Fig. S1. Amino acid sequences alignment and Neighbor-joining phylogenetic tree of mTERF27 ortholog genes in plants.

(A) Amino acid sequences alignment of mTERF27 ortholog genes in plants.
(B) Neighbor-joining phylogenetic tree of Fig. S1A. Numbers on the nodes refer to bootstrap support values.

Species abbreviations are Achn, Actinidia chinensis; AH, Amaranthus hypochondriacus; ATR, Amborella trichopoda; AL, Arabidopsis lyrata; Araip, Arachis ipaensis; AT, Arabidopsis thaliana; Bv, Beta vulgaris; Bo, Brassica oleracea; Brara, Brassica rapa; C.cajan, Cajanus cajan; Carub, Capsella rubella; CAN, Capsicum annuum; Cpa, Carica papaya; AUR, Chenopodium quinoa; Ca, Cicer arietinum; Cla, Citrullus lanatus; Ciele, Citrus clementina; Cc, Coffea canephora; COL, Corchorus olitorius; MELO, Cucumis melo; Cucsa, Cucumis sativus L.; DCAR, Daucus carota; Migut, Erythranthe guttata; Eucgr, Eucalyptus grandis; FVE, Fragaria vesca; Glyma, Glycine max; Gorai, Gossypium raimondii; HBR, Hevea brasiliensis; MDO, Malus domestica; Manes, Manihot esculenta; Mapoly, Marchantia polymorpha; Medtr, Medicago truncatula; NNU, Nelumbo nucifera; Os,
Oryza sativa ssp. japonica; Peaxi, Petunia axillaris; PAB, Picea abies; Potri, Populus trichocarpa; Prupe, Prunus persica; Pbr, Pyrus bretschneideri; RCO, Ricinus communis; Tp, Schrenkia parvula; SMO, Selaginella moellendorffii; Solye, Solanum lycopersicum; PGSC, Solanum tuberosum; THA, Tarenaya hassleriana; TCA, Theobroma cacao; TPR, Trifolium pratense; UGI, Utricularia gibba; Vradi, Vigna radiata var. radiata; GSVIV, Vitis vinifera; Zm, Zea mays; and ZJU, Ziziphus jujuba. Integrative orthologs data of mTERF27 was from PLAZA.
Fig. S2. Sequences the transfer DNA (T-DNA) insertion point in the mterf27 mutant.

(A) Structure of Arabidopsis mTERF27 showing the T-DNA insertion site in the mterf27 mutant. LP and RP indicate the forward and reverse PCR primers, respectively. LB1, plasmid primer.

(B) PCR amplifications confirming the presence of the T-DNA insertion site in the mterf27 mutant. gDNA, genomic DNA.

(C) The T-DNA sequence in mterf27.
Fig. S3. Chlorophyll fluorescence analysis of the wild-type (WT) and mterf27 plants shown in Fig. 2D.
mTERF27-complemented lines (Com1 and Com2). $F_m$, maximal fluorescence; $F_o$, minimal fluorescence; $F_v/F_m$, maximum efficiency of PSII photochemistry; NPQ, non-photochemical quenching.
Fig. S4. Negative controls for the yeast two-hybrid assay used to determine protein interactions in Fig. 4A.
### Table S1. Primers used in this study.

| Names       | Primers                                                                 |
|-------------|-------------------------------------------------------------------------|
| mTERF27-F   | ATGTCGAGCTTTATTACACTGTGTAGAAATGTTC                                       |
| mTERF27-R   | TCATCGATTACTTGTATAAGGTGGTGTAAGGT                                       |
| LP          | CTCGTCATAGGCAGCTCTTC                                                    |
| RP          | ATTCACTCGTGCAATCAAAGG                                                    |
| LB1         | GCCTTTTCAGAAATTGATATAATACCTGTTC                                        |
| mTERF27-BP-F| GGGGACAAGTTTTGTACAAAAAAGGCAGGCTCTA                                     |
| mTERF27-BP-R| TGTCGAGCTTTATTACACTGTTC                                                 |
| mTERF27-qPCR-F | ACCATGCTTTCACCAATGACCA                                                  |
| mTERF27-qPCR-R | TACATCTTTCGGGGCTACGTGC                                                  |
| MORF1-BP-F  | GGGGACAAGTTTTGTACAAAAAAGGCAGGCTCTA                                     |
| MORF1-BP-R  | GCCTTTTCAGAAATTGATATAATACCTGTTC                                        |
| MORF3-BP-F  | GGGGACAAGTTTTGTACAAAAAAGGCAGGCTCTA                                     |
| MORF3-BP-R  | CACTGGGCTTTGTTCGA                                                      |
| MORF4-BP-F  | GGGGACAAGTTTTGTACAAAAAAGGCAGGCTCTA                                     |
| MORF4-BP-R  | GCATGTGTTCTTCTTCCTGC                                                   |
| MORF5-BP-F  | GGGGACAAGTTTTGTACAAAAAAGGCAGGCTCTA                                     |
| MORF5-BP-R  | GCATGTGTTCTTCTTCCTGC                                                   |
| MORF6-BP-F  | GGGGACAAGTTTTGTACAAAAAAGGCAGGCTCTA                                     |
| MORF6-BP-R  | GCATGTGTTCTTCTTCCTGC                                                   |
| MORF8-BP-F  | GGGGACAAGTTTTGTACAAAAAAGGCAGGCTCTA                                     |
| MORF8-BP-R  | GCATGTGTTCTTCTTCCTGC                                                   |
| mTERF27-GFP-F | CGGGATCCATGTGAGAGCTTATTACACTGTAGA                                      |
| mTERF27-GFP-R | ATGTCGAGCTTTATTACACTGTTC                                                 |
|        |                     |                     |
|--------|---------------------|---------------------|
| mTERF27-LUC-F | GCGTCGACATGTCGAGCTTATTACACTGTAGA AATGTC |                     |
| mTERF27-LUC-R | GCGTCGACTCATCGATTACTTTGTAAAGGGTTGTAGT |                     |
| MORF8-LUC-F   | GGGGTACCATGGCGACGCATACCATTCTTC |                     |
| MORF8-LUC-R   | GGACTAGTACCCTGGTAGGGGTTGCC |                     |
| MEF13-LUC-F   | GCGTCGACATGGCGGAGAGTCTCAGATTAT |                     |
| MEF13-LUC-R   | GCGTCGACGCAGTAACACCATTGGTTGCC |                     |
| MORF1-LUC-F   | GGGGTACCATGGCTATGATATCTCACCGTCTC |                     |
| MORF1-LUC-R   | GGACTAGTATGCTGAGGATATCAAAAAAG |                     |