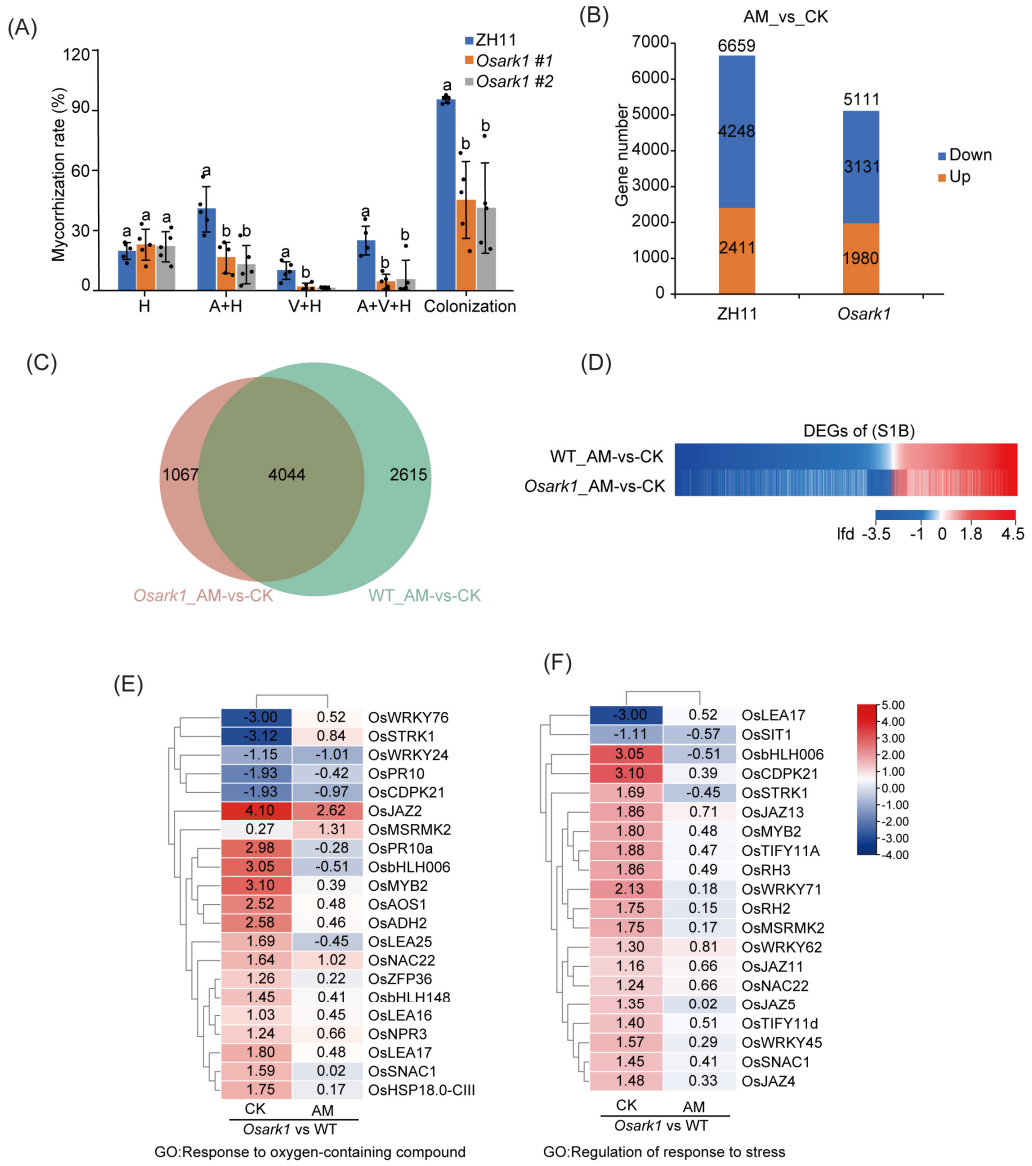


Figure S1. Analysis of differentially expressed genes (DEGs) between *Osark1* and ZH11 under AM fungi treatment. (A) Mycorrhization rate of ZH11 and *Osark1* mutant lines at 6 wpi. The percentage of different fungal structures in colonized roots as indicated were counted. Error bars represent mean ± SD (n = 5 biological replicates, four plants per pot served as a biological replicate). One-way ANOVA followed by Tukey's HSD test was utilized ($p < 0.05$). Different letters indicate significant differences. (B) Numbers of genes upregulated and downregulated by AM fungi in ZH11 or *Osark1* compared to the mock treatment. (C) Venn diagram of DEGs induced by AM fungi in ZH11 and *Osark1* compared to mock treatment. (D) Hierarchical clustering of all DEGs ($|\log_2$ fold change$| > 1$, adjust $p < 0.05$) in ZH11 and *Osark1* treated with AM fungi relative to mock treatment. (E)-(F) Heatmap showing the fold change of genes associated with the GO terms "Response to oxygen-containing compound" and "Regulation of response to stress" identified in the enrichment analysis shown in (Figure 1E).

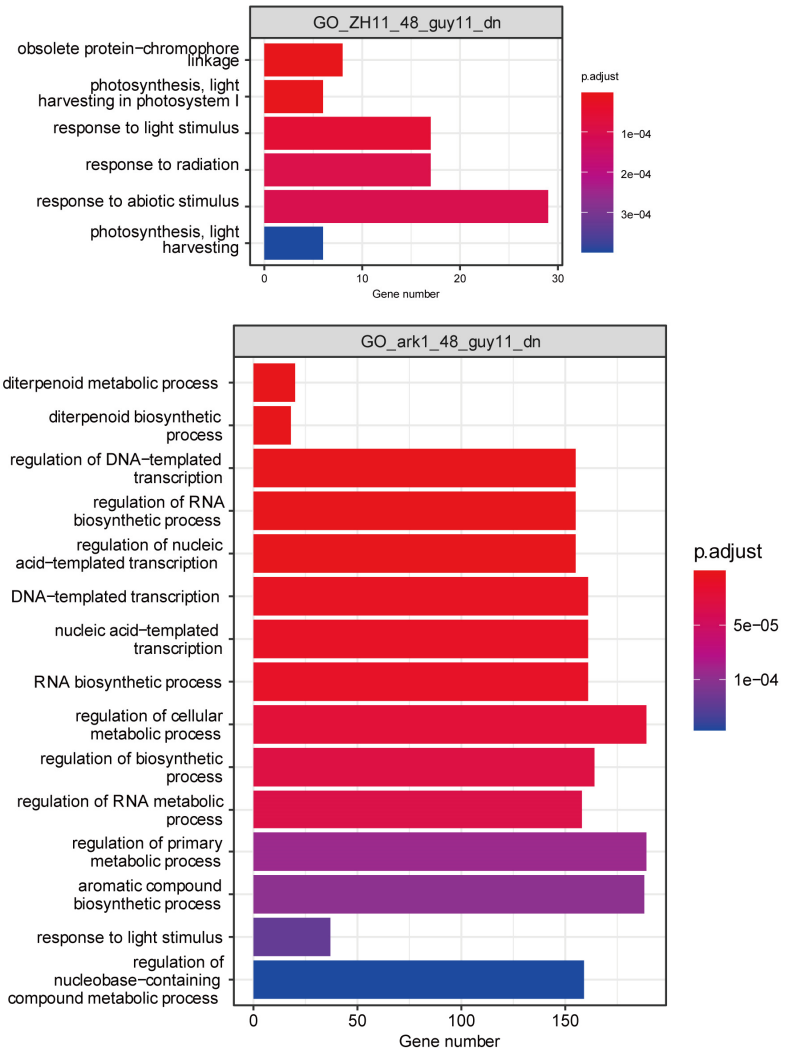


Figure S2. GO term enrichment analysis of all DEGs in ZH11 and *Osark1* treated with the *M. oryzae* at 48 hpi.