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## Appendix I

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Appendix I

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Source: NCBI Genome Project  

Source: Fungal Genome  
http://fungalgenomes.org/wiki/Main_Page

References

1. V. Wood et al., Nature 415, 871 (Feb 21, 2002).
Appendix II. Multiple sequence alignment and phylogenetic tree of bHLH TF family.

MSA of basic and helix region spanning a 29 amino acid region from 179 bHLH domain sequences produced using MUSCLE. All bHLH domains from the genomes of Candida clade, Saccharomyces clade, Y. lipolytica and S. pombe are included. The MSA was used to prepare a Neighbor-Joining tree using amino acid substitution model, with 1000 bootstrap replicates using MEGA 4. The phylogeny shows clustering of Hemiascomycetes bHLH family in six clusters (I to VI). Clusters II to VI are collapsed for representation of the tree. Cluster I shows the presence of two Candida clade-specific domain families represented by C. albicans orf19.6824 (branches colored brown) and orf19.921 (branches colored green). S. cerevisiae sequences are highlighted with Red filled circles and C. albicans using Green filled circles.
Appendix III. Multiple sequence Alignment of GATA Zinc Finger Domain.

The alignment of 102 GATA domain sequences from *Candida* clade and *Saccharomyces* clade organisms along with *A. nidulans* AreA, *G. gallus* C-terminal GATA-1 and *C. elegans* END1 was prepared using MUSCLE. The alignment highlights the conservation and differences between the different GATA domain sequences. *C. albicans* orf19.4301 and its orthologs in *Candida* clade have a non-canonical GATA domain as these sequences have four amino acid residues between the first two cysteines at position 8 and 13, and a 40 amino acid residue insert between cysteine 13 and cysteine 56. The region C-terminal to cysteine 59 shows conservation with cGATA-1 residues.