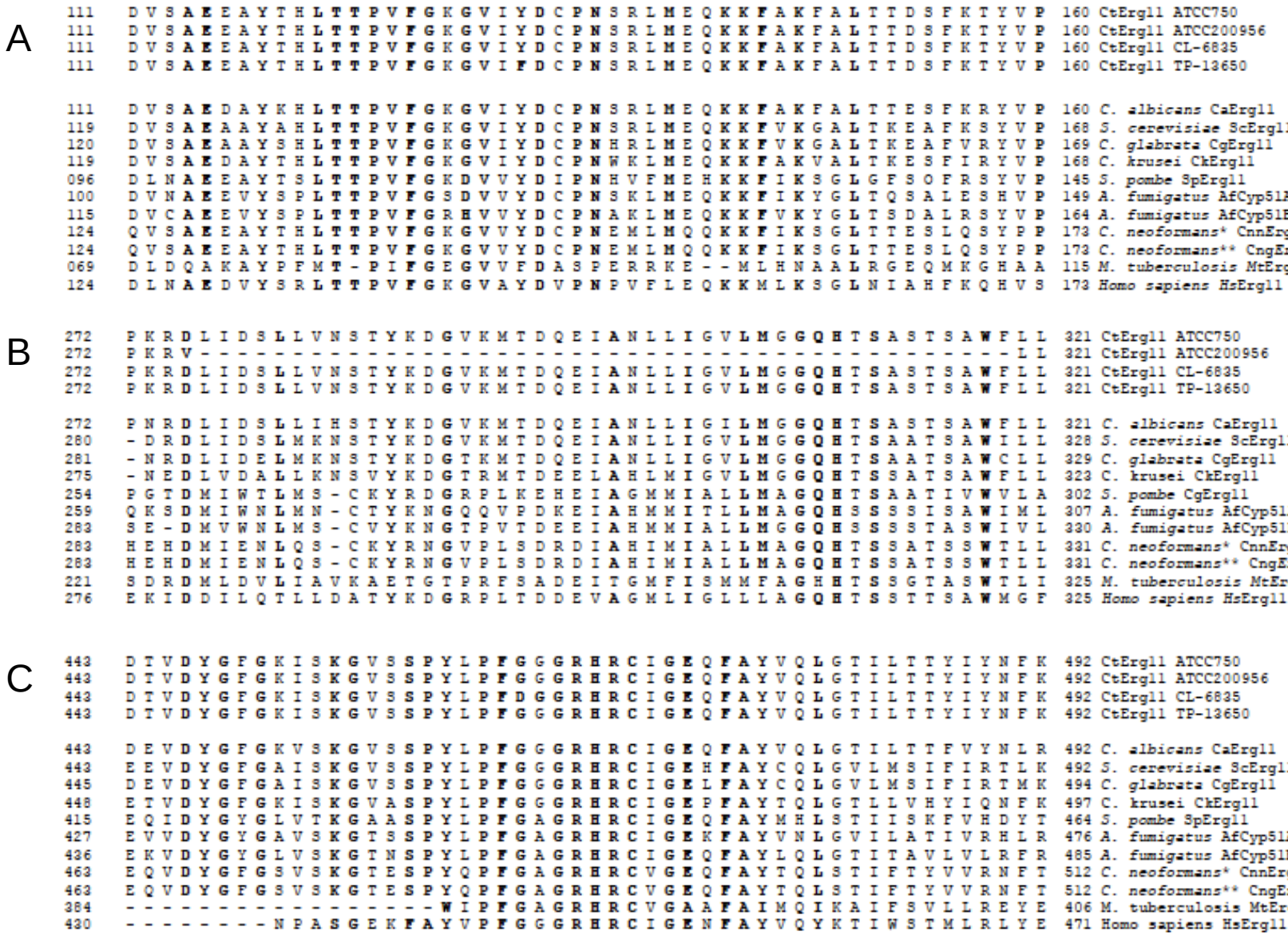
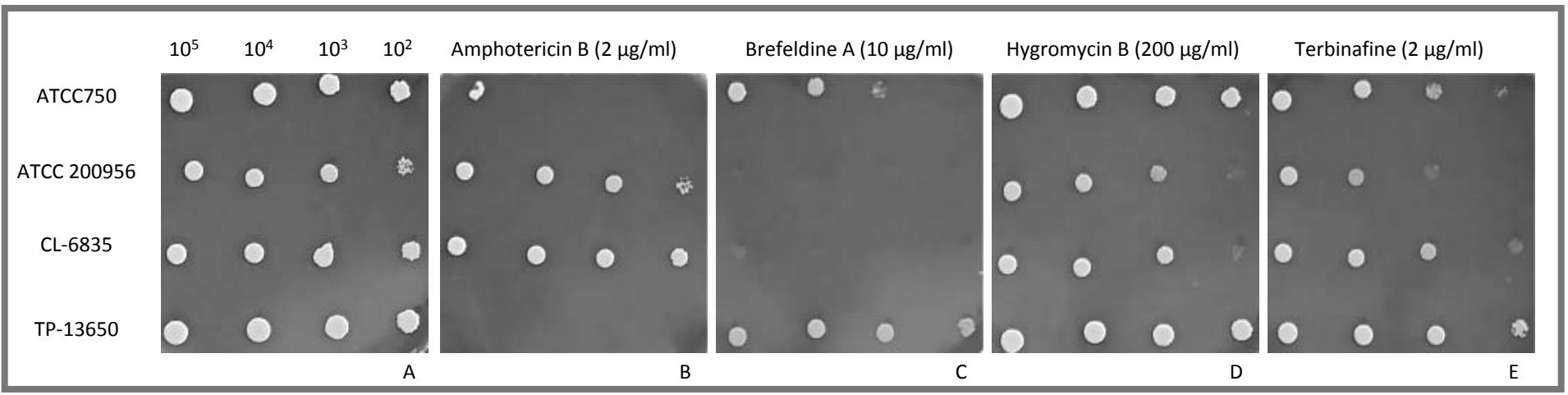
Supplementary Table 1.- Oligonucleotides used for PCR amplification and sequencing of *ERG11* and *ERG3* genes.

Name	5´- 3´	Sequences	Use given	Reference*
			Erg3 PCR amplification	
ERG3F1	sense	TGGATATCGTTCTTGAAAT TTG	PCR amplification and sequencing	This work
ERG3R1	antisense	AACTGGAATGGCTCTAGTTG	Erg3 sequencing	This work
ERG3F2	sense	TCTTATCCCTTTTCATAGTTAC	Erg3 sequencing	This work
ERG3R2	antisense	CCAATAATTACCATCATGAATC	Erg3 sequencing	This work
ERG3F3	sense	TGCTTTCCATCCAGTTGATG	Erg3 sequencing	This work
ERG3R3	antisense	GTCATCAACTTTACCTTCAAG	PCR amplification and sequencing	This work
			Erg11 PCR amplification	
ERG11F1	sense	TCTGACATGGTGTGTGTGTG	PCR amplification and sequencing	[1]
ERG11R1	antisense	ATTGATGCCATCAATGGCAG	Erg11 sequencing	[1]
ERG11F2	sense	ATCCCACAGGCTTATTTGAAA	Erg11 sequencing	[1]
ERG11R2	antisense	GGTCTCTTTCCTTGGTTTTG	Erg11 sequencing	[1]
ERG11F3	sense	TGCTGAAGAAGCTTATACCC	Erg11 sequencing	[1]
ERG11R3	antisense	CAAGGAATCAATCAAATCTCTC	Erg11 sequencing	[1]
ERG11F4	sense	GGTGGTCAACATACTTCTGC	Erg11 sequencing	[1]
ERG11R4	antisense	AGCAGGTTCTAATGGTAAGG	Erg11 sequencing	[1]
ERG11F5	sense	AAACGGTGATAAGGTTCCAG	Erg11 sequencing	[1]
ERG11R5	antisense	TCCCAAGACATCAAACCCTG	Erg11 sequencing	[1]
ERG11R5b	antisense	TGCGGTACAGGTGATCTGTG	PCR amplification and sequencing	This work

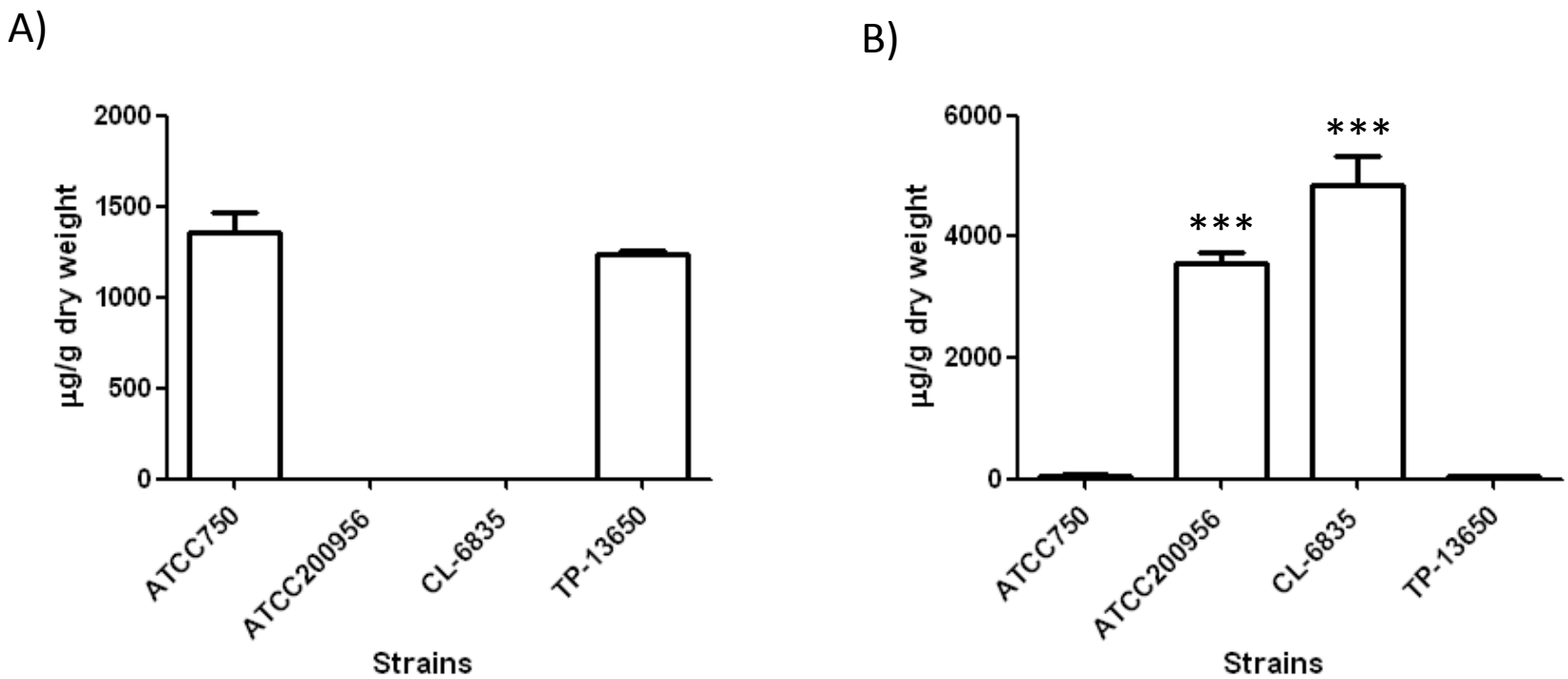
*[1] Vandeputte P, Larcher G, Bergès T, Renier G, Chabasse D, Bouchara JP. 2005. Mechanisms of azole resistance in a clinical isolate of Candida tropicalis. Antimicrob. Agents Chemother. 49:4608-4615.



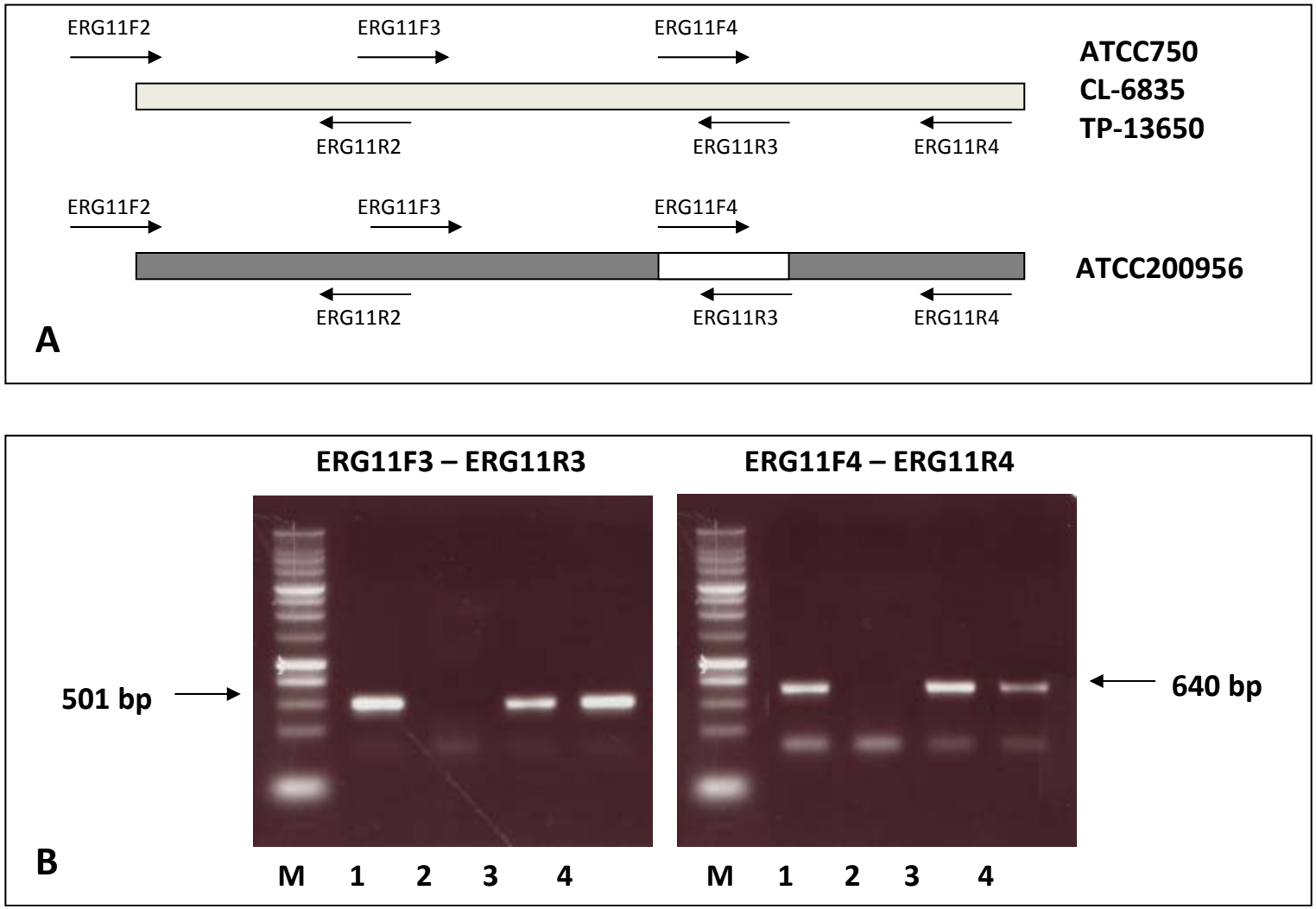
S1_Figure 1.- Alignment of the amino acid residues of Erg11p/CYP51 sequences from yeast and filamentous fungi. Mutations in the *Candida tropicalis* Erg11p are boxed: (A) *C. tropicalis* TP-13650 with Erg11p Y132F amino acid substitution; (B) C. tropicalis ATCC200956 with Erg11p amino acid deletion Δ276-319 and D275V amino acid substitution; (C) *C. tropicalis* CL-6835 with Erg11p G464D amino acid substitution. Bold letters indicate conserved amino acids.



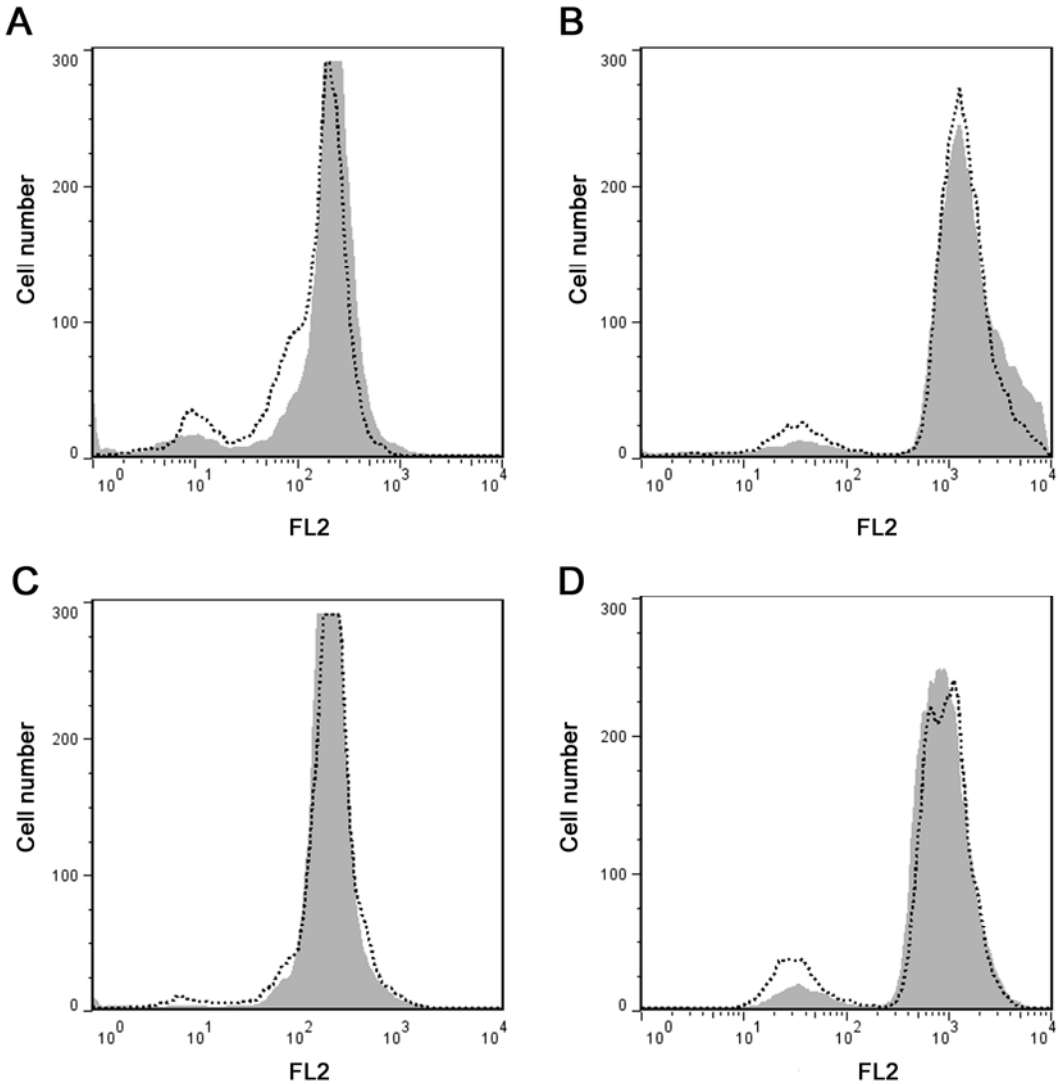
S2_Figure 2. Metabolic inhibitors susceptibility assays. Serial dilutions of *C. tropicalis* susceptible and resistant to azoles (ATCC750 and TP-13650) and *C. tropicalis* with cross-resistance to azole drugs and AmB (ATCC200956 and CL-6835) were spotted onto the agar plates containing the different drugs at the indicated concentrations (B, C, D and E). A drug-free YNB medium was included as control A). The plates were incubated for 48 h at 37°C.



S3_Figure 3.- Total amount of ergosterol (A) and 14-methyl sterols (B). Ergosterol was found in ATCC750 and TP-13650 strains (A). *Candida tropicalis* strains with cross-resistance to azole drugs and AmB, ATCC200956 and CL-6835, presented mostly 14-methyl sterols (B). C-14 methylated sterols were composed of 14-methyl fecosterol, 4,14-dimethylcholesta-8,24-dien-3β-ol, lanosterol and eburicol. ***p <0,0001.



S4_Figure 4. Agarose gel electrophoresis of amplified PCR products of *CtERG11*. (A) Forward and reverse primers (PF3 + PR3, PF4 + PR4) (Supplementary Table 1) were used to amplify a specific region of *CtERG11* sequence where the *ERG11* gene deletion was located. (B) Lane 1: ATCC750, lane 2: ATCC200956, lane 3: CL-6835 and lane 4: TP-13650. Lane M: marker (1 Kb Ladder).



S5_Figure 5. Flow cytometric quantification of Rhodamine 6G (R6G) uptake and efflux in *C. tropicalis*. Yeast cells (10^7) were incubated with R6G (10 μM) in YEPD for 30 min at 30°C, in constant shaking. Fluorescence intensity was quantified after washing with PBS (grey area). Fluorescence intensity was newly quantified (black line) following a further incubation in YEPD. A) ATCC750, B) ATCC200956, C) TP-13650, D) CL-6835.