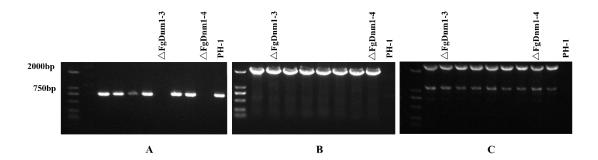
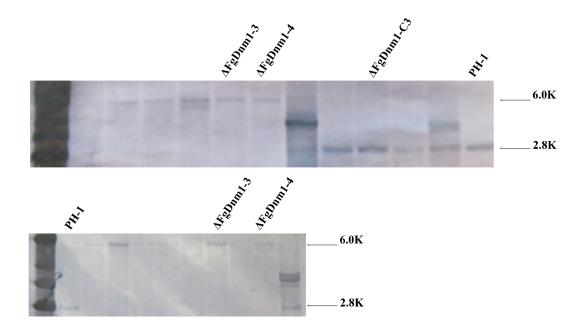


Appendix A Gene replacement strategy for FgDnm1 of Fusarium graminearum. (A) The replacement cassette is consisted of *hph* and *hsv-tk*. (B) The locus of FgDnm1 in the wild type strain PH-1. (C) The structure of the *FgDnm1* locus in the *FgDnm1* deletion mutant. (D) The complementary cassette generated by PCR amplification. (E) The structure of the *FgDnm1* locus in the complementary strain.

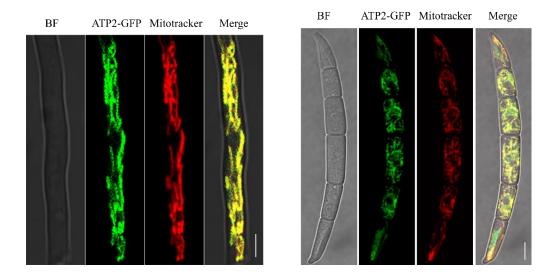


Appendix B PCR screen of *FgDnm1* deletion mutants. (A) PCR amplification of *FgDnm1* gene; a 750-bp fragment not detected indicates the replacement integration at the *FgDnm1* gene. (B) PCR amplification of the left flank, a 2000-bp fragment indicates replacement integration at the left junction.

(C) PCR amplification of the right flank, a 2100-bp fragment indicates replacement integration at the right junction.



Appendix C Southern blotting analysis of FgDnm1 deletion mutant and complementary strains. Hind III digested genomic DNA from wild type, Δ FgDnm1 and complementary strain was used for Southern blotting and probed with the 0.7-kb left flank fragment. The 6.0-kb or 2.8-kb band observed in the Δ FgDnm1 and wild type or complementary strain was diagnostic of the correct gene deletion event.



Appendix D FgAtp2 co-localize with mitochondria. FgAtp2 tagged with GFP was transformed into PH-1 and stained with mitochondrial fluorescent dye Mitotracker to visualize mitochondria, implying that FgAtp2 can be used for mitochondrial marker. Bar=5 μm.

Appendix E Growth of strains on PDA and MM medium

Strains	Mycelia growth (mm)	
	PDA	MM
PH-1	63.3± 0.5 a	74.2±0.4 a
ΔFgDnm1-3	55.2± 0.8 b	65.5±1.6 b
ΔFgDnm1-4	55.0± 0.0 b	64.5±0.8 b
ΔFgDnm1-C3	61.2± 4.8 a	75.0±1.2 a

Values in a column following the same letter are not significantly different (p < 0.05) according to Fisher's least significant difference, there were three replicates per treatment and the experiment was repeated three times.

Appendix F Conidiation and virulence assays

Strains	Conidiaton (×10 ⁵ conidia/ml)	Virulence (mm)
PH-1	7.15±1.58a	18.73±2.38a
ΔFgDnm1-3	6.62±1.88a	17.91±2.84a
ΔFgDnm1-4	6.53±2.00a	15.82±3.61a
ΔFgDnm1-C3	6.34±1.62a	17.91±3.85a

Values in a column following the same letter are not significantly different (P<0.05) according to Fisher's least significant difference, there were three replicates per treatment and the experiment was repeated three times.