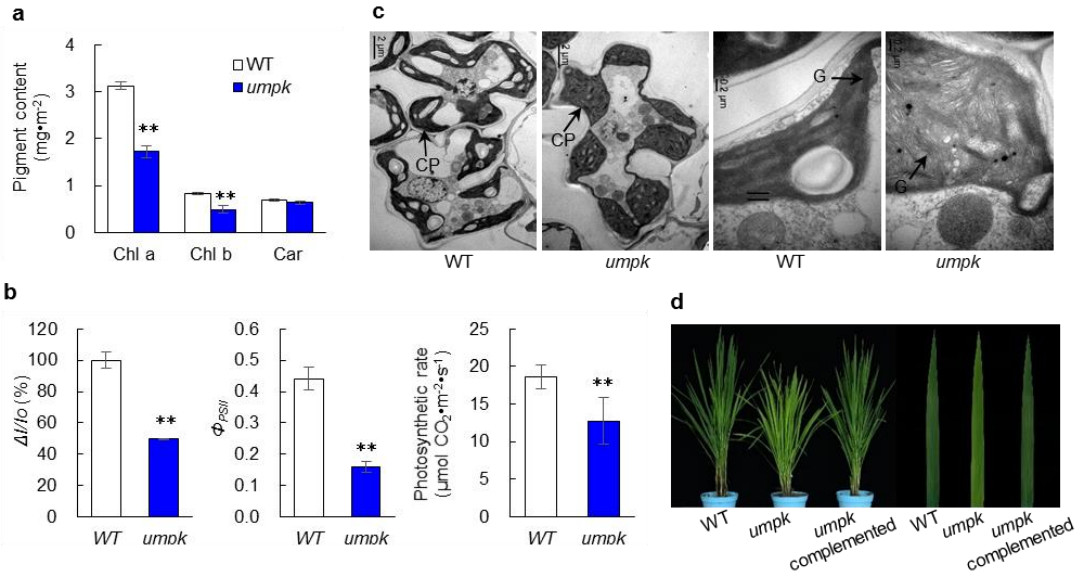


**Figure S1.** Phenotypic characterization of WT, the *umpk* mutant, and the transgenic plants. (**a**) Concentrations of chlorophyll (Chl) and carotenoid (Car) in WT and the mutant. (**b**)The light-induced P700 absorbance changes at 820 nm (*ΔI/Io*), the actual quantum efficiency (*ΦPSII*), and photosynthetic rate of WT and the mutant. (**c**) Transmission electron microscope analysis of WT and the mutant. CP, chloroplast; G, grana. (**d**) (**b**) Phenotypic complementation of the *umpk* mutant by introducing of the *UMPK* gene of WT. Data represent means ± sd ($n = 5$). Significant difference according to the Student's t test at * $P < 0.05$ and ** $P < 0.01$.

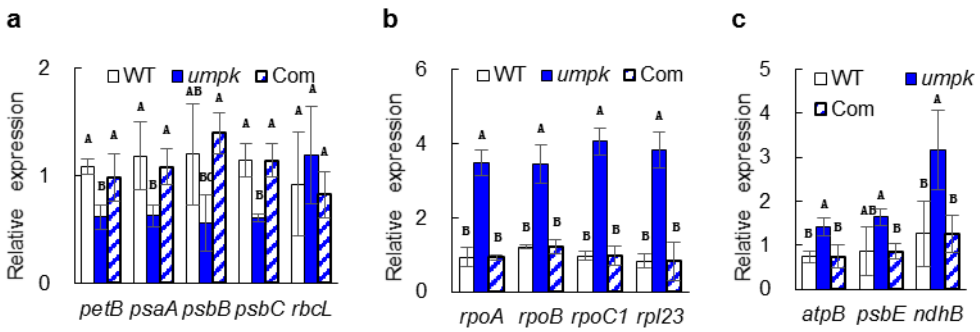


**Figure S2.** Expression of plastid genes in the complementation lines (Com) and the *umpk* mutant. (**a**) Plastid-encoded RNA polymerase (PEP)-dependent genes. (**b**) Nucleus-encoded RNA polymerase (NEP)-dependent genes. (**c**) Both PEP- and NEP-dependent genes. The *Actin1* was used as an internal control. Data represent means ± sd ($n$ = 3). Bar with different letters are significantly different at $P < 0.01$ based on Duncan's multiple range tests.

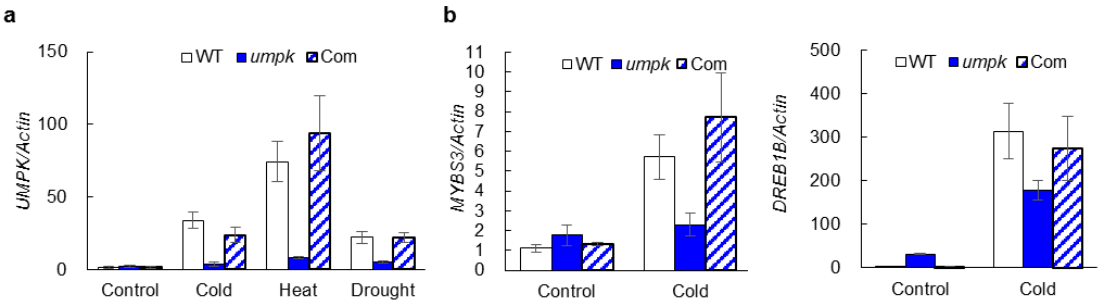


**Figure S3.** Response of *UMPK* to abiotic stresses in WT, the mutant, and the complementation lines. (**a**) Expression levels of *UMPK* under various stress treatments. (**b**) Expression levels of two cold inducible genes under control and cold conditions. $n = 3$, *Actin1* was used as the internal control. Data represent means ± sd.

Table S1 Primers used in this study.

| Name | Forward primer (5'-3') | Reverse primer (5'-3') |
|---|---|---|
| **Fine-mapping** | | |
| D1 | GCGTGCTTTTGATCCGTTG | TGCTCCCGGACGTACACTC |
| D2 | TGGGTACTGTAGCTCATTGTC | CCTTCCGTAAACTTGATCGTC |
| D3 | ATGCAACTTTGGTGATTTGGAA | AAAATGATTAGCCACCCACAT |
| D7 | TTACAATTATTAGCCACCACTTC | ATTACGAGCATTACTTGTGTA |
| Q1 | TCACAGGTAGACTGGTAGTGTTT | GTATGTTTCGTGCGGTAACTT |
| Q3 | ATTCCTCAATTACTTCTATCAGC | CATCATCAGTGAGTTGGGTA |
| Q4 | AGGAAACTAAATAAAGCGACAC | TGCACGGTTGTTATTGGCAC |
| Q5 | ATGAAATGCTCACTTACGTCT | TCCCAATTGCAAAATTACACATT |
| **Vector construction** | | |
| Complementation | CGGTACCCGGGGATCCCGGACTCCCA | CCAAGCTTGCATGCCTGCAGAGAACAATC |
| | GATACGCAAC | CGAAGCACGAGA |
| **Real-time PCR analysis** | | |
| UMPK | GATTACATTGGCATGTTGGCTAC | CTGCATTGATTTCTGCACAACG |
| OsNDPK2 | CTTTTTCAGTGCCCCAAGGA | TCGATCAGACCGGGAAAGAA |
| psaA | GCGAGCAAATAAAACACCTTTC | GTACCAGCTTAACGTGGGGAG |
| psbB | TAGTTTCTGGTTGGGCTGGCTC | CTCCAACCACCCCACGAATTG |
| psbC | GTTCCCCAACGGGAGAGGTTAT | GAGCCTAAAGGAGCATGGGTCAT |
| petB | TTCAGACCTCGCAACCAGACTG | AACAAAAGGCAAGGGTTCTTCGA |
| rbcL | CTTGGCAGCATTCCGAGTAA | ACAACGGGCTCGATGTGATA |
| rpoA | CGTGGGTTCTGTCAAGTTAGCTATAG | GGTCCTAGATACATAACTGCCCAAGA |
| rpoB | CGAGATATCCATCCGAGTCACTATG | GCTAAAGATCCAGTAAGTCCAACGT |
| rpoC1 | AATCTCCTATCTCCCGCTATTGG | CAATCGTTAATACATAAAGTCCGATAAGC |
| rpl23 | GGGTCGAACTCTTCTTTGGTGTT | GGGCCCATTCTTCTACCCTTT |
| atpB | TCGCAATTCTTGGGTTGGATGA | CAACATACTTTCCCGGAGAACCG |
| ndhB | GCGCTTATATCCATCACTGTAGGAC | CACTCCTTCGTAGACGTCAGGA |
| psbE | TGTCTGGAAGCACGGGAGAACGT | GTTTGGCCGAGGACTTCCAAACAC |
| MYBS3 | CCTTTCTGGCAAAATCAGAAAGA | ATGAACTGGAACAGGCTTGACA |
| DREB1B | AGCTCGCCGGCTCCGACA | GGGAGAAATCTGGCACATTCC |