

Table S1 : List of Oligonucleotides used in the manuscript

Table S1	
Name	Sequence
LR155F	5'-atttgAAAAATTCCAACAACTTAGGg-3'
LR155R	5'-aaaacCTTAAGTGTGGATTTC-3'
LR156F	5'TGATTTGGgATCcGTTTGAATGCACAACGTGAGAAACCCAAAAATTCCAACA ACTaAtG-3'
LR156R	5'TAATCCATTATTATTATTACTAGTATTACTACttCaTtAGTTGTGGAAAT TTT-3'
LR157F	5'- GGAAGTCTTGATAGATAC-3'
LR157R	5'- CCATTTGAAGGATTAGC-3'
LR135F	5'-CCATACACACACGTTAATTAG-3'
LR135R	5'-GCAGTTACTCTTTTGGG-3'
LR182F	atttgGTGGCCCCTGAATTGTGCG*
LR182R	aaaacGCACACAATTCAAGGGGCCAC*
LR183F	AGAAAGATGTTCCCGTAAAAGTTCAACTACCGCTTGACGGTGGCCCTtAATa GTGTGC*
LR183R	AGCATTGTATTGTAGTCGTACTCTGACAAACAAGCttGCACACtATTaAGGG GCCAC*
LR184F	GTGTTGGAGAATAGACAGCG
LR184R	CGGGTACATTATTGTGG
NPY1-S1	CCACCAAAAAAAAAATTTTCTCTTCTATTTAACATAGCTGCAATTAA CAACTGTTCTTTCTTCTTCTTCTTGTGCTTGTGagcttcgtacgctgcag gtc*
NPY1-exF	AAAACATTGACTTAAACTC
NPY1-S2	CTAAATTTTTTTTGAGCAAAAGTTGAAAAAGAAAAAGAACTCTAAAA CAACTCTAATGTATTAATAATCTATCTCTGTTCTACtctgatcatcgatgaatt cgag*
NPY1-exR	ATTTAACAAACACTGATT
X2-CaHIS1	CAACGAAATGGCCTCCCTACCACAG
X3-CaHIS1	GGACGAA TTGAAGAAAGCTGGTGCAACCG
X2-CaARG4	AAT GGA TCA GTG GCA CCG GTG
X3-CaARG4	GAGGAGTACGACCTCAAGCGC

(**Table S2** in Excel format separately)

Table S3: In general the larger chromosomes (R, 1 and 2) show higher frequencies of LOH than the smaller chromosomes (5 and 6):

Table S3: Loss of heterozygosity (LOH) is co-related with the size of chromosomes, larger chromosomes showing higher frequencies of LOH.

	Chr1	Chr2	Chr3	Chr4	Chr5	Chr6	Chr7	ChrR
Distribution of LOH	3.40%	4.15%	2.50%	3.00%	1.30%	1.20%	2.50%	4.00%
Chromosome Size	3.2	2.2	1.8	1.6	1.2	1	0.95	2.5

Table S4: Lists of Genes common to the three species examined with different drug sensitivities:

Caspofungin Sensitivity:

Genes common to <i>S.cerevisiae</i>, <i>C.albicans</i> and <i>C.glabrata</i>
MNT2

Genes Common to <i>C.albicans</i> and <i>S.cerevisiae</i>	Genes common to <i>S.cerevisiae</i> and <i>C.glabrata</i>	Genes common to <i>C.albicans</i> and <i>C.glabrata</i>
SAC7 VPS24 BSD2 GOS1 SWI4 CAT20/STE20	BCK1 ADA2 MKC1	CCH1 HEK2 SIP3

Fluconazole Sensitive:

Genes common to <i>S.cerevisiae</i>, <i>C.albicans</i> and <i>C.glabrata</i>
None

Genes Common to <i>C.albicans</i> and <i>S.cerevisiae</i>	Genes common to <i>S.cerevisiae</i> and <i>C.glabrata</i>	Genes common to <i>C.albicans</i> and <i>C.glabrata</i>
RPN4	None	None

Amphotericin B Sensitivity:

**Genes common to *S.cerevisiae*,
C.albicans and *C.glabrata***

MNT2

Genes Common to <i>C.albicans</i> and <i>S.cerevisiae</i>	Genes common to <i>S.cerevisiae</i> and <i>C.glabrata</i>	Genes common to <i>C.albicans</i> and <i>C.glabrata</i>
ATG15 RNH70 TPS1 MTG2 YUR1 RIT1 RBK1 POR1 ALG8 AYR1 HOG1 MNN10 LEN3	SSD1 DEP1 CWH41	None

Table S5: Lists of *C.albicans* strains used

Name of Strain	Genotype
CaSS1	his3::hisG/his3::hisG leu2::tetR-GAL4AD-URA3/LEU2
SN148	arg4Δ/arg4Δ, leu2Δ/leu2Δ, his1Δ/his1Δ, ura3Δ/ura3Δ
SN76	arg4Δ/arg4Δ, his1Δ/his1Δ, ura3Δ/ura3Δ

Table S6 and S7 are in Excel Format

Supplementary Figure S1:

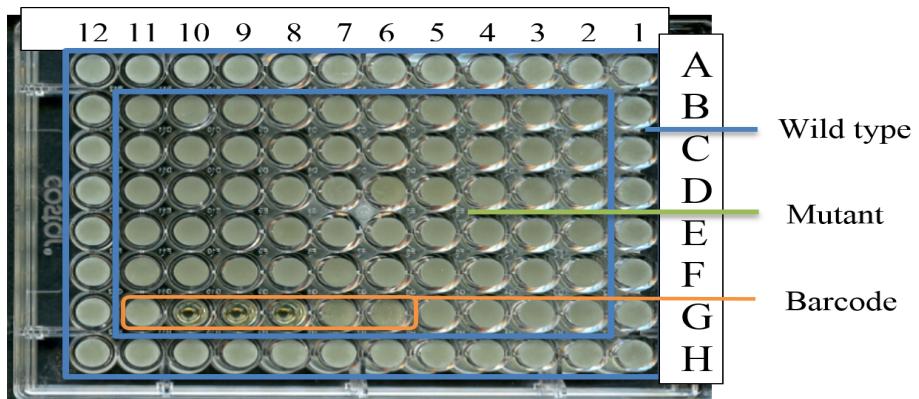
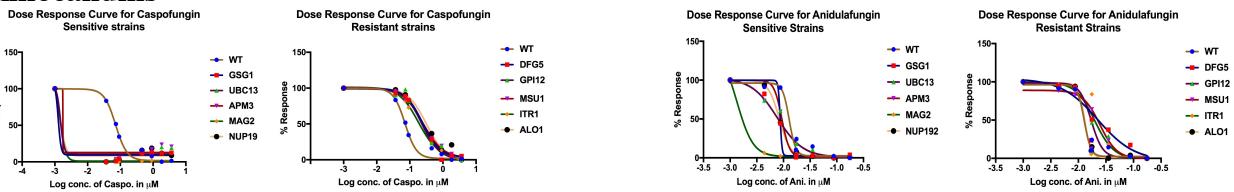


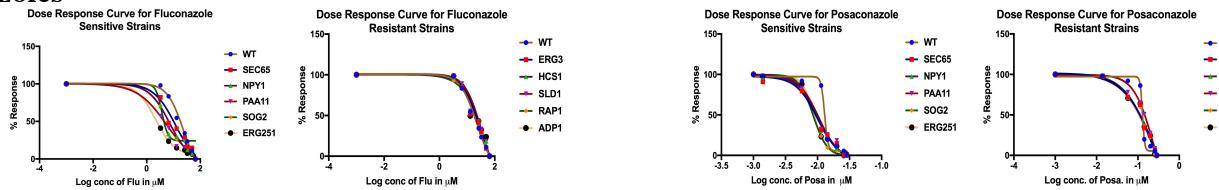
Fig. S1: A plate from Grace V1.0 collection showing the distribution of the strains in it. All the edges are occupied by the wild type parent strain CaSS1 (WT), and each plate has a unique barcode in the last 6 inner wells (G6 to G11) consisting of various patterns of CaSS1 and the morphologically distinct mutant *dig1/dig1*

Supplementary Figure S2:

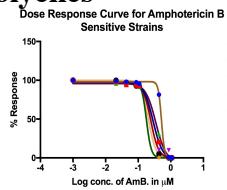
Echinocandins



Azoles



Polyenes



Pyridine Amides

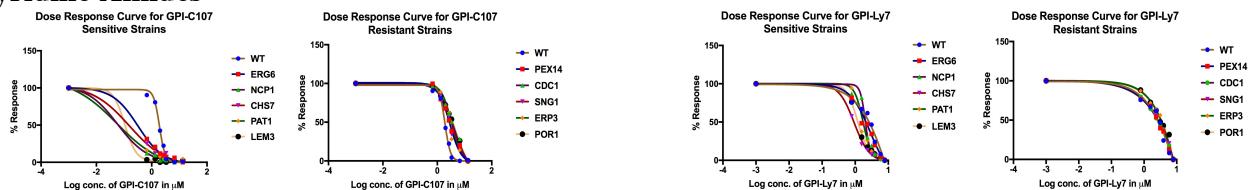


Fig S2: Dose response curves for the different drugs