Supplemental Materials

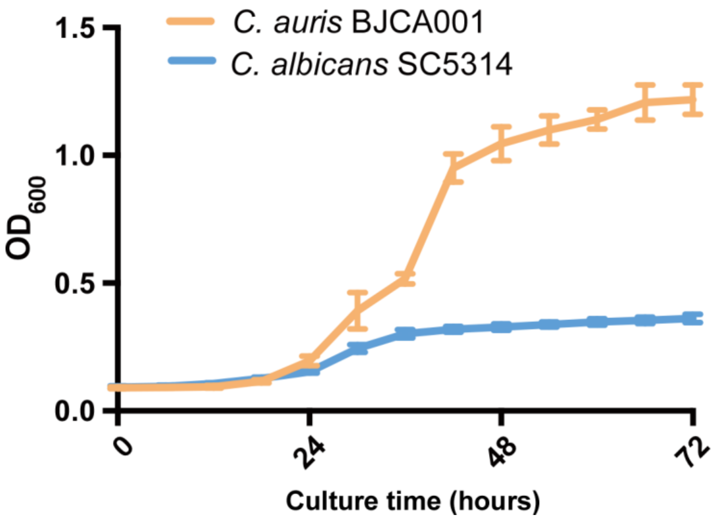

Figure S1. Growth curves of *C. auris* (BJCA001) and *C. albicans* (SC5314) in RPMI 1640 medium containing 32 mg/L fluconazole. 500 cells were inoculated into 0.2 mL fresh medium and grown at 35°C. Three biological repeats were performed. X-axis, incubation time; Y-axis, value of fungal OD600.

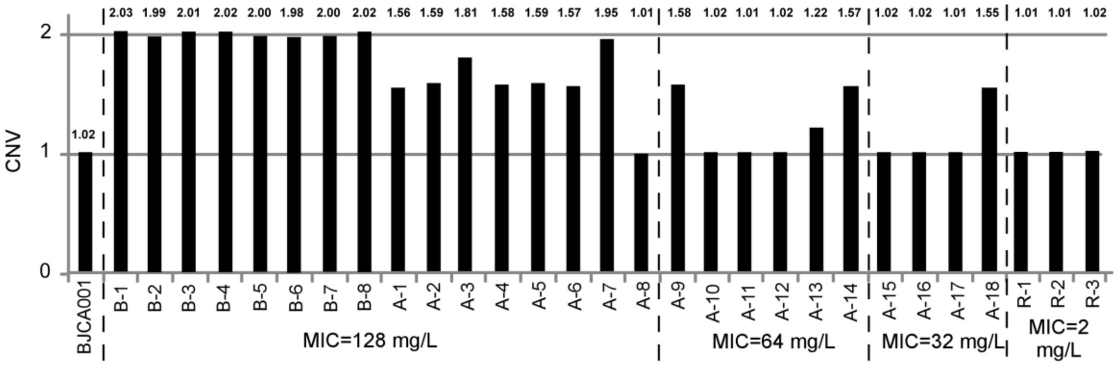

Figure S2. Copy-number variation of Scaffold 6 (Chromosome V) of experimentally evolved strains of *C. auris* A1 to A18 and B1 to B8. Fluconazole-susceptible strain BJCA001 served as a control. The MIC value to fluconazole of each isolate was shown.

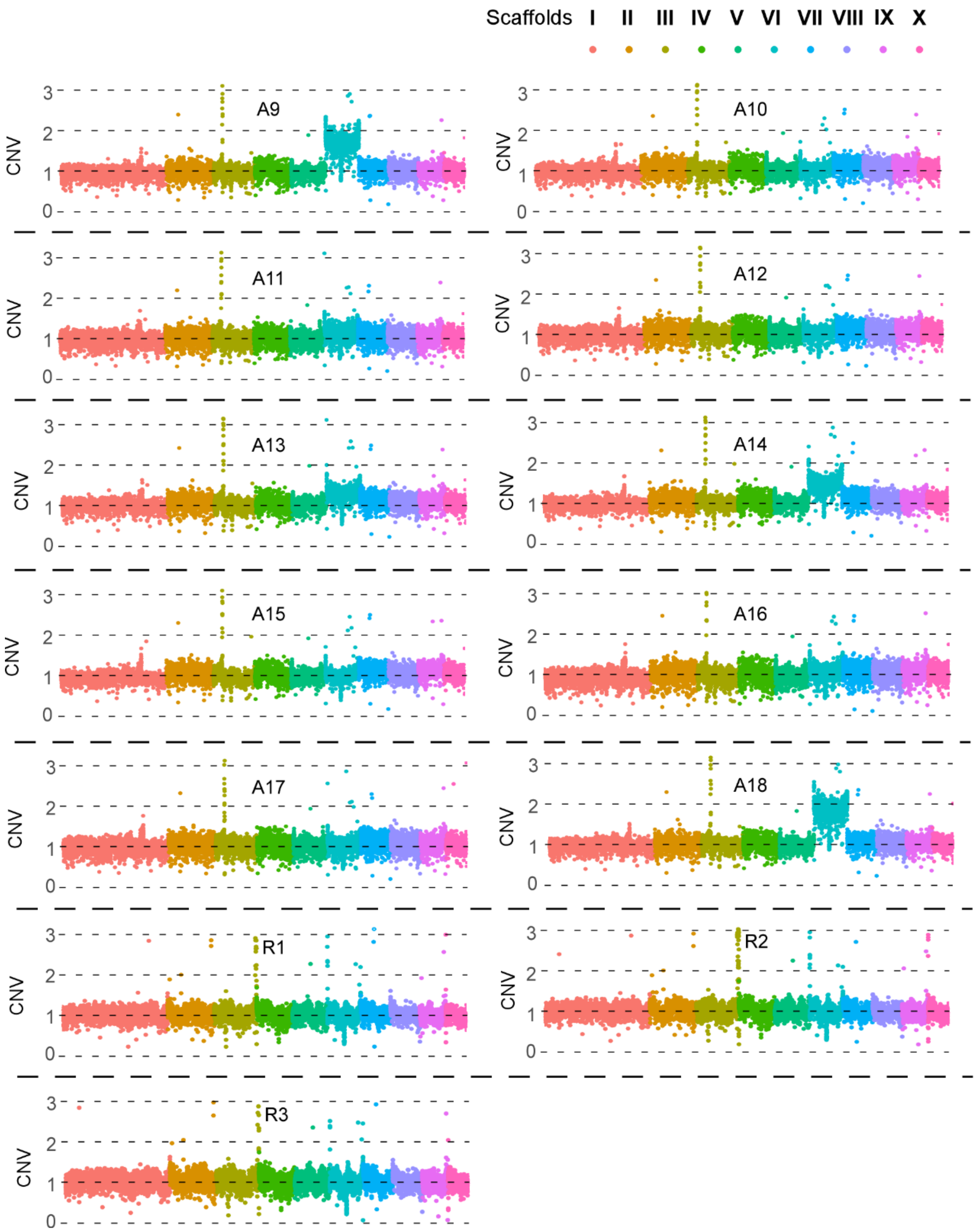

Figure S3. Genome wide Copy-number variations (CNV) for strains A9-A18, and R1-R3. A comparative genomic analysis shows a copy number variation at Scaffold 6 (Chromosome V) using the B8441 genome assembly as a reference. The x-axis indicates Scaffolds 1 to 10. The y-axis denotes the copy number of each scaffold. Each spot represents the sequence depth for a genomic segment of 500 bp across the chromosomes.

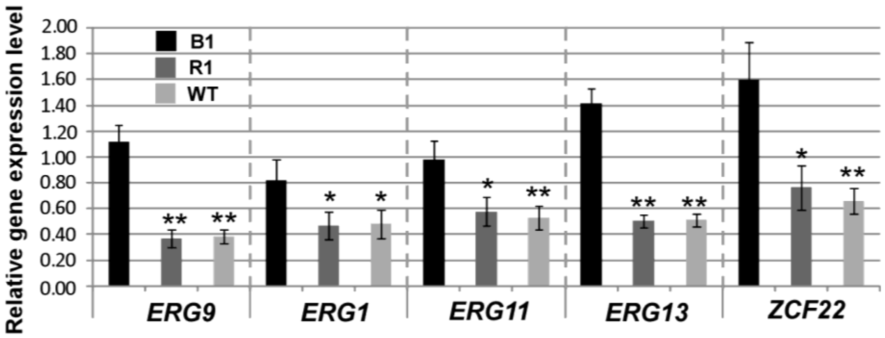

Figure S4. Relative gene expression levels of ergosterol biosynthesis-related genes in cells of strains B1, R1, and BJCA001**.** Relative transcriptional expression levels of *ERG13*, *ERG9*, *ERG1*, *ERG11*, and *ZCF22*. Error bars, standard errors of technical duplicates. *p<0.05, **p<0.01 (two tailed Student's *t*-test).

Dataset S1. Whole genomic SNPs among strains BJCA001, A1 to A18, B1 to B8, and R1 to R3.

Dataset S2. The depth of 500bp-window for strains BJCA001, A1 to A18, B1 to B8, and R1 to R3.

Dataset S3. RNA-Seq dataset.