFVGHLSTPISDSAFTR	**5**

sll0851	**CP43**	**NDIQPWQVR**	**57**
		GPNGLDLDKLR	**52**
		LGANIASAQGPTGLGK	**94**
		DLPSTGFAWWSGNAR	**87**
		GIDRETEPTLFMPDLD	**32**
		VITNPTLNPAIIFGYLLK	**58**
slr0906	**CP47**	**GYFQEEIQR**	**71**
		VHTVVLNDPGR	**18**
		GYFQEEIQRR	**24**
		LAFYDYVGNSPAK	**92**
		YQWDKGYFQEEIQR	**101**
		VDSQLAEGASLSEAWSTIPEK	**31**
		DVFAGVDPGLEEQVEFGVFAK	**122**
		AQLGEGFDFDTETFNSDGVFR	**102**
		RVDSQLAEGASLSEAWSTIPEK	**78**
		KAQLGEGFDFDTETFNSDGVFR	**149**
		FSVEQTGVTVSFYGGALDGQTFSNPSDVKK	**22**

ssl2598	psbH	**LGDILRPLNSEYGK**	**65**
ssr3451	psbE	**QELPILQER**	**57**
sll0849	psbD	**AYDFVSQELR**	**23**
		AAEDPEFETFYTK	**67**
slr1311/sll1867	psbA2/ psbA3	**VIGTWADVLNR**	**62**
		LIFQYASFNNSR	**61**
slr1326	atpA	**WDSLGRPIDGK**	**22**
		LLESPAPGIIER	**51**
slr1329	atpB	**FVQAGSEVSALLGR**	**61**
		DVNKQDVLLFIDNIFR	**47**
		MPSAVGYQPTLGTDVGDLQER	**20**
		NSAGNEVAVTCEVQQLLGDNQVR	**34**
slr1327	atpC	**LSFAETELPLFEQRFVSLISSQPVVQ**	**48**
		TLFPLSPQGLEAPDDEIFR	**13**
slr0228	FtsH2	**SRVDLPTNAPELIAR**	**22**
		LVDLLIEKETIDGEEFR	**41**

		TPGFSGADLANLLNEAAILTAR	**7**
sll1463	**FtsH4**	**AAEEIVFDSITTGAANDLQR**	**70**
		TPGFAGADLANLVNEAALLEER	**25**
sll0247	**isiA**	**RVEQAFDSLQT**	**83**
sll1578	**cpcA**	**FLSSTELQIAFGR**	**103**
slr1128	**hypothetical**	**DSAINSAQGDAQAR**	**18**