

**Reconstruction of gene innovation associated with major evolutionary transitions in the
kingdom Fungi**

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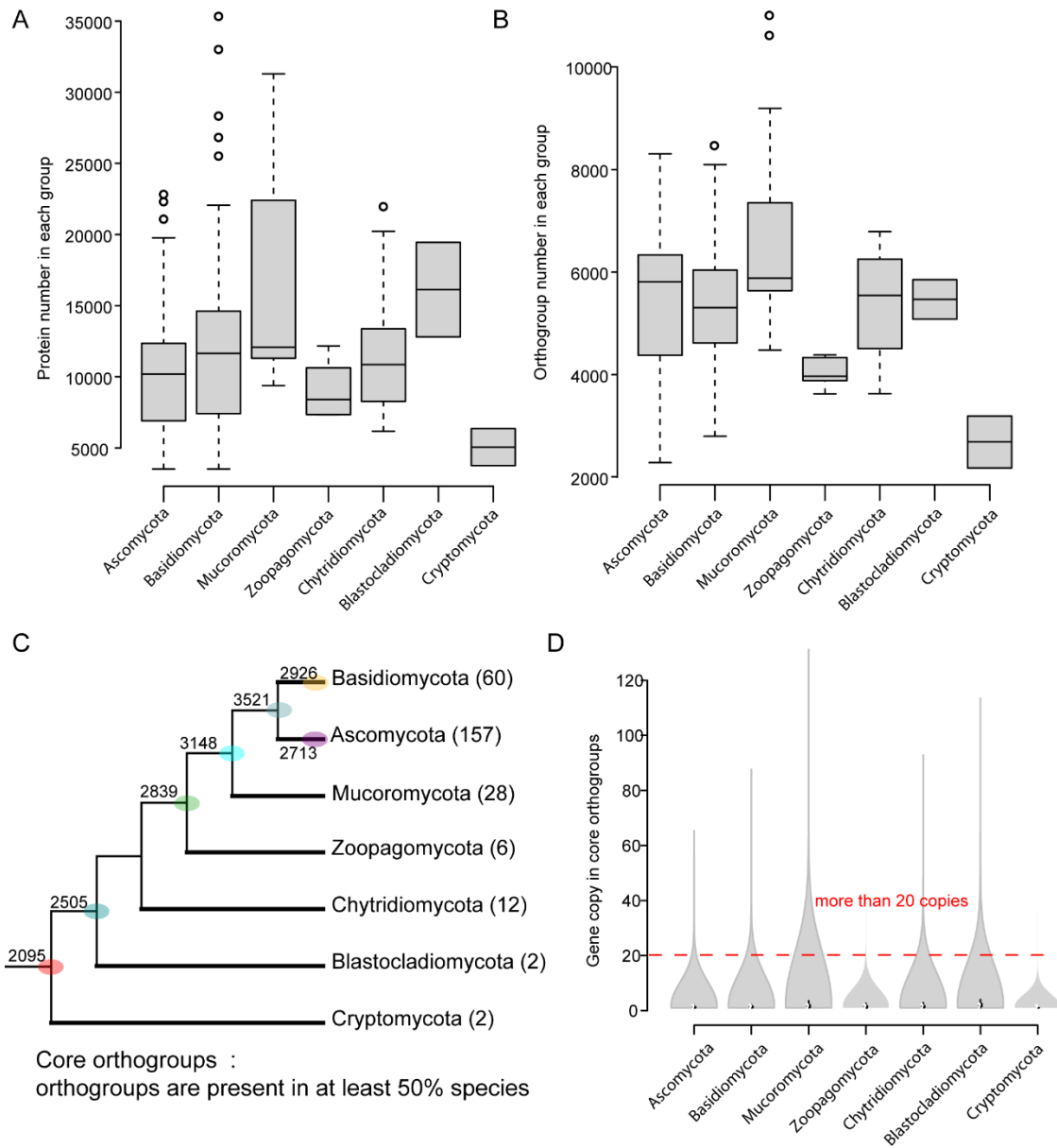


Figure S1. Protein number (A), orthogroup number (B), core orthogroup number (C) and copy number (D). Protein number and orthogroup number are shown for each phylum; core orthogroup number refers to orthogroups that are present in at least 50% of species after their emergence; copy number is the protein number in each core orthogroup.

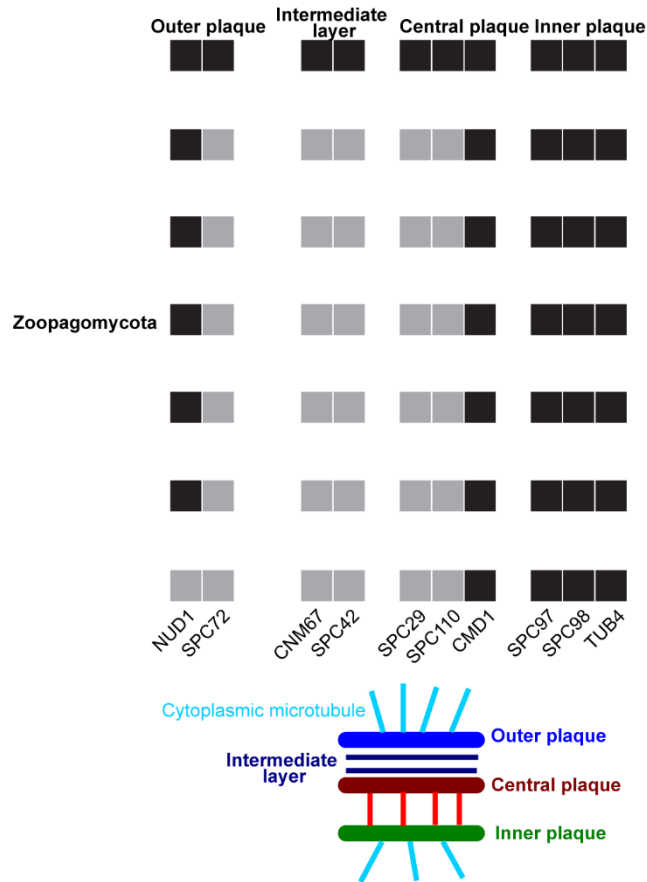


Figure S2. Distribution of proteins involved in formation of the spindle pole body. Black boxes represent “presence”; gray boxes represent “absence”.

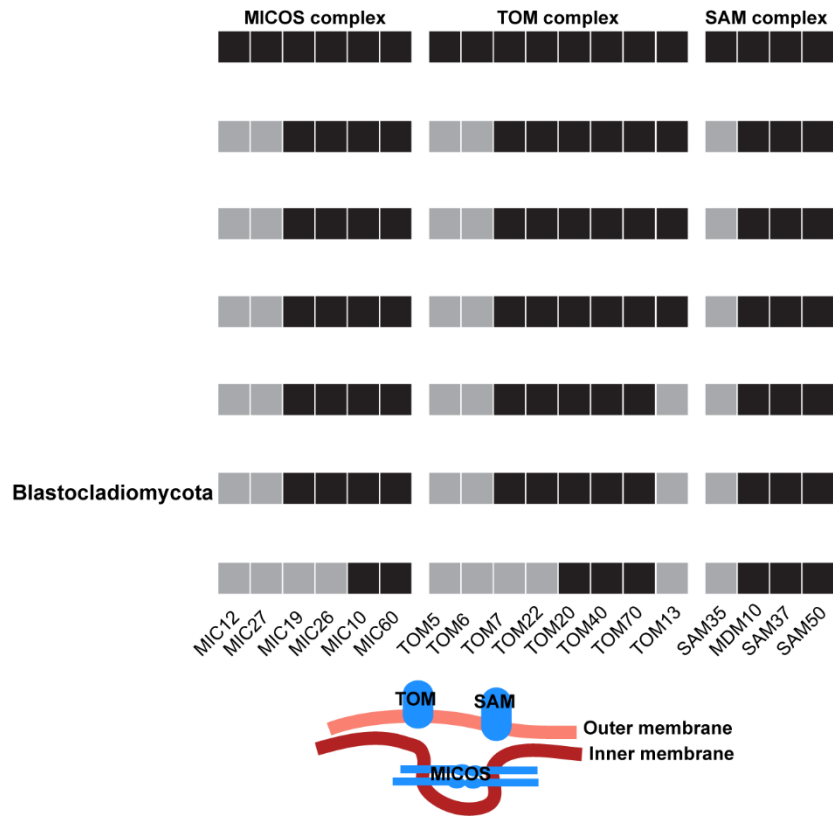


Figure S3. Distribution of proteins involved in three mitochondrial ultrastructure complexes. Black boxes represent “presence”; gray boxes represent “absence”.

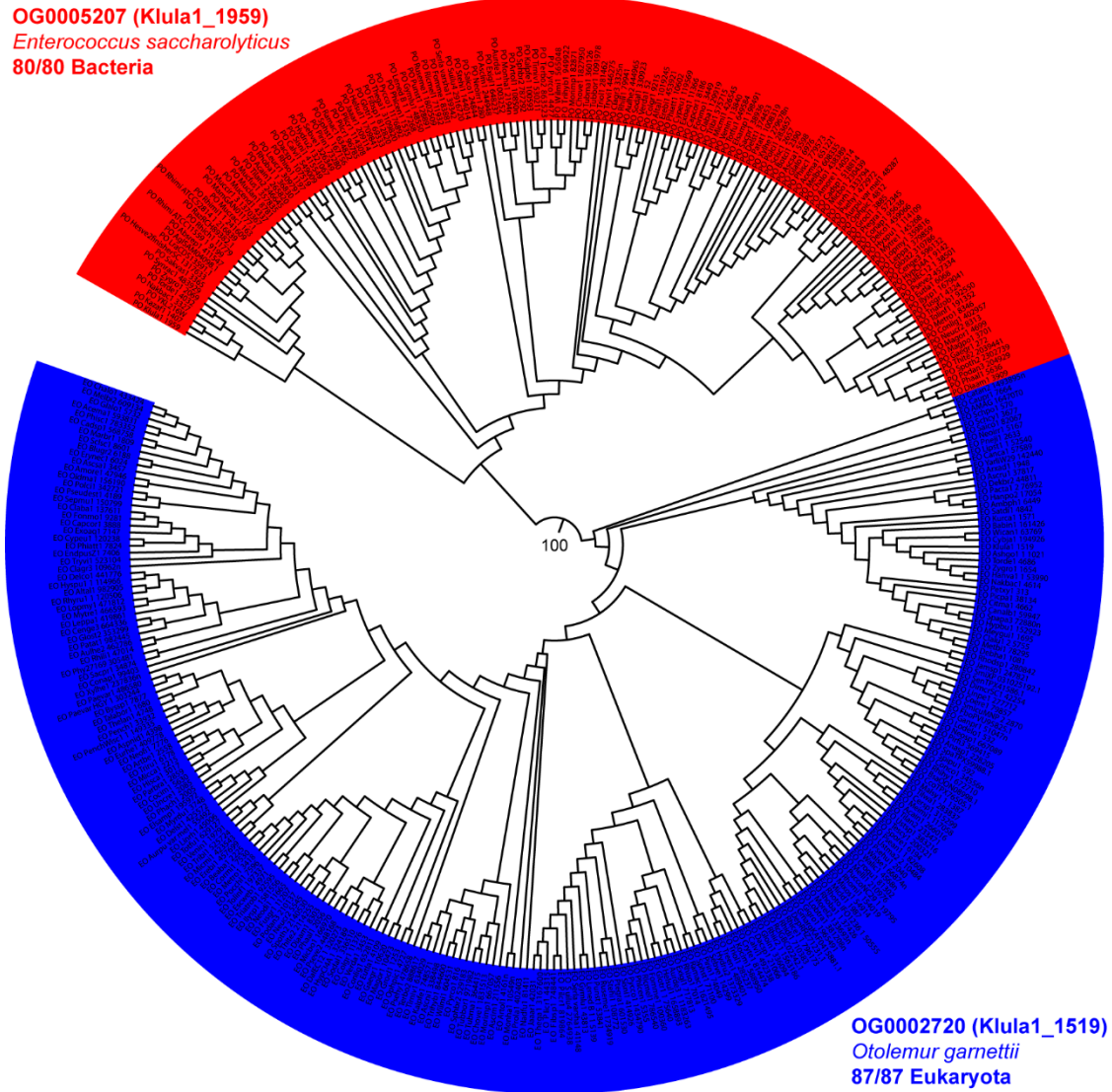


Figure S4. Maximum likelihood tree of 382 fungal dihydroorotate dehydrogenases (142 prokaryotic origin and 240 eukaryotic origin). The tree is midpoint rooted. Klula1_1519 and Klula1_1959 were used to determine the origin of each orthogroup. The best hit and frequency of organisms among the top 100 best hits are also shown.