Figure S7 Synteny analysis of Rcn1 and Rcn2. NCBI tBLASTx (Altschul *et al.*, 1997) and Artemis programs (Carver *et al.*, 2008) were used to conduct synteny analysis. Red and blue blocks (lines) represent forward and reverse matches of the DNA sequence (tBLASTx based) among *S. cerevisiae* (*Sc*), *C. glabrata* (*Cg*), and *C. albicans* (*Ca*).

REFERENCES

Altschul, S.F., Madden, T.L., Schaffer, A.A., Zhang, J., Zhang, Z., Miller, W., and Lipman, D.J. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* **25**: 3389-3402.

Carver, T., Berriman, M., Tivey, A., Patel, C., Bohme, U., Barrell, B.G., Parkhill, J., and Rajandream, M.A. (2008) Artemis and ACT: viewing, annotating and comparing sequences stored in a relational database. *Bioinformatics* **24**: 2672-2676.