

Figure S1. Structures of FpRtfA/FpRtfA and Homologyhomology comparison between *F. pseudograminearum* and *A. nidulans*. (A) The FpRtfA gene consists of 2031-bp, interrupted by three intron, and encodes a predicted protein of 597 amino acids with a Plus-3\_dom domains. (B) Phylogenetic analysis of FpRtf of *V. mali* and its homologs from other fungi. The amino acid sequences were analyzed by using MEGA 6 with Neighbor-neighbor-joining analysis with 1,000 bootstrap replicates. Numbers on the branches represent the percentage of replicates supporting each branch. The bar represents 20% sequence divergence.

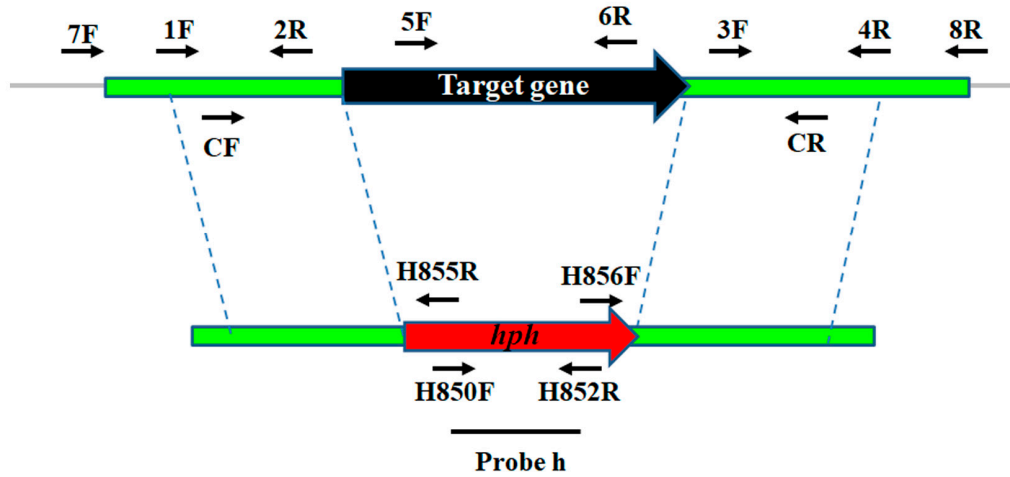


Figure S2. Gene deletion schematic of *FpRtfA*. The double-joint method was used to generate the replacement of *FpRtfA* gene. The small arrows sign the directions and positions of primers used for amplifying recombinant fragment and detecting target gene.

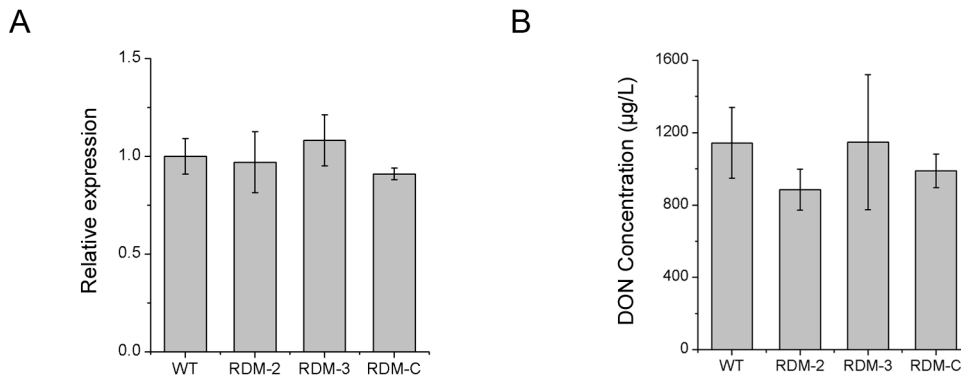


Figure S3. Transcription level of *TRI5* gene and DON concentration in inducing medium. (A) Relative transcript abundances of *TRI5* gene in mycelium at inducing medium were compared between the wild-type and *FpRtfA* mutants at 7 dpi. Expression level of *TUB* gene was used to normalize different samples. Transcript levels of wild type were arbitrary given assigned to 1. (B) DON concentration of culture solution at inducing medium. The mean and standard deviation were calculated with data from three independent biological replicates.