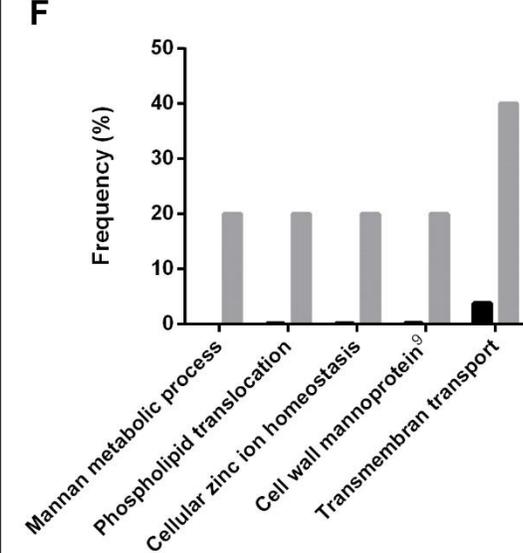
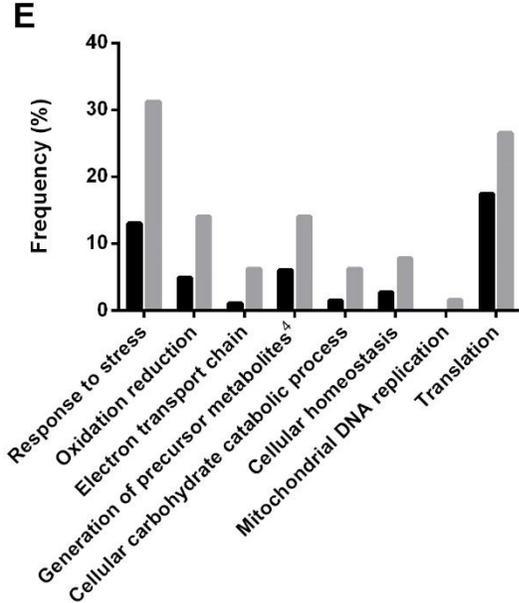
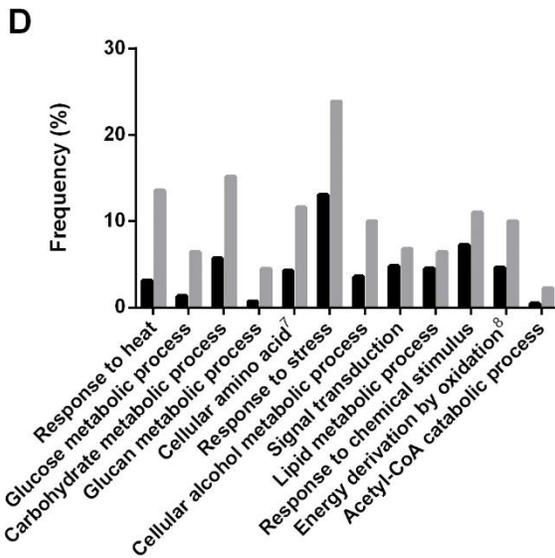
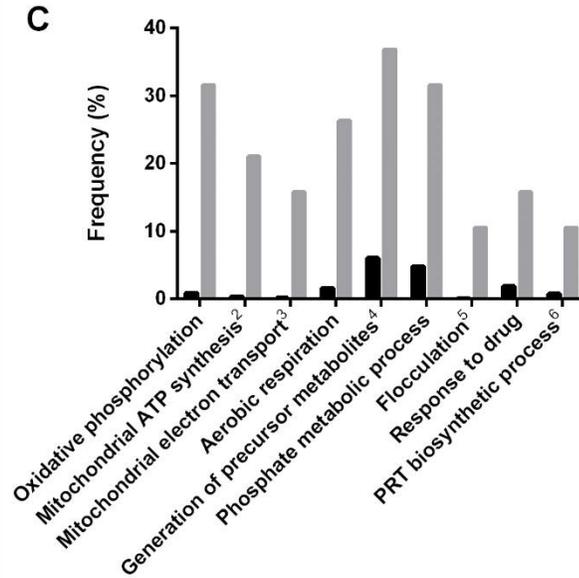
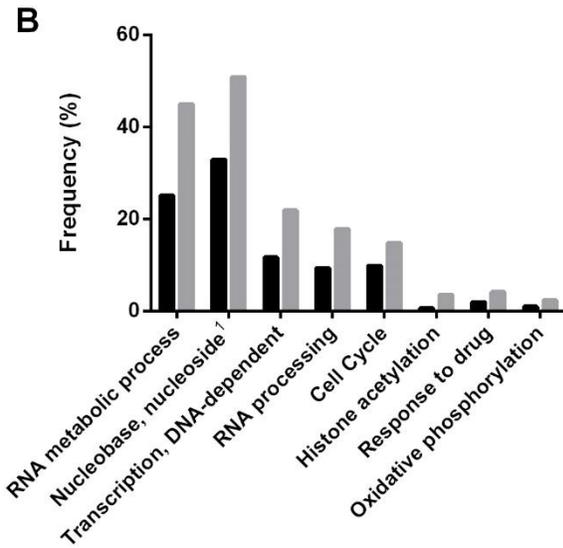
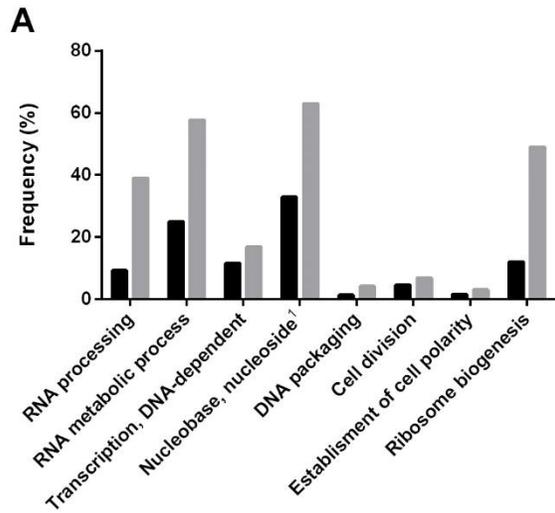


**Figure S1.** Venn diagrams for the overlap of genes up-regulated (A) and down-regulated (B) in 044Fluco21 strain (green), 044Fluco31 strain (blue) and 044Fluco45 strain (pink) comparatively to the 044 clinical isolate. The total number of genes in each list is also indicated.

044Fluco21 Strain

044Fluco31 Strain

044Fluco45 Strain



■ RF genome    ■ DF data set    p-value < 0.05

Up regulated genes

Down regulated genes

**Figure S2 –Gene Ontology terms found to be over-represented in up- or down-regulated genes in azole resistance evolved strains.** Frequency of *Candida glabrata* genes found to be up- (A,B,C) or down-regulated (D,E,F) in the *C. glabrata* 044Fluco21 (A,D), 044Fluco31 strain (B,E) or 044Fluco45 (C,F) resistant strains, when compared to the parental 044 clinical isolate, associated to the displayed GO terms (determined by GO Toolbox - <http://genome.crg.es/GOToolBox/>). RF – Reference Frequency; DF – Dataset Frequency.

**Table S1** – Evolution of the clotrimazole, fluconazole, posaconazole and voriconazole MIC values exhibited by the 044 *C.glabrata* clinical isolate during prolonged exposure to therapeutic serum concentrations of fluconazole (16µg/ml), as described in the M&M section.

Time (days)	MIC values (mg/mL)			
	FLC	VRC	PSC	CLOT
0	4	0,125	0,5	0,125
5	2	0,125	1	1
10	4	0,125	1	2
15	4	0,125	1	2
20	2	0,125	1	2
25	8	0,125	16	2
30	8	0,125	16	2
35	8	0,5	16	8
40	32	0,25	16	8
45	64	8	16	32
50	64	8	16	32
55	64	8	16	32
60	64	8	16	32
70	64	8	16	32
R (-30)	64	8	16	32







	CAGL0100789	CAF20	Phosphoprotein of the mRNA cap-binding complex involved in translational control, repressor of cap-dependent translation initiation, complexes with eIF4E for binding to eIF4E	0.895791751
Translation	CAGL0000836	DCD1	Genetic variant of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2, activity subsequently regulated by phosphorylated eIF2. Not identified as a negative regulator of GCW expression	0.868020305
	CAGL0020208	PLF6	Purkinje-homology domain protein that binds ASH1 mRNA at 3' UTR and represses its translation, resulting in proper asymmetric localization of ASH1 mRNA	0.948621308
	CAGL0K13745	MPP19	Mitochondrial ribosomal protein of the small subunit, contains two conserved e-cysteine motifs	0.940089945
	CAGL0113350	MPP19	Mitochondrial ribosomal protein of the large subunit	0.871497008
	CAGL0100030	GCN5	Alpha subunit of the translation initiation factor eIF2B, the guanine-nucleotide exchange factor for eIF2, activity subsequently regulated by phosphorylated eIF2. First identified as a positive regulator of GCW expression	0.824474681
	CAGL0087030	YDR115W	Putative mitochondrial ribosomal protein of the large subunit, has similarity to E. coli L34 ribosomal protein, required for respiratory growth, see also mitochondrial ribosomal proteins	0.820203073
	CAGL0027076	MPP13	Mitochondrial ribosomal protein of the large subunit	0.831691047
	CAGL0112268	MPP14	Mitochondrial ribosomal protein of the large subunit	0.722232937
	CAGL0112259	RPS3	Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic (AP) endonuclease activity, essential for viability, has similarity to E. coli S3 and rat S3 ribosomal proteins	1.460795493
	CAGL0020090	ASJ1	G-protein beta subunit and guanine nucleotide dissociation inhibitor for Galpha2, ortholog of RACK1 that inhibits translation; core component of the small (40S) ribosomal subunit, represses Gcn5p in the absence of amino acid starvation	1.317769712
CAGL0049044	RPS3A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rps3b and has similarity to E. coli L3 and rat L3 ribosomal proteins	1.292520204	
CAGL0037340	SRP46	Polypeptide release factor (SRP) in translation termination; mutant form acts as a recessive component suppressor; methylated by Mup2-Tim172 in urinary complex eIF4F-eIF4G-GTP; mutation of methylation site confers resistance to zymosan	1.736242518	
CAGL0087030	SRD1	RNA-binding protein that associates with translating ribosomes; involved in home regulation of Hsp70 as a component of the Hsp70 complex; also involved in the organization of actin filaments; contains a Lxx motif	1.473268185	
CAGL0100709	BTN2	v-SNARE binding protein possibly recruited from a late endosome to the Golgi; modulates arginine output, possible role in mediating pH homeostasis between the vacuole and plasma membrane H <sup>+</sup> -ATPase	1.234683335	
CAGL0030476	NPA3	Essential, conserved, cytoplasmic ATPase, phosphorylated by the PtpN-Pho85 kinase complex	1.605202521	
CAGL0057429	SRP22	Putative serine/threonine protein kinase, involved in the adaptation to low concentrations of glucose independent of the SNF1 regulated pathway	1.075164645	
CAGL0076833	MBO2	Core component of the signal recognition particle (SRP) ribonucleoprotein (RNP) complex that functions in targeting nascent secretory proteins to the endoplasmic reticulum (ER) membrane	0.940089945	
CAGL0K114629	HTB1	Histone H2B, core histone protein required for chromatin assembly and chromosome function; nearly identical to HTB2. Rst1p-Bra1p-Lop1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation	2.301445743	
CAGL0044178	HTA2	Histone H2A, core histone protein required for chromatin assembly and chromosome function; one of two nearly identical (see also HTA1) subtypes; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nup2	2.123482761	
CAGL0K114469	HTA1	Histone H2A, core histone protein required for chromatin assembly and chromosome function; one of two nearly identical subtypes (see also HTA2); DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nup2	2.301445743	
CAGL0K083446	HPF1	Histone H4, core histone protein required for chromatin assembly and chromosome function; one of two identical histone proteins (see also HPF2); contributes to histone silencing; N-terminal domain involved in maintaining genomic integrity	1.744847588	
CAGL0M060778	HPF2	Histone H4, core histone protein required for chromatin assembly and chromosome function; one of two identical histone proteins (see also HPF1); contributes to histone silencing; N-terminal domain involved in maintaining genomic integrity	1.474717709	
CAGL0M066550	HPF2	Histone H4, core histone protein required for chromatin assembly, part of heterochromatin-mediated silencing and HM silencing; one of two identical histone H4 proteins (see HPF1); regulated by acetylation, methylation, and phosphorylation	1.554180284	
CAGL0041980	HPF1	Histone H4, core histone protein required for chromatin assembly and chromosome function; one of two identical histone proteins (see also HPF2); contributes to histone silencing; N-terminal domain involved in maintaining genomic integrity	1.474717709	
CAGL0001718	PCO30	Proliferating cell nuclear antigen (PCNA), functions as the sliding clamp for DNA polymerase delta, may function as a docking site for other proteins required for mitotic and meiotic chromosomal DNA replication and for DNA repair	1.453180286	
CAGL0L05918	DTF1	eIF2beta, catalyzes hydrolysis of eIF2p1 to eIF2p1 and PP1, thereby preventing incorporation of Leu118 into eIF2 during translation; critical for the maintenance of genetic stability	1.263209308	
CAGL0E19258	TRM11	Catalytic subunit of an adenosine-dependent RNA methyltransferase complex [Tim17p-Tim112p], required for the methylation of the guanine nucleotide at position 110 (m1G110) in rRNAs; contains a THUMP domain and a methyltransferase domain	1.290546284	
CAGL0K041449	HTF1	Histone H3, core histone protein required for chromatin assembly, part of heterochromatin-mediated silencing and HM silencing; one of two identical histone H3 proteins (see HTF2); regulated by acetylation, methylation, and phosphorylation	1.246817888	
CAGL0E030774	QLA1	GMP synthase, an enzyme that catalyzes the second step in the biosynthesis of GMP from inosine 5-phosphate (IMP); transcription is not subject to regulation by guanine but is negatively regulated by nutrient starvation	1.220329492	
CAGL0005650	PR51	Sytoproto-ribonucleo-Hsp90a-sytoproto-phosphatase, synthetase PRP5, which is required for nucleotide, histidine, and tyrosine biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes	1.103232433	
CAGL0007090	PRH1	Essential protein with a highly acidic N-terminal domain; PRH1 enables genetic interactions with HTA1; overexpression interferes with silencing at heterochromatin and HM; not essential for viability	1.473092659	
CAGL0K086658	HPF1	Histone H3, core histone protein required for chromatin assembly, part of heterochromatin-mediated silencing and HM silencing; one of two identical histone H3 proteins (see HTF2); regulated by acetylation, methylation, and phosphorylation	1.600500604	
CAGL0E030689	CDC5	Dimeric histone/histone-guanine phosphotransferase, catalyzes the formation of both nucleoside monophosphate and guanine monophosphate; mutations in the human homolog PRF11 can cause Leish-Nyman syndrome and Kelly-Segalmer syndrome	1.660711105	
CAGL0005650	CDC5C	Essential eIF2-binding protein required for DNA replication, component of the pre-replicative complex (pre-RC), which requires CDC5, which requires CDC5C, to associate with cyclins and growth phase; early degraded; core entry into quiescence via SCF and the proteasome	1.053294423	
CAGL0K011450	CTF19	Subunit of the CBF3 complex, which binds to the CDE II element of centromeres, binding the DNA upon binding, and may be involved in sister chromatid cohesion during mitosis	0.953096433	
CAGL0E03510	FYJ17	Protein component required for meiotic recombination; essential for normal core exposure to a 1 kb loop	1.076308338	
CAGL0K097929	RPS16A	Protein component of the small (40S) ribosomal subunit, identical to Rps16B and has similarity to E. coli S9 and rat E18 ribosomal proteins	0.976308338	
CAGL0M115538	CDC45	DNA replication initiation factor; crucial to MCM pre-RC complexes as replication origin; promotes release of MCM from Mtrp10; vacuole elongation machinery; mutants in human homolog may cause neurofibromatosis and DGoGuvere syndromes	0.953096433	
CAGL0K097489	EAF7	Subunit of the NAA14 histone acetyltransferase complex, which acetylates the N-terminal tails of histones H4 and H2A	1.022878331	
CAGL0026286	SMC2	Subunit of the condensin complex; essential SMC2 chromosomal ATPase family member that forms a complex with Smc4p to form the active ATPase; Smc2p/Smc4p complex binds DNA, required for clustering of rDNA genes at the nucleolus	1.043309033	
CAGL0M080178	MET1	Putative nucleoside hemethyltransferase, has a role in DNA silencing and in R-loop determination	0.902538125	
CAGL0K071771	F0B1	Nuclear protein that binds the RNA replication fork barrier (RFB) site; required for replication fork blocking, recombinational hotspot activity, condensin recruitment to RFB and DNA repair; association related to retroviral integrases	0.921118546	
CAGL0005946	AH41	Adenosine deaminase (adenine aminopyrimidine), converts adenosine to hypoxanthine; involved in purine salvage; essential for viability and growth phase; early degraded; core entry into quiescence via SCF and the proteasome	1.565186724	
CAGL0K026420	RSC8	Component of the RSC chromatin remodeling complex; essential for viability and mitotic growth; homolog of SWI5/SMF subunit Swb3, H4 urtic acid; does not activate transcription of reporters	0.845471205	
CAGL0E04578	DSF4	Protein involved in Cdc12p kinase complex; required for Cdc12p kinase activity; initiation of DNA replication; phosphorylates the Min2p 7 domain; of proteins; cell cycle regulation	0.820203078	
CAGL0004249	MCM8	Protein involved in DNA replication; component of the Min2p-7 heptameric complex that binds chromatin as a part of the pre-replicative complex	0.818517019	
CAGL0M06388	FRF4	Peptidyl-prolyl co-trans isomerase (PPIase) (proline isomerase) localized to the nucleus; catalyzes isomerization of proline residues in histones H3 and H4, which affects lysine methylation of these histones	0.791776021	
CAGL0002794	MNB1	Transcriptional co-repressor of HSF1; MCB2 binding factor-regulated gene expression; tightly associates stably with promoters; has MNB1 to HSF1 and H4, which affects lysine methylation of these histones	1.565186724	
CAGL0E034340	TEA1	Ty1 enhancer activator required for full levels of Ty1 enhancer-mediated transcription; C8 zinc cluster DNA-binding protein	1.300200104	
CAGL01002178	FST1	Transcription factor (TF) (TFIIIA), essential protein with two C2H2 zinc fingers; binds the 5S rRNA gene through its zinc finger domain and directs assembly of a midribosomal ribosomal complex for RNA polymerase III; also binds DNA	1.005445862	
CAGL0002020	CTK1	Transcription factor that contains expression of ribosome biogenesis genes in response to nutrient starvation; regulates CDM2 transcription during mitotic cell cycle and DNA damage response; increases cell size; regulated by TORC1 and Mtdp1	1.077202368	
CAGL0006620	SPF1	Transcription factor involved in glucose repression; sequence specific DNA binding protein operating two C2H2 zinc finger motifs; regulated by the DAF1 kinase and the GALT2 phosphatase	0.926714047	
CAGL0M01628	MOC1	Transcriptional activator of genes involved in glycolysis; interacts and functions with the DNA-binding protein Gcn1p	0.926806864	
CAGL0E023739	GCR2	Transcription factor involved in glucose repression; sequence specific DNA binding protein operating two C2H2 zinc finger motifs; regulated by the DAF1 kinase and the GALT2 phosphatase	0.811789333	
CAGL0101076	MCM3	Transcription factor involved in cell-type-specific transcription and chromosome repressor; plays a central role in the formation of both repressor and activator complexes	0.811789333	
CAGL0E03289	TF483p	Translation initiation factor eIF4G, subunit of the mRNA cap-binding protein complex (eIF4F) that also contains eIF4E (Cdc33); associates with the poly(A)-binding protein Pab1p; also interacts with eIF4A (Tf1p); homologous to TF483p	0.802090298	
CAGL0E03709	ATC1	Nuclear protein, possibly involved in regulation of carbon source responses and/or in the establishment of liquid budding pattern	1.583724466	
CAGL0M09349	ZM17	Heat shock protein with a zinc finger motif; essential for protein import into mitochondria; may act with Pim1p to facilitate recognition and feeding of imported proteins by Sic1p (mPp70) in the mitochondrial matrix	1.147124484	
CAGL0E022879	PLC1	LM domain-containing protein that localizes to sites of polarized growth; required for selection and/or maintenance of polarized growth sites; may modulate signaling by the GTPases Cdc42p and Rho1p; has similarity to melanocan protein	0.892520285	
CAGL0E04650	IMP2	Putative serine/threonine receptor important for peroxisome inheritance; co-localizes with peroxisomes and co-localizes with peroxisomes in vivo; physically interacts with the protein P motor Mtdp2; RFP1 is not an essential gene	1.025490479	
CAGL0K041469	MARR1	Phosphorylated protein of the mitochondrial outer membrane; localizes only to mitochondria of the bud; interacts with Mtdp2 to mediate mitochondrial distribution to buds; mRNA is targeted to the bud via the transport system involving Shp2p	0.915248854	
CAGL0E03036	EMF2	Essential nuclear protein of unknown function; contains WD repeats; interacts with Mtp10p and Bfp2p; has homology to Bfp2p	1.272376179	
CAGL0005500	HEH1	Nonsensical protein of unknown function; predicted to be involved in ribosome biogenesis; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; similar to mammalian BRP16 (Brain protein 16)	1.511282096	
CAGL0E03036	EM21	Protein of unknown function; localized in the nucleoplasm and the nucleolus; specifically interacts with MTR1 in 60S ribosomal protein subunit export	1.583220976	
CAGL0E049839	YLR303W-A	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus	1.437317084	
CAGL0040849	EFJ1	Putative protein of unknown function	1.330886077	
CAGL0012778	YML250C	Putative protein of unknown function; YML250C is not an essential gene	1.308806654	
CAGL0004900	JRP4	Essential protein of unknown function; interacts with proteins involved in RNA processing; ribosome biogenesis, ubiquitination and demethylation; tagged protein localizes to nucleus and nucleolus; similar to WDR55, a human WD repeat protein	1.385930258	
CAGL0003895	FBH1	Essential eIF2-binding protein required for DNA replication; component of the pre-replicative complex (pre-RC), which requires CDC5, which requires CDC5C, to associate with cyclins and growth phase; early degraded; core entry into quiescence via SCF and the proteasome	1.284323258	
CAGL0E028778	RRT14	Putative protein of unknown function; identified in a screen for mutants with decreased levels of tRNA transcription; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus; predicted to be involved in ribosome biogenesis	1.287897504	
CAGL0M139159	YMR10C	Putative protein of unknown function; predicted to be involved in ribosome biogenesis; green fluorescent protein (GFP)-fusion protein localizes to the nucleolus; YMR10C is not an essential gene	1.260300834	
CAGL0E04490	SET3	Protein of unknown function; contains a SET domain	1.525372258	
CAGL0E03078	G9A_YG08_Ara_7_248	Cytosolic protein of unknown function; non-essential gene that is induced in a GDN1 deleted strain with altered nucleic acid metabolism; GFP-fusion protein is induced in response to the DNA-damaging agent MMS	1.2572704	
CAGL0E03078	YPL108W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the membrane of the vacuole; physical interaction with Ypp2p suggests a possible role in autophagy; YML018C is not an essential gene	1.051190429	
CAGL0E03078	YML018C	Mitochondrial intermembrane space protein; contains twin cysteine-dip-cysteine motifs; MCT17 is not an essential gene	1.045218511	
CAGL0115468	MCT17	Mitochondrial intermembrane space protein; contains twin cysteine-dip-cysteine motifs; MCT17 is not an essential gene	1.125341787	
CAGL0E02878	PRY1	Protein of unknown function	1.105848778	
CAGL0E028169	ORC3	Protein of unknown function; required for cell growth and possibly involved in RNA processing; mRNA is cell cycle regulated	0.964850222	
CAGL0E04906	CSB1	Protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nuclear envelope and the vacuole; YGC007C is not an essential gene	0.928885156	
CAGL0M047190	RFP38	Putative protein of unknown function; may play a role in the ribosome and rRNA biogenesis based on expression profiles and mutant phenotype	0.971420817	
CAGL0E03086	TD47	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole	1.005100442	
CAGL0E03086	TD47	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole	0.842424545	
G9A_YG08_KD2144	-	-	-	0.857397779
G9A_YG08_KD203181	-	-	-	0.934523203
CAGL0M04434	CCW12	Putative protein of unknown function	0.962877816	
CAGL0M04328	YA1328-A	Highly acidic cytoplasmic DDX2 domain-containing protein of unknown function; interacts with Rps2p and Gcn5p; associates with translating ribosomes; putative intrinsically unstructured protein	0.940760984	
CAGL0E03271	QSR2	Putative protein of unknown function	0.862177103	
CAGL0E03159	NA1	Putative protein of unknown function; YLR143W is not an essential gene	0.845140008	
G9A_YG08_YL102C	-	-	-	0.845140008
CAGL0E04640	FLO1	Protein of unknown function; mutant localizes to a specialized [delta] and genetically acidic [beta]	0.903804563	
CAGL0E03078	DLT1	Putative protein of unknown function; mutant localizes to a specialized [delta] and genetically acidic [beta]	0.871188683	
CAGL0E03036	DRN1	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the nucleus	0.82471393	





**Table S6** - List of genes found to be down-regulated in the *C. glabrata* 044Fluco45 population, when compared to the parental 044 clinical isolate. Genes were clustered into functional categories. *C. glabrata* gene ID, *S. cerevisiae* homolog, CCD-based gene description, and level of expression change in 044Fluco21 vs 044 is provided.

	<i>C. glabrata</i> ORF	<i>S. cerevisiae</i> Homolog	Description	Fluconazole vs. Susceptible (Log <sub>2</sub> FC)
Cell Wall	CAGL0F0297g	HDC1	Alpha-1,6-mannosyltransferase involved in cell wall mannann biosynthesis, subunit of a Golgi-localized complex that also contains Arp1p, Mnn6p, Mnn11p, and Mnn10p; identified as a suppressor of a cell lysis sensitive <i>plc1-371</i> allele	-0.842777378
	CAGL0E0177g	YPS1	Putative aspartic protease; predicted GPI-anchor; member of a YPS gene cluster that is repressed for virulence in mouse genes is downregulated in azole-resistant strains	-1.18175387
Ion Homeostasis	CAGL0Q0481g	IZH1	Membrane protein involved in zinc ion homeostasis, member of the four-protein IZH family; transcription is regulated directly by Zap1p; expression induced by zinc deficiency and fatty acids; deletion increases sensitivity to elevated zinc	-0.84191206
Cell Cycle	CAGL0Q0381g	POM152	Nuclear pore membrane glycoprotein; may be involved in duplication of nuclear pores and nuclear pore complexes during S phase.	-1.003745251
Transport	CAGL0Q0805g	DNF2	Aminophospholipid translocase (flippase) that localizes primarily to the plasma membrane; contributes to endocytosis, protein transport and cell polarity; type 4 P-type ATPase	-0.981474527
Unknown Function	CAGL0Q0486g	PUN1	Putative protein of unknown function; localizes to bud and cytoplasm; co-localizes with Sur7p in punctate patches in the plasma membrane; <i>nut</i> mutant displays decreased thermotolerance; transcription induced on cell wall damage	-1.294931493

**Table S7** - List of genes found to be up-regulated in the *C. albicans* 044Fluc45 population, when compared to the parental 044 clinical isolate. Genes were clustered into functional categories. *C. albicans* gene ID, *S. cerevisiae* homolog, CGD-based gene description, and level of expression change in 044Fluc21 vs 044 is provided.

	<i>C. albicans</i> ORF	<i>S. cerevisiae</i> Homolog	Description	Fluconazole vs Susceptible Log2FC Average
Carbon and Energy Metabolism	CagM08_ATP8	ATP8	ATP synthase subunit 8	1.30226135
	CagM011_COX2	COX2	cytochrome-c oxidase subunit II	1.330905441
	CagM012_COX3	COX3	cytochrome-c oxidase subunit III	1.238468657
	CagM009_ATP6	ATP6	ATP synthase subunit 6	1.181956838
	CagM004_COX1	COX1	cytochrome-c oxidase subunit I	1.12182479
Drug Resistance	CagM010_ATP9	ATP9	ATP synthase protein 9	1.130752985
	CAGL02026p	FET117	Protein required for assembly of cytochrome c oxidase	0.786502788
	CAGL0M0760g	PDR5 (CDR1)	Multidrug transporter of ATP-binding cassette (ABC) superfamily. Involved in resistance to azoles; expression regulated by Pdr1p; increased abundance in azole resistant strains; expression increased by loss of the mitochondrial genome	1.663594468
	CAGL0R02717g	PDR19 (CDR2)	Plasma membrane ATP binding cassette (ABC) transporter, multidrug transporter and general stress response factor implicated in cellular detoxification; regulated by Pdr1p, Pdr3p and Pdr5p; promoter contains a PDR responsive element	1.302221031
	CAGL0K0110g	STA1	Adhesin-like protein with internal repeats; predicted GPI-anchor. It has a C-terminal fragment of a single ORF in CAGL0K0110g.	1.465279375
Cell Wall	CAGL0G10219g	FLO5	Adhesin-like protein with 5 tandem repeats; predicted GPI anchor, similarity to <i>S. cerevisiae</i> flocculins, cell wall proteins that mediate adhesion	1.393971377
	CAGL0E00219g	-	Putative adhesin-like protein; contains tandem repeats and a predicted GPI-anchor	1.028272366
Stress Adaptation	CAGL0H10026g	FLO1	Predicted cell wall adhesin with a predicted role in adhesion; predicted GPI anchor; contains tandem repeats	0.82179517
	CAGL0E04359g	SOD2	Mitochondrial superoxide dismutase; protects cells against oxygen toxicity; phosphorylated	0.886409552
Unknown Function	CAGL0M11704g	AHP1	Thiol-specific peroxidase; induces hydroperoxides to protect against oxidative damage; function in vivo requires covalent conjugation to Urm1p	0.82751685
	CAGL0M12947g	YLD77C	Mitochondria-localized protein; gene is upregulated in azole-resistant strain	1.815041402
	CAGL0R0641g	YML018C	Has domain(s) with predicted membrane localization	1.571137176
	CAGL0M00713g	YHM1	Protein of unknown function; null mutant displays sensitivity to DNA damaging agents; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	1.228466673
	CAGL0G07183g	-	-	1.032979548
	CagM003_cyB	COB	-	1.04652315
	CagM007_Cga3	A14	-	1.02513851
	CagM005_Cga1	-	-	1.026176891
	CAGL0L00157g	-	-	0.910369446
	CAGL0H10054g	YB053C	Putative protein of unknown function; induced by cell wall perturbation	0.873787021
CAGL0E03499g	-	-	0.803713659	
CAGL0G07183g1	-	-	0.815212697	
CAGL0K06734g	YR014W	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the vacuole; expression directly regulated by the metabolic and meiotic transcriptional regulator Ume6p; YR014W is a non-essential gene	0.789550414	