

# Supplementary Information File

**Title of Manuscript: Multilocus sequence analyses reveal extensive diversity and multiple origins of fluconazole resistance in *Candida tropicalis* from tropical China**

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**Short title:** *Candida tropicalis* in Hainan, China

**Key words:** Multilocus sequence typing, novel genotypes, fluconazole resistance, geographic pattern

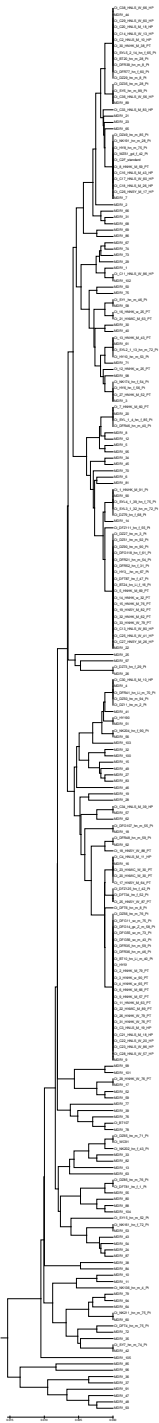
Supplementary Table S1. Locations of the six analyzed DNA fragments within the assembled genome sequence of *C. tropicalis* strain MYA-3404.

Gene name	Chromosomal scaffold ID	Scaffold length (bp)	Gene location within scaffold (bp)
<i>ICL1</i>	NW_003020058.1	1,255,791	959,343-959789
<i>MDR1</i>	NW_003020055.1	2,216,334	754,510-754086
<i>SAPT2</i>	NW_003020038.1	2,474,448	1,573,960-1,574,484
<i>SAPT4</i>	NW_003020049.1	2,308,670	2,274,975-2,274,586
<i>XYR</i>	NW_003020040.1	419,327	35,519-35,150
<i>ZWF</i>	NW_003020056.1	1,654,078	515,841-516,360

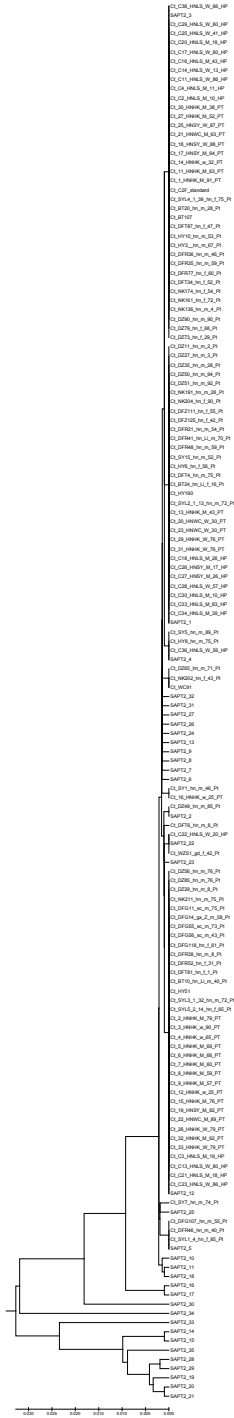
The GenBank accession number for this genome sequence is AAFN01000000. The relevant information about this genome can be accessed at:

[www.ncbi.nlm.nih.gov/bioproject/13675](http://www.ncbi.nlm.nih.gov/bioproject/13675). The above six scaffolds are among 23 chromosomal scaffolds assembled for this *C. tropicalis* genome.

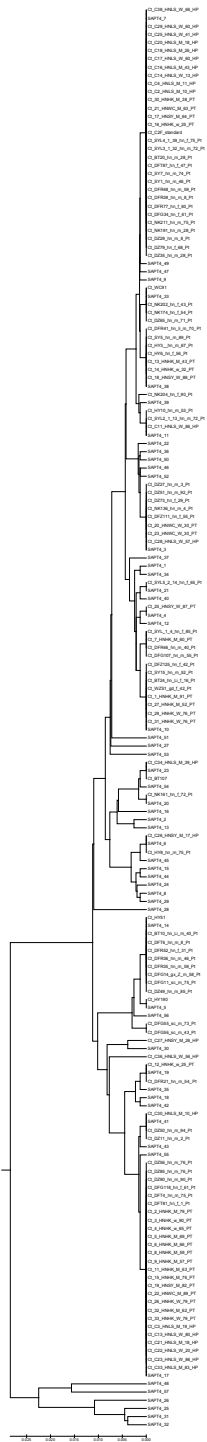




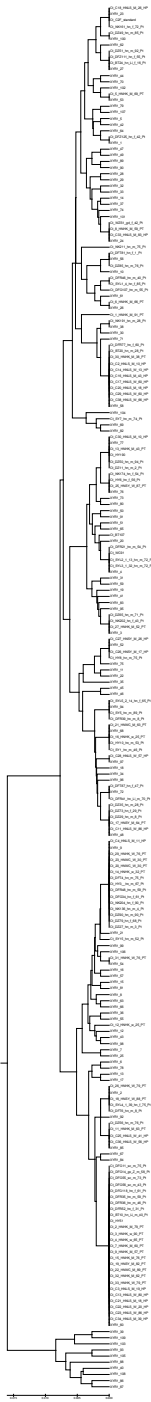
Supplementary Figure S2. Relationships among the unique genotypes at the *MDR1* locus in the *Candida tropicalis* MLST database and those of our 116 strains from Hainan Island.



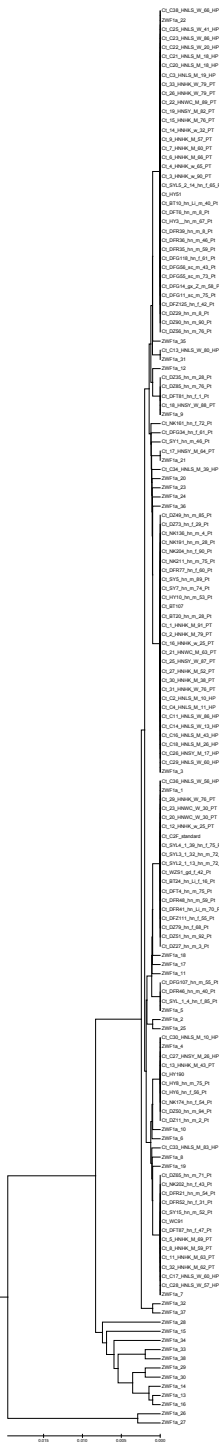
Supplementary Figure S3. Relationships among the unique genotypes at the *SAPT2* locus in the *Candida tropicalis* MLST database and those of our 116 strains from Hainan Island.



Supplementary Figure S4. Relationships among the unique genotypes at the *SATP4* locus in the *Candida tropicalis* MLST database and those of our 116 strains from Hainan Island.



Supplementary Figure S5. Relationships among the unique genotypes at the *XYRI* locus in the *Candida tropicalis* MLST database and those of our 116 strains from Hainan Island.



Supplementary Figure S6. Relationships among the unique genotypes at the *ZWF1a* locus in the *Candida tropicalis* MLST database and those of our 116 strains from Hainan Island.