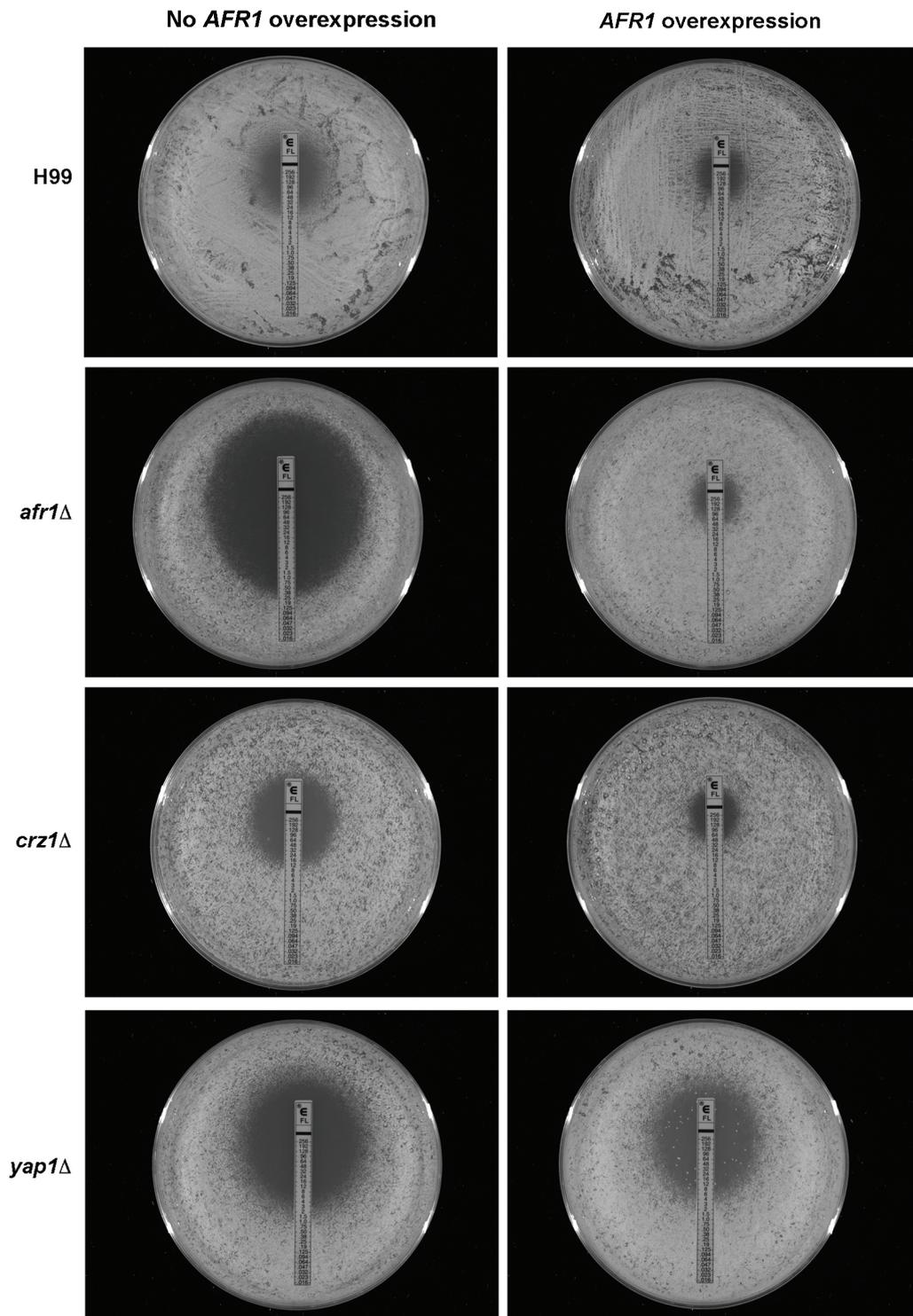


**Fig. S1.** The expression levels of *AFR1*, *AFR2*, *MDR1* and *ERG11* in the FLC resistance mutants (A-D) and mutants with increased frequency of FLC heteroresistance (E-H). The exponential growth phase cells of transcription factor mutant strains were either untreated (NT) or treated (FLC) with 32g/ml FLC for 2h. RNA was isolated and the expression levels of each gene were determined by RT-qPCR. The expression levels of each gene were normalized with that of actin gene and compared to the wild type without FLC treatment. Values represent the means  $\pm$  standard deviation of three biological replicates. \* represents  $p < 0.0476$ ; \*\*\* represents  $p < 0.0006$ ; \*\*\*\* represents  $p < 0.0001$  (uncorrected Fisher's LSD)



**Fig. S2.** Overexpression of *AFR1* results in a decrease of susceptibility to FLC. *AFR1* was placed under the control of *GPD1* promoter and transformed into indicated strains. E-test was used to measure the FLC susceptibility and photographs were taken after 3 days of incubation.

**Table S1.** List of strains used in this study.

Strain	Genotype	Parent	Reference
H99 ( <i>C. neoformans</i> )	MAT $\alpha$ serotype A		(1)
<i>afr1</i> $\Delta$	MAT $\alpha$ <i>afr1</i> $\Delta$ ::NEO	H99	(2)
<i>afr2</i> $\Delta$	MAT $\alpha$ <i>afr2</i> $\Delta$ ::NEO	H99	This study
<i>mdr1</i> $\Delta$	MAT $\alpha$ <i>mdr1</i> $\Delta$ ::NEO	H99	This study
<i>afr1</i> $\Delta$ / <i>afr2</i> $\Delta$	MAT $\alpha$ <i>afr1</i> $\Delta$ ::NEO <i>afr2</i> $\Delta$ ::HYG	H99	This study
<i>afr1</i> $\Delta$ / <i>mdr1</i> $\Delta$	MAT $\alpha$ <i>afr1</i> $\Delta$ ::NEO <i>mdr1</i> $\Delta$ ::NAT	H99	This study
<i>afr2</i> $\Delta$ / <i>mdr1</i> $\Delta$	MAT $\alpha$ <i>afr2</i> $\Delta$ ::NEO <i>mdr1</i> $\Delta$ ::NAT	H99	This study
<i>afr1</i> $\Delta$ / <i>afr2</i> $\Delta$ / <i>mdr1</i> $\Delta$	MAT $\alpha$ <i>afr1</i> $\Delta$ ::NEO <i>afr2</i> $\Delta$ ::HYG <i>mdr1</i> $\Delta$ ::NAT	H99	This study
YSB815	MAT $\alpha$ <i>yap1</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB1416	MAT $\alpha$ <i>yap2</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB1099	MAT $\alpha$ <i>bzp3</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB1249	MAT $\alpha$ <i>pip2</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB1263	MAT $\alpha$ <i>crz1</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB2493	MAT $\alpha$ <i>sre1</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB2622	MAT $\alpha$ <i>zfc2</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB2702	MAT $\alpha$ <i>bzp2</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB1104	MAT $\alpha$ <i>hap2</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB2308	MAT $\alpha$ <i>hob1</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB2972	MAT $\alpha$ <i>gat1</i> $\Delta$ ::NAT	H99	Y. Bahn
YSB3096	MAT $\alpha$ <i>nrg1</i> $\Delta$ ::NAT	H99	Y. Bahn
R265 ( <i>C. gattii</i> )	MAT $\alpha$ VGII serotype B		(3)
<i>afr1</i> $\Delta$	MAT $\alpha$ <i>afr1</i> $\Delta$ ::NEO	R265	This study
<i>afr2</i> $\Delta$	MAT $\alpha$ <i>afr2</i> $\Delta$ ::NEO	R265	This study
<i>mdr1</i> $\Delta$	MAT $\alpha$ <i>mdr1</i> $\Delta$ ::NEO	R265	This study
<i>afr1</i> $\Delta$ / <i>afr2</i> $\Delta$	MAT $\alpha$ <i>afr1</i> $\Delta$ ::NEO <i>afr2</i> $\Delta$ ::NAT	R265	This study
<i>afr1</i> $\Delta$ / <i>mdr1</i> $\Delta$	MAT $\alpha$ <i>afr1</i> $\Delta$ ::NEO <i>mdr1</i> $\Delta$ ::NAT	R265	This study
<i>afr2</i> $\Delta$ / <i>mdr1</i> $\Delta$	MAT $\alpha$ <i>afr2</i> $\Delta$ ::NEO <i>mdr1</i> $\Delta$ ::NAT	R265	This study
<i>afr1</i> $\Delta$ / <i>afr2</i> $\Delta$ / <i>mdr1</i> $\Delta$	MAT $\alpha$ <i>afr1</i> $\Delta$ ::NEO <i>afr2</i> $\Delta$ ::NAT <i>mdr1</i> $\Delta$ ::HYG	R265	This study

1. **Perfect JR, Ketabchi N, Cox GM, Ingram CW, Beiser CL.** 1993. Karyotyping of *Cryptococcus neoformans* as an epidemiological tool. J Clin Microbiol **31**:3305-3309.
2. **Sionov E, Lee H, Chang YC, Kwon-Chung KJ.** 2010. *Cryptococcus neoformans* overcomes stress of azole drugs by formation of disomy in specific multiple chromosomes. PLoS Pathog **6**:e1000848.
3. **Kidd SE, Hagen F, Tschärke RL, Huynh M, Bartlett KH, Fyfe M, Macdougall L, Boekhout T, Kwon-Chung KJ, Meyer W.** 2004. A rare genotype of *Cryptococcus gattii* caused the cryptococcosis outbreak on Vancouver Island (British Columbia, Canada). Proc Natl Acad Sci U S A **101**:17258-17263.

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

Primer name	Sequence (5' to 3')	Purpose
CNAG_AFR2_A	CAAATTCGAGGAGCTTGGAG	PCR for deletion
CNAG_AFR2_B	GCTAGTTTCTACATCTCTTCCGTGCGGTCGTAAGTACCCAAACC	PCR for deletion
CNAG_AFR2_C	CGCCGCTCTCCAGCTCACATCCTCGTCTCGTTCCAGCGAAAGAC	PCR for deletion
CNAG_AFR2_D	GAAAAGGGCCTATGCAATGA	PCR for deletion
CNAG_AFR2_E	TCTTGTCGTCATTCCCCTTC	PCR for deletion
CNAG_AFR2_F	TAGGTAAAGGGCCGAAAGGT	PCR for deletion
CNAG_MDR1_A	AAATGCGTAGGTGGCAAAAA	PCR for deletion
CNAG_MDR1_B	GCTAGTTTCTACATCTCTTCCGTGGCAGTGAGTCCTGGAGAAGC	PCR for deletion
CNAG_MDR1_C	CGCCGCTCTCCAGCTCACATCCTCCGCGAGGCAGGACTACTATC	PCR for deletion
CNAG_MDR1_D	TCGCAAAGTAGCAGTGAACAA	PCR for deletion
CNAG_MDR1_E	GCTCTGTTTGATGGATTTTGC	PCR for deletion
CNAG_MDR1_F	AACGAGTGCCACACTTAAAAAG	PCR for deletion
CNBG_AFR1_A	GCGACGACAGCAATAAATGA	PCR for deletion
CNBG_AFR1_B	GCTAGTTTCTACATCTCTTCCGTGCCTGACGGATTCTGAGTGGT	PCR for deletion
CNBG_AFR1_C	CGCCGCTCTCCAGCTCACATCCTCAACCAGGTGGAGAGATTTTCG	PCR for deletion
CNBG_AFR1_D	CAACGTCATTGCTTTGATGG	PCR for deletion
CNBG_AFR1_E	GTCTTGGTCGGTTGGTGACT	PCR for deletion
CNBG_AFR1_F	GTTGCTTCGGGTGATCAAAT	PCR for deletion
CNBG_AFR2_A	GATCCCCCTCAGAGCTTTC	PCR for deletion
CNBG_AFR2_B	GCTAGTTTCTACATCTCTTCCGTGACGGTTTTCTTCCGTTTGAG	PCR for deletion
CNBG_AFR2_C	CGCCGCTCTCCAGCTCACATCCTCCGGAGGACGTACAGGAGAAG	PCR for deletion
CNBG_AFR2_D	GGATGACGATAAACGGCAAT	PCR for deletion
CNBG_AFR2_E	GCCTATGCAGACGACTGTGA	PCR for deletion
CNBG_AFR2_F	TTCGATTGCCTCAAGATTCC	PCR for deletion
CNBG_MDR1_A	ATAATGCAGCGGTGGAAAAA	PCR for deletion
CNBG_MDR1_B	GCTAGTTTCTACATCTCTTCCGTGAGAATCATGGGCAAGAGCAT	PCR for deletion
CNBG_MDR1_C	CGCCGCTCTCCAGCTCACATCCTCGAGCATGGAACACACCAAGA	PCR for deletion
CNBG_MDR1_D	TGCAGATCAAAGCAACAGGT	PCR for deletion
CNBG_MDR1_E	CGAAGCAAGGAAAGATGGAG	PCR for deletion
CNBG_MDR1_F	TCCGATCGATTACCGATGT	PCR for deletion
CNAG_AFR1_For	ACTGTCTGCTCGTGGGATAACTC	RT-PCR
CNAG_AFR1_Rev	GAAGTCGAAGAGATTTGGCGTAGT	RT-PCR
CNAG_AFR2_For	GGCCATTTACAGACACTCA	RT-PCR
CNAG_AFR2_Rev	CTTCGCGAGCACGGTGTT	RT-PCR
CNAG_MDR1_For	TCCCGGATGCGTCCAA	RT-PCR
CNAG_MDR1_Rev	CATTGTCGATGCTTCGGAAGA	RT-PCR
CNAG_ERG11_For	TGGCAAGACGCCAAAGTCT	RT-PCR
CNAG_ERG11_Rev	GGCGGCAAATCCCTTTTC	RT-PCR
CNBG_AFR1_For	GCCACTCAGCATGACGAACA	RT-PCR
CNBG_AFR1_Rev	GACCGACTTATCGCCCTCTTC	RT-PCR
CNBG_AFR2_For	CTGATTTTCTGCGGTGTATTGG	RT-PCR
CNBG_AFR2_Rev	AACGGCGAAACACGATACATAA	RT-PCR
CNBG_MDR1_For	CAAGCCGAAACGTCTTCA	RT-PCR
CNBG_MDR1_Rev	TGGAAGCGGCCGATGA	RT-PCR
CNAG_Actin_For	CTTGCTCTTTGTCTACCTTCCA	RT-PCR
CNAG_Actin_Rev	GGACGATTGAGGGACCAGACT	RT-PCR
CNBG_Actin_For	CGAGGGCGACCAACAATAGA	RT-PCR
CNBG_Actin_Rev	ATGTGCAAGGCTGGTTTCG	RT-PCR

**Table S3.** Primers used for qPCR assays.

Probe name	Chromosome location	Locus name	Primer forward	Probe
chr1A	Chr1	CNAG_00040	forward 5'-TGGCAAGACGCCAAAGTCT-3' reverse 5'-GGCGGCAAATCCCTTTTC-3'	AACCCTGCCCCG ATGGCACGA
chr3A	Chr3	CNAG_02959	forward 5'-GAAGATGGCGAGCCTGACA-3' reverse 5'-CACTTCGAGCCTTCTTCTCATG-3'	CACCCAGGAGG AGCTCGCCGA
chr5B	Chr5	CNAG_00976	forward 5'-CGGCTTTCTTTGTGTAAGTCTATCC-3' reverse 5'-CATACTGCATCGCCAAGATCA-3'	TGCTTTTCGCAC TCCA ACTGTTCCG