

Supplemental Table S1. Primers used in this study

Primer name	Sequence (5'-3')
Knockout mutant strains construction primers	
Hyg-F	CTTGGCTGGAGCTAGTGGAGGT
Hyg-R	CCCGGTCGGCATCTACTCTATTC
HY-F	CGTTGCAAGACCTGCCTGAA
YG-R	GGATGCCTCCGCTCGAAGTA
MCD4-LF1	GCGAAAGTGGCAGCATTGACTA
MCD4-LR1	ACCTCCACTAGCTCCAGCCAAGAATGGTACTGTCCTCGGCTCTCG
MCD4-LF2	GTATCTTGGTGGCTCGGCTCA
MCD4-RF1	GAATAGAGTAGATGCCGACCGGGGCTCGTGGTTAGAGATTGGCTCC
MCD4-RR1	TGAATGGGTTGGTCAAGGTGC
MCD4-RR2	GGTGGGTGCCGAGAATGATAA
GPI13-LF1	CCATTGTTGGAGAGGGCTACGAT
GPI13-LR1	ACCTCCACTAGCTCCAGCCAAGGGGTGATGTGGGCAGGAAGTAA
GPI13-LF2	ATAGCCGTCGCTTTCCAGTGG
GPI13-RF1	GAATAGAGTAGATGCCGACCGGGCGATGGCTGTCAGTGAGGTCTTT
GPI13-RR1	CCTACGAAGAACAACGGCATAACG
GPI13-RR2	GGATTGAAGGAGGTGATGAAGGC
GPI7-LF1	AAATGGGAGGAGACCACACAGC
GPI7-LR1	ACCTCCACTAGCTCCAGCCAAGGGGTTTCAACGACTGGAAGAGG
GPI7-LF2	TCTCGCACAGTCACTTTCACCC
GPI7-RF1	GAATAGAGTAGATGCCGACCGGG
GPI7-RR1	GATTGAAGGCGAAGAGGACGAA
GPI7-RR2	CGAGCAAAGGCTGTCAAGGAG
Knockout mutant strain checking primers	
MCD4-F	CCAGTCCTTTCCAGAACCCTACC
MCD4-R	ACAAGTGAATGACGCCGAGC
GPI13-F	TCATTGACGCTCTGCGATACG
GPI13-R	CGAGTGACTGGCTAACCGTGAA
GPI7-F	GAATCTTGATGAAGCCGACACG
GPI7-R	TGAGCCACTGCGGGATGTTA
GPI7-L-F	TCATTCCCCCTTCAACGTGC
GPI7-R-R	GGATCATGGGACAAGGGAGC
hyg-f	CAGCTTCGATGTAGGAGGGC
hyg-r	CGAAATTGCCGTCAACCAAG
Complementary and subcellular localization strains construction primers	

C-GPI7-F	AGGGAACAAAAGCTGGGTACCTCTCGCACAGTCACTTTCACCC
C-GPI7-R	AGTAACGTTAAGTGCGGCCGCCAGGCTGATCTCCGACACAAC
Sub-GPI7-R	CATTCTAGAACTAGTGGATCCCGCAGATCCCAGTCGGTACAAGA
Complementary and subcellular localization strains checking primers	
pGTN-cx-F	CATTAGGCACCCCAGGCTTT
pGTN-cx-R	TCGTGACCA CCCTGACCTAC
qRT-PCR primers	
GPI7-qPCR-F	TCTGCGGAGACCACGGTATG
GPI7-qPCR-R	GTCCTCTTTGAACGCAGCAGG
GLRG_02726-F	CGTTGGTTCTTGGGTTTCCTC
GLRG_02726-R	CGTGGTGATGATGGCGAGTA
GLRG_03399-F	GCGGCAGCGAGGAGTTTAT
GLRG_03399-R	CAGCAGCACCTTGTCTTCGTT
GLRG_04171-F	GGTTCTTCCAGGCATTCGG
GLRG_04171-R	TGGGTTGAGGAGGTGCTTTC
GLRG_05787-F	TGGTTGGCAGAAGATTGTGGT
GLRG_05787-R	TGAGGTCAGAGTCAAGGGACAC
GLRG_08319-F	GCGTTCAGCCGACTTCAGT
GLRG_08319-R	AATCTCCATCCAGCACCGTT
GLRG_04217-F	AGCCGAAACCACCTTGACC
GLRG_04217-R	CATCGTCGCTACCGCAGTT
GLRG_05084-F	GCCGACATTGCTGAACTGC
GLRG_05084-R	GGTGAAGAAGATAGGCACGGG
GLRG_05478-F	AGGCGGAAGCGATGAAGA
GLRG_05478-R	TCCCTGAACCTCCCAGTTAGAG
GLRG_06327-F	CCCATTCCCGTCGGTTACT
GLRG_06327-R	TTGAAGTCAGAGTCGCCGC
GLRG_07610-F	TGCGTGCTTGTCCTAATCC
GLRG_07610-R	TGTGCTTGCGGTCGTGTT
CgH3-F	TCAAGAAGCCTCACCGCTACAA
CgH3-R	GAAGTCCTGGGCAATCTCACG
ZmActin-F	GATTCTGGGATTGCCGAT
ZmActin-R	TCTGCTGCTGAAAAGTGCTGAG

Supplemental Table S2. The genes involved in this study

<i>Colletotrichum graminicola</i>	<i>Saccharomyces cerevisiae</i>	Annotation of putative protein
<i>GLRG_02030</i>	<i>GPI1</i>	Phosphatidylinositol N-acetylglucosaminyltransferase subunit
<i>GLRG_02457</i>	<i>GPI2</i>	Phosphatidylinositol N-acetylglucosaminyltransferase subunit
<i>GLRG_06888</i>	<i>GPI3</i>	Phosphatidylinositol N-acetylglucosaminyltransferase subunit
—	<i>GPI15</i>	Phosphatidylinositol N-acetylglucosaminyltransferase subunit
<i>GLRG_01976</i>	<i>ERI1</i>	Phosphatidylinositol N-acetylglucosaminyltransferase subunit
<i>GLRG_00650</i>	<i>GPI19</i>	Phosphatidylinositol N-acetylglucosaminyltransferase subunit
<i>GLRG_00461</i>	<i>GPI12</i>	N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase
<i>GLRG_00746</i>	<i>GWT1</i>	GPI-anchored wall transfer protein
<i>GLRG_07009</i>	<i>GPI14</i>	GPI mannosyltransferase
<i>GLRG_00172</i>	<i>PBN1</i>	Protein PBN1 that probably acts by stabilizing the mannosyltransferase
<i>GLRG_10659</i>	<i>GPI18</i>	GPI mannosyltransferase 2
<i>GLRG_02707</i>	<i>MCD4</i>	GPI ethanolamine phosphate transferase 1
<i>GLRG_00195</i>	<i>GPI10</i>	GPI mannosyltransferase 3
<i>GLRG_00022</i>	<i>SMP3</i>	GPI mannosyltransferase 4
<i>GLRG_00125</i>	<i>GPI13</i>	GPI ethanolamine phosphate transferase 3
<i>GLRG_10201</i>	<i>GPI11</i>	Glycosylphosphatidylinositol anchor biosynthesis protein 11
<i>GLRG_03783</i>	<i>GPI7/LAS21</i>	ethanolamine phosphate transferase 2
<i>GLRG_05637</i>	<i>GAA1</i>	GPI transamidase component
<i>GLRG_06189</i>	<i>GPI8</i>	GPI-anchor transamidase
<i>GLRG_07420</i>	<i>GPI16</i>	GPI transamidase component
<i>GLRG_07072</i>	<i>GPI17</i>	GPI transamidase component
<i>GLRG_00756</i>	<i>GAB1</i>	GPI transamidase component
<i>GLRG_02701</i>	<i>BST1</i>	GPI inositol-deacylase
<i>GLRG_04171</i>	<i>CHS1</i>	Chitin synthase I
<i>GLRG_03399</i>	<i>CHS2</i>	Chitin synthase II
<i>GLRG_05787</i>	<i>CHS2</i>	Chitin synthase II
<i>GLRG_02726</i>	<i>CHS3</i>	Chitin synthase III
<i>GLRG_08319</i>	<i>CHS3</i>	Chitin synthase III
<i>GLRG_05478</i>	<i>GAS1</i>	1,3-beta-glucanosyltransferase

<i>GLRG_05084</i>	<i>GAS2</i>	1,3-beta-glucanosyltransferase
<i>GLRG_06327</i>	<i>GAS3</i>	1,3-beta-glucanosyltransferase
<i>GLRG_07610</i>	<i>GAS4</i>	1,3-beta-glucanosyltransferase
<i>GLRG_04217</i>	<i>GAS5</i>	1,3-beta-glucanosyltransferase