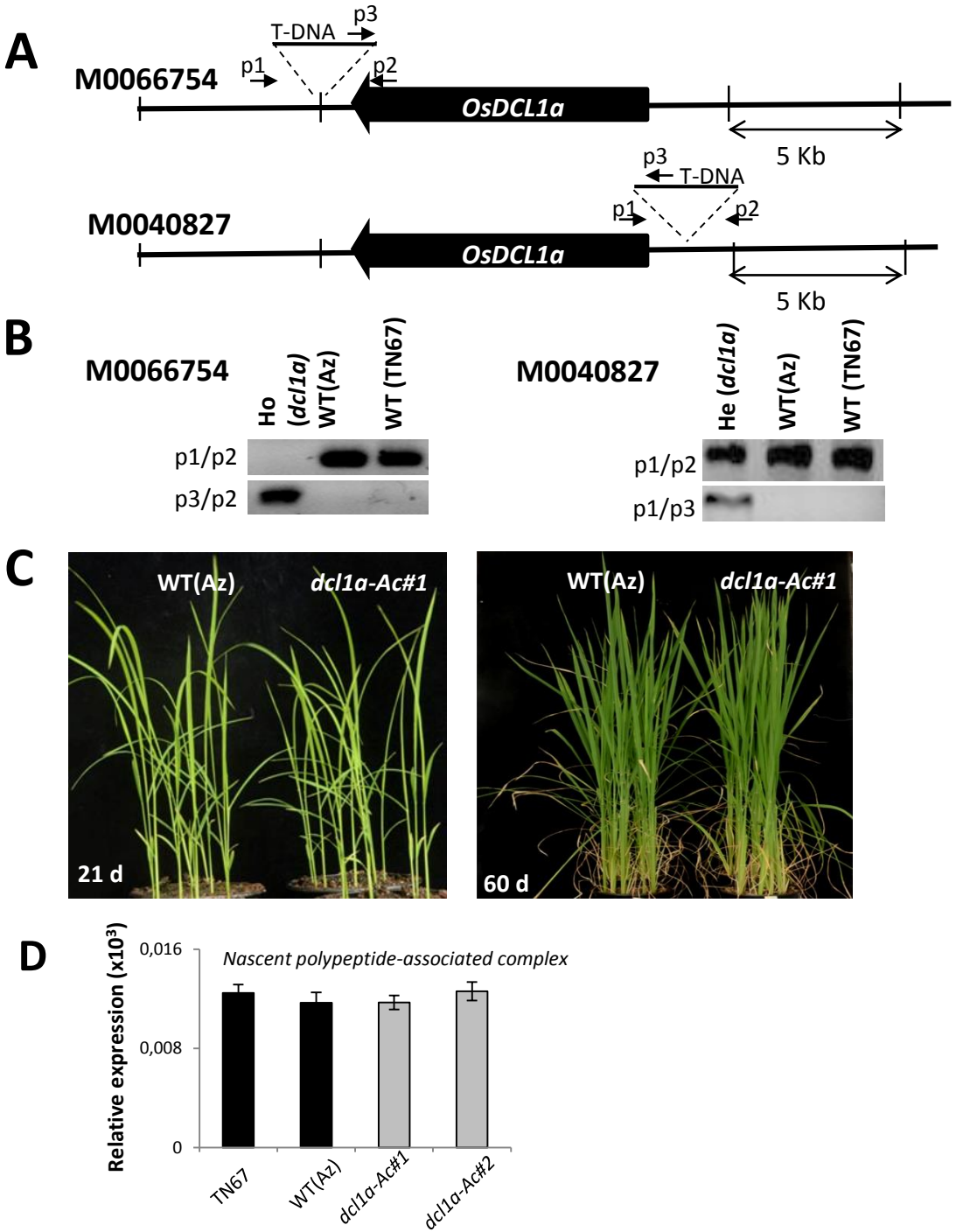

Fig. S1. Analysis of *OsDCL1a-Ac* mutant plants. (A) Schematic representation of the T-DNA insertion rice mutants (TRIM collection, M0066754 and M0040827 mutants). The position of primers used for the analysis of T-DNA integration is shown (p1, p2, p3). (B) PCR-amplified DNA fragments for homozygous (Ho), hemizygous (He) and azygous (Az, segregated) plants. The nucleotide sequence of the amplification fragments was confirmed. (C) Appearance of wild-type (segregated azygous plants) and *dcl1a-Ac* plants at the indicated developmental stages. (D) Accumulation of *Nascent polypeptide-associated complex* transcripts in *dcl1a-Ac* plants. Differences were not statistically significant (ANOVA test).

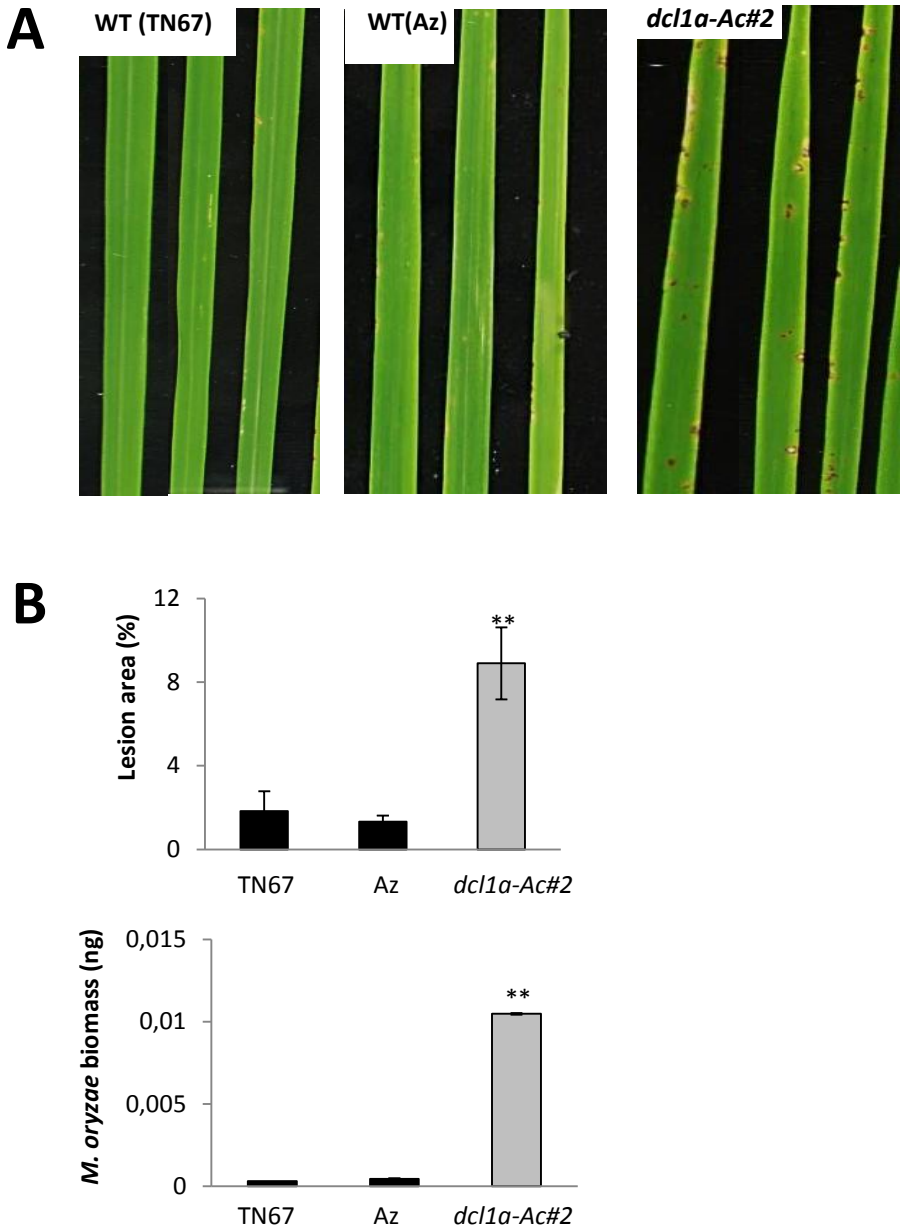

Fig. S2. Susceptibility of *dcl1a-Ac#2* plants to infection by the fungal pathogen *M. oryzae*. (A) Disease symptoms at 7 days post-inoculation (dpi) with *M. oryzae* spores (1 x 10^5 spores/ml). (B) Lesion area of *M. oryzae*-infected leaves and quantification of *M. oryzae* DNA by qPCR, at 7 dpi. (**, $p \leq 0.01$ by ANOVA).

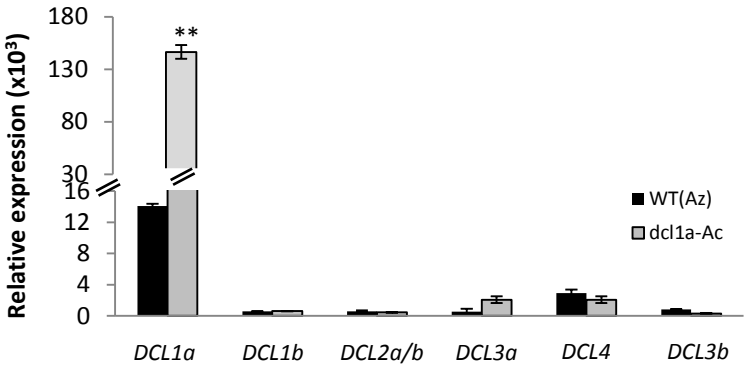

Fig. S3. Expression of *OsDCL* genes in wild-type and *dcl1a-Ac* plants grown under normal conditions. The expression of *OsDCL1a* (Os03g02970), *OsDCL1b* (Os06g25250), *OsDCL2a/b* (Os03g38740/Os09g14610), *OsDCL3a* (Os01g68120), *OsDCL4* (Os04g43050) and *OsDCL5* (Os10g34430) was examined by RT-qPCR. Data are mean ± SD of 3 biological replicates, each with 12 plants per genotype. (**, $P \leq 0.01$ by ANOVA). Except for *DCL1a*, no significant differences were observed in the expression of other *OsDCL* genes between wild-type and *dcl1a-Ac* plants.

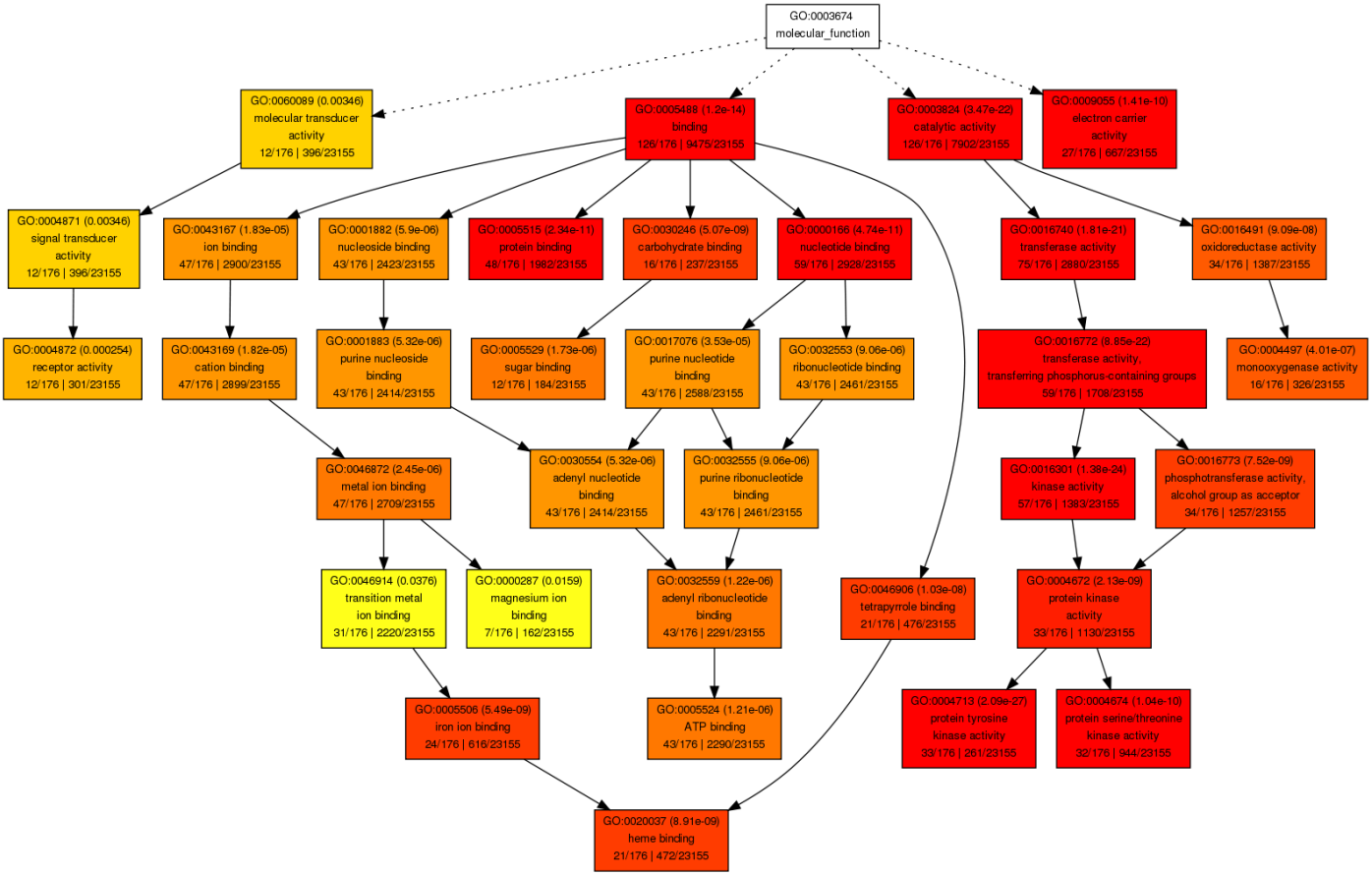

Fig. S4. Distribution of differentially expressed genes in *dcl1a-Ac* plants (*Osdcl1a-Ac#1* mutant) according to their molecular function determined by using AgriGO. The following parameters were used: (1) Fisher's exact test with Bonferroni multiple comparison correction; (2) significance level $\alpha = 0.05$, and the *Oryza sativa* NCBI database

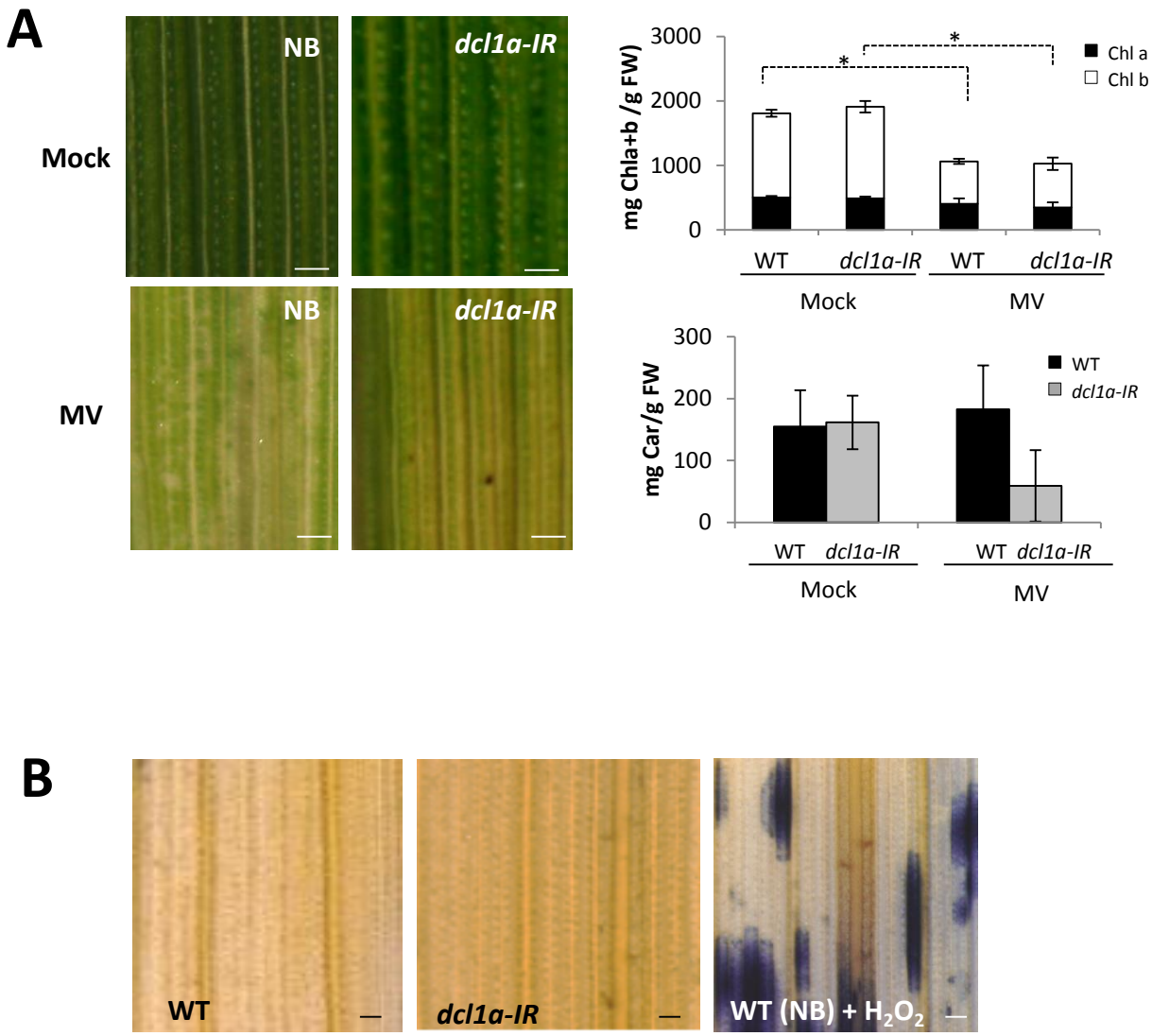

Fig. S5. Effect of methyl viologen on chlorophylls and carotenoids, and detection of $O_2^{\bullet-}$ in *dcl1a-IR* plants. (A) Leaves of 3-week-old knock-down *DCL11a* (*dcl1a-IR)* and wild-type (Nipponbare) plants were treated with methyl viologen (MV) for 72 h. Right panels: quantification of chorophyls (Chla+Chlb) and carotenoids (Car) in mock-inoculated and MV-treated wild-type and *dcl1a-IR* plants. Data shown correspond to wild-type and *dcl1a-IR* plants (*, $P \leq 0.05$ by ANOVA). (B) Detection of superoxide ion ($O_2^{\bullet-}$) by nitroblue tetrazolium (NBT) staining in leaves of wild-type and *dcl1a-IR* plants. As a control, leaves were treated with H_2O_2 for 6 h. Bars = 250 µm.

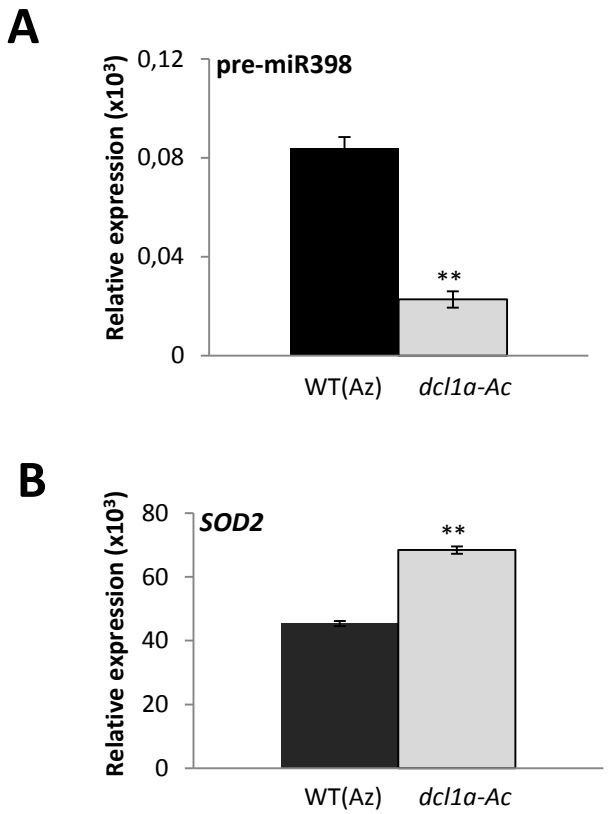

Fig. S6. Accumulation of miR398 precursor (A) and miR398-targeted *OsSOD2* (Os07g46990) transcripts (B). Transcript levels were determined by RT-qPCR (**, $P \leq 0.01$ by ANOVA).