

B

		1	10	20	30	40	50	60
AnrtfA	XP_662174.1	MADLLDAELTALAGDDASSEDETSPFRKHTSASPQASASFRSPEFTSTMGKKNAPAR						
FpRtfA	XP_009254491.1	MSDVEDDLALAGR..SSDDEGSDNFSRRGSASPPVKRSGSKREHGSKARRGGDDSE						
		70	80	90	100	110		
AnrtfA	XP_662174.1	RSRKSRRDDEEEDGEISADSLNSASMSSEAPSD.SESSDAAGVDEEGPIYPYKLYHSA						
FpRtfA	XP_009254491.1EEGEASSAPGTPNSLESPMDESDSDAEP.SRGRAAAADDDEDENYPVDGRYKSA						
		120	130	140	150	160	170	
AnrtfA	XP_662174.1	QKQELMALPEIQREQILSERAOEVDRHNQDLALRRLLASREEREARAKKNKRKASAN						
FpRtfA	XP_009254491.1	KKAEELMALPELEREQIISERAOEVDNRHNQDLALRRLLASREEREARAKKNKRKAGTA						
		180	190	200	210	220	230	
AnrtfA	XP_662174.1	IDEGRKSSSRQKTLGGGRKVEASEAIEAYKRQREQKGRDELRRLDITATKDHKSKSRVS						
FpRtfA	XP_009254491.1	LEDGRKASRPRITETKRETDMSLRQAKAPKARR.....REDLELRKKNDYSSRRGDSGAE						
		240	250	260	270	280	290	
AnrtfA	XP_662174.1	DEDAEGESEVEWDDRESRPTP...PKDDPPAELRDIQRARVGRNFAQVCFYPGFEDTM						
FpRtfA	XP_009254491.1	DSDD.....YNRGSRPTPDVDEARDQPPAELRDYDVRVLRNFAQVCFHPGFEGQL						
		300	310	320	330	340	350	
AnrtfA	XP_662174.1	VCCYVRLNVGPNFN.GVNEYRLAMITEIKEGKKYALGANCRTFTDOYVLAHGKTTA						
FpRtfA	XP_009254491.1	IGCYVRLIAGFHPETGLEQYRMAYIKGFSTSRPYALQGPQG.VLVTDOYVLAHGKAIKE						
		360	370	380	390	400	410	
AnrtfA	XP_662174.1	FPFVACSDSPFTEAEFNRRYQVMAVECDCKMPTKSOIAKQVMDINRLINHQTPEEENEKL						
FpRtfA	XP_009254491.1	FPFLAASSGKPTDSEFNRRYVTCHEGVTLPKAYITDQVMDINRLINHSWTEEIKTRL						
		420	430	440	450	460		
AnrtfA	XP_662174.1	RKQGLDITKTTFFKRVDEKCKKIAQELGDDDEVGRLOVELANLGS.....SAKPP						
FpRtfA	XP_009254491.1	AKISDILKRRFDPAERERLAKLDEAQRGDDDEVAEELOVELDNLGSQRLAFRTSLGSKHS						
		470	480	490	500	510	520	
AnrtfA	XP_662174.1	RTEKKLTEHERLAQLNLRNOKLNYENVRRAOIEERKASRKAAAAARGEGSLNPFLL.VK						
FpRtfA	XP_009254491.1	EETKAKSEODRLAERNRENRRLNABAVRKAQIKERAKSKETIEAAIKRGETYQGDMSRRLR						
		530	540	550	560	570		
AnrtfA	XP_662174.1	TRAKTHYDANE ¹⁰⁰ STPK..SENGSP ¹⁰⁰ SVTPA ¹⁰⁰ SST ¹⁰⁰ PNPSTPARSS..TPSN ¹⁰⁰ SQNK ¹⁰⁰ QSKG ¹⁰⁰ GG ¹⁰⁰ K ¹⁰⁰ I						
FpRtfA	XP_009254491.1	TKAKFVHDANE ¹⁰⁰ KVEQKSAANG ¹⁰⁰ AGTPG ¹⁰⁰ NST ¹⁰⁰ SKSAAKSQLLPHMVKLQEE ¹⁰⁰ KL ¹⁰⁰ KE ¹⁰⁰ G ¹⁰⁰ IP ¹⁰⁰ TI						
		580	590	600				
AnrtfA	XP_662174.1	RHRNMDDENIAALDLDDIDIEI						
FpRtfA	XP_009254491.1	HKPLMDDVIGS ¹⁰⁰ LDLDDIDVEI						

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.

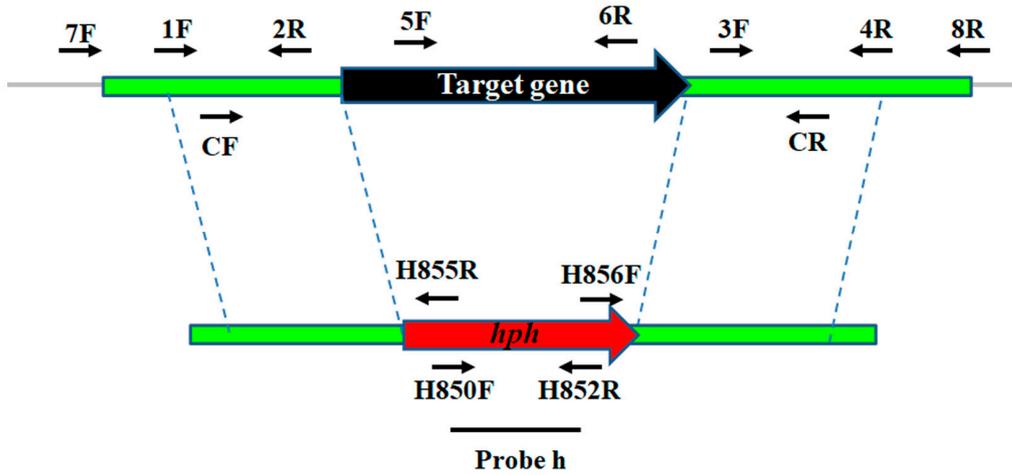


Figure S2. Gene deletion schematic of FpRtfA. The double-joint method was used to generate the replacement of FpRtfA gene. The small arrows sign the directions and positions of primers used for amplifying recombinant fragment and detecting target gene.

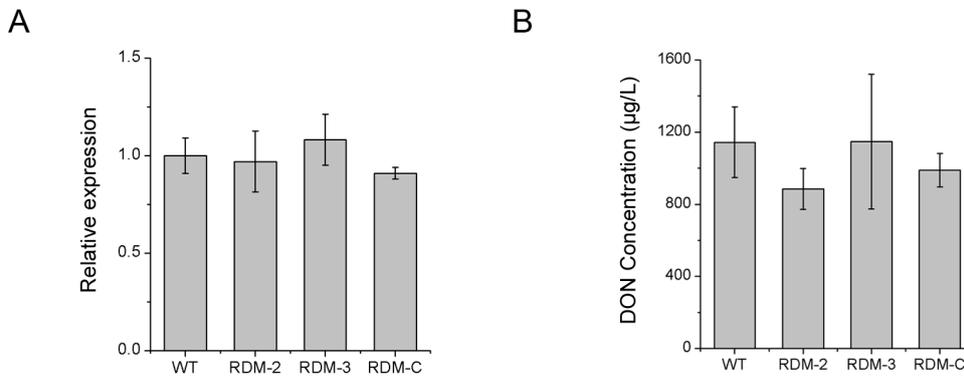


Figure S3. Transcription level of TRI5 gene and DON concentration in inducing medium. (A) Relative transcript abundances of TRI5 gene in mycelium at inducing medium were compared between the wild-type and FpRtfA mutants at 7 dpi. Expression level of TUB gene was used to normalize different samples. Transcript 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.