

Table S1. Homeobox transcription factors in genomes of eukaryotic microbes.

Species name	Phylum /Subphylum	Expected number			Homeobox TF /TF (%)	References
		ORFs	TFs	Homeobox TFs		
<i>Magnaporthe oryzae</i>	Pezizomycotina	11,069	462	8	1.73%	(Dean et al., 2005)
<i>Aspergillus fumigatus</i>	"	9,887	562	9	1.60%	(Nierman et al., 2005)
<i>A. nidulans</i>	"	10,701	638	7	1.10%	(Galagan et al., 2005)
<i>Fusarium graminearum</i>	"	13,321	660	13	1.97%	(Cuomo et al., 2007)
<i>F. oxysporum</i>	"	17,608	814	13	1.60%	-
<i>F. verticillioides</i>	"	14,199	629	10	1.59%	-
<i>F. solani</i>	"	15,707	992	22	2.22%	-
<i>Neurospora crassa</i>	"	9,842	420	8	1.90%	(Galagan et al., 2003)
<i>Podospora anserina</i>	"	10,596	477	7	1.47%	(Espagne et al., 2008)
<i>Stagonospora nodorum</i>	"	16,597	516	13	2.52%	(Hane et al., 2007)
<i>Trichoderma reesei</i>	"	9,129	513	8	1.56%	(Martinez et al., 2008)
<i>Candida albicans</i>	Saccharomycotina	6,090	308	5	1.62%	(Jones et al., 2004) (van het Hoog et al., 2007)
<i>C. glabrata</i>	"	5,165	262	10	3.82%	(Dujon et al., 2004)
<i>Saccharomyces cerevisiae</i>	"	6,692	295	11	3.73%	(Goffeau et al., 1996)
<i>Schizosaccharomyces pombe</i>	Taphrinomycotina	5,058	223	2	0.90%	(Wood et al., 2002)
<i>Cryptococcus neoformans</i>	Basidiomycota	6,475	307	9	2.93%	(Loftus et al., 2005)
<i>Laccaria bicolor</i>	"	20,614	501	15	2.99%	(Martin et al., 2008)
<i>Phanerochaete chrysosporium</i>	"	10,048	387	11	2.84%	(Martinez et al., 2004)
<i>Ustilago maydis</i>	"	6,689	332	7	2.11%	(Kamper et al., 2006)
<i>Encephalitozoon cuniculi</i>	Microsporidia	1,996	108	13	12.04%	(Katinka et al., 2001)
<i>Phytophthora ramorum</i>	Oomycetes	15,743	641	8	1.25%	(Tyler et al., 2006)
<i>P. sojae</i>	"	19,027	919	7	0.76%	(Tyler et al., 2006)
Total		242,253	10,966	216	1.97%	