

Figure S1. Multiple sequence alignment of FgNhp6 with homologs from other fungi. Sequence alignment was conducted using MAFFT. The sequence for analysis was as follows:

FgNhp6 from *Fusarium graminearum*, Nhp6B from *Saccharomyces cerevisiae*, Nhp6A from *Saccharomyces cerevisiae*, Mnh6 from *Pyricularia oryzae*, XP_018743258.1 from *Fusarium verticillioides*, XP_023424625.1 from *Fusarium fujikuroi*, XP_024551858.1 from *Botrytis cinerea*, XP_011393295.1 from *Neurospora crassa*, XP_754458.1 from *Aspergillus fumigatus*, XP_660489.1 from *Aspergillus nidulans*, XP_042995499.1 from *Ustilagoidea virens*, XP_016594384.1 from *Penicillium expansum*.

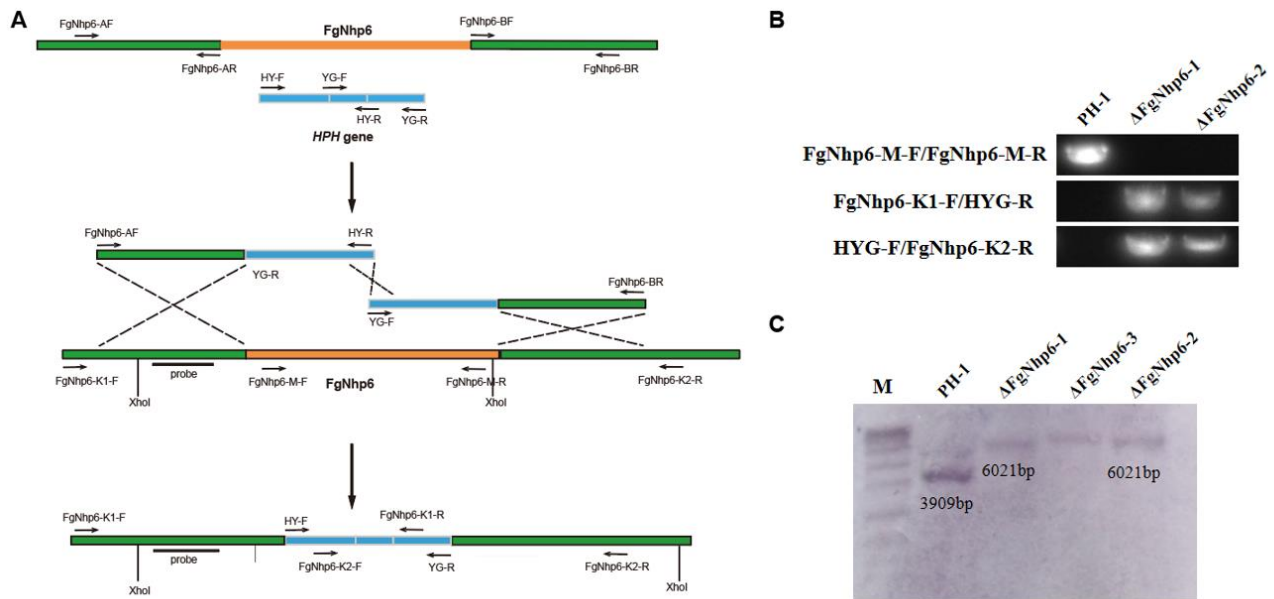


Figure S2. Generation and identification of *FgNhp6* deletion mutants. (A) Schematic representation of the gene deletion strategy. The *FgNhp6* gene was replaced by the hygromycin gene (*HPH*) through homologous recombination. Primer binding sites are labeled by arrows. (B) PCR analysis of transformants showed ΔFgNhp6-1, -2 might be the correct *FgNhp6* deletion mutants. (C) Southern blot analysis of *FgNhp6* deletion mutants and the wild-type strain PH-1 confirmed the ΔFgNhp6-1 and ΔFgNhp6-2 were corrected. A 708 bp downstream fragment was used as a probe. The genomic DNA sample of each strain was digested with *Xho*I.