

## Supplementary material

### **MoNap1, a nucleosome assemble protein 1, regulates growth, development and pathogenicity in *Magnaporthe oryzae***

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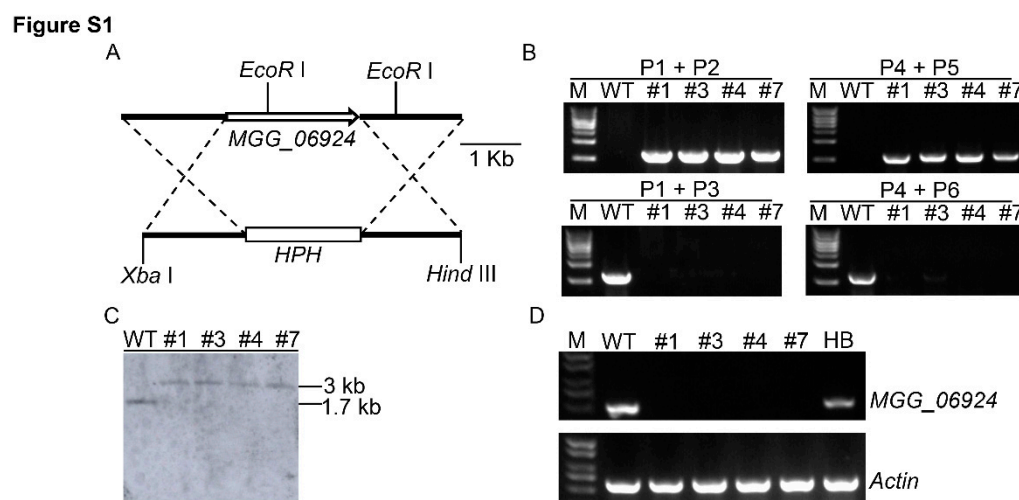
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**This PDF file includes**

Figure and Table

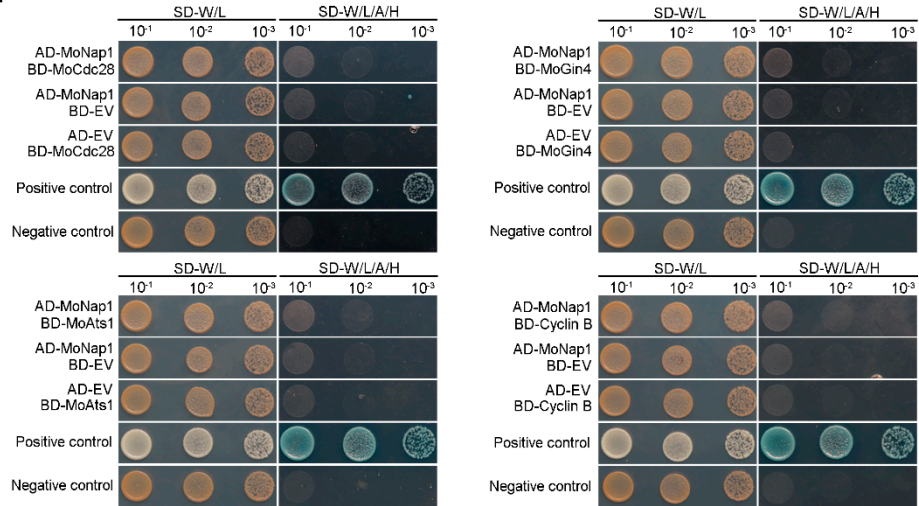
**Figure S1 Targeted gene deletion of *MoNAP1* in *M.oryzae*.** (A) Schematic presentation of targeted deletion of *MoNAP1* using homologous recombination method. (B) PCR verification of knockout transformants. (C) Southern blot assay showing the successful replacement of *MoNAP1* by a single insertion of hygromycin fragment. (D) RT-PCR verification of mutant and complemented strains.



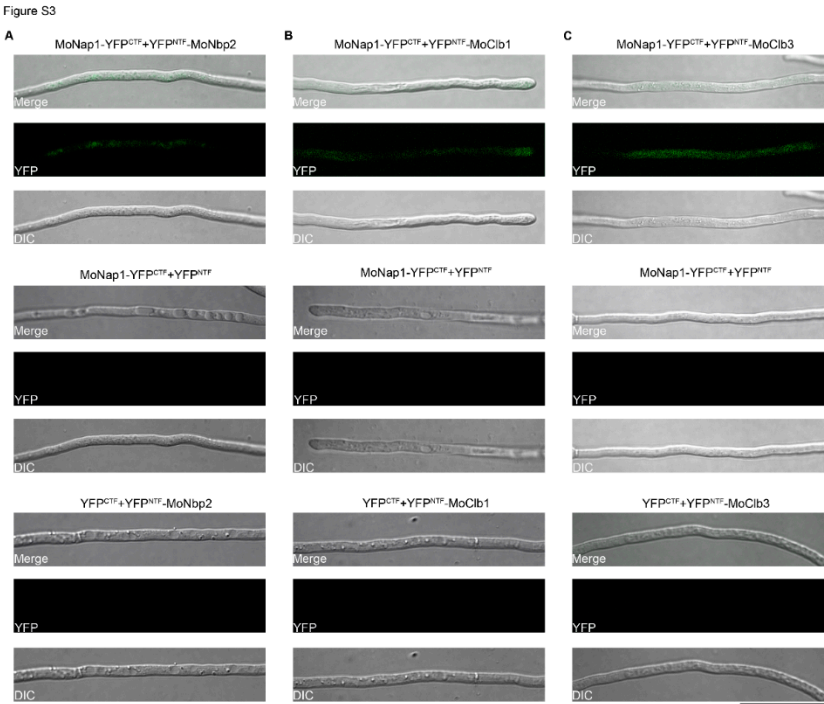
**Figure S2 MoNap1 has no interaction with MoCdc28, MoGin4, MoAts1 and MoCyc1 in *M.oryzae*.**

Yeast two hybrid (Y2H) assay. Yeast strains co-expressing prey and bait constructs were cultured on SD-Leu-Trp and SD-Ade-Leu-Trp-His plates supplemented with X- $\alpha$ -GAL respectively.

**Figure S2**

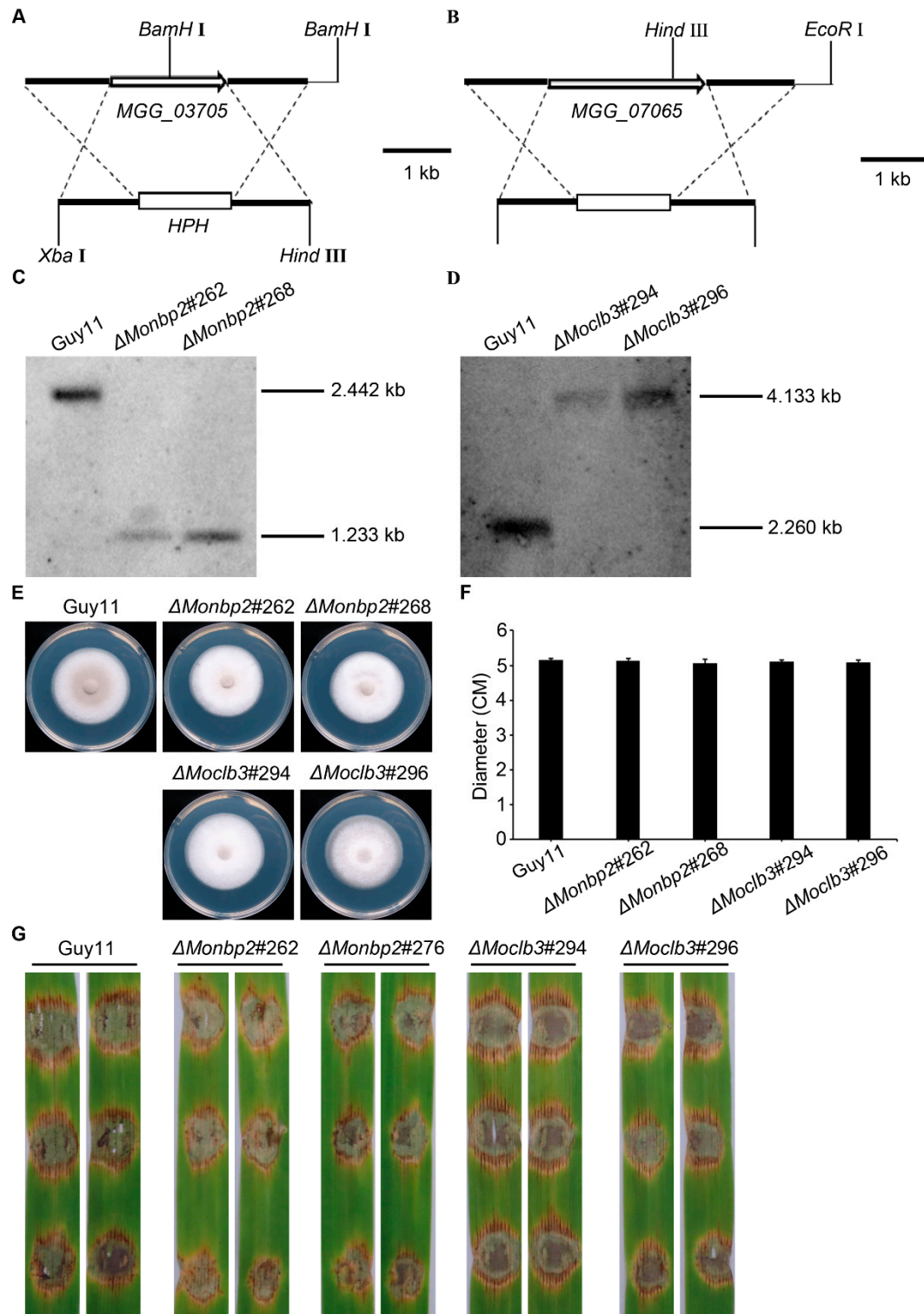


**Figure S3. BiFC results between MoNap1-YFP<sup>CTF</sup> and YFP<sup>NTF</sup>-MoNbp2, YFP<sup>NTF</sup>-MoCib1 or YFP<sup>NTF</sup>-MoCib3. YFP signals were observed in vegetative hyphae under laser scanning confocal microscope (NIKON, Japan). The negative control transformants harbor MoNap1-YFP<sup>CTF</sup> and YFP<sup>NTF</sup>, YFP<sup>CTF</sup> and YFP<sup>NTF</sup>-MoNbp2, YFP<sup>CTF</sup> and YFP<sup>NTF</sup>-MoCib1, YFP<sup>CTF</sup> and YFP<sup>NTF</sup>-MoCib3. Bar=25  $\mu$ m.**

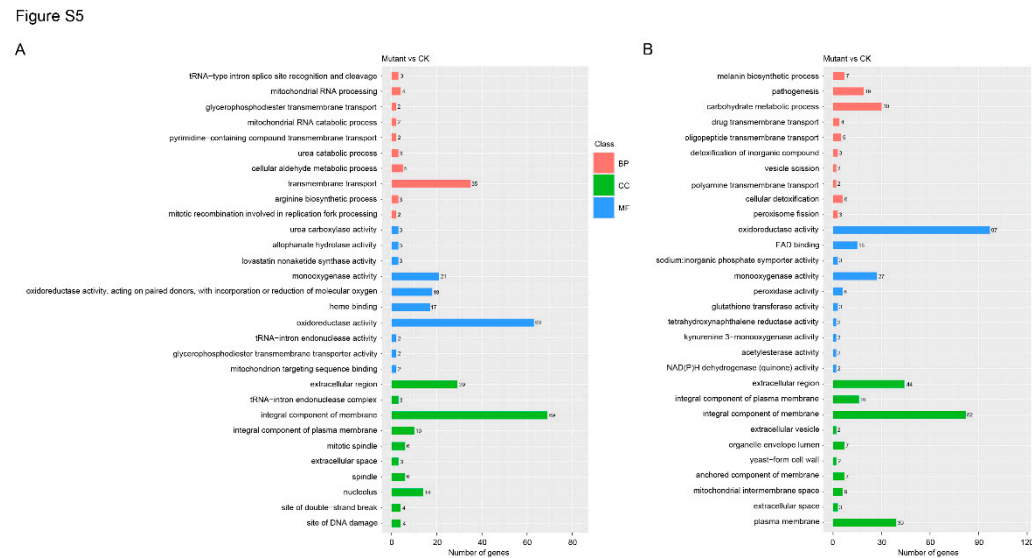


**Figure S4 Knockout and phenotype analysis of MoNap1-interacted proteins.** (A) and (B) Schematic presentation of targeted deletion of *MoNBP2* and *MoCLB3* using homologous recombination method. (C) and (D) Gene knockout verification of  $\Delta Monbp2$  and  $\Delta Moclb3$  mutants by Southern blot analysis. (E) Colony morphology of WT,  $\Delta Monbp2$  and  $\Delta Moclb3$  mutant strains on CM were observed and photographed after 7 days at 28 °C. (F) The colony diameters were measured and subjected to statistical analysis. For each strain, three independent biological experiments with four replicates each time were carried out. Error bars represent standard deviation, and asterisks above the columns indicate significant differences between WT and  $\Delta Monbp2$ , WT and  $\Delta Moclb3$  estimated by Student's t test (\*\* $P < 0.01$ ). (G) Virulence of WT,  $\Delta Monbp2$  and  $\Delta Moclb3$  mutant strains performed on detached barley leaves. Lesions formed on barley leaves inoculated with mycelial blocks of WT,  $\Delta Monbp2$  and  $\Delta Moclb3$  and observed at 5dpi.

**Figure S4**

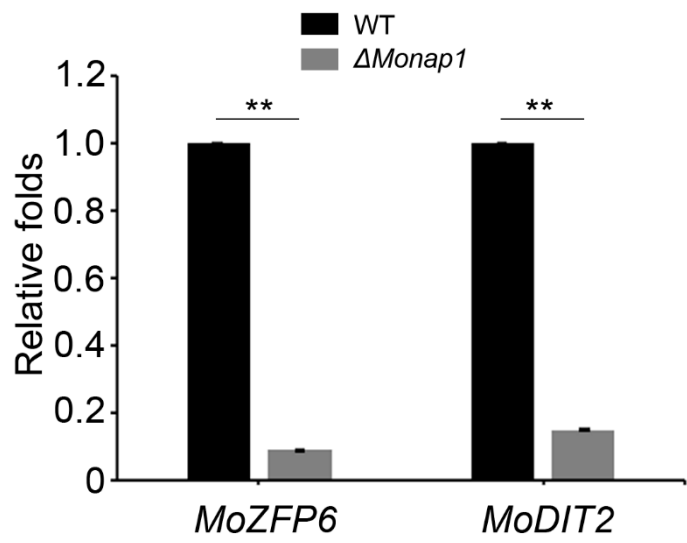


**Figure S5. Gene Ontology terms of biological processes, cellular components, and molecular functions enriched in wild-type strain Guy11 and *ΔMonap1* mutant. (A) Gene Ontology (GO) analysis of up-regulated genes ( $P<0.05$ ). (B) Gene Ontology (GO) analysis of down-regulated genes ( $P<0.05$ ).**



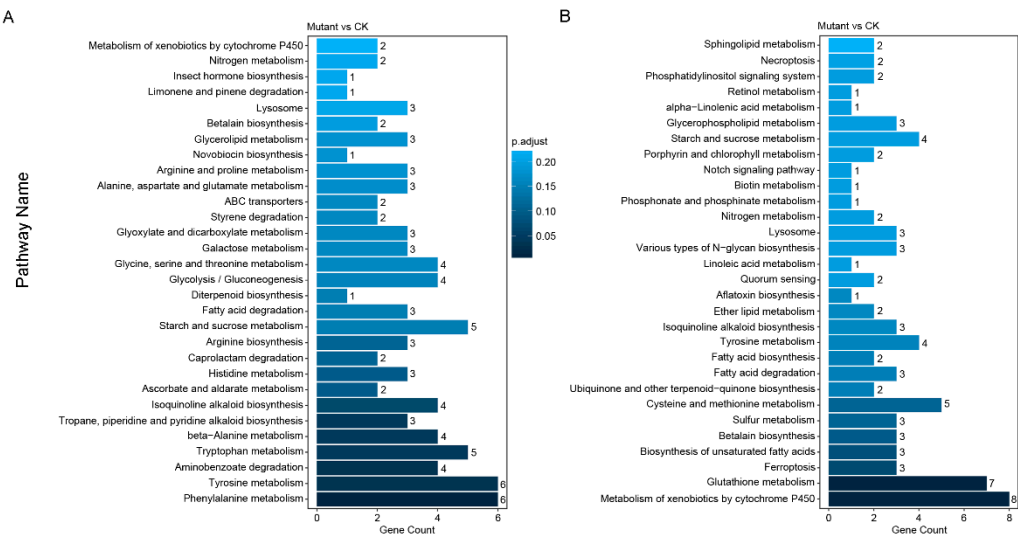
**Figure S6. Expression level of *MoZFP6* and *MoDIT2* in WT and *ΔMonap1* mutant. The expression level of different genes in WT was set as 1.**

Figure S6



**Figure S7** Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of the DEGs. (A) Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of the genes up-regulated. (B) Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis of the genes down-regulated.

Figure S7



**Table S1. Primers used in this study**

**Table S2. Differentially expressed genes related to melanin biosynthesis and pathogenesis in *ΔMonap1* mutant using  $|\log_2\text{FoldChange}| > 1.5$  and  $P < 0.05$ .**