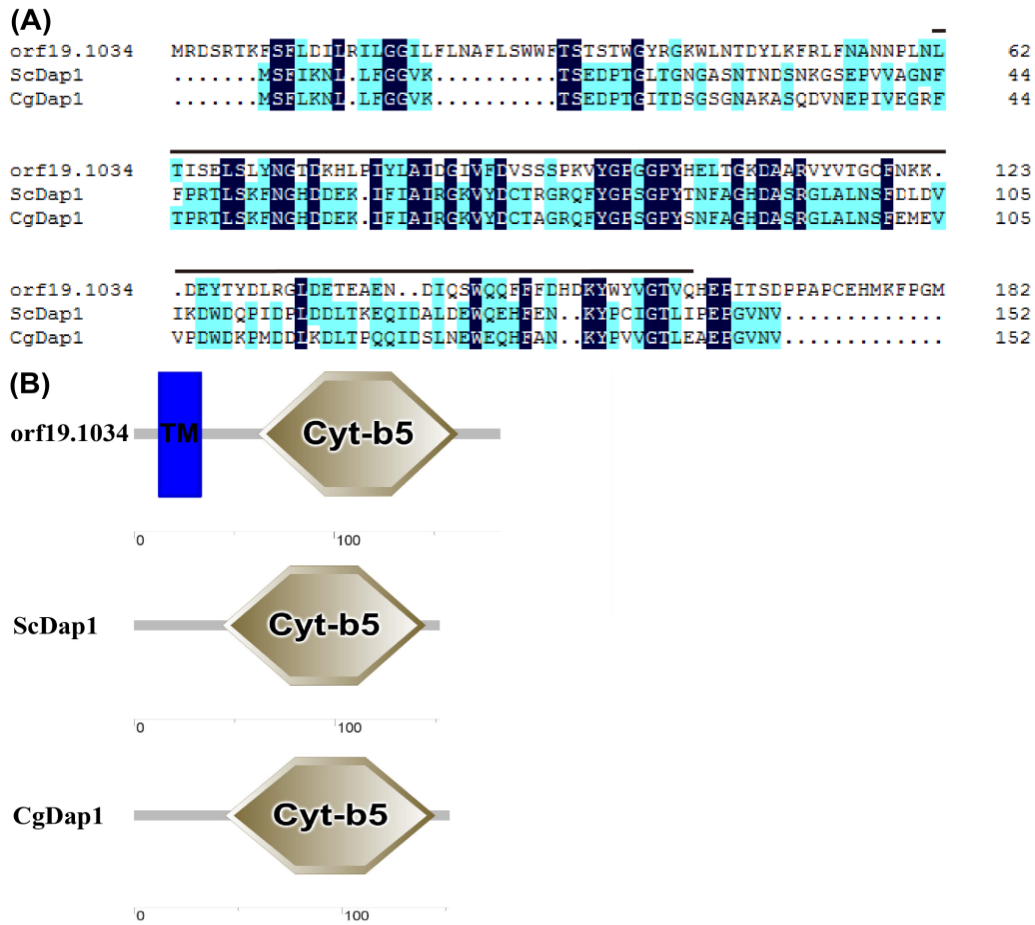
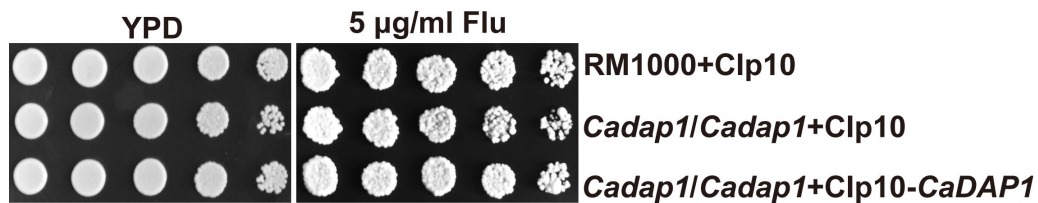


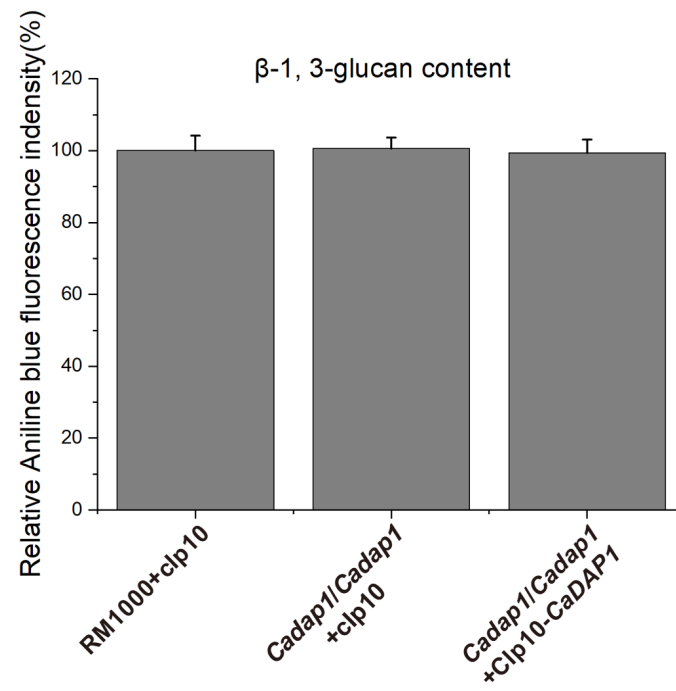
## Supplemental file



**Figure S1. Predicted yeast Dap1 ortholog, CaDap1 (orf19.1034) in *Candida albicans*.** (A) Amino acid sequence alignment of *C. albicans* CaDap1 (orf19.1034) and its homologous sequences from *Saccharomyces cerevisiae* (ScDap1) and *C. glabrata* (CgDap1). The horizontal line represents the predicted cytochrome *b5*-like heme-binding domain of the CaDap1 (orf19.1034). (B) Predicted cytochrome *b5*-like heme-binding and transmembrane (TM) domains in CaDap1 (orf19.1034), ScDap1, and CgDap1, based on a SMART protein search (<http://smart.embl-heidelberg.de/>).



**Figure S2.** The *Cadap1/Cadap1* mutant exhibited insensitive to fluconazole (Flu). Growth phenotypes of the WT, *Cadap1/Cadap1* mutant, and *CaDAP1* RS were evaluated following exposure to 5 µg/ml fluconazole. The cells cultured overnight were renewed in YPD medium and grown to exponential phase at 30°C. Following this, they underwent a tenfold serial dilution and were then spotted sequentially onto plates supplemented with fluconazole. Phenotypic characteristics were examined following incubation at 30°C for 48-72 hours.



**Figure S3.** Deletion of *CaDAP1* leads to unchanged  $\beta$ -1,3-glucan content in cell walls.