

A. List of Supplementary Figures and Tables

Figure S1 The glucosylceramide pathway mutants grow normally at neutral and alkaline pH

Figure S2 Variability in the infectivity assay

Table S1 *C. albicans* mutants with previously reported virulence and morphogenesis phenotypes

Table S2 *C. albicans* with previously reported virulence and kidney burden phenotypes

Table S3 Results of the Infectivity, Morphogenesis, and Proliferation Screens (Excel file)

Table S4 Mutants with abnormal infectivity (Excel file)

Table S5 Mutants with abnormal morphogenesis (M score >1) (Excel file)

Table S6 Analysis of hyphal formation among infectivity-defective mutants

Table S7 Analysis of chromosome ploidy in 12 mutants and the parent strain by quantitative PCR

Table S8 Primers used for mutant construction and validation (Excel file)

Table S9 *C. albicans* strains used in this study

Table S10 $\log_2(R/I)$ ratios of mutants tested in the infectivity screen (Excel file)

Table S11 $\log_2(R/I)$ ratios of wild type *C. albicans* tested in the infectivity screen (Excel file)

Table S12 *C. albicans* mutants with reported virulence phenotypes that were recreated in this study

B. Legends for Supplementary Tables in Excel

Table S4. Mutants with abnormal infectivity. Data are presented for the 115 mutants that displayed abnormal infectivity phenotypes, as defined in the text. Mutant is the code for each gene knockout in the homozygous gene disruption library. Systematic name is the systematic numerical designation for the disrupted gene. Gene name is the standard name for named ORFs, as they appear in the Candida Genome Database. Process is the known or predicted cellular process associated with the protein encoded by the disrupted gene. Activity is the known or predicted function of the protein encoded by the disrupted gene; predictions were based on closest BLAST hits and/or SMART motifs. Under Infectivity, t-test p value is the t test result of comparing $\log_2(R/I)$ measurements for each mutant with those of wild type *C. albicans* across the screen, and Median (R/I) is the R/I corresponding to the median $\log_2(R/I)$ value of each mutant. Under Morphology, C represents the morphology of the center of a colony for a particular mutant grown on Spider medium for 14 days, compared to that of wild type *C. albicans*, and can range from -3 (hypofilamentous) through 0 (wild type) to 3 (hyperfilamentous), as described in the text. P represents the periphery of the colony. M score is the absolute value of C plus P. DT is the doubling time in minutes of each mutant in Synthetic Complete liquid medium at 37°C. Published virulence phenotype is the reported phenotype of a mutant in the tail vein model of disseminated Candidiasis, and PMID is the PubMed unique identifier for the reference.

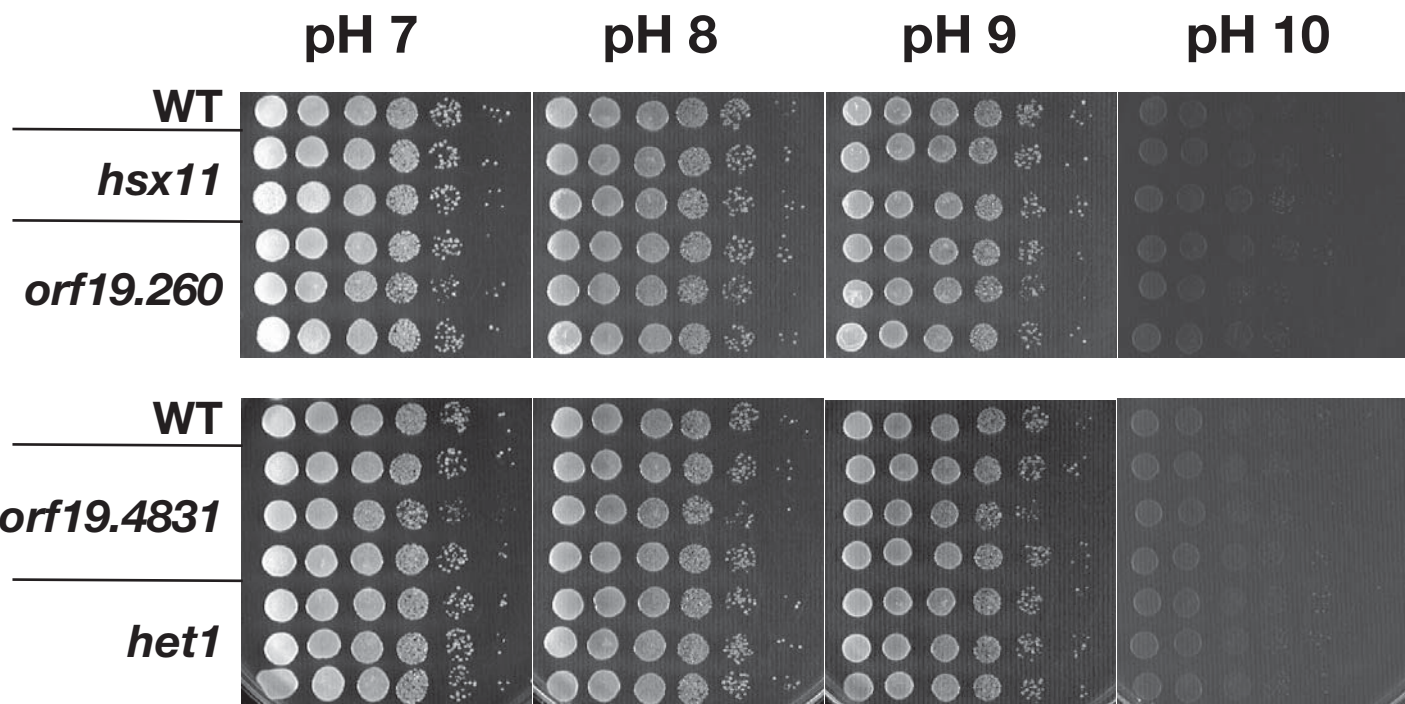
Table S10. $\log_2(R/I)$ ratios of mutants tested in the infectivity screen. Rows correspond to data from individual mutants. Columns give the identity of the mutant in the library, the systematic name of the deleted gene, and $\log_2(R/I)$ values from separate experiments. Note that some mutants have more than 6 values. Mutants numbering 1-96 were tested multiple times while the assay was vetted. In addition, data were combined if mutants with different numbers were subsequently discovered to target the same gene. Mutants have fewer than 6 values if some of the quantitative PCR reactions failed.

C. Supplementary References

1. Aono, R. Taxonomic distribution of alkali-tolerant yeasts. *Syst Appl Microbiol* **13**, 394-397 (1990).
2. Saito, K., Takakuwa, N., Ohnishi, M. & Oda, Y. Presence of glucosylceramide in yeast and its relation to alkali tolerance of yeast. *Appl Microbiol Biotechnol* **71**, 515-21 (2006).
3. Arbour, M. et al. Widespread occurrence of chromosomal aneuploidy following the routine production of *Candida albicans* mutants. *FEMS Yeast Research* **9**, 1070-7 (2009).

D. Supplementary Figures and Tables

Figure S1



The glucosylceramide pathway mutants grow normally at neutral and alkaline pH.

The glucosylceramide pathway mutants and wild type *C. albicans* were spotted onto plates buffered at neutral and alkaline pH and allowed to grow at 37°C in the presence of 5% CO₂, as described.^{1,2}

Figure S2

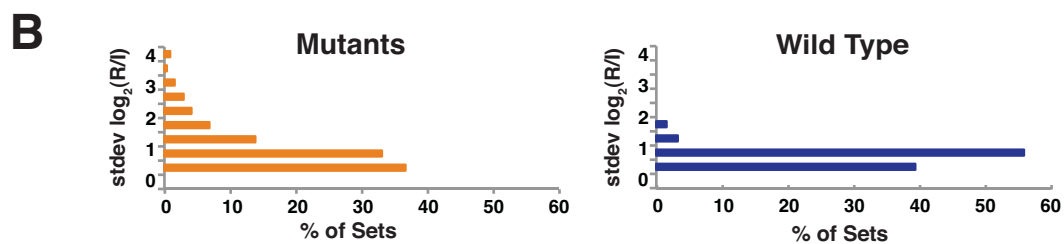
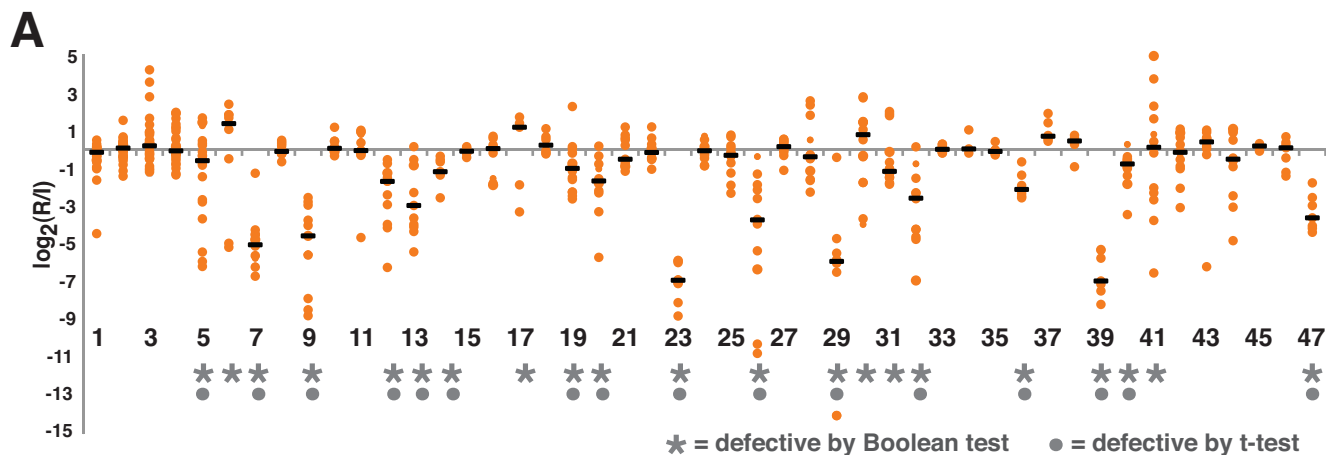


Figure S2. Statistical tests and variability in the infectivity assay.

A) This version of Figure 2C designates which infectivity-defective mutants were detected by Boolean criteria (grey asterisks) versus the t-test (grey dots). Orange circles represent the $\log_2(R/I)$ values from individual strains in different mice. Black bars represent the median $\log_2(R/I)$ value for each mutant. Mutants in this set were newly constructed isolates of 47 published strains previously reported to have virulence defects in the murine model of disseminated candidiasis. Mutants 1-47 were homozygous disruptants of *LIP8*, *NAG1*, *DAC1*, *HWP2*, *AAF1*, *KRE5*, *CDC10*, *SAP7*, *HOG1*, *CHK1*, *MNS1*, *MAD2*, *INP51*, *UTR2*, *RAS1*, *YPT72*, *CHS7*, *CEK1*, *MTLA1*, *CDC19*, *YHB1*, *YHB5*, *PHR1*, *GLN3*, *CST20*, *HSL1*, *PHO100*, *CAS5*, *KEX2*, *PTC1*, *CPP1*, *CLA4*, *NIK1*, *SIT4*, *IFF11*, *PEP7*, *SAP1*, *SAP3*, *ACE2*, *RBT4*, *NRG1*, *RIM101*, *CTA4*, *OCH1*, *IFF4*, *MKC1*, and *RFG1*, respectively.

B) Variability in the infectivity assay. Standard deviations in $\log_2(R/I)$ are presented for the first 6 measurements of each mutant and randomly generated sets of 6 ratios from the wild type dataset.

Table S1 *C. albicans* mutants with previously reported virulence and morphogenesis phenotypes

Systematic name	Gene name	Virulence phenotype	Reference	Morphology phenotype	Reference
orf19.1036	<i>MNS1</i>	Virulence defect	PMID:17933909	Filamentous growth abnormal	PMID:17933909
orf19.1093	<i>FLO8</i>	Virulence defect	PMID:16267276	Hyphal growth abnormal	PMID:16267276
orf19.1161	<i>PLD1</i>	Virulence defect	PMID:15552646	Hyphal growth abnormal	PMID:11283284
orf19.1275	<i>GAT1</i>	Virulence defect*	PMID:14617156	Wild-type hyphal growth*	PMID:14617156
orf19.1321	<i>HWP1</i>	Wild-type virulence	PMID:15817775	Wild-type filamentous growth	PMID:15817775
orf19.1358	<i>GCN4</i>	Wild-type virulence*	PMID:15302823	Filamentous growth abnormal*	PMID:15701793
orf19.1373	<i>INP51</i>	Virulence defect	PMID:18957583	Hyphal growth abnormal	PMID:18957583
orf19.147	<i>YAK1</i>	Wild-type virulence*	PMID:18321992	Filamentous growth abnormal*	PMID:18321992
orf19.1513	<i>FAB1</i>	Wild-type virulence*	PMID:12117957	Hyphal growth abnormal*	PMID:12117957
orf19.1526	<i>SNF2</i>	Virulence defect	PMID:16647065	Hyphal growth abnormal	PMID:16647065
orf19.1598	<i>ERG24</i>	Virulence defect	PMID:11897574	Hyphal growth abnormal	PMID:11897574
orf19.1621	<i>GPA2</i>	Wild-type virulence*	PMID:15302825	Filamentous growth abnormal*	PMID:15302825
orf19.1671	<i>UTR2</i>	Virulence defect	PMID:15042589 PMID:17074760	Hyphal growth abnormal	PMID:15042589
orf19.1716	<i>URA3</i>	Virulence defect	PMID:14500538	Hyphal growth abnormal	PMID:14500538
orf19.1760	<i>RAS1</i>	Virulence defect	PMID:11722734	Hyphal growth abnormal	PMID:10515923
orf19.1779	<i>MP65</i>	Virulence defect	PMID:17217426	Hyphal growth abnormal	PMID:17217426
orf19.1822	<i>UME6</i>	Virulence defect	PMID:19054126	Hyphal growth abnormal	PMID:19054126
orf19.2012	<i>NOT3</i>	Wild-type virulence*	PMID:14500538	Hyphal growth abnormal*	PMID:14500538
orf19.2154	<i>HXK1</i>	Virulence defect	PMID:11298769	Hyphal growth abnormal	PMID:11298769
orf19.2156	<i>NAG1</i>	Virulence defect	PMID:11298769	Hyphal growth abnormal	PMID:11298769
orf19.2157	<i>DAC1</i>	Virulence defect	PMID:11298769	Hyphal growth abnormal	PMID:11298769
orf19.2179	<i>SIT1</i>	Wild-type virulence	PMID:12060662 PMID:12183576	Wild-type hyphal growth	PMID:12183576
orf19.2245	<i>YPT72</i>	Virulence defect	PMID:19364843	Filamentous growth abnormal	PMID:19364843
orf19.2277	<i>TPK2</i>	Virulence defect	PMID:10652099	Hyphal growth abnormal	PMID:10652099
orf19.2334	<i>BIG1</i>	Virulence defect	PMID:16552067	Hyphal growth abnormal	PMID:16552067
orf19.2347	<i>MNN2</i>	Virulence defect	PMID:16467465	Hyphal growth abnormal	PMID:16467465
orf19.2379	<i>NOT4</i>	Virulence defect	PMID:14702416	Hyphal growth abnormal	PMID:14702416

orf19.2444	<i>CHS7</i>	Virulence defect	PMID:16079341	Filamentous growth abnormal	PMID:16079341
orf19.2614	<i>RSR1</i>	Virulence defect	PMID:9308185	Hyphal growth abnormal	PMID:9308185
orf19.2770.1	<i>SOD1</i>	Virulence defect	PMID:12427960	Hyphal growth abnormal	PMID:12427960
orf19.2809	<i>CTN3</i>	Wild-type virulence	PMID:18227254	Wild-type hyphal growth	PMID:18227254
orf19.2823	<i>RFG1</i>	Virulence defect	PMID:11259598	Filamentous growth abnormal	PMID:11259598
orf19.2849	<i>AQY1</i>	Wild-type virulence	PMID:11746601	Wild-type hyphal growth	PMID:11746601
orf19.2881	<i>MNN4</i>	Wild-type virulence	PMID:15271989	Wild-type hyphal growth	PMID:15271989
orf19.2886	<i>CEK1</i>	Virulence defect	PMID:9596738	Hyphal growth abnormal	PMID:9596738
orf19.290	<i>KRE5</i>	Virulence defect	PMID:15590817	Hyphal growth abnormal	PMID:15590817
orf19.2972	<i>PDE2</i>	Virulence defect	PMID:17614954	Filamentous growth abnormal	PMID:14523128
orf19.3010.1	<i>ECM33</i>	Virulence defect	PMID:15470113 PMID:18546157	Hyphal growth abnormal	PMID:15470113
orf19.3256	<i>SLN1</i>	Virulence defect	PMID:10572127	Hyphal growth abnormal	PMID:10572127
orf19.3340	<i>SOD2</i>	Wild-type virulence	PMID:12898709	Wild-type hyphal growth	PMID:12898709
orf19.3366	<i>CSH3</i>	Virulence defect	PMID:14756779	Hyphal growth abnormal	PMID:14756779
orf19.3523	<i>CRK1</i>	Virulence defect	PMID:11073971	Hyphal growth abnormal	PMID:11073971
orf19.3524	<i>CRK1</i>	Virulence defect	PMID:11073971	Filamentous growth abnormal	PMID:12773383
orf19.3642	<i>SUN41</i>	Virulence defect	PMID:17873081	Hyphal growth abnormal	PMID:17905924
orf19.3680	<i>SEP7</i>	Wild-type virulence*	PMID:12819094	Hyphal growth abnormal*	PMID:12819094
orf19.3707	<i>YHB1</i>	Virulence defect	PMID:15189992	Filamentous growth abnormal	PMID:16030247
orf19.3802	<i>PMT6</i>	Virulence defect	PMID:10809683	Hyphal growth abnormal	PMID:15659169
orf19.3829	<i>PHR1</i>	Virulence defect	PMID:7591097	Filamentous growth abnormal	PMID:10974097
orf19.3912	<i>GLN3</i>	Virulence defect	PMID:17950010	Filamentous growth abnormal	PMID:17369441
orf19.4064	<i>GPI7</i>	Virulence defect	PMID:11994163	Hyphal growth abnormal	PMID:11994163
orf19.4109	<i>PMT4</i>	Virulence defect	PMID:15659169	Hyphal growth abnormal	PMID:15659169
orf19.4208	<i>RAD52</i>	Virulence defect	PMID:16299301	Filamentous growth abnormal	PMID:16468988
orf19.4242	<i>CST20</i>	Virulence defect	PMID:8917571	Hyphal growth abnormal	PMID:8917571
orf19.4257	<i>INT1</i>	Virulence defect	PMID:10444345	Filamentous growth abnormal	PMID:9478896
orf19.4284	<i>BUR2</i>	Wild-type virulence	PMID:14500538	Wild-type hyphal growth	PMID:14500538
orf19.4304	<i>GAP1</i>	Wild-type virulence*	PMID:12949183	Filamentous growth abnormal*	PMID:12949183
orf19.4308	<i>HSL1</i>	Virulence defect	PMID:15659158	Filamentous growth abnormal	PMID:15659158
orf19.4339	<i>VPS4</i>	Virulence defect	PMID:18814053	Filamentous growth	PMID:15590834

				abnormal	
orf19.4401	<i>YVH1</i>	Virulence defect	PMID:16000712	Hyphal growth abnormal	PMID:16000712
orf19.454	<i>SFL1</i>	Virulence defect	PMID:17715361	Hyphal growth abnormal	PMID:17715361
orf19.4551	<i>CTN1</i>	Wild-type virulence	PMID:18227254	Wild-type hyphal growth	PMID:18227254
orf19.4565	<i>BGL2</i>	Virulence defect	PMID:9043114	Hyphal growth abnormal	PMID:9043114
orf19.4590	<i>RFX2</i>	Virulence defect	PMID:19252121	Filamentous growth abnormal	PMID:19252121
orf19.4591	<i>CAT2</i>	Wild-type virulence	PMID:18281597	Wild-type hyphal growth	PMID:18227254
orf19.469	<i>HST7</i>	Wild-type virulence*	PMID:8917571	Hyphal growth abnormal*	PMID:8917571
orf19.4719	<i>CWH41</i>	Virulence defect	PMID:17933909	Filamentous growth abnormal	PMID:17933909
orf19.4755	<i>KEX2</i>	Virulence defect	PMID:12419804	Hyphal growth abnormal	PMID:9360967
orf19.4773	<i>AOX2</i>	Wild-type virulence	PMID:11368790	Wild-type hyphal growth	PMID:11368790
orf19.4774	<i>AOX1</i>	Wild-type virulence	PMID:11368790	Wild-type hyphal growth	PMID:11368790
orf19.4785	<i>PTC1</i>	Virulence defect	PMID:18708562	Hyphal growth abnormal	PMID:18708562
orf19.4866	<i>CPP1</i>	Virulence defect	PMID:9398674	Hyphal growth abnormal	PMID:9398674
orf19.4890	<i>CLA4</i>	Virulence defect	PMID:9259554	Hyphal growth abnormal	PMID:9259554
orf19.4927	<i>BNI1</i>	Virulence defect	PMID:15914538	Filamentous growth abnormal	PMID:16215178
orf19.4958	<i>ECM25</i>	Virulence defect	PMID:18368314	Filamentous growth abnormal	PMID:18368314
orf19.5031	<i>SSK1</i>	Virulence defect	PMID:10639412	Hyphal growth abnormal	PMID:10639412
orf19.505	<i>SRV2</i>	Virulence defect	PMID:11325951	Filamentous growth abnormal	PMID:11325951
orf19.5061	<i>ADE5,7</i>	Virulence defect	PMID:17600079	Hyphal growth abnormal	PMID:17600079
orf19.5083	<i>DRG1</i>	Virulence defect	PMID:17159222	Filamentous growth abnormal	PMID:17159222
orf19.5107	<i>NOT5</i>	Virulence defect	PMID:12787355 PMID:14500538	Hyphal growth abnormal	PMID:14500538
orf19.5148	<i>CYR1</i>	Virulence defect	PMID:11694594	Filamentous growth abnormal	PMID:11694594
orf19.5171	<i>PMT1</i>	Virulence defect	PMID:9694829	Hyphal growth abnormal	PMID:15659169
orf19.5181	<i>NIK1</i>	Virulence defect	PMID:11270409 PMID:10572127	Hyphal growth abnormal	PMID:9618540
orf19.5200	<i>SIT4</i>	Virulence defect	PMID:14731272	Hyphal growth abnormal	PMID:14731272
orf19.5343	<i>ASH1</i>	Virulence defect	PMID:12446785	Filamentous growth abnormal	PMID:12446785
orf19.548	<i>CDC10</i>	Virulence defect	PMID:12819094	Hyphal growth abnormal	PMID:12819094
orf19.5657	<i>SWI1</i>	Virulence defect	PMID:16647065	Hyphal growth abnormal	PMID:16647065
orf19.5662	<i>PEP7</i>	Virulence defect	PMID:17005990	Hyphal growth abnormal	PMID:17005990
orf19.5691	<i>CDC11</i>	Virulence defect	PMID:12819094	Filamentous growth abnormal	PMID:12181342

orf19.5741	<i>ALS1</i>	Virulence defect	PMID:15042589	Hyphal growth abnormal	PMID:15256583
orf19.5798	<i>LIG4</i>	Virulence defect	PMID:16299301	Filamentous growth abnormal	PMID:11119499
orf19.589	<i>VPS21</i>	Virulence defect	PMID:19364843	Filamentous growth abnormal	PMID:19364843
orf19.5908	<i>TEC1</i>	Virulence defect	PMID:11069668	Hyphal growth abnormal	PMID:11069668
orf19.5962	<i>SNF3</i>	Virulence defect	PMID:17030998	Filamentous growth abnormal	PMID:17030998
orf19.6009	<i>SET1</i>	Virulence defect	PMID:16629671	Filamentous growth abnormal	PMID:16629671
orf19.6033	<i>CMP1</i>	Virulence defect	PMID:16790813	Hyphal growth abnormal	PMID:12753189
orf19.6040	<i>SNF7</i>	Virulence defect	PMID:16299290	Filamentous growth abnormal	PMID:15590834
orf19.6091	<i>RIM8</i>	Virulence defect	PMID:10992507	Filamentous growth abnormal	PMID:10601209
orf19.6092	<i>KEL1</i>	Wild-type virulence*	PMID:14500538	Hyphal growth abnormal*	PMID:14500538
orf19.610	<i>EFG1</i>	Virulence defect	PMID:15760450	Hyphal growth abnormal	PMID:11595734
orf19.6109	<i>TUP1</i>	Virulence defect	PMID:12576958	Filamentous growth abnormal	PMID:9204892
orf19.6124	<i>ACE2</i>	Virulence defect	PMID:15255906	Filamentous growth abnormal	PMID:15255906
orf19.6214	<i>ATC1</i>	Virulence defect	PMID:17464051	Hyphal growth abnormal	PMID:17464051
orf19.6229	<i>CAT1</i>	Virulence defect	PMID:9573075	Hyphal growth abnormal	PMID:18352908
orf19.6243	<i>VPS34</i>	Virulence defect	PMID:11065354	Hyphal growth abnormal	PMID:11065354
orf19.6362	<i>SPA2</i>	Virulence defect	PMID:12940995	Hyphal growth abnormal	PMID:12940995
orf19.6515	<i>HSP90</i>	Virulence defect	PMID:19327993	Filamentous growth abnormal	PMID:19327993
orf19.6598	<i>WAL1</i>	Virulence defect	PMID:17139615	Hyphal growth abnormal	PMID:15075276
orf19.6640	<i>TPS1</i>	Virulence defect	PMID:9683476	Hyphal growth abnormal	PMID:10577485
orf19.6734	<i>TCC1</i>	Virulence defect	PMID:16998076	Filamentous growth abnormal	PMID:16998076
orf19.6760	<i>MDS3</i>	Virulence defect	PMID:12524333	Hyphal growth abnormal	PMID:16087754
orf19.6798	<i>SSN6</i>	Virulence defect	PMID:12581357	Hyphal growth abnormal	PMID:12581357
orf19.6844	<i>ICL1</i>	Virulence defect*	PMID:17158734	Wild-type filamentous growth*	PMID:11452311
orf19.6953	<i>IRS4</i>	Virulence defect	PMID:16151204	Hyphal growth abnormal	PMID:16151204
orf19.7089	<i>PMR1</i>	Virulence defect	PMID:15843378	Filamentous growth abnormal	PMID:15843378
orf19.7150	<i>NRG1</i>	Virulence defect	PMID:11532939	Filamentous growth abnormal	PMID:11532939
orf19.7247	<i>RIM101</i>	Virulence defect	PMID:12524333 PMID:10992507	Filamentous growth abnormal	PMID:10074081
orf19.7391	<i>OCH1</i>	Virulence defect	PMID:16263704	Hyphal growth abnormal	PMID:16263704
orf19.7479	<i>NTH1</i>	Wild-type virulence*	PMID:9421900	Hyphal growth abnormal*	PMID:9421900
orf19.7523	<i>MKC1</i>	Virulence defect	PMID:9009353	Hyphal growth	PMID:9493378

				abnormal	
orf19.7549	<i>PMT5</i>	Wild-type virulence	PMID:15659169	Wild-type hyphal growth	PMID:15659169
orf19.7551	<i>ALO1</i>	Virulence defect	PMID:11349062	Hyphal growth abnormal	PMID:11349062
orf19.7622	<i>SPT3</i>	Virulence defect	PMID:12072450	Filamentous growth abnormal	PMID:12072450
orf19.767	<i>ERG3</i>	Virulence defect	PMID:16436713	Filamentous growth abnormal	PMID:16436713
orf19.806	<i>VMA7</i>	Virulence defect	PMID:15870472	Hyphal growth abnormal	PMID:15870472
orf19.881	<i>DFG16</i>	Virulence defect	PMID:17367383	Filamentous growth abnormal	PMID:17367383
orf19.895	<i>HOG1</i>	Virulence defect	PMID:10322006	Filamentous growth abnormal	PMID:16339080
orf19.896	<i>CHK1</i>	Virulence defect	PMID:10572127	Hyphal growth abnormal	PMID:10572127
orf19.96	<i>TOP1</i>	Virulence defect	PMID:9043115	Hyphal growth abnormal	PMID:9043115
orf19.971	<i>SKN7</i>	Virulence defect	PMID:15039366	Hyphal growth abnormal	PMID:15039366
orf19.974	<i>ROT2</i>	Virulence defect	PMID:17933909	Filamentous growth abnormal	PMID:17933909

* Denotes discordance between virulence and morphology phenotypes

Table S2 *C. albicans* mutants with previously reported virulence and kidney burden phenotypes

Systematic name	Gene name	Virulence	Kidney burden	Reference
orf19.5741	<i>ALS1</i>	Decreased	Decreased	PMID:15042589
orf19.2849	<i>AQY1</i>	Wild-type	Wild-type	PMID:11746601
orf19.4565	<i>BGL2</i>	Decreased	Decreased	PMID:9043114
orf19.4670	<i>CAS5</i>	Decreased	Decreased	PMID:19463063
orf19.4328	<i>CCC2</i>	Wild-type	Wild-type	PMID:12067343
orf19.548	<i>CDC10</i>	Decreased	Decreased	PMID:12819094
orf19.5691	<i>CDC11</i>	Decreased	Decreased	PMID:12819094
orf19.4890	<i>CLA4</i>	Decreased	Decreased	PMID:9259554
orf19.6033	<i>CMP1</i>	Decreased	Decreased	PMID:12753189
orf19.4009	<i>CNB1</i>	Decreased	Decreased	PMID:12796287
orf19.367	<i>CNH1</i>	Decreased*	Wild-type*	PMID:10832630
orf19.4866	<i>CPP1</i>	Decreased	Decreased	PMID:9398674
orf19.4242	<i>CST20</i>	Decreased	Decreased	PMID:8917571
orf19.5083	<i>DRG1</i>	Decreased	Decreased	PMID:17159222
orf19.4958	<i>ECM25</i>	Decreased	Decreased	PMID:18368314
orf19.7219	<i>FTR1</i>	Decreased	Decreased	PMID:10807578
orf19.7231	<i>FTR2</i>	Wild-type	Wild-type	PMID:10807578
orf19.4308	<i>HSL1</i>	Decreased	Decreased	PMID:15659158
orf19.4257	<i>INT1</i>	Decreased*	Increased*	PMID:10444345
orf19.4755	<i>KEX2</i>	Decreased	Decreased	PMID:12419804
orf19.1040	<i>MAD2</i>	Decreased	Decreased	PMID:12100546
orf19.7523	<i>MKC1</i>	Decreased	Decreased	PMID:9009353
orf19.2881	<i>MNN4</i>	Wild-type	Wild-type	PMID:15271989
orf19.1665	<i>MNT1</i>	Decreased	Decreased	PMID:9636208
orf19.7391	<i>OCH1</i>	Decreased*	Wild-type*	PMID:16263704
orf19.689	<i>PLB1</i>	Decreased	Decreased	PMID:9748287
orf19.1161	<i>PLD1</i>	Decreased	Decreased	PMID:15552646
orf19.5171	<i>PMT1</i>	Decreased	Decreased	PMID:9694829
orf19.4208	<i>RAD52</i>	Decreased	Decreased	PMID:16299301
orf19.7247	<i>RIM101</i>	Decreased	Decreased	PMID:10992507
orf19.6091	<i>RIM8</i>	Decreased	Decreased	PMID:10992507
orf19.2614	<i>RSR1</i>	Decreased	Decreased	PMID:18281602
orf19.6009	<i>SET1</i>	Decreased	Decreased	PMID:16629671
orf19.5962	<i>SNF3</i>	Decreased*	Wild-type*	PMID:17030998
orf19.2060	<i>SOD5</i>	Decreased	Decreased	PMID:14617819
orf19.1671	<i>UTR2</i>	Decreased	Decreased	PMID:15042589
orf19.6243	<i>VPS34</i>	Decreased	Decreased	PMID:11065354
orf19.4339	<i>VPS4</i>	Decreased	Decreased	PMID:18814053

* Denotes discrepancy between virulence and kidney burden

Table S6 Analysis of hyphal formation among infectivity-defective mutants

Mutant	Systematic name	Gene name	M score	Hyphal formation
57	orf19.2500		S	Normal
58	orf19.2570	<i>MCI4</i>	S	Normal
62	orf19.2821		S	Normal
70	orf19.3290		0	Normal
71	orf19.3335		0	Normal
75	orf19.3611		0	Normal
93	orf19.4758		S	Normal
101	orf19.4831		0	Normal
103	orf19.4933	<i>FAD3</i>	2	Normal
111	orf19.5234	<i>RBD1</i>	2	Normal
118	orf19.5499		0	Normal
119	orf19.5509		0	Normal
129	orf19.6035		S	Normal
133	orf19.6249	<i>HAK1</i>	0	Normal
134	orf19.6327	<i>HET1</i>	0	Normal
136	orf19.6607		S	Normal
144	orf19.7288		0	Normal
147	orf19.7436	<i>AAF1</i>	2	Normal
150	orf19.7590		S	Normal
193	orf19.30		5	Normal
200	orf19.101	<i>RIM9</i>	2	Defective
209	orf19.191	<i>KIC1</i>	6	Defective
211	orf19.194		0	Normal
225	orf19.290	<i>KRE5</i>	4	Defective
229	orf19.328	<i>NPR2</i>	4	Normal
241	orf19.449		0	Normal
247	orf19.529		0	Normal
249	orf19.548	<i>CDC10</i>	1	Normal
251	orf19.557		0	Normal
263	orf19.649		3	Defective
265	orf19.663	<i>GIN4</i>	6	Defective
275	orf19.723	<i>BCR1</i>	5	Defective
276	orf19.726	<i>PPZ1</i>	4	Normal
281	orf19.753		0	Normal
287	orf19.783		5	Defective
293	orf19.807	<i>CHS5</i>	2	Normal
299	orf19.844	<i>STE11</i>	3	Normal
307	orf19.895	<i>HOG1</i>	4	Normal
319	orf19.1040	<i>MAD2</i>	0	Normal
324	orf19.1092		3	Defective
340	orf19.1264	<i>CFL2</i>	0	Normal
344	orf19.1276		0	Normal
360	orf19.1373	<i>INP51</i>	3	Normal
362	orf19.1392		0	Normal
367	orf19.1445	<i>ESC4</i>	0	Normal
372	orf19.1490	<i>MSB2</i>	4	Normal
379	orf19.1567		4	Normal
388	orf19.1621	<i>GPA2</i>	4	Normal
397	orf19.1671	<i>UTR2</i>	2	Normal
440	orf19.2013	<i>KAR2</i>	0	Normal
442	orf19.2021	<i>HGT8</i>	0	Normal
459	orf19.2094	<i>PDR6</i>	1	Normal
486	orf19.2315		0	Normal
497	orf19.2444	<i>CHS7</i>	0	Normal

504	orf19.2484		IC	Normal
517	orf19.2653		0	Normal
526	orf19.2726		0	Normal
540	orf19.2842	<i>GZF3</i>	2	Normal
552	orf19.2961		0	Normal
582	orf19.3201	<i>MTLA1</i>	0	Normal
585	orf19.3212	<i>MID1</i>	0	Normal
590	orf19.3283		0	Normal
599	orf19.3384		0	Normal
624	orf19.3575	<i>CDC19</i>	0	Normal
650	orf19.3753	<i>SEF1</i>	0	Normal
655	orf19.3794	<i>CSR1</i>	3	Normal
660	orf19.3829	<i>PHR1</i>	4	Defective
670	orf19.3895	<i>CHT2</i>	0	Normal
678	orf19.3995	<i>RIM13</i>	3	Defective
680	orf19.4002	<i>DUN1</i>	0	Normal
692	orf19.4084	<i>KIS1</i>	3	Normal
706	orf19.4182		4	Defective
709	orf19.4188	<i>NMD5</i>	0	Normal
726	orf19.4292		4	Normal
728	orf19.4308	<i>HSL1</i>	2	Normal
750	orf19.4471		3	Normal
769	orf19.4593	<i>RGA2</i>	0	Normal
770	orf19.4603	<i>ARL1</i>	4	Normal
774	orf19.4640	<i>PWP1</i>	S	Defective
783	orf19.4720	<i>CTR2</i>	3	Normal
786	orf19.4729		4	Normal
791	orf19.4755	<i>KEX2</i>	S	Defective
796	orf19.4785	<i>PTC1</i>	3	Normal
805	orf19.4844		3	Normal
809	orf19.4866	<i>CPP1</i>	2	Normal
812	orf19.4890	<i>CLA4</i>	4	Normal
814	orf19.4905		0	Normal
831	orf19.5068		4	Defective
855	orf19.5241	<i>SNT1</i>	2	Normal
881	orf19.5445	<i>GLO3</i>	4	Normal
904	orf19.5662	<i>PEP7</i>	5	Normal
918	orf19.5776	<i>TOM1</i>	2	Normal
919	orf19.5782		0	Normal
942	orf19.5994	<i>RHB1</i>	0	Normal
944	orf19.6011	<i>SIN3</i>	6	Normal
956	orf19.6124	<i>ACE2</i>	5	Normal
960	orf19.6202	<i>RBT4</i>	0	Normal
969	orf19.6293		3	Normal
980	orf19.6411		0	Normal
1018	orf19.6736		S	Normal
1023	orf19.6784	<i>PGA32</i>	0	Normal
1031	orf19.6842		2	Normal
1050	orf19.7049	<i>CYB5</i>	0	Normal
1055	orf19.7094	<i>HGT12</i>	0	Normal
1063	orf19.7150	<i>NRG1</i>	4	Normal
1064	orf19.7186	<i>CLB4</i>	3	Normal
1090	orf19.7349	<i>CHS4</i>	0	Normal
1092	orf19.7359	<i>CRZ1</i>	0	Normal
1098	orf19.7388	<i>PBS2</i>	3	Normal
1100	orf19.7397		0	Normal
1132	orf19.10080	<i>TRP2</i>	0	Normal
1133	orf19.10341	<i>RFG1</i>	3	Normal
1138	orf19.11256	<i>PPG1</i>	4	Normal

1139	orf19.11257	SSK2	3	Normal
1149	orf19.13191	SNF4	S	Defective

Legend for Table S6 The ability of the 115 infectivity-defective mutants to form hyphae was determined using the clinical germ tube assay. Small colonies of each mutant and of the wild type comparator SN250 were inoculated into 500 μ l bovine serum, mixed by vortexing, and incubated at 35°C for 2.5 hours. Cells were fixed by addition of 1 drop of 10% formaldehyde and examined under 40x magnification. Scoring for germ tube formation was as follows: “normal” was defined as the presence of at least 5 true hyphae (short lateral extensions from the yeast cell with parallel sides and no constriction at the junction with the parent; typically, 5-10 hyphae were seen within 10 microscopic fields); “defective” was defined as 0-4 hyphae with wild type morphology on the entire slide (>10 microscopic fields).

Table S7 Analysis of chromosome ploidy in 12 mutants and the parent strain by quantitative PCR

Chromosome	Strain	Experiment 1		Experiment 2		Average Ploidy	Chromosome	Strain	Experiment 1		Experiment 2		Average Ploidy
		Ploidy	Std dev	Ploidy	Std dev				Ploidy	Std dev	Ploidy	Std dev	
Ch1	SN152	1.11	0.13	1.14	0.26	1.12	Ch1	SN152	1.10	0.05	1.12	0.07	1.11
	4 (<i>slid1</i>)	1.00	0.03	1.00	0.04	1.00		650	1.00	0.04	0.85	0.11	0.93
	90 (<i>hsx11</i>)	0.98	0.06	1.00	0.06	0.99		960	0.96	0.05	0.99	0.09	0.97
	101 (<i>orf19.4831</i>)	0.98	0.07	0.91	0.09	0.94		72	0.99	0.02	1.00	0.06	0.99
	m134 (<i>het1</i>)	1.14	0.05	1.12	0.10	1.13		122	0.97	0.03	0.99	0.04	0.98
	40	0.96	0.02	0.91	0.07	0.93		143	1.00	0.06	1.00	0.03	1.00
	47	1.02	0.06	1.05	0.05	1.04		1070	1.13	0.05	1.20	0.05	1.17
Ch2	SN152	1.16	0.05	1.19	0.10	1.18	Ch2	SN152	1.15	0.05	1.14	0.10	1.15
	4 (<i>slid1</i>)	0.95	0.06	1.00	0.06	0.98		650	0.95	0.04	0.97	0.11	0.96
	90 (<i>hsx11</i>)	1.00	0.05	1.00	0.03	1.00		960	0.98	0.06	0.94	0.04	0.96
	101 (<i>orf19.4831</i>)	0.94	0.03	0.97	0.03	0.96		72	1.00	0.05	1.00	0.07	1.00
	m134 (<i>het1</i>)	1.09	0.08	1.17	0.01	1.13		122	0.98	0.04	1.00	0.04	0.99
	40	0.98	0.05	1.00	0.05	0.99		143	1.04	0.04	1.03	0.03	1.04
	47	1.01	0.04	1.07	0.14	1.04		1070	1.00	0.02	1.09	0.12	1.04
Ch3	SN152	1.04	0.03	1.14	0.04	1.13	Ch3	SN152	1.12	0.03	1.19	0.04	1.16
	4 (<i>slid1</i>)	0.91	0.02	0.99	0.02	0.99		650	1.03	0.02	0.95	0.08	0.99
	90 (<i>hsx11</i>)	0.90	0.05	1.00	0.05	0.99		960	1.00	0.03	0.94	0.10	0.97
	101 (<i>orf19.4831</i>)	0.97	0.05	0.89	0.04	0.97		72	0.98	0.02	0.96	0.07	0.97
	m134 (<i>het1</i>)	1.01	0.05	1.06	0.04	1.07		122	0.98	0.04	1.00	0.02	0.99
	40	1.00	0.08	0.92	0.05	1.00		143	1.00	0.05	1.04	0.04	1.02
	47	1.14	0.10	1.01	0.03	1.12		1070	1.10	0.08	1.40	0.19	1.25
Ch4	SN152	0.93	0.29	0.92	0.24	0.91	Ch4	SN152	0.91	0.30	1.00	0.25	0.95
	4 (<i>slid1</i>)	1.06	0.15	0.99	0.11	1.01		650	1.00	0.12	1.00	0.20	1.00
	90 (<i>hsx11</i>)	1.00	0.44	1.03	0.17	1.00		960	1.03	0.04	1.00	0.20	1.01
	101 (<i>orf19.4831</i>)	1.06	0.15	1.05	0.14	1.04		72	1.02	0.03	1.09	0.27	1.06
	m134 (<i>het1</i>)	1.00	0.12	0.97	0.19	0.97		122	0.97	0.03	1.06	0.09	1.01
	40	0.98	0.16	1.00	0.16	0.98		143	0.84	0.07	1.00	0.12	0.92
	47	1.01	0.16	1.05	0.19	1.02		1070	1.10	0.03	1.13	0.12	1.11
Ch5	SN152	0.91	0.14	0.85	0.34	0.90	Ch5	SN152	1.01	0.15	1.00	0.15	1.00
	4 (<i>slid1</i>)	1.00	0.10	1.00	0.11	1.02		650	0.85	0.16	1.00	0.15	0.92
	90 (<i>hsx11</i>)	1.02	0.12	0.94	0.17	1.00		960	1.03	0.12	1.04	0.14	1.04
	101 (<i>orf19.4831</i>)	0.94	0.09	1.01	0.11	0.99		72	0.94	0.06	0.94	0.10	0.94
	m134 (<i>het1</i>)	1.02	0.14	1.16	0.04	1.11		122	1.00	0.08	1.03	0.09	1.01
	40	1.00	0.18	1.02	0.11	1.03		143	1.13	0.10	1.24	0.10	1.19
	47	0.97	0.17	0.98	0.08	0.99		1070	0.98	0.15	0.97	0.09	0.98
Ch6	SN152	1.07	0.04	1.06	0.02	1.06	Ch6	SN152	1.04	0.04	1.12	0.02	1.08
	4 (<i>slid1</i>)	0.97	0.05	1.01	0.03	0.99		650	1.02	0.01	1.00	0.04	1.01
	90 (<i>hsx11</i>)	0.98	0.02	1.02	0.02	1.00		960	0.98	0.03	0.99	0.07	0.99
	101 (<i>orf19.4831</i>)	1.01	0.02	0.99	0.02	1.00		72	0.96	0.00	0.96	0.06	0.96
	m134 (<i>het1</i>)	1.00	0.02	1.00	0.04	1.00		122	1.00	0.08	1.00	0.04	1.00
	40	1.01	0.08	1.00	0.04	1.01		143	1.04	0.02	1.09	0.02	1.06
	47	0.99	0.07	0.94	0.02	0.97		1070	0.97	0.06	1.00	0.17	0.98
Ch7	SN152	0.98	0.04	1.00	0.22	0.99	Ch7	SN152	1.06	0.08	1.03	0.10	1.04
	4 (<i>slid1</i>)	0.96	0.12	1.03	0.03	1.00		650	1.06	0.05	0.98	0.13	1.02
	90 (<i>hsx11</i>)	1.02	0.05	1.04	0.06	1.04		960	1.06	0.08	1.05	0.18	1.06
	101	1.05	0.03	0.99	0.10	1.02		72	0.93	0.05	1.04	0.06	0.99

	(<i>orf19.4831</i>)												
	m134 (<i>het1</i>)	0.98	0.16	0.97	0.07	0.98		122	1.00	0.09	0.97	0.03	0.99
	40	1.05	0.09	1.02	0.05	1.04		143	0.98	0.02	1.00	0.04	0.99
	47	1.00	0.07	0.94	0.11	0.97		1070	1.00	0.08	0.97	0.14	0.98
ChR	SN152	0.93	0.10	0.76	0.12	0.85	ChR	SN152	1.03	0.10	0.98	0.06	1.00
	4 (<i>sld1</i>)	1.05	0.06	1.06	0.10	1.05		650	1.12	0.10	0.99	0.11	1.05
	90 (<i>hsx11</i>)	1.00	0.07	1.00	0.11	1.00		960	1.06	0.06	1.04	0.08	1.05
	101 (<i>orf19.4831</i>)	1.00	0.05	1.09	0.08	1.05		72	1.00	0.06	1.08	0.04	1.04
	m134 (<i>het1</i>)	0.83	0.03	0.89	0.06	0.86		122	0.93	0.08	1.00	0.05	0.96
	40	1.01	0.04	1.06	0.08	1.04		143	0.74	0.02	0.87	0.03	0.80
	47	0.82	0.06	0.94	0.10	0.88		1070	0.84	0.03	1.01	0.05	0.93

Legend for Table S7 Analysis of the eight *C. albicans* chromosomes was performed on the parental strain (SN152), six strains that demonstrated abnormal infectivity (mutants 4 (*sld1/orf19.260*), 90 (*hsx11*), 101 (*orf19.4831*), 134 (*het1*), 650, and 960), and 6 strains with normal infectivity (mutants 40, 47, 72, 122, 143, and 1070). Results of two experiments are presented.

The aneuploidy assay was adapted from that of Arbour et al.³ using published Primer Set A to monitor the copy number of *C. albicans* Chromosomes 1, 2, 3, 4, 5, 6, 7, and R. Modifications were as follows: Rather than performing mixed reactions with TaqMan probes to all eight chromosomes, SYBR green was used to monitor the appearance of PCR products in individual reactions for each chromosome. 20 μ l reactions were assembled containing ~200 ng of genomic DNA of the strain being tested, 2 μ M of each diagnostic primer, 2 mM MgCl₂, 50 mM KCl, 10 mM Tris 8.3, 0.075x SYBR Green (Sigma), and 0.2 units of Taq polymerase. In a 384 well plate, SN152 (diploid control) and 6 mutant strains were tested in sextuplicate, along with sextuplicate reactions of SN152 used for calibration with a standard curve. Each experiment was repeated, such that 12 replicates of each sample were represented in the final analysis. Data for each primer set were median-centered and the wild-type sample was analyzed identically to each mutant sample.

Table S9 *C. albicans* strains used in this study

Strain	Phenotype	Genotype	Reference
SN152	Reference strain His ⁻ Leu ⁻ Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴</i>	Noble and Johnson (2005)
SN87	Reference strain His ⁻ Leu ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴</i>	Noble and Johnson (2005)
QMY23	Reference strain prototroph	<i>his1Δ/his1Δ, leu2Δ::C.dubliniensis HIS1/leu2Δ::C.maltosa LEU2, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴</i> Note: QMY23 was derived from SN87 by integration of <i>C. dubliniensis HIS1</i> and <i>C. maltosa LEU2</i> at the disrupted <i>leu2</i> loci.	Mitrovich et al. (2007)
SN250	Reference strain Arg ⁻	<i>his1Δ/his1Δ, leu2Δ::C.dubliniensis HIS1/leu2Δ::C.maltosa LEU2, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴</i>	This work
SN255	<i>orf19.260</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.260Δ::C.dubliniensisHIS1/orf19.260Δ::C.maltosaLEU2</i> (Isolate 1)	This work
SN256	<i>orf19.260</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.260Δ::C.dubliniensisHIS1/orf19.260Δ::C.maltosaLEU2</i> (Isolate 2)	This work
SN257	<i>orf19.260</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.260Δ::C.dubliniensisHIS1/orf19.260Δ::C.maltosaLEU2</i> (Isolate 3)	This work
SN285	<i>orf19.4592 (HSX11)</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.4592Δ::C.dubliniensisHIS1/orf19.4592Δ::C.maltosaLEU2</i> (Isolate 1)	This work
SN286	<i>orf19.4592 (HSX11)</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.4592Δ::C.dubliniensisHIS1/orf19.4592Δ::C.maltosaLEU2</i> (Isolate 2)	This work
SN290	<i>orf19.4831</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.4831Δ::C.dubliniensisHIS1/orf19.4831Δ::C.maltosaLEU2</i> (Isolate 1)	This work
SN291	<i>orf19.4831</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.4831Δ::C.dubliniensisHIS1/orf19.4831Δ::C.maltosaLEU2</i> (Isolate 2)	This work
SN292	<i>orf19.4831</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.4831Δ::C.dubliniensisHIS1/orf19.4831Δ::C.maltosaLEU2</i> (Isolate 3)	This work

SN296	<i>orf19.6327 (HET1)</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.6327Δ::C.dublinsiensisHIS1/orf19.6327Δ::C.maltosaLEU2</i> (Isolate 1)	This work
SN297	<i>orf19.6327 (HET1)</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.6327Δ::C.dublinsiensisHIS1/orf19.6327Δ::C.maltosaLEU2</i> (Isolate 2)	This work
SN298	<i>orf19.6327 (HET1)</i> mutant Arg ⁻	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.6327Δ::C.dublinsiensisHIS1/orf19.6327Δ::C.maltosaLEU2</i> (Isolate 3)	This work
SN425	Reference strain prototroph	<i>his1Δ/his1Δ, leu2Δ::C.dublinsiensisHIS1/leu2Δ::C.maltosaLEU2, arg4Δ/arg4Δ::C.dublinsiensisARG4, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴</i>	This work
SN426	<i>orf9.4592 (HSX11)</i> Complemented strain prototroph	<i>his1Δ/his1Δ, leu2Δ/leu2Δ::ORF19.4592-C.dublinsiensisARG4, arg4Δ/arg4Δ4, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.4592Δ::C.dublinsiensisHIS1/orf19.4592Δ::C.maltosaLEU2</i>	This work
SN428	<i>orf19.260</i> Complemented strain prototroph	<i>his1Δ/his1Δ, leu2Δ/leu2Δ::ORF19.260-C.dublinsiensisARG4, arg4Δ/arg4Δ4, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.260Δ::C.dublinsiensisHIS1/orf19.260Δ::C.maltosaLEU2</i>	This work
SN430	<i>orf19.4831</i> Complemented strain prototroph	<i>his1Δ/his1Δ, leu2Δ/leu2Δ::ORF19.4831-C.dublinsiensisARG4, arg4Δ/arg4Δ4, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.4831Δ::C.dublinsiensisHIS1/orf19.4831Δ::C.maltosaLEU2</i>	This work
SN432	<i>orf9.6327 (HET1)</i> Complemented strain prototroph	<i>his1Δ/his1Δ, leu2Δ/leu2Δ::ORF19.6327-C.dublinsiensisARG4, arg4Δ/arg4Δ4, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.6327Δ::C.dublinsiensisHIS1/orf19.6327Δ::C.maltosaLEU2</i>	This work
SN442	<i>orf19.4592 (HSX11)</i> mutant prototroph	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ::C.dublinsiensisARG4, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.4592Δ::C.dublinsiensisHIS1/orf19.4592Δ::C.maltosaLEU2</i>	This work
SN444	<i>orf19.260</i> mutant prototroph	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ::C.dublinsiensisARG4, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.260Δ::C.dublinsiensisHIS1/orf19.260Δ::C.maltosaLEU2</i>	This work
SN446	<i>orf19.4831</i> mutant prototroph	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ::C.dublinsiensisARG4, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.4831Δ::C.dublinsiensisHIS1/orf19.4831Δ::C.maltosaLEU2</i>	This work
SN448	<i>orf19.6327 (HET1)</i> mutant prototroph	<i>his1Δ/his1Δ, leu2Δ/leu2Δ, arg4Δ/arg4Δ::C.dublinsiensisARG4, URA3/ura3Δ::imm⁴³⁴, IRO1/iro1Δ::imm⁴³⁴, orf19.6327Δ::C.dublinsiensisHIS1/orf19.6327Δ::C.maltosaLEU2</i>	This work

Table S12 *C. albicans* mutants with reported virulence phenotypes that were recreated in this study

Mutant	Systematic name	Gene name	Published virulence phenotype	Reference	Infectivity Screen	
					Defect in Boolean test?	t-test p value
27	orf19.1345	<i>LIP8</i>	Virulence defect	PMID:17646357	no	2.1E-03
45	orf19.2156	<i>NAG1</i>	Virulence defect	PMID:11298769	no	9.8E-01
46	orf19.2157	<i>DAC1</i>	Virulence defect	PMID:11298769	no	5.5E-03
73	orf19.3380	<i>HWP2</i>	Virulence defect	PMID:19616419	no	1.0E-01
147	orf19.7436	<i>AAF1</i>	Virulence defect	PMID:10377090	Yes	1.3E-12
225	orf19.290	<i>KRE5</i>	Virulence defect	PMID:15590817	Yes	4.1E-01
249	orf19.548	<i>CDC10</i>	Virulence defect	PMID:16858141	Yes	0.0E+00
282	orf19.756	<i>SAP7</i>	Virulence defect	PMID:16177393	no	9.4E-01
307	orf19.895	<i>HOG1</i>	Virulence defect	PMID:10322006	Yes	0.0E+00
308	orf19.896	<i>CHK1</i>	Virulence defect	PMID:10417206	no	4.1E-01
318	orf19.1036	<i>MNS1</i>	Virulence defect	PMID:17933909	no	5.3E-01
319	orf19.1040	<i>MAD2</i>	Virulence defect	PMID:12100546	Yes	0.0E+00
360	orf19.1373	<i>INP51</i>	Virulence defect	PMID:18957583	Yes	0.0E+00
397	orf19.1671	<i>UTR2</i>	Virulence defect	PMID:15042589 PMID:17074760	Yes	6.8E-06
406	orf19.1760	<i>RAS1</i>	Virulence defect	PMID:11722734	no	6.7E-01
473	orf19.2245	<i>YPT72</i>	Virulence defect	PMID:19364843	no	8.6E-02
497	orf19.2444	<i>CHS7</i>	Virulence defect	PMID:16079341	Yes	5.7E-01
544	orf19.2886	<i>CEK1</i>	Virulence defect	PMID:9596738	no	2.4E-01
582	orf19.3201	<i>MTLA1</i>	Virulence defect	PMID:17555440	Yes	3.4E-07
624	orf19.3575	<i>CDC19</i>	Virulence defect	PMID:16681837	Yes	2.2E-16
642	orf19.3707	<i>YHB1</i>	Virulence defect	PMID:15189992	no	5.6E-01
643	orf19.3710	<i>YHB5</i>	Virulence defect	PMID:15189992	no	6.4E-01
660	orf19.3829	<i>PHR1</i>	Virulence defect	PMID:7591097	Yes	0.0E+00
671	orf19.3912	<i>GLN3</i>	Virulence defect	PMID:17950010	no	5.1E-01
716	orf19.4242	<i>CST20</i>	Virulence defect	PMID:8917571	no	1.4E-02
728	orf19.4308	<i>HSL1</i>	Virulence defect	PMID:15659158	Yes	0.0E+00
742	orf19.4424	<i>PHO100</i>	Virulence defect	PMID:19151328	no	6.3E-01

779	orf19.4670	CAS5	Virulence defect	PMID:19463063	no	7.3E-01
791	orf19.4755	KEX2	Virulence defect	PMID:12419804	Yes	0.0E+00
796	orf19.4785	PTC1	Virulence defect	PMID:18708562	Yes	6.8E-01
809	orf19.4866	CPP1	Virulence defect	PMID:9398674	Yes	2.3E-03
812	orf19.4890	CLA4	Virulence defect	PMID:9259554	Yes	0.0E+00
847	orf19.5181	NIK1	Virulence defect	PMID:11270409 PMID:10572127	no	8.4E-01
851	orf19.5200	SIT4	Virulence defect	PMID:14731272	no	4.2E-01
873	orf19.5399	IFF11	Virulence defect	PMID:17371861	no	8.5E-01
904	orf19.5662	PEP7	Virulence defect	PMID:17005990	Yes	5.4E-12
908	orf19.5714	SAP1	Virulence defect	PMID:9284116	no	3.1E-04
943	orf19.6001	SAP3	Virulence defect	PMID:9284116	no	2.2E-01
956	orf19.6124	ACE2	Virulence defect	PMID:15255906	Yes	0.0E+00
960	orf19.6202	RBT4	Virulence defect	PMID:10978273	Yes	1.1E-07
1063	orf19.7150	NRG1	Virulence defect	PMID:11532939	Yes	2.1E-01
1074	orf19.7247	RIM101	Virulence defect	PMID:12524333 PMID:10992507	no	8.7E-02
1094	orf19.7374	CTA4	Virulence defect	PMID:18083829	no	5.9E-01
1099	orf19.7391	OCH1	Virulence defect	PMID:16263704	no	3.1E-04
1107	orf19.7472	IFF4	Virulence defect	PMID:19347602	no	4.9E-01
1112	orf19.7523	MKC1	Virulence defect	PMID:9009353	no	3.3E-01
1133	orf19.10341	RFG1	Virulence defect	PMID:11259598	Yes	0.0E+00
95	orf19.4774	AOX1	Wild-type virulence	PMID:11368790	no	3.1E-03
123	orf19.5636	RBT5	Wild-type virulence	PMID:10978273	no	7.9E-01
207	orf19.173		Wild-type virulence	PMID:19463063	no	5.6E-01
245	orf19.469	HST7	Wild-type virulence	PMID:8917571	no	8.4E-01
388	orf19.1621	GPA2	Wild-type virulence	PMID:15302825	Yes	6.0E-09
395	orf19.1665	MNT1	Wild-type virulence	PMID:15519997	no	8.9E-01
630	orf19.3618	YWP1	Wild-type virulence	PMID:15870471	no	6.9E-01
638	orf19.3680	SEP7	Wild-type virulence	PMID:12819094	no	3.7E-01
724	orf19.4284	BUR2	Wild-type virulence	PMID:14500538	no	2.9E-12
1134	orf19.10507	XOG1	Wild-type virulence	PMID:9308184	no	2.7E-03

