

Figure S1. Phylogenetic analysis of PMI proteins among filamentous fungi. PMI Protein sequences from *F. oxysporum* f. sp. cubense TR4 (N1RBD6 and X0IZ75), *F. oxysporum* f. sp. pisi HDV247 (W9P4S7), *F. oxysporum* f. sp. vasinfectum (X0L7N5), *F. oxysporum* f. sp. lycopersici 4287 (A0A0D2YBQ5), *F. oxysporum* f. sp. rapae (A0A8J5TPK4), *F. oxysporum* graminearum PH-1 (A0A2H3GKK5), *Pyricularia oryzae* Y34 (L7IAR8), *Colletotrichum musicola* (A0A8H6NVI0), *Verticillium dahlia* Vdls.17 (G2WYC6), *Pterula gracilis* (A0A5C3QJ10), *F. oxysporum* f. sp. cubense race 1 (N4UUG0) and *Neurospora crassa* (Q7S4U2) sequences were downloaded from NCBI and analyzed by MEGA 11 Neighbor joining method with a bootstrap value of 5,000 replicates.

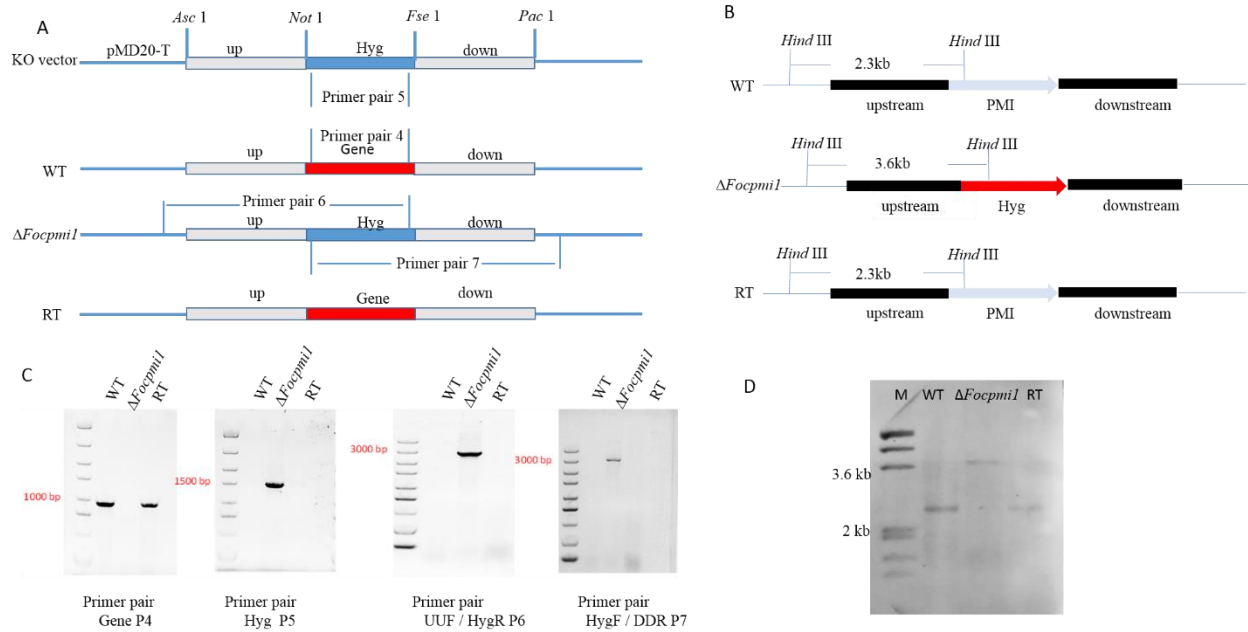


Figure S2. Schematic representation of strategies for the production and confirmation of $\Delta Focpmi1$ and RT strains. A, Strategies to generate the $\Delta Focpmi1$ mutant and revertant (RT) strains by homologous recombination. WT is wild-type, $\Delta Focpmi1$ is the mutant, and RT is the revertant strain. B, Genomic cutting sites for southern blotting. C, PCR analysis using four pairs of primers indicated in A. D, verification of the $\Delta Focpmi1$ mutant and RT strains by southern blotting.

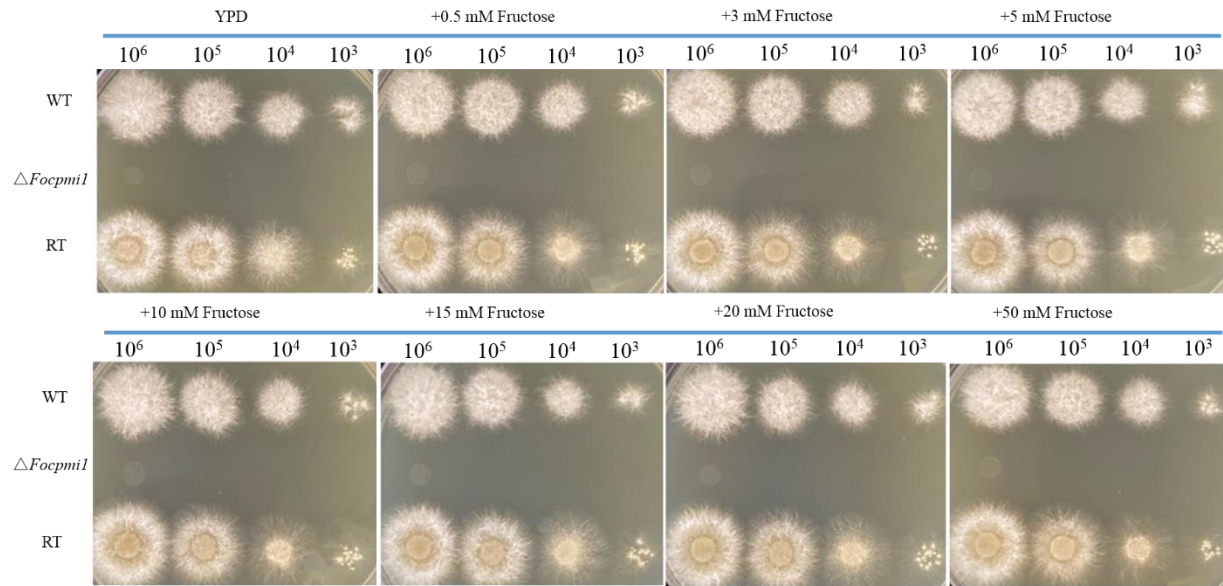


Figure S3. Growth characterization of the $\Delta Focpmi1$ at different concentrations of fructose. Freshly harvested conidia of all the three strains were serially diluted (10^6 - 10^3) and point inoculated on YPD medium amended with different concentrations (0.5, 3, 5, 10, 15, 20 and 50mM) of fructose. The plates were incubated at 28 °C for 48 hours.

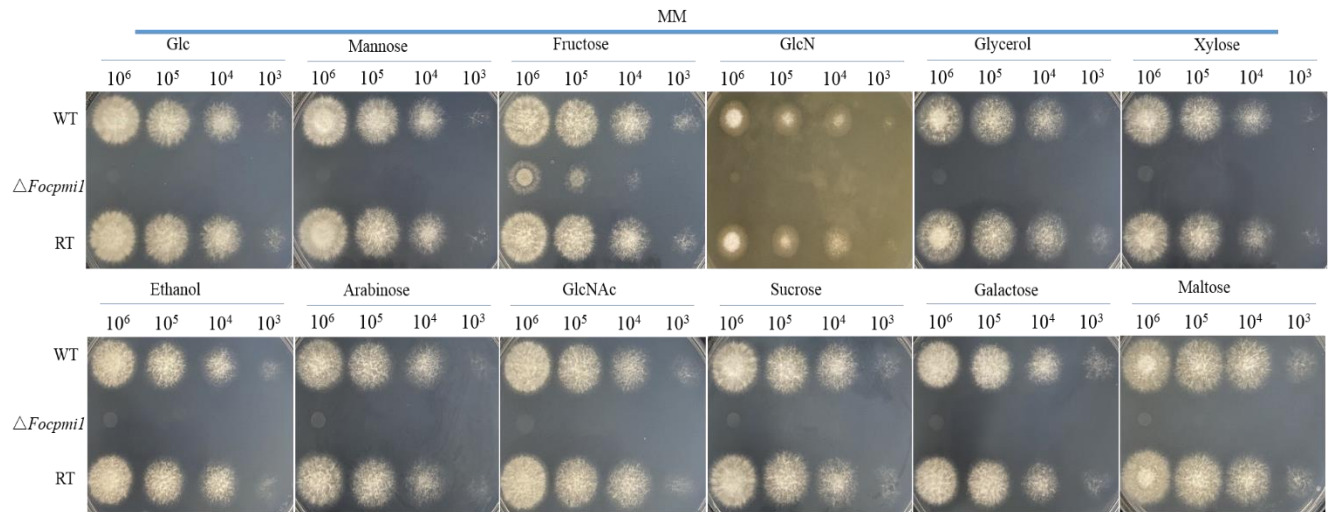


Figure S4. Growth characterization of the *Focpmi1* mutant on different sugars as sole carbon sources.

Freshly harvested conidia from all the three strains were point inoculated on MM solid medium plates containing Glc, mannose, fructose, GlcN, glycerol, xylose, ethanol, arabinose, N-acetylglucosamine (GlcNAc), Sucrose, galactose and maltose. The plates were incubated at 28 °C for 48 hours.

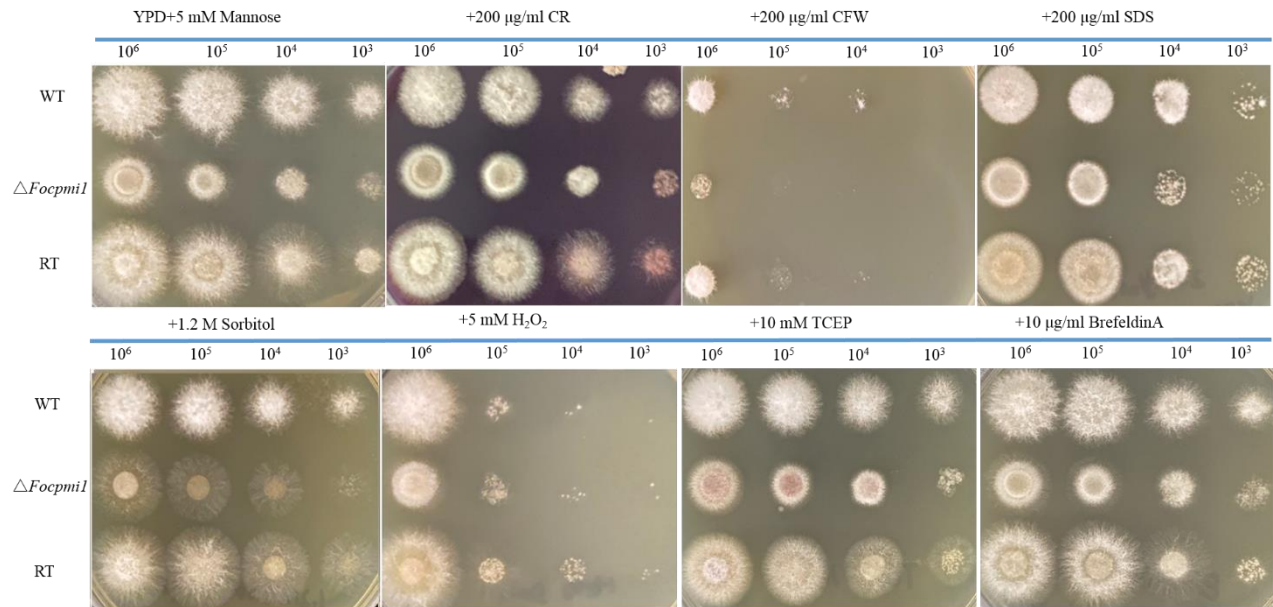


Figure S5. Cell wall integrity analysis and sensitivity towards osmotic, and ER stress in YPD medium.

Freshly harvested serially diluted conidia 10⁶-10³ were point inoculated onto YPD medium plates supplemented with 300 µg/ml CR, 50 µg/ml CFW, 200 µg/ml SDS, 1.2 M sorbitol, 5 mM H₂O₂, 10 mM TCEP and 10 µg/ml Brefeldin A. The plates were photographed after 48 hours of incubation at 28 °C.

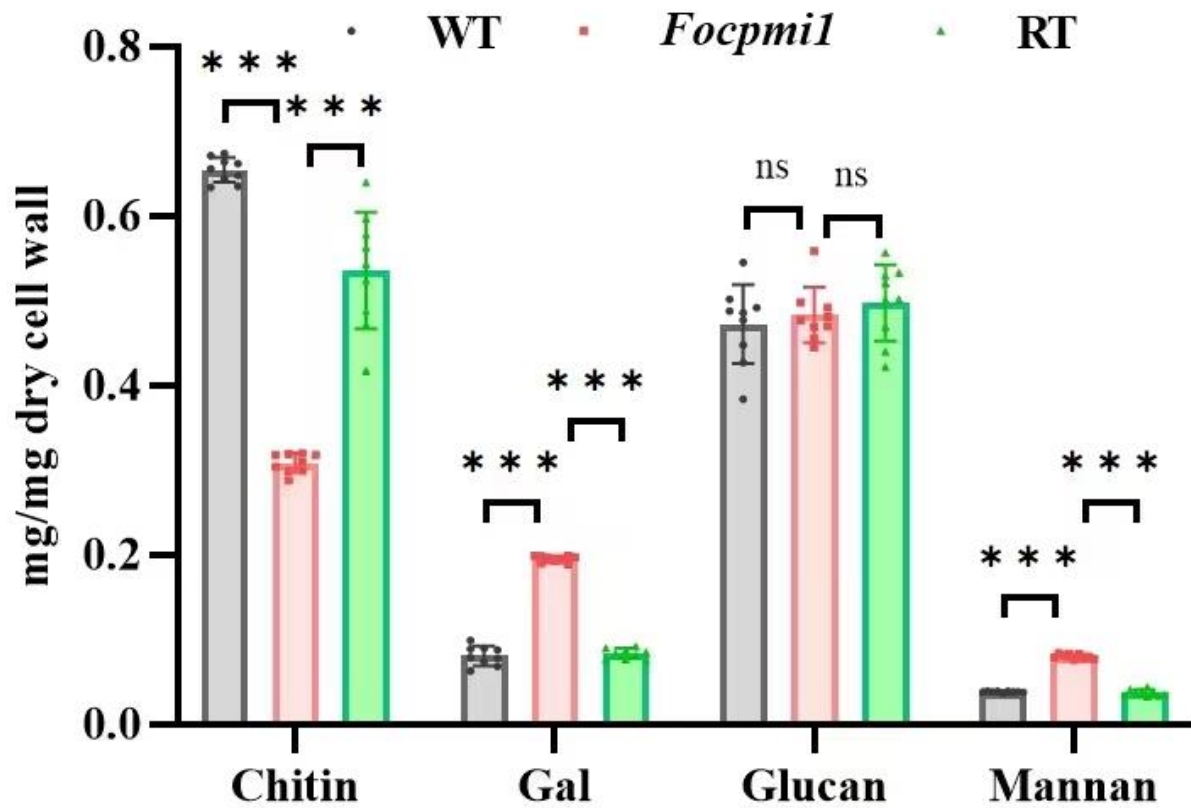


Figure S6. Cell wall content analysis of $\Delta Focpmi1$ strain. 2×10^8 conidia of WT, $\Delta Focpmi1$ and RT strains were inoculated in MMM liquid medium and incubated at 28 °C for 72 hours. Dried mycelia (10 mg) were used for the cell wall contents quantification. The experiment was conducted in three biological replicates.

Table S1. Primers used in the study

Primers	Primer sequences (5'-3')	Length (bp)	Remark
P1			
<i>Focpmi1</i> -up-F (<i>AscI</i>)	TT GGC GCGCC GAA GCA CAT CAA GCG TTG GTT	1185	<i>Focpmi1</i> mutant construction
<i>Focpmi1</i> -up-R (<i>NotI</i>)	ATAAGAATGCGGCCGCATTTGCGATGTTTCGTTGTTGG		
P2			
Hyg-F (<i>NotI</i>)	ATAAGAATGCGGCCGCGACAGAAGATGATATTGAAGG	1429	<i>Focpmi1</i> mutant construction
Hyg- R (<i>FseI</i>)	TATGGCCGGCCGATTTTCAGTAACGTTAAGTGG		
P3			
<i>Focpmi1</i> -down-F (<i>FseI</i>)	TAT GGCCGGCC ATGATATTGGAGTGATGTGAG	1119	<i>Focpmi1</i> mutant construction
<i>Focpmi1</i> -down-R (<i>PacI</i>)	CC TTAATTAA CGA CGT AAT ATC TCG ACT ATG		
P4			
<i>Focpmi1</i> Gene-F	TCTCCTCCCACTACGGCAACA	944	Mutant and revertant confirmation
<i>Focpmi1</i> Gene-R	AGCGATCCTTCCCTTCCACT		
P5			
Hyg-F	GACAGA AGATGATATTGAAGG	1429	Mutant and revertant confirmation
Hyg-R	GATTTTCAGTAAC GTTAAGTGG		
P6			
<i>Focpmi1</i> -UUF	GGGCATTCCACTGTCTGTTGT	2865	Mutant and revertant

Hyg-R	GAT TTC AGT AAC GTT AAG TGG		confirmation
P7			Mutant and
Hyg-F	GAC AGA AGA TGA TAT TGA AGG	2874	revertant
<i>Focpmi1</i> -DDR	CCTGTCCGACATAGCTGTTCCA		confirmation
P8			
<i>Focpmi1</i> -UUF	GGGCATTCCACTGTCTGTTGT	4286	Revertant
<i>Focpmi1</i> -DDR	CCTGTCCGACATAGCTGTTCCA		construction
P9			
<i>Focpmi1</i> RT-F	AAGGTGTTACGGATGAGAAGAAGAAGT	236	qRT-PCR
<i>Focpmi1</i> RT-R	GAAGAAGAGCACAAAGCAACCAAT		
P10			
<i>Focpmi2</i> RT-F	TACGCCAGAAGCCTTTGAGAC	246	qRT-PCR
<i>Focpmi2</i> RT-R	TAGGTTGCCAGGGTCGTTTGC		
P11			
<i>FocEF1α</i> - F	CCCAAGGCTGTCGCTTTCGTC	191	qRT-PCR
<i>FocEF1α</i> -R	AGACGGAGGGGCTTGTC AACG		
P12			
<i>Focpmi2</i> -up-F (<i>AscI</i>)	TT GGCGCGCC GACATTTGCAATACTTAGACG	1147	<i>Focpmi2</i> mutant construction

<i>Focpmi2</i> -up-R (<i>NotI</i>)	ATAAGAATGCGGCCGCATGACTATGACGATTAAC GAA		
P13			
<i>Focpmi2</i> -down-F (<i>FseI</i>)	TAT GGCCGGCC CGA CAT TTT GAG ATT CAA TGC	1190	<i>Focpmi2</i> mutant construction
<i>Focpmi2</i> -down-R (<i>PacI</i>)	CC TTAATTAA ATC GAC ATC CTG AGT TTA TAG		

Table S2. Genes responsible for plant cell wall degrading enzymes.

Gene ID	FDR	log2FC	Predicted function
Focb16_v004426	2.10E-06	-7.2308	Carboxylic ester hydrolase
Focb16_v000085	2.38E-11	-2.44834	Carboxylic ester hydrolase
Focb16_v011188	1.22E-06	-7.33859	Acetylxylan esterase 2
Focb16_v014173	3.95E-05	-2.41913	Alpha-glucosidase 2
Focb16_v000244	0.000414	-3.42482	Beta-glucosidase 4
Focb16_v000177	6.41E-12	-2.80639	Glycerophosphodiester phosphodiesterase
Focb16_v003281	1.22E-16	-3.98028	Beta-glucosidase
Focb16_v011585	9.11E-09	-2.50828	Putative beta-glucosidase C
Focb16_v002629	5.63E-16	-2.5294	Mannan endo-1,6-alpha-mannosidase
Focb16_v014263	3.40E-10	-5.97382	Beta-mannosidase B

Focb16_v015639	1.19E-35	-5.91848	Mannan endo-1,6-alpha-mannosidase
Focb16_v002729	1.77E-23	-6.59788	Endo-beta-1,4-glucanase D
Focb16_v004733	2.41E-08	-4.95047	Putative endo-beta-1,4-glucanase D
Focb16_v007553	9.92E-24	-4.15232	Endoglucanase-4
Focb16_v009544	7.22E-23	-2.35588	chitinase
Focb16_v005330	1.06E-15	-6.31701	Beta-L-arabinobiosidase
Focb16_v004994	0.002243	-5.13582	alpha-L-fucosidase
Focb16_v011413	0.000117	-4.32552	Alpha-L-fucosidase 2
Focb16_v000310	1.08E-56	-4.63723	Putative pectin lyase D
Focb16_v003939	2.07E-63	-3.33653	Glycosidase
Focb16_v008003	2.80E-05	-3.76292	Peptidoglycan deacetylase

Focb16_v011761	3.17E-37	-4.11241	Glycosidase
Focb16_v012948	7.03E-07	-7.4379	Unsaturated glucuronyl hydrolase
Focb16_v013479	2.70E-45	-2.96048	Phosphotransferase
Focb16_v013482	2.16E-17	-4.11972	N-acetylglucosamine-6-phosphate deacetylase