

Fourteen genomes used in this study.

Species ^a	Genome size/ gene number	Sources and accession numbers
Fungi [Saccharomycotina (hemiascomycetes)]		
<i>Yarrowia lipolytica</i> (Yl)	20.5 Mb/ 6,700	European Molecular Biology Laboratory [http://www.ebi.ac.uk/genomes/]
<i>Candida albicans</i> (Ca)	15.6 Mb/ 6,090	CandidaDB [http://genolist.pasteur.fr/CandidaDB/]
<i>Debaryomyces hansenii</i> (Dh)	12 Mb/ 7,000	European Molecular Biology Laboratory [http://www.ebi.ac.uk/genomes/]
<i>Ashbya gossypii</i> ^b (Ag)	9.2 Mb/ 4,718	NCBI ^c : NC005782, NC005788 (Chromosomes 1-7)
<i>Candida glabrata</i> (Cg)	12.3 Mb/ 5,283	NCBI ^c : NC005967, NC005968, NC006026, NP006037 (Chromosomes A-M)
<i>Saccharomyces cerevisiae</i> (Sc)	12.1 Mb/6,294	<i>Saccharomyces</i> Genome Database [http://www.yeastgenome.org/]
Fungi [Pezizomycotina (euascomycetes)]		
<i>Aspergillus fumigatus</i> (Af)	29.4 Mb/ 9,926	Sanger Institute [http://www.sanger.ac.uk/Projects/Fungi/]
<i>Neurospora crassa</i> (Nc)	40 Mb/ 10,082	Fungal Genome Initiative [http://www.broad.mit.edu/annotation/]
<i>Fusarium graminearum</i> ^b (Fg)	40 Mb/ 11,640	Fungal Genome Initiative [http://www.broad.mit.edu/annotation/]
<i>Magnaporthe grisea</i> (Mg)	37.8 Mb/ 11,109	Fungal Genome Initiative [http://www.broad.mit.edu/annotation/]
Fungi [Taphrinomycotina (archaeascomycetes)]		
<i>Schizosaccharomyces pombe</i> (Sp)	14 Mb/ 4,824	NCBI ^c : NC003424, NC003423, NC003421 (Chromosomes 1-3)
Plant		
<i>Arabidopsis thaliana</i> (At)	120 Mb/ 25,498	MIPS Arabidopsis genome database [http://mips.gsf.de/]
Animals		
<i>Mus musculus</i> (Mm)	2.5 Gb/ 24,174	NCBI ^c
<i>Drosophila melanogaster</i> (Dm)	165 Mb/ 13,600	FlyBase [http://flybase.bio.indiana.edu/]

^aSpecies abbreviations used in this study are shown in parentheses.

^b*Fusarium graminearum* is known also as *Gibberella zeae*. *Ashbya gossypii* is known also as *Eremothecium gossypii*.

^cNational Center for Biotechnology Information [<http://www.ncbi.nlm.nih.gov/>]