

Supplementary Materials:

Figure S1. Fluorescence labelling of conidia surface carbohydrates with FITC-conjugated lectins.

Table S1. Nucleotide sequence of constructs and primers used in the study

Table S2. Summary of RNA-Seq quality data of M1 and its $\Delta KU70$ parental strain. Four biological repeats were performed for each isolate.

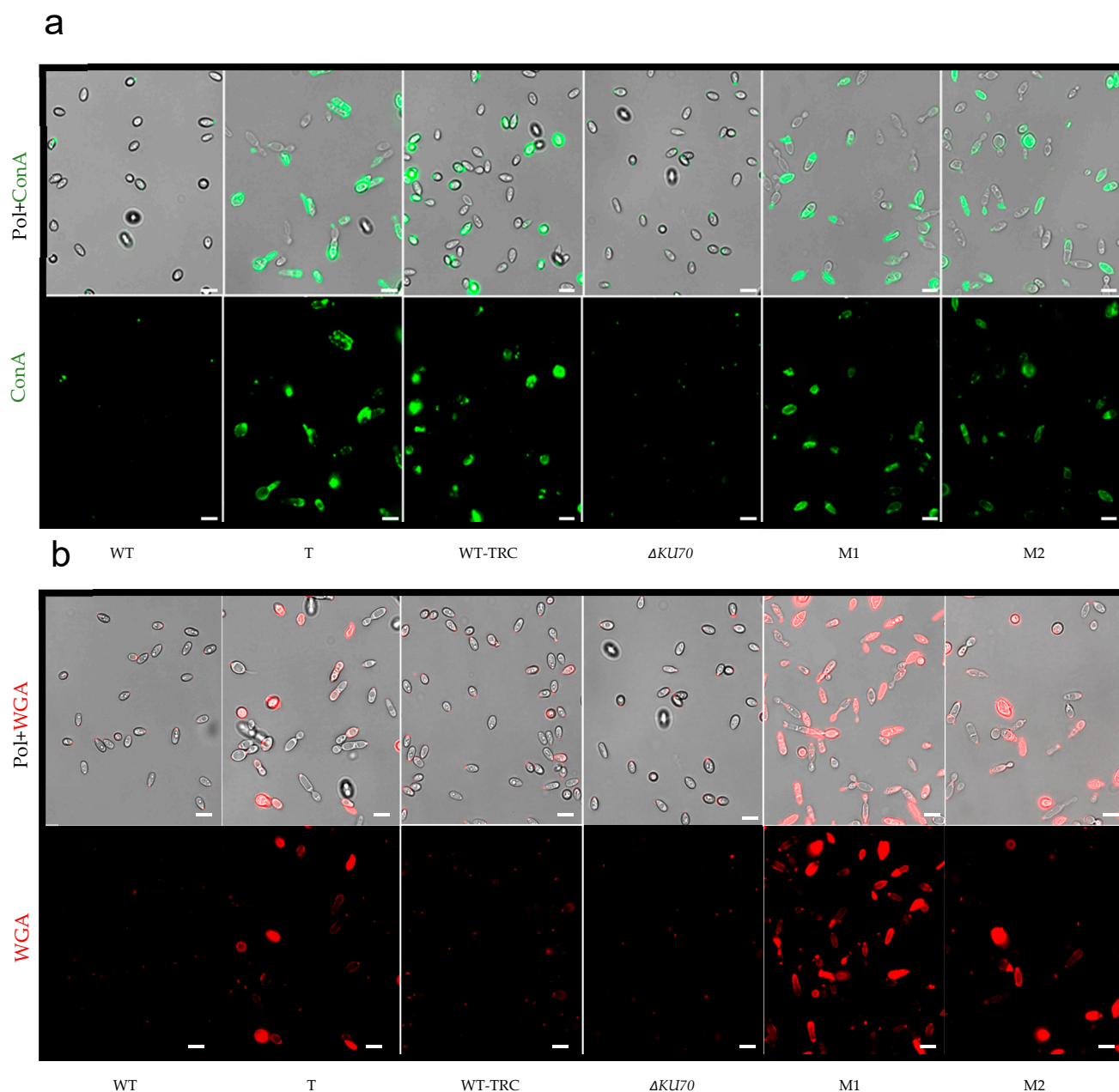


Figure S1. Fluorescence labelling of conidia surface carbohydrates with FITC-conjugated lectins. Representative images from fluorescence acquisition of conidia stained with Concanavalin A (**a**) or WGA (**b**), which bind to mannosyl and glucosyl residues and N-acetylglucosamine residues, respectively. Image acquired using an Olympus IX71 widefield inverted fluorescence microscope using a 20 \times magnification lens. Scale bar: 10 μ m.

Table S1. Nucleotide sequence of constructs and primers used in the study

Gene target	Sequence (5'-3')	Application
crRNA protospacer (<i>PIG1</i>)	GACGGCCAAGCAACTTGTGG	CrispR-Cas9 construction
tracrRNA	GTTTATAGAGCTAGAAATAGCAAGTT AAAATAAGGCTAGTCCGTTATCAAC TTGAAAAAGTGGCA CCGAGTCGGTGCT	
Up-stream and down-stream region of <i>PIG1</i> (SAPIO_CDS8655)	F- TGTGACACAAGGCTTATACC R- TACGAGCGAGCCTTTTGTCT	PCR (verification of <i>PIG1</i> deletion)
<i>FIS1</i> (SAPIO_CDS7496)	F-GATCAGTTCGAGAAGGAGGG R- GGAAGATGTCGGAGAGGAGA	RT-qPCR (RNA-seq validation)
<i>UBC6</i> Ubiquitin-conjugating enzyme E2 J2 (SAPIO_CDS4581)	F-GAGAACCCGCCACCATACA R-CAATACTGGCCGCCATGGTA	
<i>PIG1</i> (SAPIO_CDS8655)	F-TTTGGGTGCTTGGAGTGGGGATAA R-GCCGTATCGTGGAACAAGCTCAAT	
Tetrahydroxynaphthalene reductase (SAPIO_CDS8657)	F-GGGCAAGGTCGCTGTAGTCA R-TGGGGTTGGTGCCGAAAGAC	
Polyketide synthase (SAPIO_CDS8658)	F- AGAAGTCGATGGCTTGACGAGG R- GGCAGTCCAATCTTCAGGCTCT	
Iron transport multicopper oxidase (<i>abr1</i> , SAPIO_CDS8659)	F-CCACCGGGCGAAAGTATTGTGT R-CGTCGGGGTATTGTGCCATGTT	
Scytalone deshydratase (SAPIO_CDS5047)	F- CACCCTCAAGACGCAGCACT R- CCCGTCCACCCTCCTATACCAA	
Peptidase C2, calpain family (SAPIO_CDS8079)	F-AGGTTTGCCTCGTGCTGCAT R-ATCATGCGCCTTTTCATGCCCT	
Conidiation specific protein-6 (SAPIO_CDS6958)	F-AGATTGACACCTCTCCTAGCGCC R-TGCTTCCCGTTTGGCCTCCT	
Thioredoxin reductase (SAPIO_CDS1830)	F-GACGTGAATCCTGCCACTTT R-ACCGAGAATGTCACCCTGTA	

F: forward primer, R: reverse primer

Table S2. Summary of RNA-Seq quality data of M1 and its $\Delta KU70$ parental strain. Four biological repeats were performed for each isolate.

Index	$\Delta KU70$				M1			
	1	2	3	4	1	2	3	4
Total reads (millions)	17.6	20.6	20.8	20.7	19.8	12.7	20.6	17.3
Total assigned reads (millions)	11.7	12.3	15.0	14.6	10.4	9.4	14.6	11.2
% assigned reads	66.2	59.8	71.8	70.3	70.7	74.1	70.4	64.7
Q30%	95.7	95.6	95.4	95.5	95.8	95.5	95.7	95.7
GC%	53.0	52.0	53.7	53.5	53.3	55.0	53.5	52.9

Q30%: proportion of reads with a quality value > 30 after filtering. GC%: proportion of guanine and cytosine nucleotides among total nucleotides after filtering.