Supporting Information

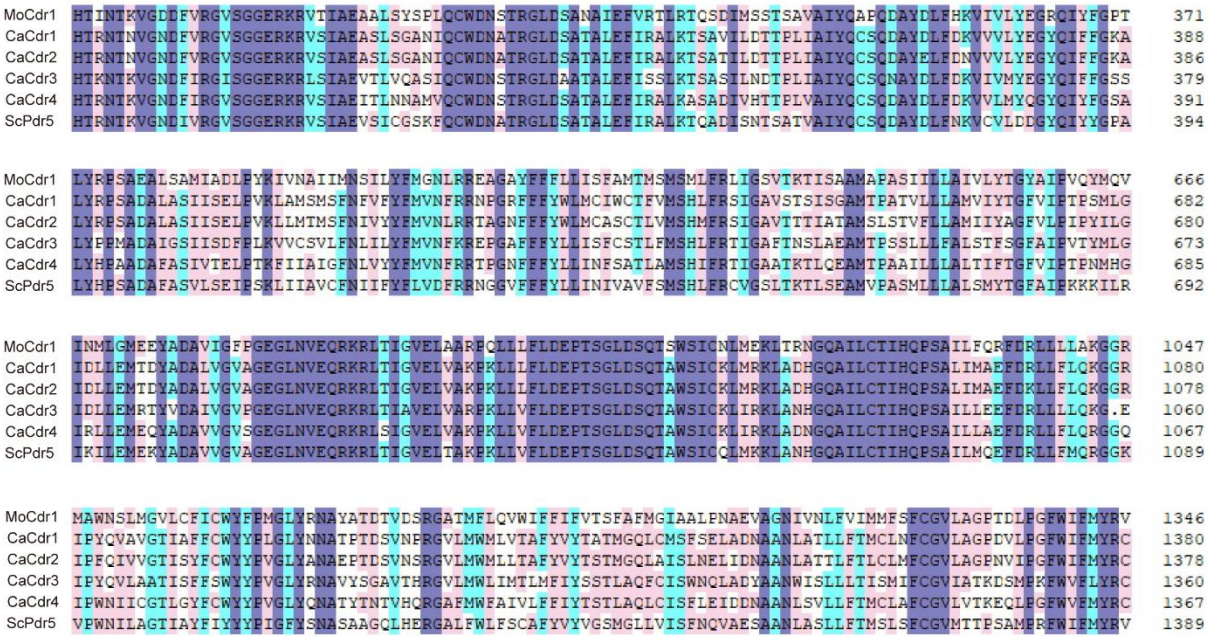

Fig. S1 Alignment of Cdr1 homologues in *M. oryzae*, *S. cerevisiae*, *C. albicans* using DANMAN software, and the sequences are from BLAST search using the MoCdr1 sequences in NCBI.

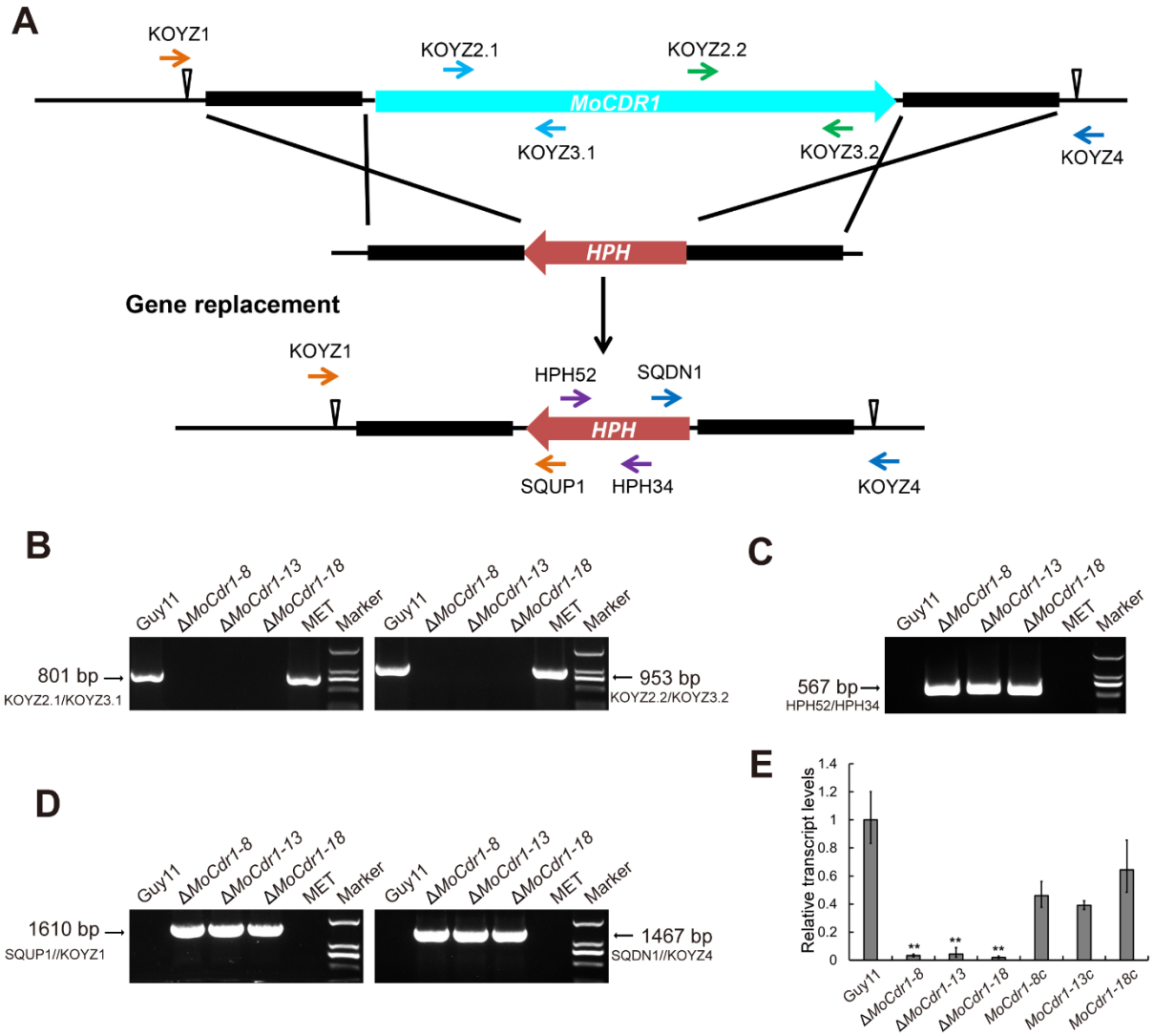

Fig. S2 Knockout of *MoCDR1* in *M.oryzae*. (**A**) The diagram shows the targeted gene replacement strategy. *MoCDR1* was replaced by the hygromycin-resistance gene (*HPH*) fused into the p1300 vector. Another 4 ABCG-1 genes were performed with a similar strategy. (**B-D**) The mutants were confirmed by using multiple PCR. Two pairs of primer sets (KOYZ2.1/KOYZ3.1 and KOYZ2.2/KOYZ3.2) were used to amplify fragments of the targeted gene in transformants. The primer set (HPH52/HPH34) was used to clone the fragment of *HPH* in mutants. Two pairs of primer sets (KOYZ1/SQUP1and SQDN1/KOYZ4) were used to amplify the recombinational DNA fragments in mutants. (**E**) The quantitative RT-PCR was used to test the relative transcript levels of the *MoCDR1* in the wild type Guy11, Δ*Mocdr1* mutants and the complement strains. Asterisks indicate statistically significant differences between Guy11 and Δ*Mocdr1* (**$P < 0.01$).

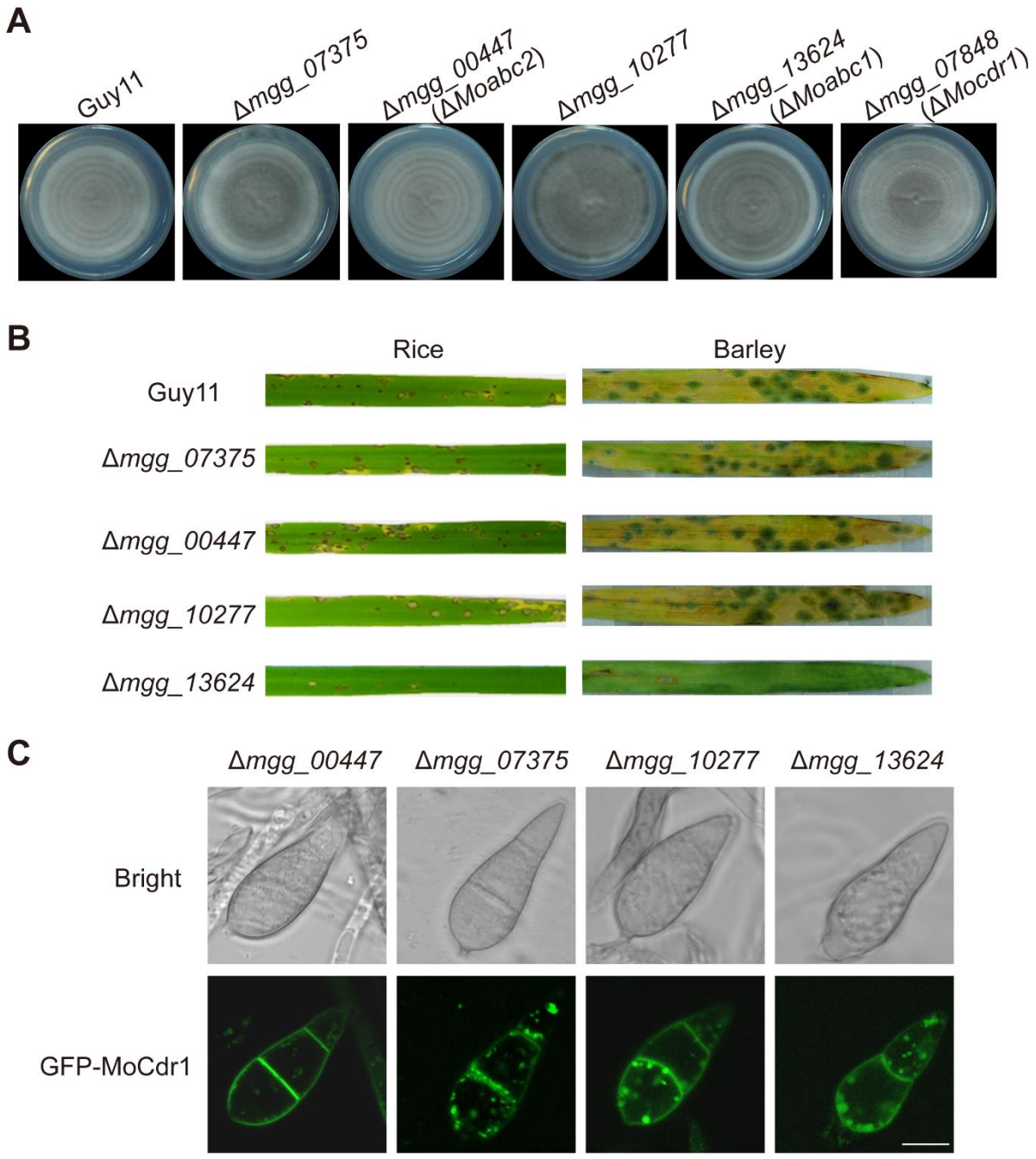

Fig. S3 The colonial morphology and pathogenicity of the ABCG-1 mutants in *M.oryzae*. (**A**) The wild type Guy11 and ABCG-1 mutants were cultured on CM for 9 days. (**B**) The pathogenicity of Guy11 and ABCG-1 mutants were test by spray-inoculated on the rice and barley leaves. (**C**) The deletion of the other 4 ABCG-1 did not affect the localization of MoCdr1. Bar = 5 μm.

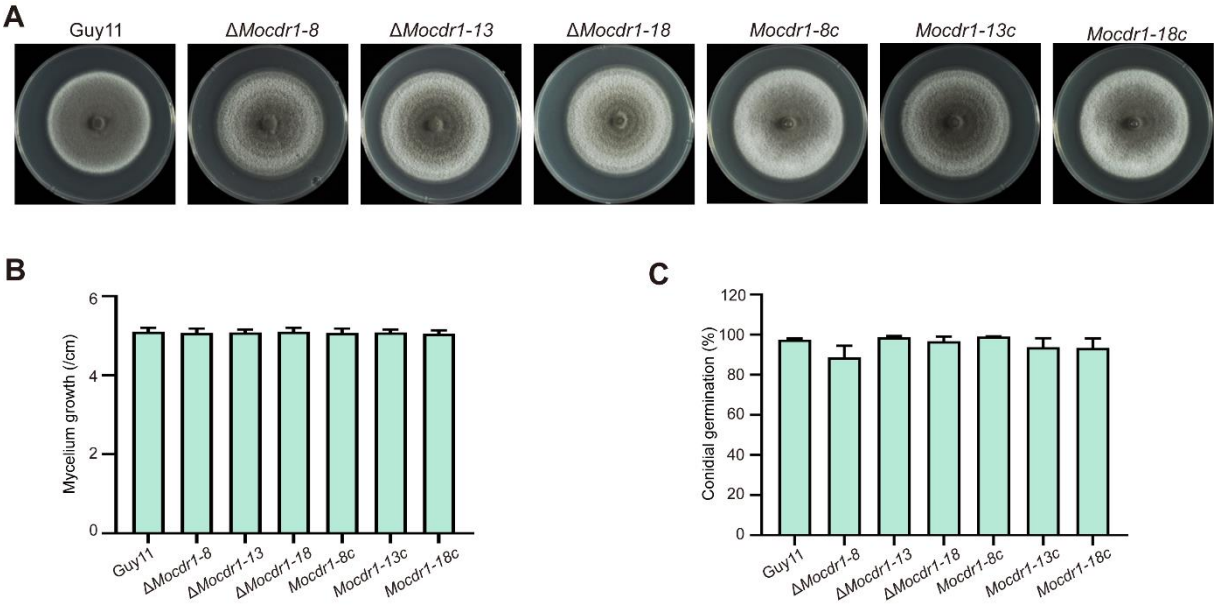

Fig. S4 The growth and conidial germination of Δ*Mocdr1* mutants. (**A**) The colony morphology of the wild type Guy11, Δ*Mocdr1* mutants and the complement strains in CM for 9 days. (B) The mycelial diameters of Guy11, Δ*Mocdr1* mutants and the complement strains when cultured on CM for 9 days. (**C**) The conidial germination rate of Guy11, Δ*Mocdr1* mutants and the complement strains at 4 h post incubation.

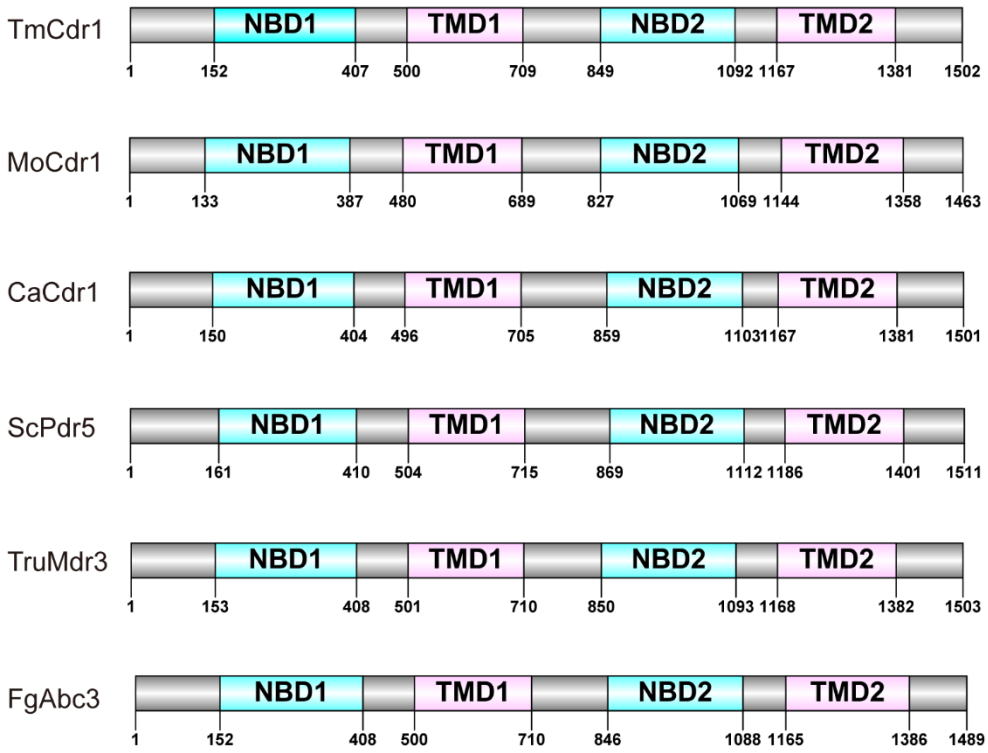

Fig. S5 The sequence structures of TmCdr1, MoCdr1, CaCdr1, ScPdr5, TruMdr3, FgAbc3 proteins. Blue boxes were ATP-binding domains (NBDs), and pink boxes were transmembrane domains (TMDs).

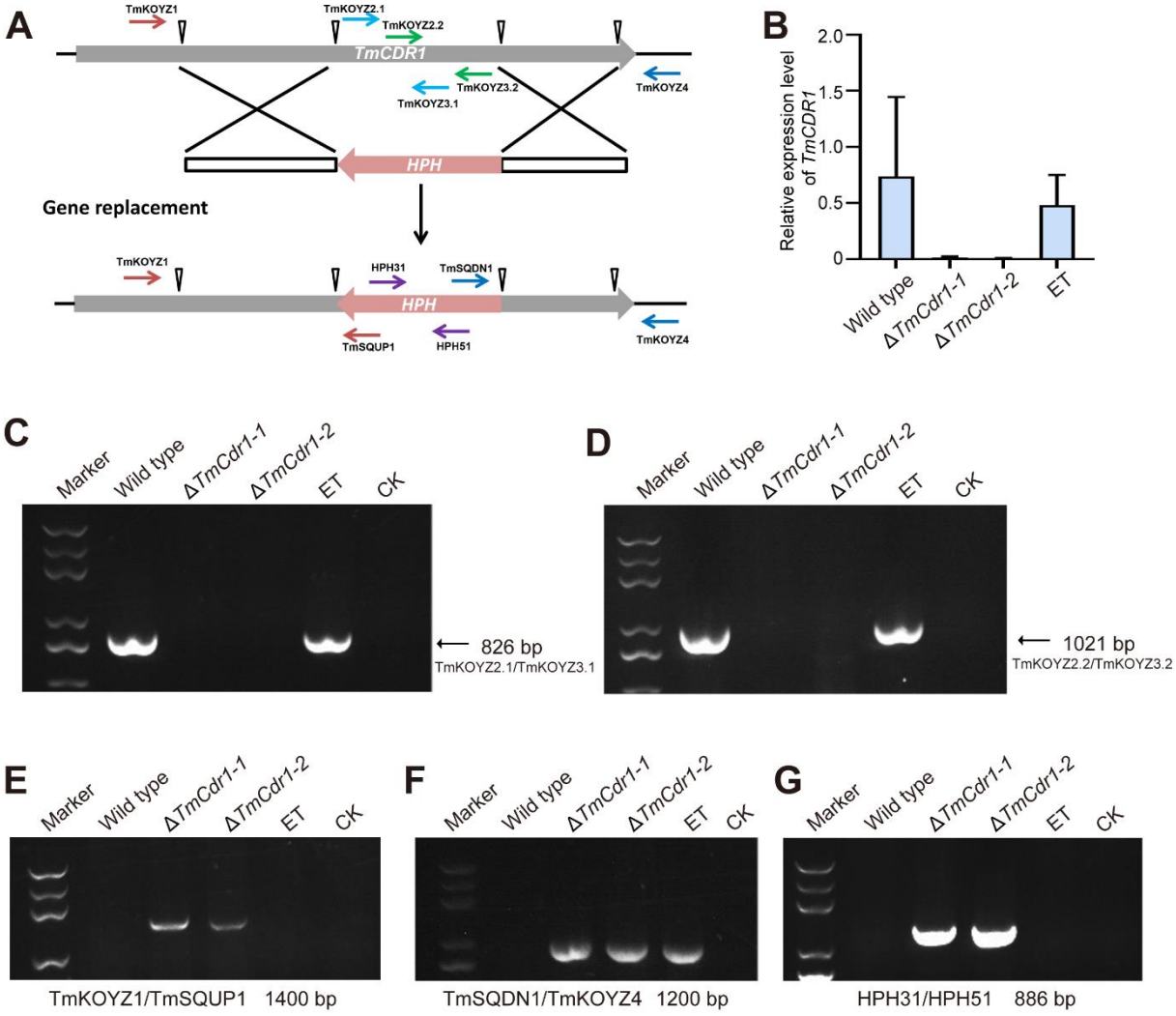

Fig. S6 Knockout of *TmCDR1* in *T. mentagrophytes*. (**A**) The diagram shows the targeted gene replacement strategy. *TmCDR1* was replaced by the hygromycin-resistance gene (*HPH*) fused into the p1300 vector. (**B**) The quantitative RT-PCR was used to test the relative transcript levels of the *TmCDR1* in the wild type ZJA-1, Δ*Tmcdr1* mutants and an ectopic transformant (ET). (**C-G**) The mutants were confirmed by using multiple PCR. Two pairs of primer sets (TmKOYZ2.1/TmKOYZ3.1 and TmKOYZ2.2/TmKOYZ3.2) were used to amplify fragments of the targeted gene in transformants. Two pairs of primer sets (TmKOYZ1/TmSQUP1and TmSQDN1/TmKOYZ4) were used to amplify the recombinational DNA fragments in mutants. The primer set (HPH31/HPH51) was used to clone the fragment of *HPH* in mutants.

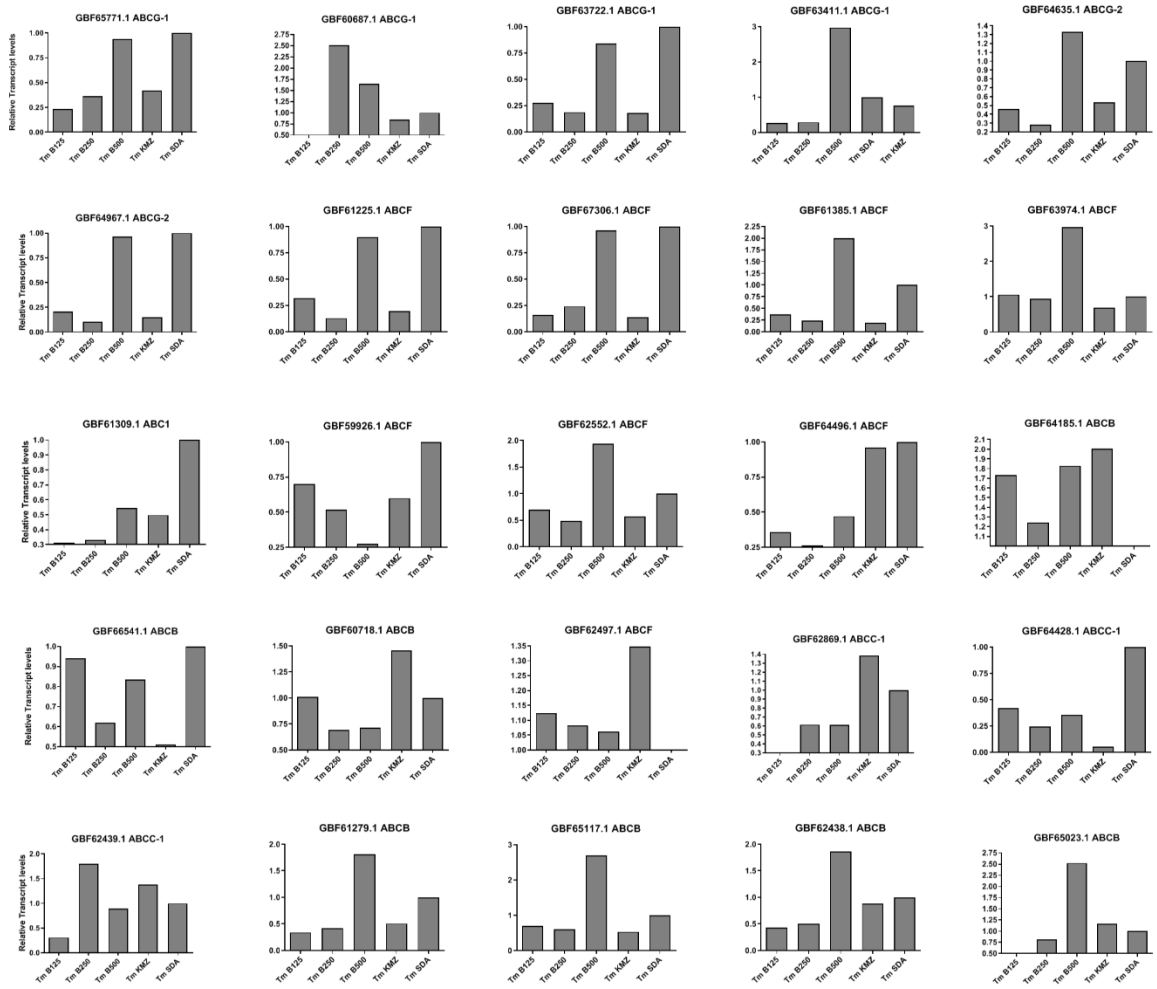

Fig. S7 The relative transcript levels 25 ABC genes in *T. mentagrophytes* were tested by quantitative RT-PCR upon the induction of berberine in 125, 250 and 500 μg mg^{-1}(B125, B250 and B500) or clotrimazole (CMZ) in 0.1 μg ml^{-1}. The 18S rRNA gene was as internal reference gene and the transcription levels on SDA were defined as one for each gene. The identifier numbers of the genes and the subfamilies were marked.

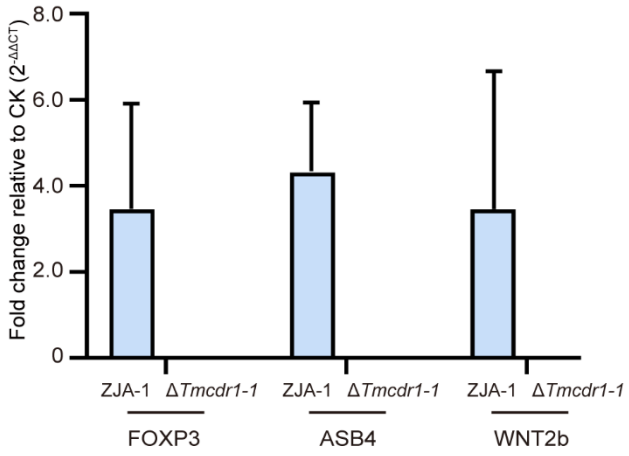

Fig. S8 The relative transcripts of FOXP3, ASB4, WNT2B in mouse macrophages treated with wild type and Δ*Tmcdr1* strains compared with untreated mouse macrophages.

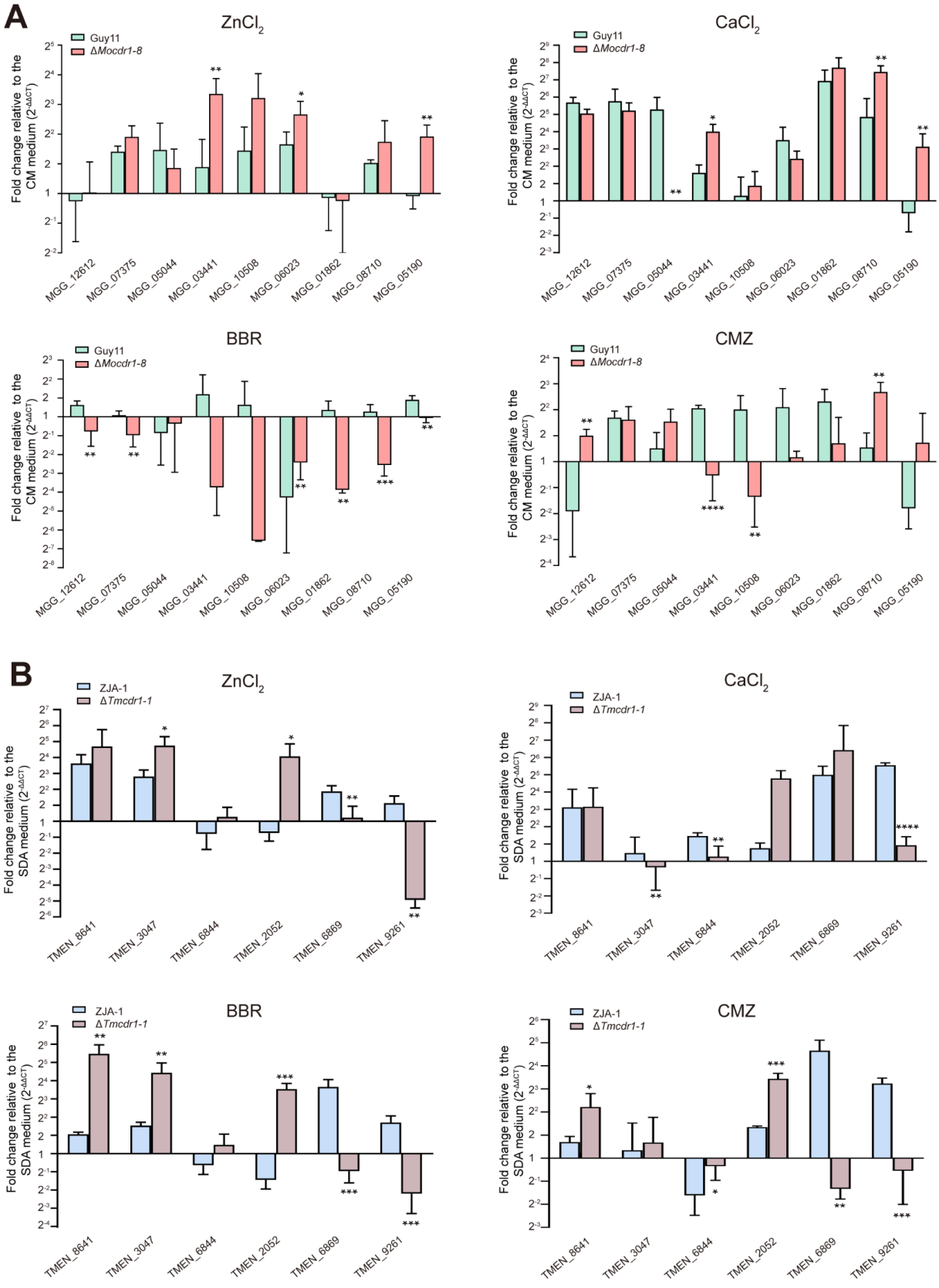

Fig. S9 Relative expression levels of transport genes in response to different drugs. (A) After the wild type Guy11, Δ*Mocdr1-8* mutant cultured in CM medium and CM containing 0.5 mg/mL $ZnCl_2$, 18 mg/mL $CaCl_2$, 100 μg/mL berberine (BBR) and 50 ng/mL clotrimazole (CMZ) for 8 days, total RNAs were extracted from hyphae samples, and qRT-PCR was performed to obtain transporter gene expression levels. (B) After the wild type ZJA-1, Δ*Tmcdr1-1* mutant cultured in SDA and SDA containing 1.6 mg/mL $ZnCl_2$, 50 mg/mL $CaCl_2$, 0.5 mg/mL BBR and 0.1 μg/mL CMZ for 8 days, total RNAs were extracted from hyphae samples, and qRT-PCR was performed to obtain transporter gene expression levels**.**