

Table S1. Transcription factors encoded by 23 fungal and Oomycete genomes

Species name	Phylum/ Subphylum	No. of ORFs	No. of TF families	No. of TFs	Ratio	Ref.*
<i>Magnaporthe oryzae</i>	Pezizomycotina	11,069	44	495	4.49%	(1)
<i>Fusarium graminearum</i>	Pezizomycotina	13,339	44	659	4.94%	(2)
<i>Fusarium oxysporum</i>	Pezizomycotina	17,735	43	795	4.48%	NA
<i>Neurospora crassa</i>	Pezizomycotina	9,842	44	420	4.27%	(3)
<i>Podospora anserina</i>	Pezizomycotina	10,596	41	477	4.50%	(4)
<i>Stagonospora nodorum</i>	Pezizomycotina	15,893	39	442	2.77%	(5)
<i>Uncinocarpus reesii</i>	Pezizomycotina	7,798	44	321	4.12%	
<i>Aspergillus fumigatus</i>	Pezizomycotina	9,887	44	562	5.68%	(6)
<i>Aspergillus nidulans</i>	Pezizomycotina	10,568	44	608	5.75%	(7)
<i>Yarrowia lipolytica</i>	Saccharomycotina	6,524	42	289	4.43%	(8)
<i>Saccharomyces cerevisiae</i>	Saccharomycotina	6,700	36	295	4.41%	(9)
<i>Candida glabrata</i>	Saccharomycotina	5,165	38	262	5.07%	(8)
<i>Debaryomyces hansenii</i>	Saccharomycotina	6,354	42	324	5.10%	(8)
<i>Candida albicans</i>	Saccharomycotina	6,185	39	317	5.13%	(10, 11)
<i>Schizosaccharomyces pombe</i>	Taphrinomycotina	5,058	38	222	4.39%	(12)
<i>Cryptococcus neoformans</i>	Basidiomycota	6,475	34	307	4.74%	(13)
<i>Phanerochaete chrysosporium</i>	Basidiomycota	10,048	37	387	3.85%	(14)
<i>Laccaria bicolor</i>	Basidiomycota	20,614	39	494	2.40%	(15)
<i>Ustilago maydis</i>	Basidiomycota	6,689	40	331	4.95%	(16)
<i>Rhizopus oryzae</i>	Mucoromycotina	17,482	41	1,110	6.35%	(17)
<i>Encephalitozoon cuniculi</i>	Microsporidia	1,996	22	108	5.41%	(18)
<i>Phytophthora sojae</i>	Oomycetes	19,027	42	919	4.83%	(19)
<i>Phytophthora ramorum</i>	Oomycetes	15,743	40	641	4.07%	(19)
<b>Total</b>		240,787		10,785	4.46%	-

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