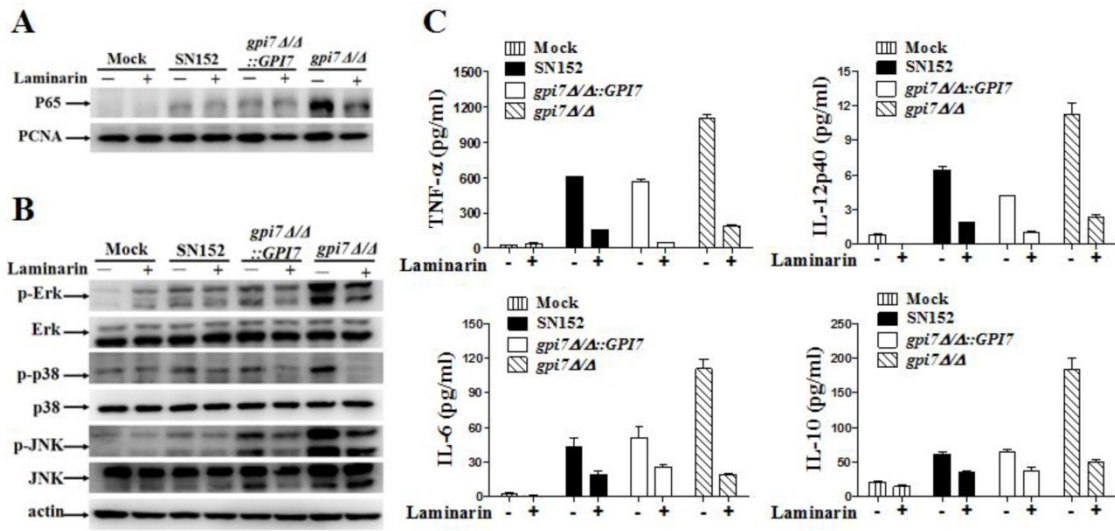
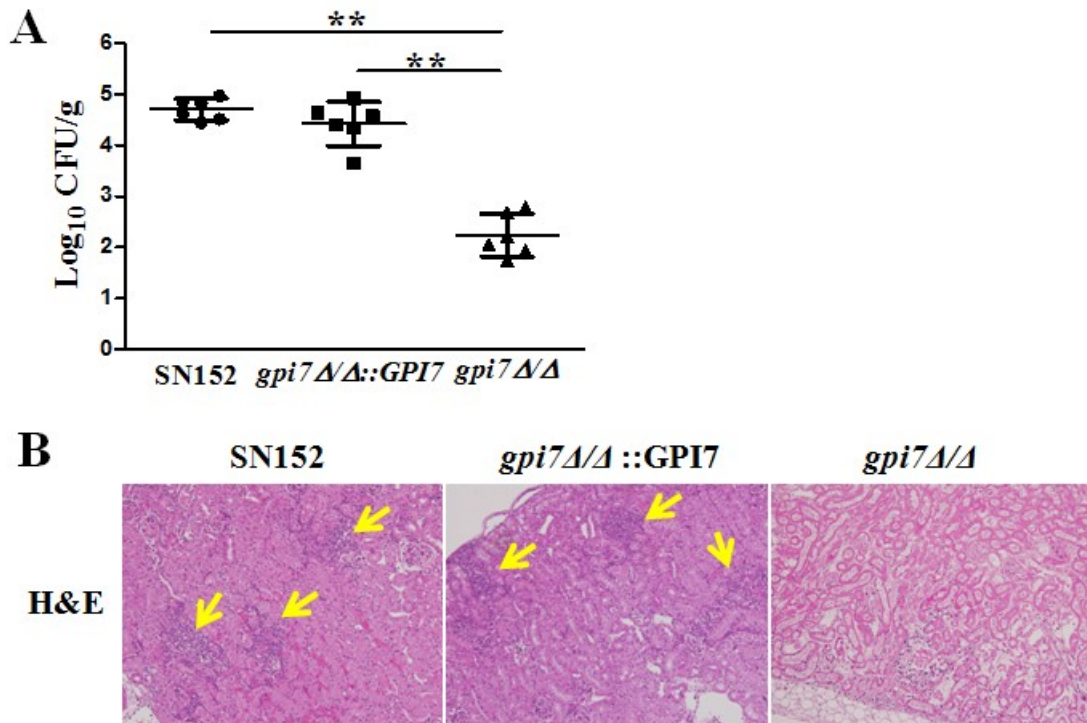


**FIG. S1. Construction of strains.** (A) Strategy for deletion of *C.albicans* *GPI7* based on two-step homologous recombination using a fusion-PCR-based strategy (1,2). (B) Strategy for construction of the *C.albicans* *GPI7* reconstituted strain based on SAT1 flipping method (3). (C) Strategy for construction of strains expressing HA-tag fused *Als1p* (*gpi7Δ/Δ als1Δ/ALS1-HA* and *als1Δ/ALS1-HA*) in strain *gpi7Δ/Δ* and SN152.



**FIG. S2. NF-κB and MAPK activation and inflammatory responses stimulated by *C.albicans* yeast *gpi7Δ/Δ*, which was abolished GPI-CWPs, were dectin-1 dependent.**

Thioglycollate-elicited peritoneal macrophages from wild type mice with or without 500 μg/ml laminarin preincubation were stimulated with *C.albicans* yeasts (MOI=5) of SN152, *gpi7Δ/Δ::GPI7* or *gpi7Δ/Δ* for 1 hour (A) or 30 minutes (B). The nuclear extracts (A) and cell lysates (B) were analyzed by immunoblotting with the indicated antibodies. (C) ELISA assays for TNF-α, IL-6, IL-12p40 and IL-10 in supernatants of thioglycollate-elicited peritoneal macrophages from wild type mice in the presence or absence of 500 μg/ml laminarin, which were stimulated with the indicated *C. albicans* yeasts (MOI =5) for 6 hours. Data shown are representative of three independent experiments. Data are means± SD.



**FIG. S3. *GPI7* gene is required for normal virulence during hematogenously disseminated candidiasis.** Mice were inoculated via the tail vein with  $2 \times 10^5$  CFU yeast-phase cells of the indicated strains of *C. albicans*. (A) Kidney fungal burdens of mice after infection with the parent, revertant and *gpi7Δ/Δ* mutant strains for 7 days, respectively. Data are representative of three independent experiments. \*\*,  $P < 0.01$  (Kruskal-Wallis nonparametric One-way ANOVA with Dunns post-test). (B) Hematoxylin and eosin (H&E) staining with thin sections of kidneys after infection with the parent, revertant and *gpi7Δ/Δ* mutant strains for 7 days, respectively.

**TABLE S1. *C. albicans* strains used in this study**

Strain	Relevant genotype	Source or reference
SC5314	Wild type	Dominique Sanglard
SN152	<i>arg4</i> $\Delta$ / <i>arg4</i> $\Delta$ <i>leu2</i> $\Delta$ / <i>leu2</i> $\Delta$ <i>his1</i> $\Delta$ / <i>his1</i> $\Delta$ <i>URA3/ura3</i> $\Delta$ :: <i>imm</i> <sup>434</sup> <i>IRO1/iro1</i> $\Delta$ :: <i>imm</i> <sup>434</sup>	Noble
<i>gpi7</i> $\Delta$ / $\Delta$	<i>gpi7</i> $\Delta$ :: <i>HIS1</i> / <i>gpi7</i> $\Delta$ :: <i>LEU2</i> <i>arg4</i> $\Delta$ / <i>arg4</i> $\Delta$ <i>URA3/ura3</i> $\Delta$ :: <i>imm</i> <sup>434</sup> <i>IRO1/iro1</i> $\Delta$ :: <i>imm</i> <sup>434</sup>	This study
<i>gpi7</i> $\Delta$ / $\Delta$ :: <i>GPI7</i>	<i>gpi7</i> $\Delta$ :: <i>HIS1</i> / <i>gpi7</i> $\Delta$ :: <i>GPI7</i> :: <i>SAT1-FLIP</i> <i>arg4</i> $\Delta$ / <i>arg4</i> $\Delta$ <i>URA3/ura3</i> $\Delta$ :: <i>imm</i> <sup>434</sup> <i>IRO1/iro1</i> $\Delta$ :: <i>imm</i> <sup>434</sup>	This study
<i>gpi7</i> $\Delta$ / $\Delta$	<i>gpi7</i> $\Delta$ :: <i>HIS1</i> / <i>gpi7</i> $\Delta$ :: <i>LEU2</i> <i>ALS1</i> :: <i>HA</i> :: <i>SAT1-FLIP</i> /	This study
<i>als1</i> $\Delta$ / <i>ALS1-HA</i>	<i>als1</i> $\Delta$ :: <i>ARG4</i> <i>URA3/ura3</i> $\Delta$ :: <i>imm</i> <sup>434</sup> <i>IRO1/iro1</i> $\Delta$ :: <i>imm</i> <sup>434</sup>	
<i>als1</i> $\Delta$ / <i>ALS1-HA</i>	<i>ALS1</i> :: <i>HA</i> :: <i>SAT1-FLIP</i> / <i>als1</i> $\Delta$ :: <i>ARG4</i> <i>leu2</i> $\Delta$ / <i>leu2</i> $\Delta$ <i>his1</i> $\Delta$ / <i>his1</i> $\Delta$ <i>URA3/ura3</i> $\Delta$ :: <i>imm</i> <sup>434</sup> <i>IRO1/iro1</i> $\Delta$ :: <i>imm</i> <sup>434</sup>	This study

**TABLE S2. Primers used in this study**

Primer	Sequence
eGPI7L	TCTATGTGGGGGAGGTCAAA
GuR	cacggcgcgcctagcagcggTGTGTGGATGGGTCTGAAAA
GdL	gtcagcggcccatccctgcGGATCTCTGAAATGAGGTTGG
eGPI7R	TGGATGGTGATGGTGAAGAA
oGL1	TCACCACAGGAGGTACACCA
oGR1	TCATCCCATGATCTCCCATT
oGL2	TCTAGCCGTGATTGTGGTGT
oGR2	TGCAAATGTTGGCACTAAGC
oGL3	CCTGGTGGGTTGATTCATT
oGR3	ACCCACCAAAAACACATTG
GuL	GGCATCAATTATTGGGCAT
GdR	CTGCTGAAGCTGCAAGAGAA
eHISR	TCAAGCCCTGTAGCTCCATT
eHISL	TCCGCTCATTGATTCCTC
eLEUR	GCACGCCGTTACAGGAGTTA
eLEUL	GAAGTTGGTGACGCGATTGT
Primer2	ccgctgctaggcgcgccgtgACCAGTGTGTGATGGATATCTGC
Primer5	ccagggatgcggccgctgacAGCTCGGATCCACTAGTAACG

GPI7rup L	ATAAGGGCCC CCATAATCCTCTCCCCTGGT
GPI7rup R	CCGCTCGAGTGTGTGGATGGGTCTGAAAA
GPI7rdown L	CCCACCGCGGCACACTACAAACCCCAACATC
GPI7rdown R	CCATAGAGCTCTGGATGGTGATGGTGAAGAA
oS1	GGAGTCACCGAACAACACAA
oS2	TGTGGCTCTCTTGATTGCTG
oS3	GACGCTCAGTGCACACAACCT
oS4	TCGCAAATTCGATGAGACTG
uA1	TTGCAAAAATTTCCAACCTGGT
dA2	CAACTTGCTTTGCTCTGCAC
oA1	ATTTGCCACAACCACCACAG
oA2	TCATTTGAAGCACTGGCAAC
uAG1	CTCAATAAAACAATCCTGGGT
dAG2	TTCAAAATAGGTATCACGGGC
ASA1	GCACGCTAGACAAATTCTTCC
ASA2	CAGCTCCTTGGCATAACGATT

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## SUPPLEMENTAL REFERENCES

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