



Genus	Genome Size (Mb)	Protein Homology (%)
Mucor circinelloides	4407/10300	37.5%
CBE27.49	10300 genes, 3.70 Mb	
Phycomyces blakesleeanus	6658/10300	64.5%
NRL1555	14702 genes, 4p	
Rhizopus oryzae	6658/10300	64.5%
RA-99-880	17467 genes, 4p	
Ashbya gossypii	6039/10300	58.6%
ATCC 10895	4720 genes, 2p	
Candida glabrata	6039/10300	58.6%
CBS 138	5111 genes, 2p	
Saccharomyces cerevisiae	6039/10300	58.6%
SC288c	5880 genes, 2p	
Kluyveromyces lactis	6039/10300	58.6%
NRL Y-1140	5300 genes, 2p	
Debaryomyces hansenii	6039/10300	58.6%
CBS67	6524 genes, 2p	
Pichia stipitis	6039/10300	58.6%
CBS6054	5818 genes, 2p	
Yarrowia lipolytica	6039/10300	58.6%
QAB122	6417 genes, 2p	
Schizosaccharomyces pombe	6039/10300	58.6%
972h	5003 genes, 2p	
Neurospora crassa	6039/10300	58.6%
CF74A	9524 genes, 2p	
Ustilago maydis	6039/10300	58.6%
521	6538 genes, 2p	
Trichoderma reesei	6039/10300	58.6%
QM6a	9144 genes, 2p	
Aspergillus oryzae	6039/10300	58.6%
RB-40	12074 genes, 2p	
Aspergillus niger	6039/10300	58.6%
ATC 1015	11197 genes, 2p	
Aspergillus fumigatus	6039/10300	58.6%
AF293	9025 genes, 2p	
Aspergillus nidulans	6039/10300	58.6%
FGSC44	7082 genes, 2p	
Penicillium chrysogenum	6039/10300	58.6%
Wilson54-1255	12811 genes, 2p	

Figure S1. Proteome comparison of genomes in *Fungi*. ALR (the ratio of alignment length to query sequence length): >0.50, identity: >0.40. The red shades refer to protein homology that can be found within a genome (paralog). The green shades refer to protein homology that can be found between two genomes (ortholog).