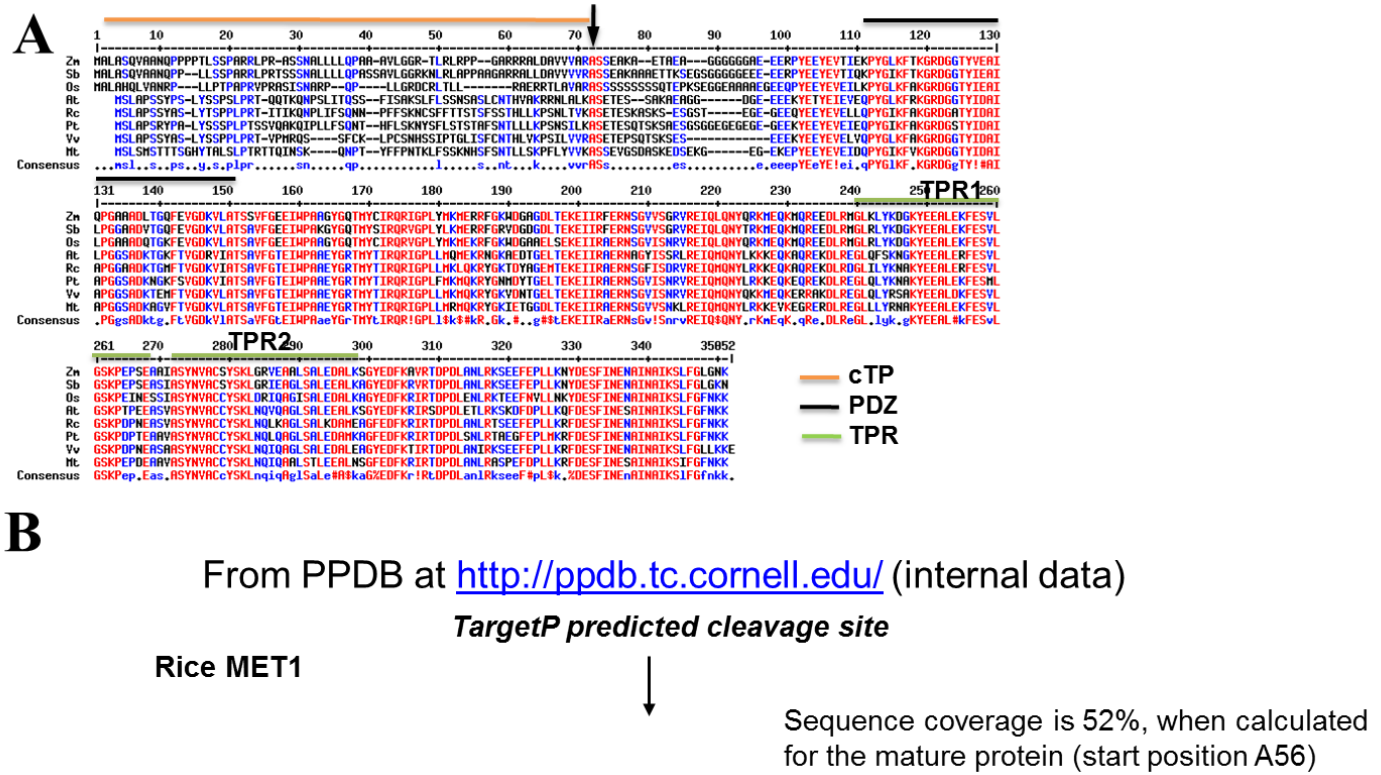
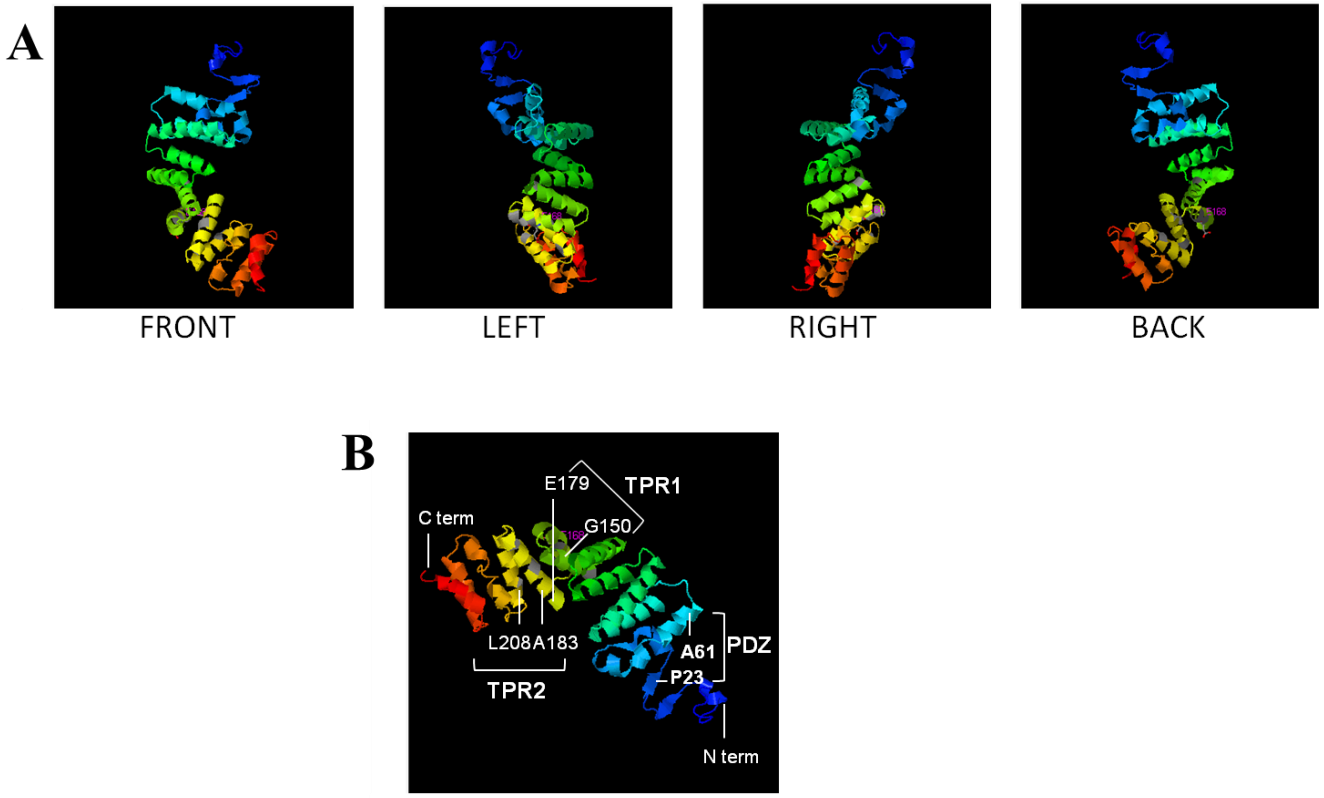


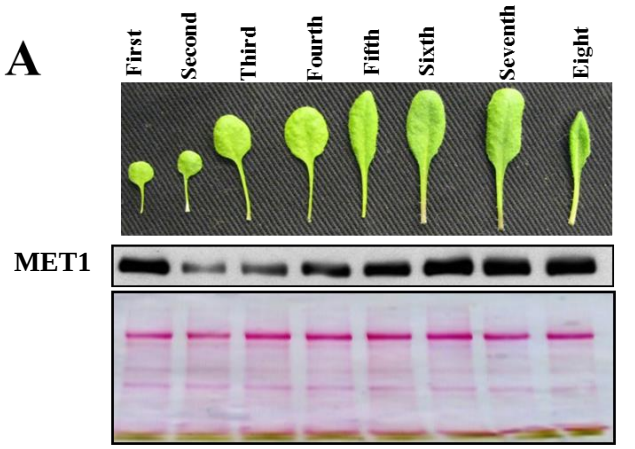
Supplemental Figure 1. Sequence alignment of the MET1 homologs in selected monocots and dicots and experimental sequence coverage of rice MET1.

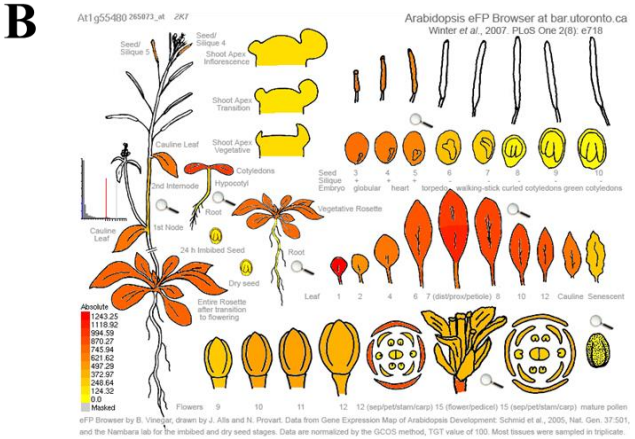
(A) Sequence alignment of the MET1 homologs in 4 selected monocots (*Sorghum bicolor - Sb*, *Oryza sativa - Os*, *Zea mays - Zm)* and 6 dicots (*Arabidopsis thaliana - At*, *Glycine max - Gm*, *Populus trichocarpa - Pt*, *Vitis vinifera - Vv*, *Medicago truncatula - Mt*, *Ricinus communis - Rc*). The alignment was created using Multialin (Corpet, 1988). High and low consensus residues are shown in red and blue, respectively. cTP – chloroplast transit peptide.

(B) Protein sequence coverage of rice MET1 (Os07g07540) determined by MS/MS of the proteome of isolated chloroplasts and total leaf samples.

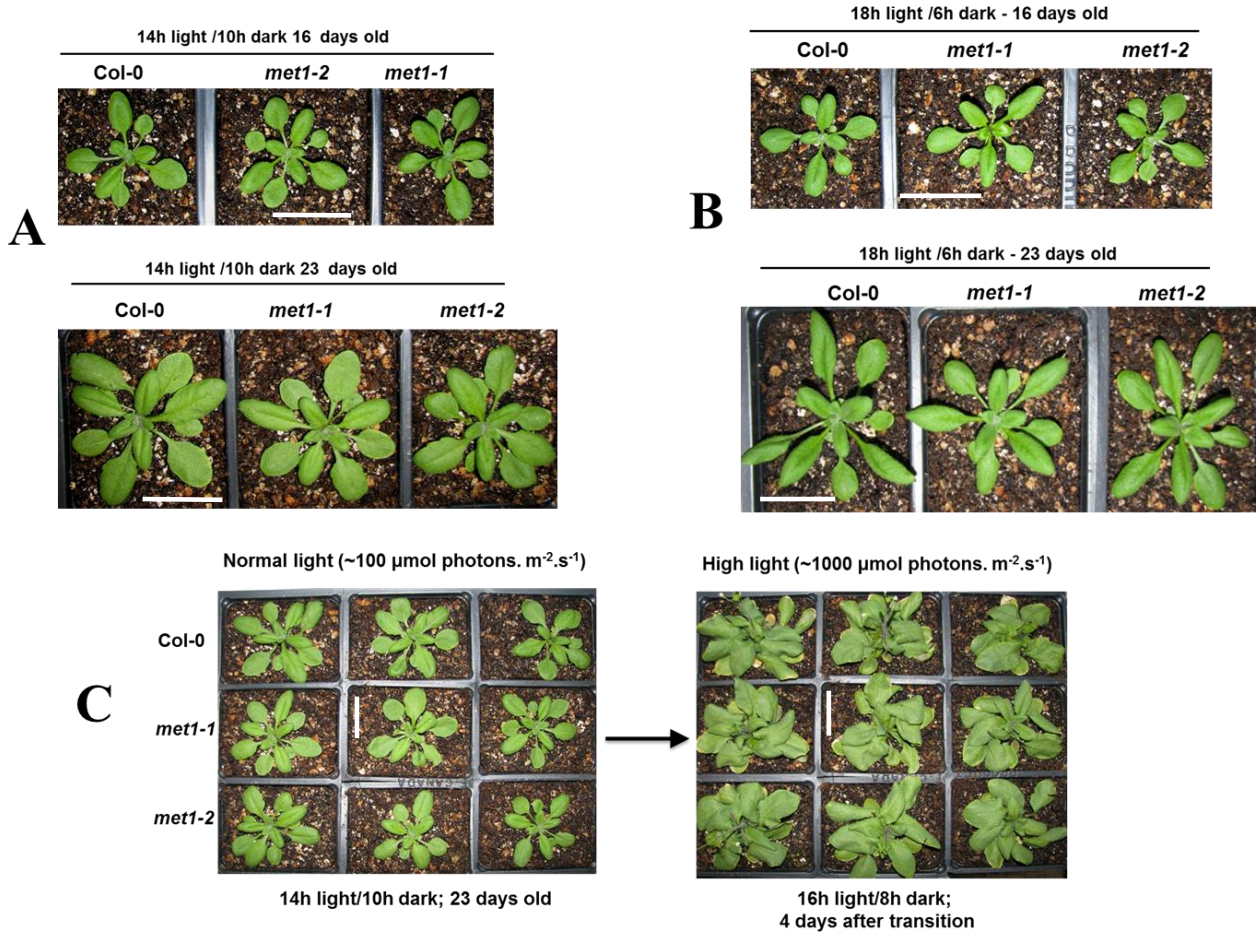


Supplemental Figure 2. Structural model for mature MET1 generated by i-TASSER (http://zhanglab.ccmb.med.umich.edu/I-TASSER/). The best model (confidence score -2.10) was selected among five predicted models.
(A) Different side views of the model
(B) PDZ (from P23 to A61) and TPR domains (from G150 to E179: TPR1 and from A183 to L208: TPR2) in the structure. MET1 does not have any predicted transmembrane domain but the C-terminal end is rich in hydrophobic amino acids and conserved among all species.

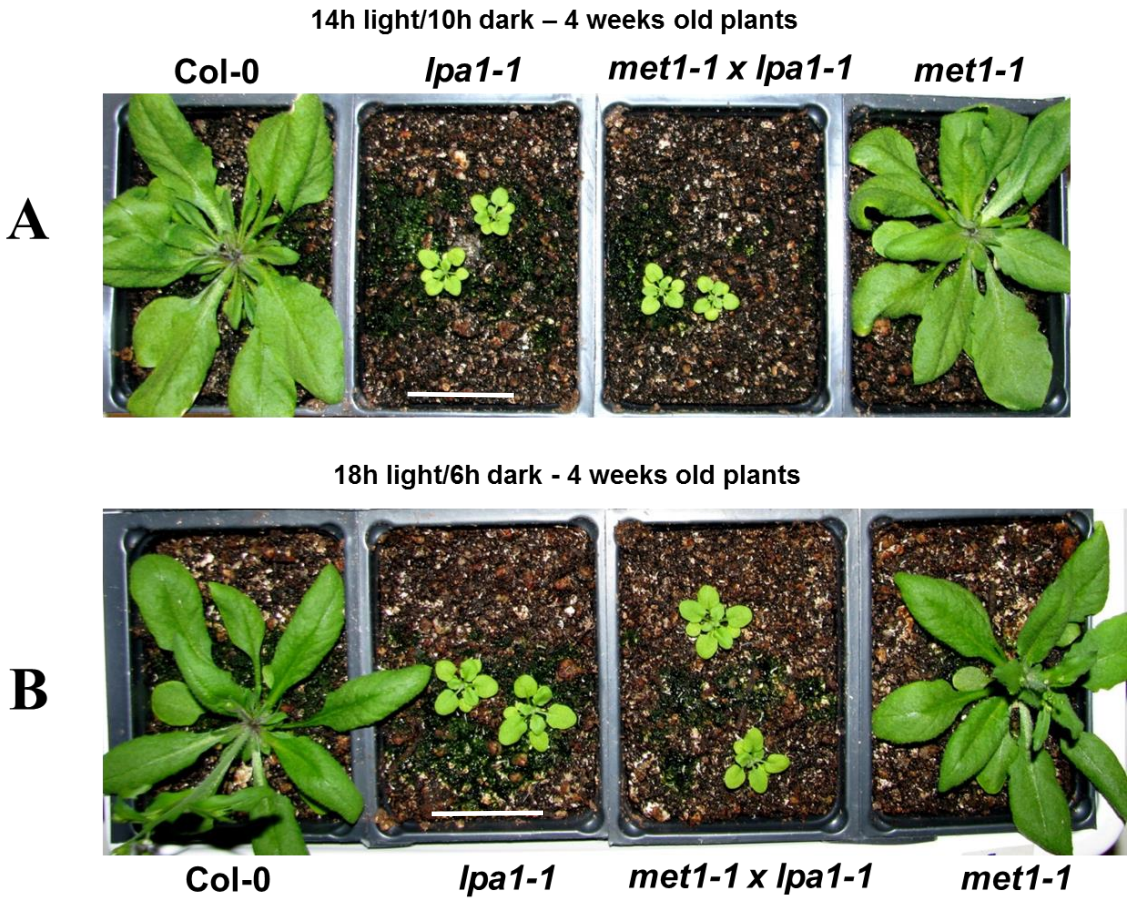




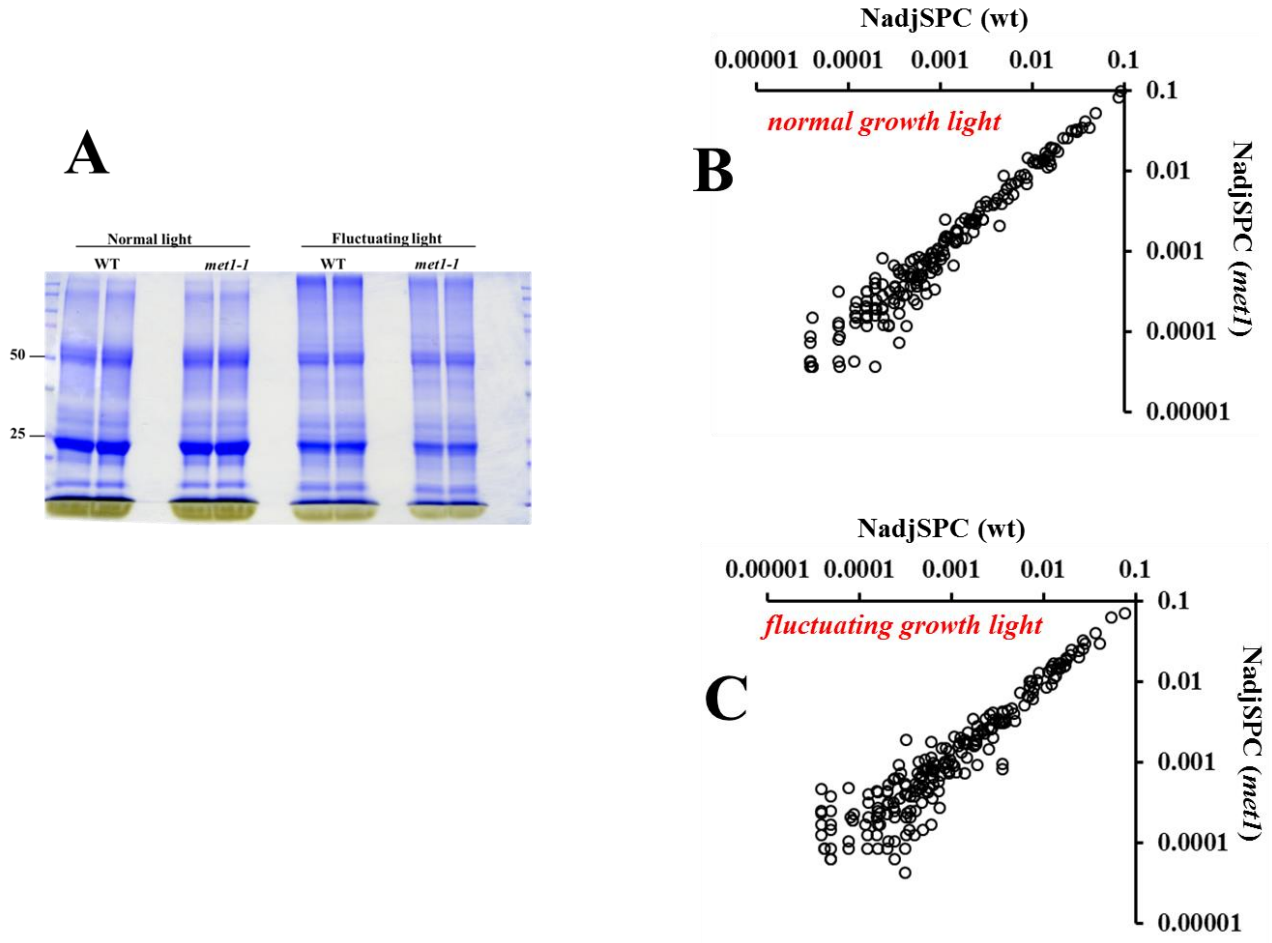
Supplemental Figure 3. Protein and mRNA accumulation patterns during Arabidopsis development in leaves and other organs.
(A) MET1 protein accumulation in at different developmental stages in wt Arabidopsis. Rosettes of soil grown plants grown at a 16/8 h light/dark cycle were collected at stage 1.08. Individual leaves from >10 rosettes with the same position of each rosette were pooled, and total protein extracted in presence of SDS.
(B) Accumulation of *MET1* mRNA in different organs and developmental stages from eFP browser at http://bar.utoronto.ca/welcome.htm.



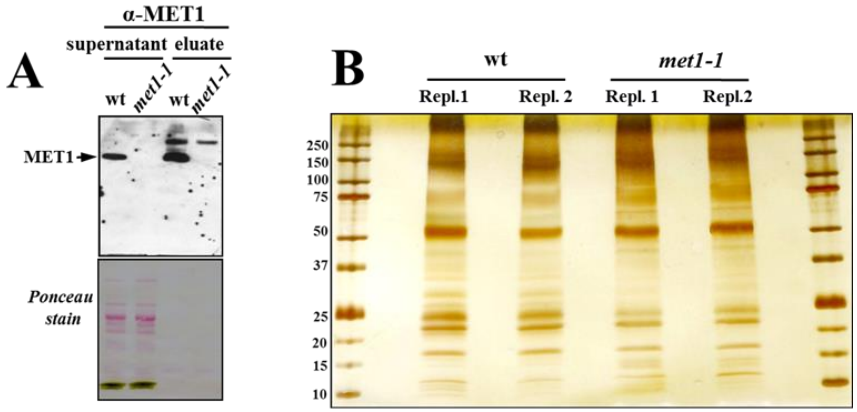
Supplemental Figure 4. Testing the effect of different light regimes on growth and development of *met1-1* and *met1-2*. The size bars correspond to 3 cm.
(A,B) Phenotypes of wt, *met1-1, met1-2* plants at 16 days and 23 days old grown under a light/dark cycle of 14h light/10 h dark **(A)** or 18 h light/6 h dark **(B)** with light intensity of ~100 µmol photon.$m^{-2}.s^{-1}$.
(C) Phenotypes of wt, met*1-1, met1-2* plants grown at ~100 µmol photon.$m^{-2}.s^{-1}$ at 14h light/10 h dark and 4 days after transfer to 10-fold higher light intensity and an increased light period (18 h light/6 h dark).



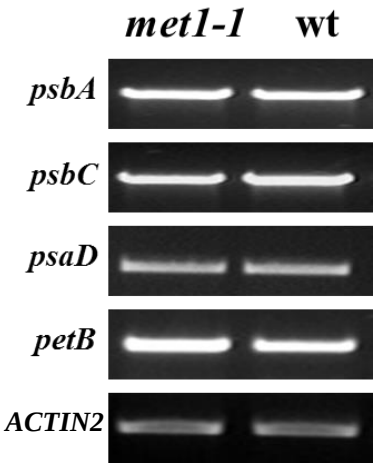
Supplemental Figure 5. Growth and developmental phenotypes of single and double mutants in *LPA1* and *MET1*.
(A,B) Phenotypes of 4 week old wt, *lpa1-1*, *met1-1*, and *met1-1 x lpa-1* at 14h light/10 h dark **(A)** and 18 h light/6 h dark **(B)** grown at ~80 µmol photons m^{-2} s^{-1} light intensity. The size bars correspond to 3 cm.



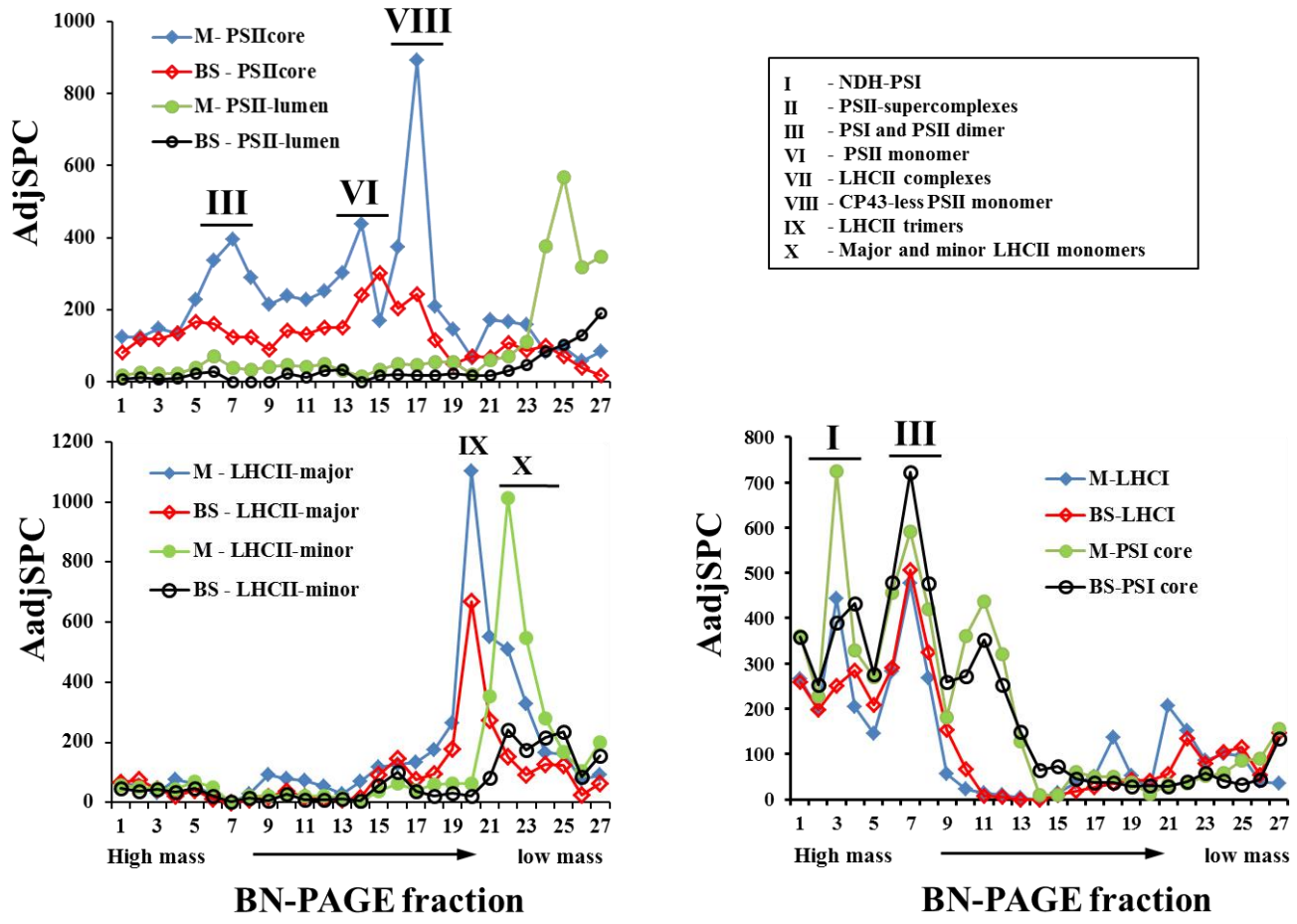
Supplemental Figure 6. Scatter plots and Coomassie stained SDS-PAGE gel with 60 µg proteins of isolated thylakoid proteins of wt and *met1-1* grown on soil under normal light or fluctuating growth light used for MS/MS analysis and quantification by label-free spectral counting. **(A)** SDS-PAGE gels of thylakoid proteins. **(B,C)** Scatter plots of normalized protein abundances (as measured by NadjSPC) for wt and *met1-1* of plants grown under normal light conditions **(B)** or fluctuating light conditions **(C)**.



Supplemental Figure 7. Identification of MET1-1 candidate protein interactors.
(A) High enrichment of MET1 using anti-MET1 serum against thylakoids solubilized by DM.
(B) Silverstain of an SDS-PAGE gel with co-immunoprecipitates with anti-MET1 serum used for MS/MS analysis in wt. *met1-1* was used as negative control.



Supplemental Figure 8. Accumulation of selected plastid gene transcripts in wt and *met1-1* mutant as determined by RT-PCR.



Supplemental Figure 9. MS/MS analysis of BN-PAGE gel lanes of maize mesophyll and bundle sheath thylakoids. Original mass spectrometry data are from (Majeran et al., 2008). Profiles for the integral membrane proteins of the PSII core, thylakoid lumen proteins of the water splitting complex of PSII, the minor LHCs (CP24,26,29) and major LHCs, PSI core proteins and LHI proteins are shown.

Supplemental Table 1. Primers used for genotyping, RT-PCR analysis and cloning of the MET1 antigen.

Primer name	Sequence (5'-3') Forward	Sequence (5'-3') Reverse
MET1 antiserum	GGATCCATGTCTTTAGCTCCGAGCAGTTATCCA	TCTCGAGATACTTACCATTCTTGGAAAATTGCAG
MET1 RT-PCR	ATGTCTTTAGCTCCGAGCAGTTATC	TTTCTTGTTAAAGCCAAACAAGGAT
ACTIN2 RT-PCR	CAAACGAGGGCTGGAACAAGACT	GCAACTGGGATGATATGGAAAAGA
LPA1 RT-PCR	ATGGCTGTGGCTACAGCTCCGT	TCTTTCTAACTTGCTGAGAACGTCA
LPA1 genotyping (Gene specific)	TAGTTCCTGTGGTATGGGGTG	TCTTCTCTTCCAACGACCATG
LPA1 genotyping (Gene specific and TDNA)	TAGTTCCTGTGGTATGGGGTG	AACGTCCGCAATGTGTTATTAAGTTGTC
MET1-1 genotyping (Gene specific)	GGACAATGTACACAATTCGTCAG	TTTCTTGTTAAAGCCAAACAAGGAT
MET1-1 genotyping (Gene specific and TDNA)	GGACAATGTACACAATTCGTCAG	TAGCATCTGAATTTCATAACCAATCTCGATACAC
MET1-2 genotyping (Gene specific)	TTTCTTGTTAAAGCCAAACAAGGAT	GGACAATGTACACAATTCGTCAG
MET1-2 genotyping (Gene specific and TDNA)	TTTCTTGTTAAAGCCAAACAAGGAT	TGATCCATGTAGATTTCCCGGACATGAAG
psaD RT-PCR	GCCGAGAAAACAGAGTCCTCCTC	CAAATCATAAGATTGTTTCCCA
psbC RT-PCR	GGAGCTCATG TAGCCCATG	GTTAAGAGGAGTCATGGAAAG
psbA RT-PCR	GAGAGACGCGAAAGCGAAAG	TCCATTTGTAGATGGAGCCTCA
petB RT-PCR	GTAGCTACGGGATTTGCTATGACT	TAAGGGACCAGAAATACCTTGCTT