

Fig. S1. qRT-PCR validation of the RNA-Seq data.

WT	AAAGAATTATGTTTGGTATGCTTACGC-TAA	TGGCGTTTATTTAGGTCGGCGACGCAA	355
$\Delta Pdw03_3762-1$	AAAGAATTATGTTTGGTATGCTTACGC	CTAATGGCGTTTATTTAGGTCGGCGACGCAA	356
$\Delta Pdw03_3762-13$	AAAGAATTATGTTTGGTATGCTTACGC	-AATGGCGTTTATTTAGGTCGGCGACGCAA	354
WT	GCGTACTCTTCCCCGGCCGACCAGCCTC	TGGCCGGCAGTGCTCCCCCGGGCCCCCAATC	178
$\Delta Pdw03_3571-10$	GCGTACTCTTCCCCGGCCGACCAGCCTC	TGGCCGGCAGTGCT	177
WT	CACCTCACCTCCCAACCTGTCAGCCCC-G		269
$\Delta Pdw03_2654-5$	CACCTCACCTCCCAACCTGTCAGCCCC-G	TCCCGAGCAAAAAGGATTGGAGGAGGAGGAG	300
$\Delta Pdw03_2654-6$	CACCTCACCTCCCAACCTGTCAGCCCC	CG	270
WT		GGCGGCAAGGCATCTCGAACGAAACCGC	298
$\Delta Pdw03_2654-5$	GAAGGTGAGAGTGAGACAAAGAGCGAAATAG	GGCGGCAAGGCATCTCGAACGAAACCGC	360
$\Delta Pdw03_2654-6$		GGCGGCAAGGCATCTCGAACGAAACCGC	299

Fig. S2. Sequence alignment of gene locus in the selected mutants. Protospacers were marked in red. Protospacer-adjacent motifs (PAM) were underlined. Nucleotide alterations are highlighted in yellow.

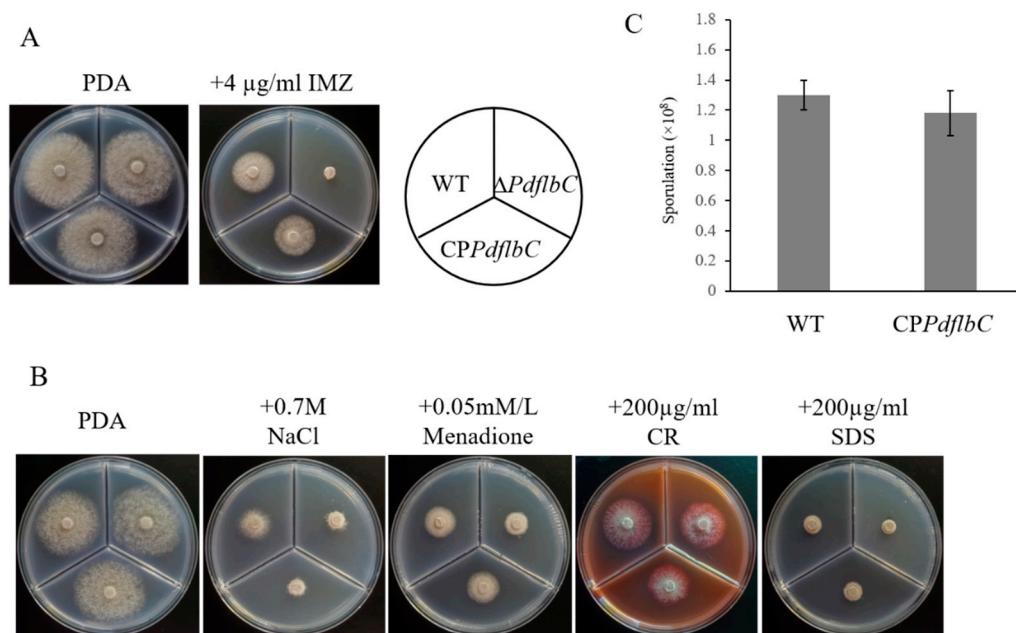


Fig. S3. Phenotypes of the complemented strain $CPPdw03$. A) Sensitivity of the wild type, the gene

deletion mutant ΔP_{dfbC} and the complemented strain CPP_{dfbC} to IMZ. B) Sensitivity of the wild type, the gene deletion mutant ΔP_{dfbC} and the complemented strain CPP_{dfbC} to environmental stresses. C) Sporulation of the wild type and the complemented strain CPP_{dfbC} .