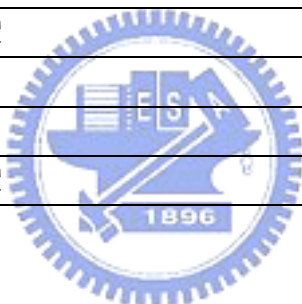


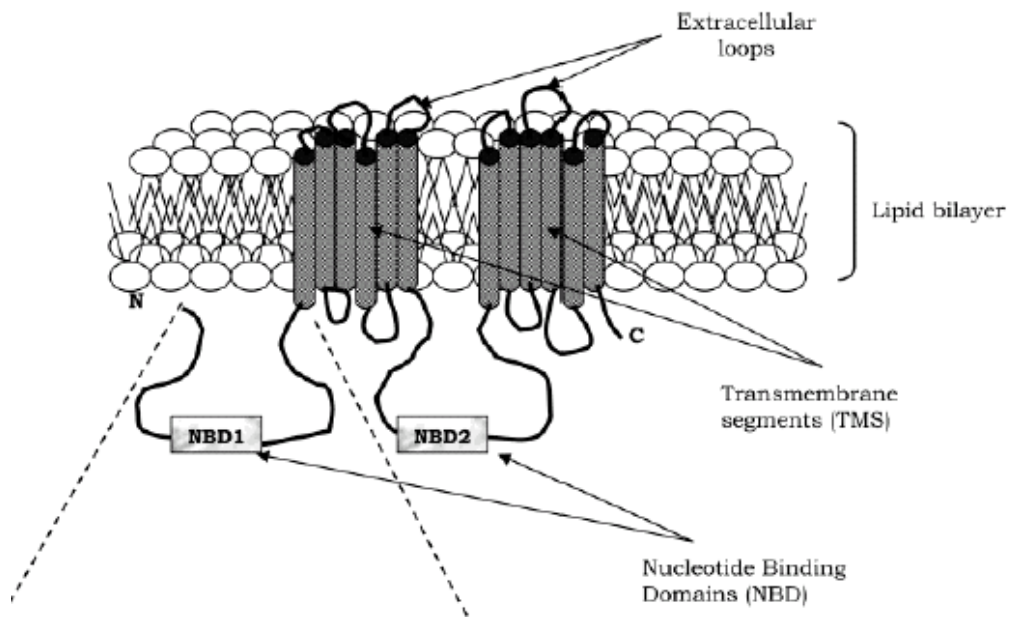
Table 1. The relevant information of the isolated ORFs

Candidate plasmids	ORFs in Candidate plasmid inserts	Size of ORFs (amino acids)	Location of ORFs in Stanford database	Analysis and research of ORFs relevant to this study
C13	13a ( <i>REP3</i> )	380	Contig 6-2308	● Protein containing six C2H2 type zinc finger domains, predicted as a transcriptional factor
	13b	345	Contig 6-2021	
C19	19a ( <i>REP4</i> )	694	Contig 6-2505	● Protein with weak similarity to <i>S. cerevisiae</i> Mnn4p, which is required for transfer of mannosylphosphate
	19b	340	Contig 6-2505	
C82	82 ( <i>REP5</i> )	785	Contig 6-2197	● Protein with weak similarity to <i>S. pombe</i> Gti1p, which is involved in gluconate transport induction
C92	92 ( <i>REP6</i> )	507	Contig 6-2488	<ul style="list-style-type: none"> <li>● Protein containing two zinc finger C2H2 type repeats, which bind nucleic acids</li> <li>● mRNA abundance is greater in <i>C. albicans</i> strains highly resistant to azole (MIC &gt;64 mg/ml) than in strains weakly resistant to azole (MIC &lt;0.25 mg/ml)</li> </ul>

Table 2. The differences in *CDR1* promoter sequence between SC5314 and Ym990348 strains. \* means no nucleic acids. Taking second line for example, there are no nucleotides in Ym990348 promoter corresponding to T in SC5314*CDR1* promoter at –803 position.

The position at <i>CDR1</i> promoter	SC5314 <i>CDR1</i> promoter sequence	Ym990348 <i>CDR1</i> promoter sequence
-803	T	*
-526	C	G
-516~ -511	GAATC	*
-481~ -480	*	TCCT
-436	T	G
-431~ -429	GCA	*
-377	G	*
-235~ -234	*	AA
-234	C	T
-110~ -99	*	TTGTTACTTAC
-184	*	T
-9	C	G





Appendix 1. Predicted structural organization of Cdr1p and nucleotide binding domain (NBD). The topological model of Cdr1p shows two putative transmembrane domains (TMD) and two NBDs. Each TMD comprises six R-helices spanning the lipid membrane. The cytoplasmic domains of Cdr1p, i.e., NBD1 and NBD2, are located at the N- and C-terminus, respectively. (Jha *et al.*, 2003)