

Appendix A Annotation of protein kinase (PK) families/subfamilies*

Familis/groups	NCBI ACCESSION	Fungi	Description
AGC	NP_116620	Saccharomyces cerevisiae S288C	RIM15; YFL033C Serine/threonine protein kinase; positive regulator of IME2 expression and of sporulation
AGC/AKT	NP_012075	Saccharomyces cerevisiae S289C	SCH9/KOM1/YHR205W Serine/threonine protein kinase that is activated by cAMP, overproduction can suppress cdc25 mutant.
AGC/DMPK	XP_011390382	Ustilago maydis	NCBI NOTE: Related to Serine/threonine-protein kinase CBK1
AGC/DMPK/GEK	KNE92030	Puccinia striiformis	NCBI NOTE: ATP binding site
AGC/DMPK/ROCK	XP_014567070	Mixia osmundae	NCBI NOTE: Glycosyltransferase sugar-binding region containing DXD motif
AGC/NDR	NP_011606	Saccharomyces cerevisiae S290C	DBF2/G4643/YGR092W Serine/threonine protein kinase Similar to Dbf20p, required for events in anaphase/telophase.
AGC/NDR/NDR	NP_014238	Saccharomyces cerevisiae S290C	CBK1/N1727/YNL161W Putative serine/threonine protein kinase of unknown function.
AGC/NDR/NDR-UNCLASSIFIED	XP_011389907	Ustilago maydis	NCBI NOTE: Putative protein kinase DBF2
AGC/PDK1	NP_014541	Saccharomyces cerevisiae S290C	YDR490C/D8035.33/PKH1 Serine/threonine protein kinase functions similarly to mammalian 3-phosphoinositide-dependent protein kinase; phosphorylates and activates Ypk1p

AGC/PKA	NP_015121	Saccharomyces cerevisiae S290C	TPK2/PKA2/YKR1/P1855/YPL203W/PKA3 cAMP-dependent protein kinase 2, catalytic chain.
AGC/PKC	NP_009445	Saccharomyces cerevisiae S291C	PKC1/STT1/HPO2/CLY15/YBL0807/YBL105C Protein kinase C, regulates MAP kinase cascade involved in regulating cell wall metabolism.
AGC/RSK	CCU81475	Blumeria graminis	NCBI NOTE: Serine/threonine-protein kinase
AGC/RSK/RSKP70	NP_009584	Saccharomyces cerevisiae S290C	YBR028C/YBR0312 Serine/threonine protein kinase with similarity to Ypk2p/Ykr2p and Ypk1p.
AGC/RSK/RSKP90	XP_007409802	Melampsora larici-populina	NCBI NOTE: Hypothetical protein MELLADRAFT_35870
AGC/RSK/RSK-UNCLASSIFIED	NP_010015	Saccharomyces cerevisiae S290C	KIN82/YCR1153/YCR091W Serine/threonine protein kinase of unknown function.
AGC/SGK	XP_007810341	Metarhizium acridum	NCBI NOTE: Protein kinase domain-containing protein
AGC/YANK	XP_011390435	Ustilago maydis	NCBI NOTE: Catalytic domain of the Serine/Threonine Kinase, Yank1
Atypical/ABC1	NP_015216	Saccharomyces cerevisiae S290C	YPL109C; LPH17 Protein of unknown function
Atypical/ABC1/ABC1-A	NP_011396	Saccharomyces cerevisiae S290C	ABC1; G2920; YGL119W Protein likely to be involved in assembly of ubiquinol cytochrome-c reductase complex
Atypical/ABC1/ABC1-B	NP_013354	Saccharomyces cerevisiae S290C	YLR253W/L9672.2/YL53 Protein with weak similarity to Abc1p
Atypical/ABC1/ABC1-C	XP_011386479	Ustilago maydis	NCBI NOTE:
Atypical/BCR	XP_003330885	Puccinia graminis	NCBI NOTE: atypical/BCR protein kinase
Atypical/HISK	XP_002617611	Clavispora lusitaniae	NCBI NOTE:
Atypical/PI4K	XP_003319638	Puccinia graminis	NCBI NOTE: atypical/PI4K protein kinase

Atypical/PIKK	KNE98704	Puccinia graminis	NCBI NOTE: Atypical/PIKK protein kinase
Atypical/PIKK/FRAP	XP_013018086	Schizosaccharomyces octosporus	NCBI NOTE: phosphatidylinositol kinase Tor1
Atypical/RIO	NP_014192	Saccharomyces cerevisiae S290C	NCBI NOTE: Essential serine kinase involved in the processing of 20S pre-rRNA; involved in the processing of the 20S pre-rRNA into mature 18S rRNA; has similarity to Rio1p
Atypical/RIO/RIO1	NP_014762	Saccharomyces cerevisiae S290C	RIO1; YOR3266; O3266; YOR119C Protein of unknown function
Atypical/RIO/RIO2	XP_011391614	Ustilago maydis	NCBI NOTE:
CAMK	NP_010182	Saccharomyces cerevisiae S290C	DUN1/ORF2370/YDL101C Protein kinase necessary for induction of Rnr3p and DNA repair genes after DNA damage. Contains FHA domain.
CAMK/CAMK1	NP_013349	Saccharomyces cerevisiae S290C	RCK2/CMK3/CLK1/L9672.6/YLR248W Calcium/calmodulin-dependent serine/threonine protein kinase (CaM kinase).
CAMK/CAMK1/CAMK1-CMK	NP_116669	Saccharomyces cerevisiae S290C	CMK2/O2325/YOL016C Calcium/calmodulin-dependent serine/threonine protein kinase (CaM kinase), type II.
CAMK/CAMK1/CAMK1-RCK	NP_011357	Saccharomyces cerevisiae S290C	RCK1/G1854/YGL158W Serine/threonine protein kinase with similarity to Cmk1p, Cmk2p, and Cmk3p. (Seq updated)
CAMK/CAMKL	XP_011391526	Ustilago maydis	NCBI NOTE:

CAMK/CAMKL/AMPK	NP_010765	Saccharomyces cerevisiae S290C	SNF1/CAT1/CCR1/PAS14/HAF3/D8035.20/YDR477W Serine/threonine protein kinase essential for derepression of glucose-repressed genes, acts with Snf4p.
CAMK/CAMKL/BRSK	CEH18548	Ceraceosorus bombacis	NCBI NOTE: Serine threonine-protein kinase
CAMK/CAMKL/CHK1	NP_009833	Saccharomyces cerevisiae S290C	YBR274W/YBR1742/CHK1 Checkpoint kinase, required for metaphase DNA-damage checkpo (Similar to CHK1-sp, CHK1_ce, SNF1_r)
CAMK/CAMKL/GIN4	NP_010795	Saccharomyces cerevisiae S290C	GIN4/D9719.13/YDR507C Serine/threonine-protein kinase with similarity to Yc1024p, growth inhibitory protein.
CAMK/CAMKL/KIN1	NP_013197	Saccharomyces cerevisiae S290C	KIN1/YD9727.17/YDR122W Serine/threonine protein kinase, Similar to Kin2p and S. pombe KIN1.
CAMK/CAMKL/KIN4	NP_014876	Saccharomyces cerevisiae S290C	KIN4/KIN31/(KIN3)/O5220/YOR233W Serine/threonine protein kinase Similar to Kin1p and Kin2p, catalytic domain is most Similar to Snf1p.
CAMK/CAMKL/MARK	NP_015175	Saccharomyces cerevisiae S290C	YPL150W/P2597 Serine/threonine protein kinase of unknown function. (Not in YPD listing)
CAMK/CAMKL/PASK	NP_009385	Saccharomyces cerevisiae S290C	YAL017W/YAL002/FUN31 Serine/threonine protein kinase of unknown function.
CAMK/RAD53	XP_011326827	Fusarium graminearum	NCBI NOTE:
CK1	KZO95435	Calocera viscosa	NCBI NOTE:
CK1/CK1	NP_011049	Saccharomyces cerevisiae S290C	YCK3/CKI3/YER123W Casein kinase I isoform.

CK1/CK1/CK1-D	NP_015120	Saccharomyces cerevisiae S290C	HRR25/P1850/YPL204W Casein kinase I, serine/threonine/tyrosine protein kinase, associated with DNA repair and meiosis.
CK1/CK1/CK1-G	NP_014245	Saccharomyces cerevisiae S290C	YCK1/CKI2/YHR135C Casein kinase I isoform.
CMGC	XP_011323418	Fusarium graminearum	NCBI NOTE:
CMGC/CDK	NP_116624	Saccharomyces cerevisiae S290C	CAK1/CIV1/YFL029C Cdk-activating kinase (serine/threonine protein kinase) responsible for in vivo activation of Cdc28p. PHNAKFE in kinase domain III.
CMGC/CDK/CDC2	NP_009718	Saccharomyces cerevisiae S290C	CDC28/CDK1/SRM5/HSL5/YBR1211/YBR160W Cyclin-dependent protein kinase essential for completion of START and for mitosis, associates with Cks1p and cyclins. PSTAIRE in kinase domain III.
CMGC/CDK/CDK5	NP_015294	Saccharomyces cerevisiae S290C	PHO85/P7102_18A/YPL031C Cyclin-dependent protein kinase that interacts with cyclin Pho80p to regulate phosphate pathway. PSTAIRE in kinase domain III.
CMGC/CDK/CDK7	NP_010175	Saccharomyces cerevisiae S290C	KIN28/ORF2330/YDL108W CDK component of transcription initiation factor TFIIF, phosphorylates C-terminal domain (CTD) of RNA polymerase large subunit. DMSAIRE in kinase domain III.
CMGC/CDK/CDK8	NP_015283	Saccharomyces cerevisiae S290C	SSN3/UME5/SRB10/(ARE1)/P7102_08/YPL042C CDK of the RNA polymerase II holoenzyme complex and Kornberg's mediator (SRB) subcomplex. SQSACRE and TLY in kinase domains III and VIII.
CMGC/CDK/CDK9	KNF03340	Puccinia graminis	NCBI NOTE:CMGC/CDK/CDK9 protein kinase

CMGC/CDK/CRK7	NP_012783	Saccharomyces cerevisiae S290C	CTK1/YKL139W Carboxyl-terminal domain (CTD) kinase alpha subunit, CDK that phosphorylates C-terminal domain of RNA polymerase II large subunit. PITSIRE in kinase domain III.
CMGC/CDK/PITSLRE	XP_007705970	Bipolaris sorokiniana	NCBI NOTE:
CMGC/CDKL	XP_007696936	Bipolaris sorokiniana	NCBI NOTE:
CMGC/CK2	NP_014704	Saccharomyces cerevisiae S290C	CKA2/O2810/YOR061W Casein kinase II, catalytic (alpha) subunit.
CMGC/CLK	NP_013081	Saccharomyces cerevisiae S290C	KNS1/L1224/YLL019C Serine/threonine protein kinase of unknown function. (Similar to CLK_h)
CMGC/DYRK	XP_002549142	Candida tropicalis	NCBI NOTE:
CMGC/DYRK/DYRK2	XP_013016002	Schizosaccharomyces octosporus	NCBI NOTE: CMGC/DYRK/DYRK2 protein kinase Ppk5
CMGC/DYRK/PRP4	XP_013016858	Schizosaccharomyces octosporus	NCBI NOTE: CMGC/DYRK/PRP4 protein kinase Prp4
CMGC/DYRK/YAK	NP_012394	Saccharomyces cerevisiae S290C	YAK1/YJL141C Serine/threonine protein kinase that suppresses loss of Tpk1p + Tpk2p + Tpk3p. (Similar to KA23_sp, MNB_dm, MNB_h)
CMGC/GSK	NP_014513	Saccharomyces cerevisiae S290C	YOL128C/O0530/ORF1209713 Protein serine/threonine protein kinase of unknown function.
CMGC/MAPK	NP_011554	Saccharomyces cerevisiae S290C	KSS1/G4149/YGR040W Serine/threonine protein kinase of the MAP kinase family, redundant with Fus3p for cell cycle arrest. TEY in kinase domain VIII (activation loop).

CMGC/MAPK/ERK1	NP_011895	Saccharomyces cerevisiae S290C	SMK1/YP9499.10/YPR048W Sporulation-specific MAP kinase required for completion of sporulation. TNY in kinase domain VIII.
CMGC/MAPK/P38	NP_013214	Saccharomyces cerevisiae S290C	HOG1/SSK3/L9354.2/L2931/YLR113W Serine/threonine protein kinase of MAP kinase (MAPK) family, involved in high-osmolarity signal transduction pathway. TGY in kinase domain VIII.
CMGC/RCK	NP_012429	Saccharomyces cerevisiae S290C	IME2/SME1/J0817/YJL106W STK and positive regulator of sporulation genes that is essential for initiation of meiosis. TAY in kinase domain VIII (activation loop). (Similar to MAK_r, p34_h, CDK2_h)
CMGC/RCK/MAK	APA07961	Sclerotinia sclerotiorum	NCBI NOTE:
CMGC/SRPK	NP_013943	Saccharomyces cerevisiae S290C	YMR216C/YM8261.10 Putative serine/threonine protein kinase, involved in phosphorylation of Npl3p, similar to Cdc31p. (Similar to DSK1_sp, SRPK1_ce, U52111_h).
Other/AGAK1	KDQ19992	Botryobasidium botryosum	NCBI NOTE:
Other/AUR	NP_015115	Saccharomyces cerevisiae S290C	IPL1/P1820/YPL209C Serine/threonine protein kinase involved in chromosome segregation. (Similar to AUR_dm)
Other/BUB	NP_011704	Saccharomyces cerevisiae S290C	BUB1/G7542/YGR188C Serine/threonine protein kinase and checkpoint protein required for cell cycle arrest in response to loss of microtubule function. (N-terminus Similar to MAD3_sc)

Other/BUD32	NP_011778	Saccharomyces cerevisiae S291C	NCBI NOTE: Protein kinase; component of the EKC/KEOPS complex with Kae1p, Cgi121p, Pcc1p, and Gon7p; Pyrococcus Bud32 ortholog functions as a P-loop ATPase rather than a protein kinase in the context of the complex;
Other/CAMKK	NP_012876	Saccharomyces cerevisiae S292C	ELM1/YKL261/YKL048C Serine/threonine protein kinase regulating pseudohyphal growth.
Other/CAMKK/CAMKK-META	CCU82552	Blumeria graminis	NCBI NOTE: Calcium/calmodulin dependent protein kinase C
Other/CAMKK/ELM	EEQ44153	Candida albicans	NCBI NOTE:
Other/CDC7	NP_010267	Saccharomyces cerevisiae S290C	CDC7/SAS1/OAF2/D2855/YDL017W Protein kinase required for initiation of DNA synthesis, for commitment to sporulation, for DNA repair, and for meiotic recombination. (Similar to HSK1_sp)
Other/CILIATE-A1	KMU84665	Coccidioides immitis	NCBI NOTE:
Other/HAL	NP_014216	Saccharomyces cerevisiae S290C	HAL5/J0531/YJL165C Serine/threonine protein kinase involved in salt and pH tolerance.
Other/HASPIN	NP_009544	Saccharomyces cerevisiae S291C	NCBI NOTE: Protein kinase; along with its paralog, ALK1, required for proper spindle positioning and nuclear segregation following mitotic arrest, proper organization of cell polarity factors in mitosis,
Other/IKS	NP_012478	Saccharomyces cerevisiae S290C	IKS1/J1143/YJL057C Probable serine/threonine protein kinase

Other/IRE	NP_011946	Saccharomyces cerevisiae S290C	IRE1/ERN1/YHR079C Protein kinase and type I membrane protein involved in signal transduction from ER lumen to nucleus, part of the unfolded protein response. (Similar to C41C4.4_ce)
Other/NAK	NP_015088	Saccharomyces cerevisiae S290C	YPL236C/P1057 Protein of unknown function. - No GXG (Similar to C3H1.13_sp) (Not in YPD)
Other/NAK/BIKE	NP_014378	Saccharomyces cerevisiae S290C	YNL020C/N2823/ARK1 Serine/threonine protein kinase with probable involvement in cytoskeletal function
Other/NAK/MPSK	XP_002174536	Schizosaccharomyces japonicus	NCBI NOTE: NAK protein kinase Ppk13
Other/NEK	NP_009410	Saccharomyces cerevisiae S291C	KIN3/NPK1/FUN52/YAR018C Serine/threonine protein kinase, null mutation has no phenotype. TTY in kinase domain VIII (activation loop).
Other/NEK/NEK2	XP_001884793	Laccaria bicolor	NCBI NOTE: PREDICTED: phosphorylase b kinase gamma catalytic chain, skeletal muscle/heart isoform-like
Other/PEK	XP_013016069	Schizosaccharomyces octosporus	NCBI NOTE: PEK protein kinase Hri2
Other/PEK/GCN2	NP_010569	Saccharomyces cerevisiae S290C	GCN2/AAS1/D9954.16/YDR283C Serine/threonine protein kinase that regulates initiation of translation by phosphorylation of eIF2alpha (Sui2p) (Similar to EIF2aK_r, HRI_r)
Other/PLK	NP_013714	Saccharomyces cerevisiae S290C	CDC5/PKX2/MSD2/YM8270.03/YMR001C Serine/threonine protein kinase required for exit from mitosis, ts mutants block after nuclear division. (Similar to PLK-1_h, POLO_dm)

Other/PLK/PLK1	XP_001594879	Sclerotinia sclerotiorum	NCBI NOTE:
Other/PLK/SAK	CCJ29354	Pneumocystis jirovecii	NCBI NOTE:
Other/RAN	NP_015299	Saccharomyces cerevisiae S290C	SHA3/SKS1/LPB5/YPL026C Serine/threonine protein kinase that suppresses the growth defect of snf3 mutants on low glucose
Other/SCY1	NP_014755	Saccharomyces cerevisiae S290C	SCY1/G3197/YGL083W Protein involved in suppression of a GTPase mutant
Other/TTK	NP_010256	Saccharomyces cerevisiae S290C	MPS1/RPK1/D2785/YDL028C Serine/threonine/tyrosine protein kinase involved in spindle pole body duplication (Similar to ESK_m, TTK_h).
Other/ULK	NP_011335	Saccharomyces cerevisiae S290C	YGL180W/G1615/APG1/AUT3 Serine/threonine protein kinase involved in induction of autophagy after nutrient limitation (Similar to UNC-51_ce, PLO1_sp)
Other/ULK/ULK	XP_013019319	Schizosaccharomyces octosporus	NCBI NOTE: ULK/ULK protein kinase Atg1
Other/VPS15	NP_009655	Saccharomyces cerevisiae S290C	VPS15/VPT15/(VPL19)/YBR0825/YBR097W Serine/threonine protein kinase involved in vacuolar protein sorting. (Similar to ZK930.1_ce)
Other/WEE	NP_012348	Saccharomyces cerevisiae S290C	SWE1/J0406/YJL187C Serine/tyrosine dual-specificity protein kinase able to phosphorylate Cdc28p on tyrosine and inhibit its activity. (Similar to Wee1_sp, and MLK_h)
Other/WEE/WEE-UNCLASSIFIED	XP_013019271	Schizosaccharomyces octosporus	NCBI NOTE: WEE protein kinase Wee1

PAB-dependent Poly(A) specific ribonuclease subunit	XP_013019657	Schizosaccharomyces octosporus	NCBI NOTE: Serine/threonine protein kinase
Serine/Threonine protein kinase	NP_015431	Saccharomyces cerevisiae S290C	YPR106W/P8283.9/ISR1 Protein with similarity to protein kinases Gcn2p, galactosyltransferase-associated protein kinase P58/Gtap, and the Raf proto-oncogene. (Similar to none)
STE	XP_009220426	Gaeumannomyces tritici	NCBI NOTE: STE protein kinase
STE/STE11	NP_013466	Saccharomyces cerevisiae S290C	STE11/L8039.10/YLR362W Serine/threonine protein kinase of the MEKK family, component of the pheromone pathway and a pathway regulating filamentous growth.
STE/STE11/BCK1	NP_012440	Saccharomyces cerevisiae S290C	BCK1/(SLK1)/SSP31/LAS3/SAP3/J0906/YJL095W Serine/threonine protein kinase of the MEKK family, involved in the cell wall integrity pathway.
STE/STE11/CDC15	NP_009411	Saccharomyces cerevisiae S290C	CDC15/YAR019C Protein kinase of the MAP kinase kinase family essential for late nuclear division. (Similar to MESS1_m, CDC7_sp, MST1_h)
STE/STE11/SSK	NP_009998	Saccharomyces cerevisiae S290C	SSK2/N3276/YNR031C Map kinase kinase kinase of the high osmolarity signal transduction pathway.
STE/STE20	NP_594646	Schizosaccharomyces pombe	NCBI NOTE: Serine/threonine protein kinase Ppk2
STE/STE20/FRAY	CBQ69811	Sporisorium reilianum	NCBI NOTE:
STE/STE20/KHS	KDQ07215	Botryobasidium botryosum	NCBI NOTE:

STE/STE20/PAKA	NP_014528	Saccharomyces cerevisiae S291C	YOL113W/HRA655/O0722/SKM1 Serine/threonine protein kinase with similarity to Ste20p.
STE/STE20/YSK	NP_011970	Saccharomyces cerevisiae S290C	NRK1/KIC1/H8263.14/YHR102W Serine/threonine protein kinase that interacts with Cdc31p.
STE/STE7	NP_012407	Saccharomyces cerevisiae S290C	PBS2/HOG4/SFS4/SSK4/OSR1/J0699/YJL128C Tyrosine protein kinase of the MAP kinase kinase (MEK kinase) family, essential component of the high-osmolarity signal transduction pathway.
STE/STE7/MEK1	CCU81577	Blumeria graminis	NCBI NOTE: Mitogen-activated protein kinase kinase
STE/STE7/MKK	NP_014874	Saccharomyces cerevisiae S290C	MKK1/SSP32/O5095/YOR231W Serine/threonine protein kinase of the MAP kinase kinase (MEK) family involved in cell wall integrity pathway.
TKL	KDQ17892	Botryobasidium botryosum	NCBI NOTE:
TKL/LISK/LISK-DD1	CBQ69762	Sporisorium reilianum	NCBI NOTE: Related to serine/threonine protein kinase
TKL/TKL-CCIN	XP_001886931	Laccaria bicolor	NCBI NOTE:

*For the database development, some groups/familis have changed. We pick up the groups/familis can be found in new database and noted by Saccharomyces cerevisiae S290C. Other familis/groups can not be found we noted by other fungi gene.

Appendix B Fungal species used in this study

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	<i>Malassezia globosa</i>	CBS 7966	JGI	83	4286	Human	YES	Facultative	Dandruff-associated <i>Malassezia</i> genomes reveal convergent and

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										pathogenic fungi	divergent virulence traits shared with plant and human fungal pathogens.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Ustilaginomycetes</i>	<i>Ustilago maydis</i>	521	FGI	97	6522	Plant	NO	Biotrophic	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> .

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Ustilaginomycetes</i>	<i>Sporisorium reilianum</i>	SRZ2	NCBI	101	6648	Plant	NO	Biotrophic	Pathogenicity determinants in smut fungi revealed by genome comparison.
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Agaricomycetes</i>	<i>Moniliophthora perniciosa</i>	FA553	JGI	48	13560	Plant	NO	Hemibiotrophic	A genome survey of <i>Moniliophthora perniciosa</i> gives new insights into Witches' Broom Disease of cacao.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Agaricomycetes</i>	<i>Botryobasidium botryosum</i>	FD-172 v1.0	JGI	389	16526		NO	Saprophytic fungi	Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi.
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Agaricomycetes</i>	<i>Coniophora puteana</i>	RWD-64-598	JGI	175	13761		NO	Saprophytic	The Paleozoic origin of enzymatic lignin decomposition

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										fungi	reconstructed from 31 fungal genomes.
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Agaricomycetes</i>	<i>Laccaria bicolor</i>	S238N-H82 (v2.0)	JGI	220	23132		NO	Saprophytic fungi	The genome of <i>Laccaria bicolor</i> provides insights into mycorrhizal symbiosis.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Agaricomycetes</i>	<i>Hebeloma cylindrosporum</i>	H7 v2.0	NCBI	209	15382	Plant	NO	Symbiotic	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists.
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Agaricomycetes</i>	<i>Paxillus involutus</i>	ATCC 200175 v1.0	NCBI	304	17968	Plant	NO	Symbiotic	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Tremellomycetes</i>	<i>Cryptococcus neoformans</i>	JEC21	FGI	106	6475	Human	YES	Facultative pathogenic fungi	The genome of the basidiomycetous yeast and human pathogen <i>Cryptococcus neoformans</i> .
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Tremellomycetes</i>	<i>Cryptococcus gattii</i>	R265	FGI	93	6210	Human	YES	Facultative	Genome variation in <i>Cryptococcus gattii</i> , an emerging pathogen

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										pathogenic fungi	of immunocompetent hosts.
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Dacrymycetes</i>	<i>Calocera cornea</i>	(v1.0)	JGI	182	13177		NO	Saprophytic fungi	Comparative genomics of early-diverging mushroom-forming fungi provides insights into the origins of lignocellulose decay

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
											capabilities.
Basidiomycota	Agaricomycotina	Dacrymycetes	<i>Calocera viscosa</i>	(v1.0)	JGI	183	12378		NO	Saprophytic fungi	Comparative genomics of early-diverging mushroom-forming fungi provides insights into the origins of lignocellulose decay capabilities.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Dothideomycetes</i>	<i>Cochliobolus sativus</i>	ND90Pr	NCBI	119	12250	Plant	NO	Hemibiotrophic	Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen <i>Dothideomycetes</i> fungi.
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Dothideomycetes</i>	<i>Dothistroma septosporum</i>	NZE10 (v1.0)	NCBI	115	12580	Plant	NO	Hemibiotrophic	The genomes of the fungal plant pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> reveal adaptation to

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. tritici	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
											different hosts and lifestyles but also signatures of common ancestry.
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Dothideomycetes</i>	<i>Mycosphaerella graminicola</i>	(v2.0)	JGI	124	10933	Plant	NO	Hemibiotrophic	Finished genome of the fungal wheat pathogen <i>Mycosphaerella graminicola</i> reveals dispensome structure, chromosome

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
											plasticity, and stealth pathogenesis.
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Dothideomycetes</i>	<i>Phaeosphaeria nodorum</i>	Sn79	JGI	116	12379	Plant	NO	Necrotrophic	Dothideomycete-plant interactions illuminated by genome sequencing and EST analysis of the wheat pathogen <i>Stagonospora nodorum</i> .

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. tritici	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Dothideomycetes</i>	<i>Pyrenophora teres</i> f. teres		NCBI	121	11799	Plant	NO	Necrotrophic	A first genome assembly of the barley fungal pathogen <i>Pyrenophora teres</i> f. teres.
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Dothideomycetes</i>	<i>Cladosporium fulvum</i>		JGI	127	14127	Plant	NO	Biotrophic	The genomes of the fungal plant pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> reveal adaptation to

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
											different hosts and lifestyles but also signatures of common ancestry.
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Eurotiomycetes</i>	<i>Arthroderma benhamiae</i>	CBS 112371	NCBI	134	7980	Human	NO	Facultative pathogenic	Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										fungi	
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Eurotiomycetes</i>	<i>Ajellomyces capsulatus</i>	NAm1	JGI	121	9313	Insect	NO		Comparative genomic analyses of the human fungal pathogens <i>Coccidioides</i> and their relatives.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Ascomycota	Pezizomycotina	Eurotiomycetes	<i>Aspergillus clavatus</i>	NRRL 1	FGI	127	9120		NO	Saprophytic fungi	Sequencing of mitochondrial genomes of nine <i>Aspergillus</i> and <i>Penicillium</i> species identifies mobile introns and accessory genes as main sources of genome size variability.
Ascomycota	Pezizomycotina	Eurotiomycetes	<i>Coccidioides immitis</i>	H538.4	FGI	118	10593	Human	NO	Facultative	Comparative genomic analyses of the human fungal pathogens

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										pathogenic fungi	Coccidioides and their relatives.
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Eurotiomycetes</i>	<i>Penicillium marneffeii</i>	ATCC 18224	FGI	119	10689	Human	NO	Facultative pathogenic	Genome Sequence of the AIDS-Associated Pathogen <i>Penicillium marneffeii</i> (ATCC18224) and Its Near Taxonomic

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										fungi	Relative <i>Talaromyces stipitatus</i> (ATCC10500).
Ascomycota	Pezizomycotina	Eurotiomycetes	<i>Trichophyton rubrum</i>	CBS 118892	FGI	121	10418	Human	NO	Facultative pathogenic fungi	Comparative genome analysis of <i>Trichophyton rubrum</i> and related dermatophytes reveals candidate genes involved in infection.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Ascomycota	Pezizomycotina	Leotiomycetes	<i>Blumeria graminis</i> f. sp. <i>hordei</i>	DH14	JGI	92	6470	Plant	NO	Biotrophic	Genome expansion and gene loss in powdery mildew fungi reveal tradeoffs in extreme parasitism.
Ascomycota	Pezizomycotina	Leotiomycetes	<i>Botryotinia fuckeliana</i>	B05.10	NCBI	115	11028	Plant	NO	Necrotrophic	Genomic analysis of the necrotrophic fungal pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> .

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Leotiomycetes</i>	<i>Sclerotinia sclerotiorum</i>	UF-70	NCBI	115	14503	Plant	NO	Necrotrophic	Genomic analysis of the necrotrophic fungal pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> .
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Orbiliomycetes</i>	<i>Arthrobotrys oligospora</i>	ATCC 24927	FGI	118	11479	Plant	NO	Facultative pathogenic	Genomic and proteomic analyses of the fungus <i>Arthrobotrys oligospora</i> provide insights into nematode-trap formation.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										fungi	
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Pezizomyetes</i>	<i>Tuber melanosporum</i>	Mel28	FGI	100	7496	Plant	NO	Symbiotic	Perigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Ascomycota	Pezizomycotina	Sordariomycetes	<i>Chaetomium thermophilum</i>	DSM 1495	FGI	100	7180		NO	Saprophytic fungi	Insight into Structure and Assembly of the Nuclear Pore Complex by Utilizing the Genome of a Eukaryotic Thermophile.
Ascomycota	Pezizomycotina	Sordariomycetes	<i>Cordyceps militaris</i>	CM01	NCBI	160	9651	Insect	NO		Genome sequence of the insect pathogenic fungus <i>Cordyceps militaris</i> , a valued traditional Chinese medicine

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Ascomycota	Pezizomycotina	Sordariomycetes	<i>Fusarium graminearum</i>	PH-1	FGI	114	13321	Plant	NO	Hemibiotrophic	The <i>Fusarium graminearum</i> genome reveals a link between localized polymorphism and pathogen specialization.
Ascomycota	Pezizomycotina	Sordariomycetes	<i>Gaeumannomyces graminis</i> var. <i>tritici</i>	R3-111a-1	FGI	137	14650	Plant	NO	Necrotrophic	The <i>Fusarium graminearum</i> genome reveals a link between localized polymorphism and pathogen specialization.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Ascomycota	Pezizomycotina	Sordariomycetes	<i>Magnaporthe oryzae</i>		NCBI	121	12991	Plant	NO	Necrotrophic	The genome sequence of the rice blast fungus <i>Magnaporthe grisea</i> .
Ascomycota	Pezizomycotina	Sordariomycetes	<i>Metarhizium acridum</i>	CQMa 102	NCBI	146	9849	Insect	NO		Genome sequencing and comparative transcriptomics of the model entomopathogenic fungi <i>Metarhizium anisopliae</i> and <i>M.</i>

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
											<i>acridum</i> .
Ascomycota	Pezizomycotina	Sordariomycetes	<i>Metarhizium anisopliae</i>	ARSEF 549	NCBI	135	10598	Insect	NO		Genome sequencing and comparative transcriptomics of the model entomopathogenic fungi <i>Metarhizium anisopliae</i> and <i>M. acridum</i> .

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Ascomycota	Pezizomycotina	Sordariomycetes	<i>Nectria haematococca</i>	(v2.0)	JGI	162	15707	Plant	NO	Necrotrophic	The genome of <i>Nectria haematococca</i> : contribution of supernumerary chromosomes to gene expansion.
Ascomycota	Pezizomycotina	Sordariomycetes	<i>Neurospora crassa</i>	OR74A (v2.0)	JGI	145	10785		NO	Saprophytic fungi	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> .

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. tritici	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
<i>Ascomycota</i>	<i>Saccharomycotina</i>	<i>Saccharomycetes</i>	<i>Candida albicans</i>	WO-1	JGI	101	5931	Human	NO	Facultative pathogenic fungi	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes.
<i>Ascomycota</i>	<i>Saccharomycotina</i>	<i>Saccharomycetes</i>	<i>Candida lusitanae</i>		NCBI	102	5941	Human	YES	Facultative	Evolution of pathogenicity and sexual reproduction in eight

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										pathogenic fungi	Candida genomes.
<i>Ascomycota</i>	<i>Saccharomycotina</i>	<i>Saccharomycetes</i>	<i>Candida tropicalis</i>	MYA-3404	JGI	104	6258	Human	YES	Facultative pathogenic	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										fungi	
<i>Ascomycota</i>	<i>Saccharomycotina</i>	<i>Saccharomycetes</i>	<i>Debaryomyces hansenii</i>	CBS767	NCBI	105	6272		YES	Saprophytic fungi	Promiscuous DNA in the nuclear genomes of hemiascomycetous yeasts.

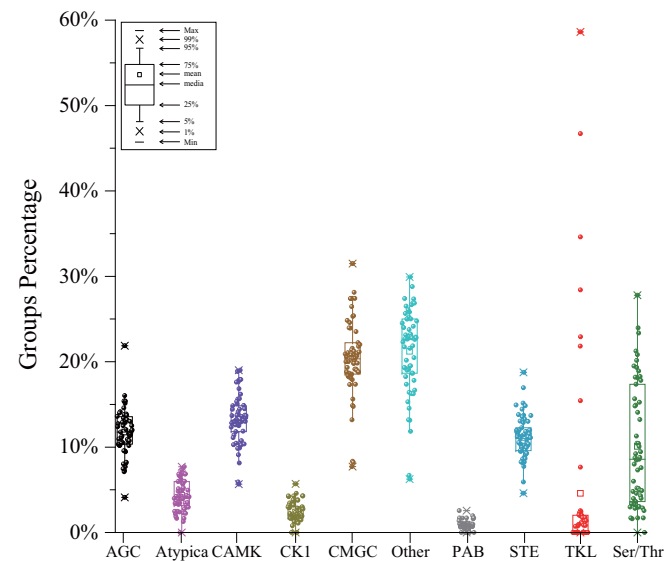
Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Ascomycota	Saccharomycotina	Saccharomycetes	<i>Lodderomyces elongisporus</i>	NRRL YB-4239	JGI	100	5799	Human	YES	Facultative pathogenic fungi	Evolution of pathogenicity and sexual reproduction in eight <i>Candida</i> genomes.
Ascomycota	Saccharomycotina	Saccharomycetes	<i>Saccharomyces</i>	S288C	NCBI	125	6575		YES	Saprophytic	Life with 6000 genes.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Microbotryomycetes</i>	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Mixiomycetes</i>	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Pucciniomycetes</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Exobasidiomycetes</i>	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
			<i>cerevisiae</i>							fungi	
<i>Ascomycota</i>	<i>Taphrinomycotina</i>	<i>Schizosaccharomycetes</i>	<i>Schizosaccharomyces cryophilus</i>	OY26	JGI	117	5180		YES	Saprophytic fungi	Comparative functional genomics of the fission yeasts.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Ascomycota	Taphrinomycotina	Schizosaccharomycetes	<i>Schizosaccharomyces japonicus</i>	yFS275	FGI	119	4878		YES	Saprophytic fungi	Comparative functional genomics of the fission yeasts.
Ascomycota	Taphrinomycotina	Schizosaccharomycetes	<i>Schizosaccharomyces octosporus</i>	yFS286	FGI	117	4986		YES	Saprophytic fungi	Comparative functional genomics of the fission yeasts.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
Ascomycota	Taphrinomycotina	Schizosaccharomycetes	<i>Schizosaccharomyces pombe</i>		JGI	117	5134		YES	Saprophytic fungi	The genome sequence of <i>Schizosaccharomyces pombe</i> .
Ascomycota	Taphrinomycotina	Pneumocystidomycetes	<i>Pneumocystis jirovecii</i>	RU7	JGI	73	3520	Human	NO	Facultative pathogenic	De novo assembly of the <i>Pneumocystis jirovecii</i> genome from a single bronchoalveolar lavage fluid specimen from a patient.

Phylum	Subphylum	Class	Fungi species	Strain(s)	Source	Kinome size	Genome size	Host	Yeast	Nutritional mode	Reference paper
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Microbotryum violaceum</i>	p1A1 Lamole	FGI	118	7819	Plant	NO	Biotrophic	Sex and parasites: genomic and transcriptomic analysis of <i>Microbotryum lychnidis-dioicae</i> , the biotrophic and plant-castrating anther smut fungus.
Basidiomycota	Pucciniomycotina	Microbotryomycetes	<i>Rhodotorula graminis</i>	WP1 (v1.1)	JGI	102	7283	Plant	YES	Symbiotic	Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1.
Basidiomycota	Pucciniomycotina	Mixiomycetes	<i>Mixia osmundae</i>	IAM 14324	JGI	101	6903	Plant	NO	Biotrophic	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> .
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Melampsora laricis-populina</i>	98AG31	NCBI	128	16694	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia graminis</i>	CRL 75-36-700-3	FGI	123	15707	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Pucciniomycotina	Pucciniomycetes	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	PST-78	FGI	131	19542	Plant	NO	Biotrophic	Obligate biotrophy features unraveled by the genomic analysis of rust fungi.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Tilletiaria anomala</i>	UBC 951 (v1.0)	NCBI	99	6810	Plant	NO	Saprophytic fungi	Draft Genome Sequence of a Rare Smut Relative, <i>Tilletiaria anomala</i> UBC 951.
Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	<i>Ceraceosorus bombacis</i>		NCBI	96	8022	Plant	NO	Hemibiotrophic	Comparative Genomics Including the Early-Diverging Smut Fungus <i>Ceraceosorus bombacis</i> Reveals Signatures of Parallel Evolution within Plant and Animal Pathogens of Fungi and Oomycetes.
										fungi	
Ascomycota	Taphrinomycotina	Taphrinomycetes	<i>Taphrina deformans</i>		JGI	67	4609	Plant	NO	Facultative pathogenic fungi	Genome sequencing of the plant pathogen <i>Taphrina deformans</i> , the causal agent of peach leaf curl.



Appendix C Group percentages of the ten protein kinase (PK) groups.

Appendix D Distribution of protein kinases in fungi

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127

<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
<i>Basidiomycota</i>	<i>Pucciniomycotina</i>	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
<i>Basidiomycota</i>	<i>Ustilaginomycotina</i>	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Cryptococcus gattii</i>	12	4	14	3	19	24	11	1	4	92
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Calocera cornea</i>	14	5	18	2	24	24	15	63	16	181
<i>Basidiomycota</i>	<i>Agaricomycotina</i>	<i>Calocera viscosa</i>	13	6	18	7	27	28	15	52	16	182
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Cochliobolus sativus</i>	13	5	15	2	22	26	12	0	23	118
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Dothistroma septosporum</i>	13	7	15	2	22	29	12	2	12	114
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Mycosphaerella graminicola</i>	13	6	17	2	34	25	11	1	14	123
<i>Ascomycota</i>	<i>Pezizomycotina</i>	<i>Phaeosphaeria nodorum</i>	13	4	15	2	21	28	12	0	21	116

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Pyrenophora teres</i> f. <i>teres</i>	13	7	16	2	21	28	12	0	21	120

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Cladosporium fulvum</i>	12	5	13	1	22	38	11	0	24	126

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Arthroderma benhamiae</i>	14	3	14	2	34	25	13	1	27	133

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Ajellomyces capsulatus</i>	14	3	13	2	32	23	11	0	22	120

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Aspergillus clavatus</i>	14	4	15	2	40	26	13	0	12	126

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Coccidioides immitis</i>	12	4	16	2	29	22	13	1	18	117

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Penicillium marneffeii</i>	14	5	15	3	28	27	13	0	12	117

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Trichophyton rubrum</i>	13	2	16	0	29	21	10	0	29	120

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis f. sp. tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Blumeria graminis f.</i>	13	6	12	2	19	24	12	0	3	91

[illegible]

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Botryotinia fuckeliana</i>	13	6	15	2	22	26	12	0	18	114

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Sclerotinia sclerotiorum</i>	11	5	15	2	23	25	12	0	21	114

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Arthrotrys oligospora</i>	12	5	14	2	22	27	12	0	23	117

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Tuber melanosporum</i>	13	3	19	2	21	25	12	0	4	99

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Chaetomium</i>	14	6	13	2	19	24	13	0	8	99

[illegible]

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Cordyceps militaris</i>	13	3	21	3	45	26	15	0	34	160

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Fusarium graminearum</i>	13	4	13	2	24	26	12	2	17	113

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Gaeumannomyces</i>	14	3	21	2	25	25	13	1	32	136

[illegible]

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Magnaporthe oryzae</i>	14	6	18	2	24	27	12	1	16	120

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Metarhizium acridum</i>	16	5	15	3	40	26	14	0	26	145

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Metarhizium anisopliae</i>	16	4	14	3	37	26	14	0	20	134

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Nectria haematococca</i>	13	4	18	3	36	27	15	0	45	161

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Pezizomycotina	<i>Neurospora crassa</i>	15	6	21	5	36	28	20	2	11	144

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Saccharomycotina	<i>Candida albicans</i>	12	7	15	3	22	25	12	0	4	100

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Saccharomycotina	<i>Candida lusitanae</i>	13	7	14	3	21	25	12	0	5	100

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Saccharomycotina	<i>Candida tropicalis</i>	13	8	15	2	22	26	12	0	5	103

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Saccharomycotina	<i>Debaryomyces hansenii</i>	13	7	17	3	21	28	12	0	3	104

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Saccharomycotina	<i>Lodderomyces</i>	12	6	13	3	22	25	12	0	6	99

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Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Saccharomycotina	<i>Saccharomyces cerevisiae</i>	17	5	22	4	23	36	14	0	2	123

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Taphrinomycotina	<i>Schizosaccharomyces</i>	18	8	16	5	22	31	13	0	2	115

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Taphrinomycotina	<i>Schizosaccharomyces</i>	18	5	16	5	23	32	14	0	4	117

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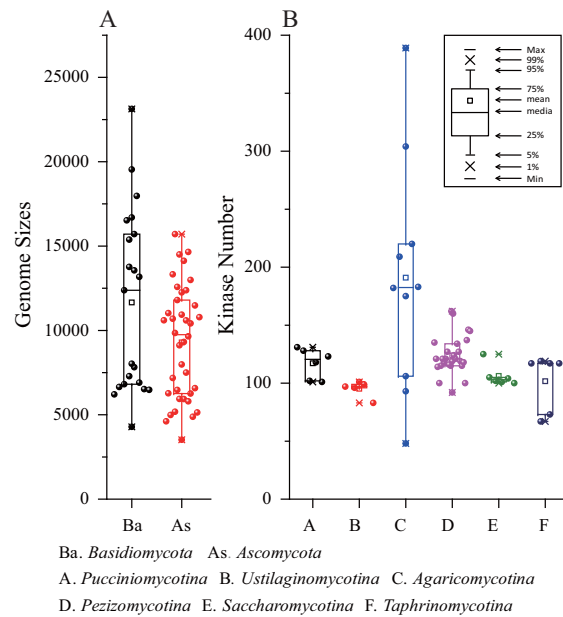
Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Taphrinomycotina	<i>Schizosaccharomyces</i>	18	8	15	5	22	30	13	0	3	114

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Taphrinomycotina	<i>Schizosaccharomyces</i>	18	6	16	5	22	32	14	0	2	115

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Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Taphrinomycotina	<i>Pneumocystis jirovecii</i>	6	5	9	2	20	20	10	0	0	72

Phylum	Subphylum	Fungi species	AGC	Atypica	CAMK	CK1	CMGC	Other	STE	TKL	Ser/Thr	Total
Basidiomycota	Pucciniomycotina	<i>Microbotryum violaceum</i>	16	5	21	2	24	23	20	3	2	116
Basidiomycota	Pucciniomycotina	<i>Rhodotorula graminis</i>	14	4	18	2	22	22	14	2	3	101
Basidiomycota	Pucciniomycotina	<i>Mixia osmundae</i>	13	5	17	2	21	24	13	2	3	100
Basidiomycota	Pucciniomycotina	<i>Melampsora laricis-populina</i>	28	5	16	3	20	21	13	3	18	127
Basidiomycota	Pucciniomycotina	<i>Puccinia graminis</i>	17	9	17	7	22	24	14	3	9	122
Basidiomycota	Pucciniomycotina	<i>Puccinia striiformis</i> f. sp. <i>tritici</i>	21	9	17	6	28	25	15	3	6	130
Basidiomycota	Ustilaginomycotina	<i>Tilletiaria anomala</i>	13	5	14	2	21	23	15	2	3	98
Basidiomycota	Ustilaginomycotina	<i>Ceraceosorus bombacis</i>	14	4	15	2	19	22	13	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Malassezia globosa</i>	10	4	13	1	21	19	11	1	3	83
Basidiomycota	Ustilaginomycotina	<i>Ustilago maydis</i>	13	6	14	2	18	22	14	2	5	96
Basidiomycota	Ustilaginomycotina	<i>Sporisorium reilianum</i>	14	4	14	2	21	23	15	2	5	100
Basidiomycota	Agaricomycotina	<i>Moniliophthora perniciosa</i>	6	0	5	0	4	3	9	11	10	48
Basidiomycota	Agaricomycotina	<i>Botryobasidium botryosum</i>	16	5	22	5	30	26	23	228	33	388
Basidiomycota	Agaricomycotina	<i>Coniophora puteana</i>	24	6	33	5	26	23	15	27	15	174
Basidiomycota	Agaricomycotina	<i>Laccaria bicolor</i>	21	5	20	8	44	32	17	48	23	218
Basidiomycota	Agaricomycotina	<i>Hebeloma cylindrosporum</i>	22	5	17	8	50	34	18	16	38	208
Basidiomycota	Agaricomycotina	<i>Paxillus involutus</i>	22	5	18	13	25	36	14	142	28	303
Basidiomycota	Agaricomycotina	<i>Cryptococcus neoformans</i>	14	6	19	4	21	24	13	1	3	105
Ascomycota	Taphrinomycotina	<i>Taphrina deformans</i>	5	4	12	2	14	18	10	0	2	67



Appendix E Distribution of genome sizes of Ascomycetes and Basidiomycetes and distribution of kinase numbers in 6 sub-phyla.

Appendix F The unique kinases families in fungi with different hosts

85 common elements in "Plant", "Insect", "Human" and "NONE":
CMGC/CK2
Other/SCY1
Other/ULK/ULK
STE/STE20/PAKA
STE/STE20/YSK
STE/STE7/MEK1
serine/threonine
CAMK/CAMKL
AGC
AGC/AKT
AGC/NDR/NDR
AGC/NDR/NDR-UNCLASSIFIED
AGC/PDK1
AGC/YANK
CAMK
CAMK/CAMK1/CAMK1-CMK
CAMK/CAMK1/CAMK1-RCK
CAMK/CAMKL/KIN1
CAMK/CAMKL/KIN4
CK1/CK1/CK1-D

CMGC/CDK
CMGC/CDK/CDK8
CMGC/CDK/CRK7
CMGC/DYRK/DYRK2
CMGC/DYRK/PRP4
CMGC/DYRK/YAK
CMGC/MAPK
CMGC/MAPK/P38
CMGC/SRPK
Other/AUR
Other/BUB
Other/HAL
Other/RAN
STE/STE11/BCK1
STE/STE11/SSK
STE/STE7
Other/CDC7
Other/VPS15
AGC/PKA
AGC/PKC
AGC/RSK/RSK-UNCLASSIFIED

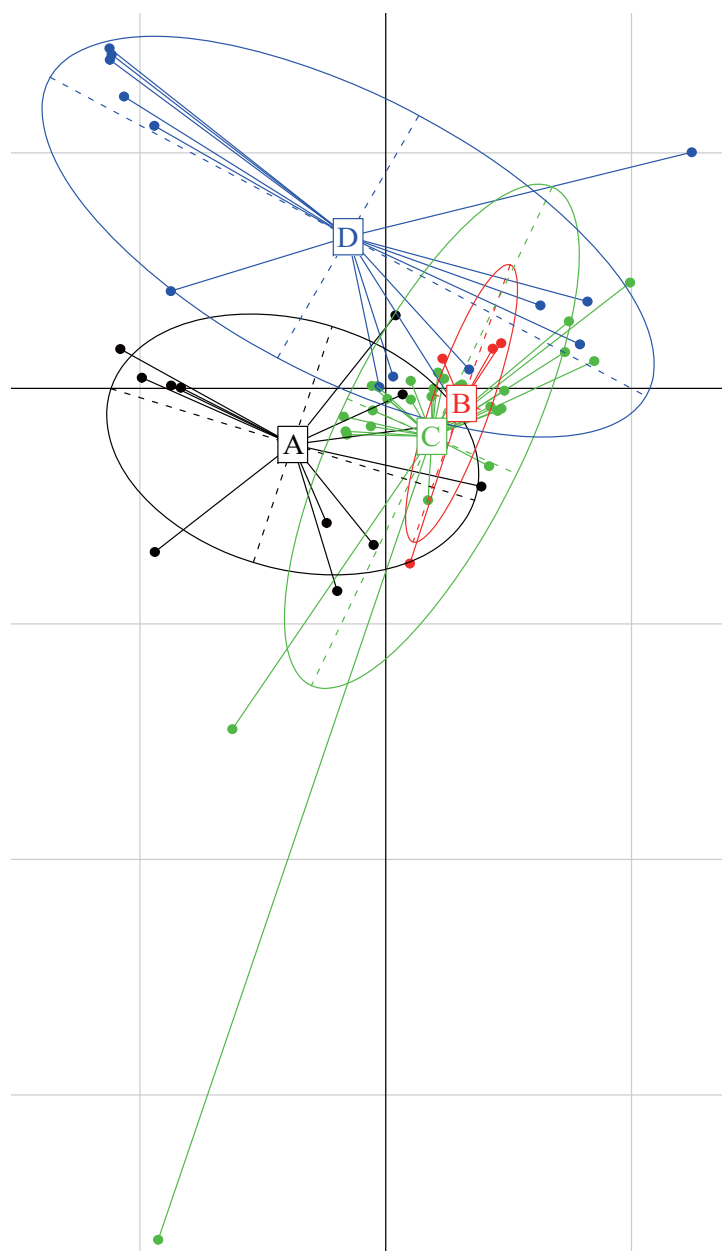
CAMK/CAMK1
CAMK/CAMKL/AMPK
CAMK/CAMKL/PASK
CK1/CK1/CK1-G
CMGC/CDK/CDC2
CMGC/CDK/CDK5
CMGC/CLK
Other/IRE
Other/NAK
Other/TTK
STE/STE11
STE/STE11/CDC15
CMGC/GSK
STE/STE7/MKK
Atypical/ABC1/ABC1-C
CMGC/CDK/CDK7
CMGC/RCK/MAK
Other/NEK
Atypical/RIO/RIO2
CAMK/CAMKL/CHK1
Other/PEK/GCN2

Other/BUD32
Other/CAMKK/CAMKK-META
PAB-dependent
Atypical/ABC1/ABC1-B
Other/HASPIN
Other/IKS
CAMK/CAMKL/GIN4
Other/PLK
Atypical/ABC1
AGC/NDR
Atypical/ABC1/ABC1-A
Atypical/RIO/RIO1
Other/WEE/WEE-UNCLASSIFIED
Other/CAMKK
Other/NAK/BIKE
AGC/RSK/RSKP70
CMGC
Other/PEK
CAMK/RAD53
CMGC/MAPK/ERK1
Other/PLK/PLK1

CAMK/CAMKL/MARK
STE/STE20
9 common elements in "Plant", "Human" and "NONE":
TKL
Other/CAMKK/ELM
Other/WEE
STE/STE20/FRAY
Atypical/PI4K
AGC/DMPK
CK1/CK1
Atypical/PIKK/FRAP
CMGC/RCK
9 common elements in "Plant", "Human" and "NONE":
TKL
Other/CAMKK/ELM
Other/WEE
STE/STE20/FRAY
Atypical/PI4K
AGC/DMPK

CK1/CK1
Atypical/PIKK/FRAP
CMGC/RCK
1 common element in "Plant", "Insect" and "Human":
AGC/RSK
5 common elements in "Plant" and "NONE":
TKL/LISK/LISK-DD1
STE
TKL/TKL-CCIN
Other/AGAK1
Other/ULK
7 elements included exclusively in "Plant":
AGC/DMPK/GEK
Atypical/PIKK
CAMK/CAMKL/BRSK
CMGC/CDKL
AGC/RSK/RSKP90
AGC/DMPK/ROCK

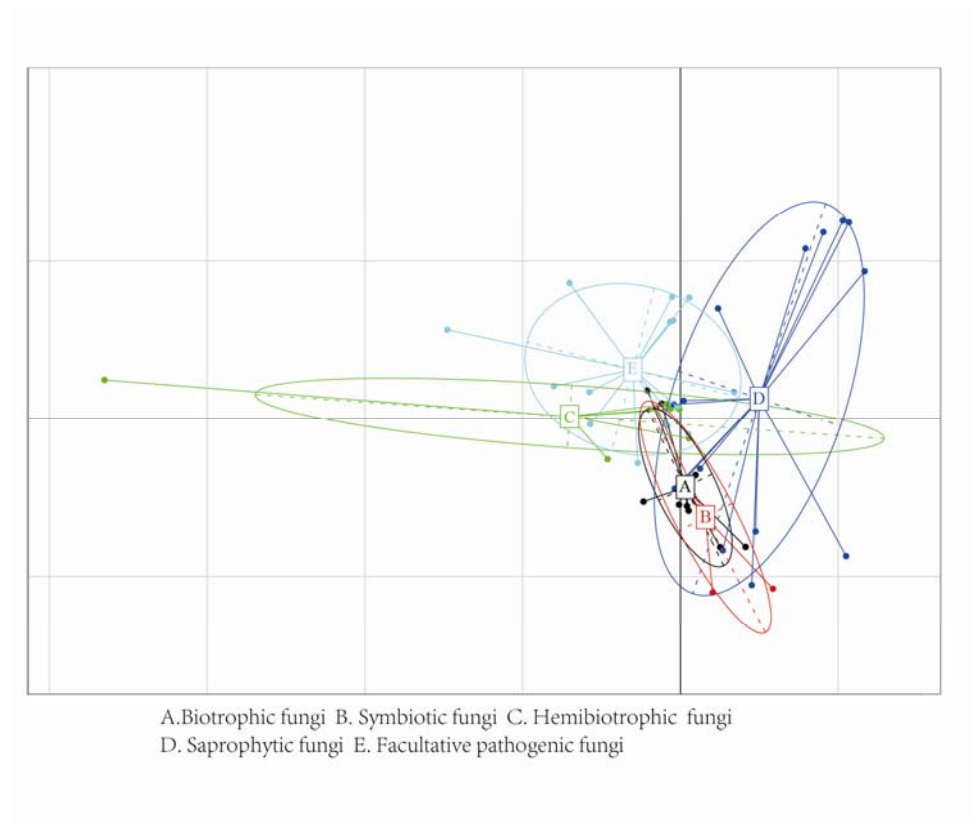
Atypical/BCR
5 elements included exclusively in "NONE":
STE/STE20/KHS
CK1
Other/NEK/NEK2
Atypical/RIO
Other/NAK/MPSK
1 common element in "Human" and "NONE":
Atypical/HISK
2 elements included exclusively in "Human":
Other/CILIATE-A1
Other/PLK/SAK
1 element included exclusively in "Insect":
AGC/SGK



A. Human pathogenic fungi B. Insect pathogenic fungi
C. Plant pathogenic fungi D. nonpathogenic fungi

Appendix G Principal component analysis (PCA) of protein kinases (PKs) from 48 fungi with different modes of nutrition.

The PCA result from 48 of the 59 fungi, including five types of nutritional modes: saprophytic, facultative parasitic, hemi-biotrophic, biotrophic, and symbiotic fungi, as well as 79 of the 119 PKs families, which can be found in at least half of these fungi, which was used to generate the PCA figure. The x-axis denotes the value of PC1, while the y-axis denotes the value of PC2, with each dot representing one cluster of PKs. The color for five types of nutritional modes, saprophytic, facultative parasitic, hemi-biotrophic, biotrophic, and symbiotic fungi are black, red, green, navy blue and light blue, respectively.



Appendix H Principal component analysis (PCA) of protein kinases (PKs) in 59 fungi for different hosts. The PCA result of all the 59 fungi including three host of pathogenic fungi (human, insect, plant) and yeast, demonstrating 76 of 119 PK families which can be found in at least half of these fungi that were used to generate the PCA figure. The x-axis denotes the value of PC1, while the y-axis denotes the value

of PC2, with each dot representing one cluster of PKs. The color for human pathogenic fungi, insect pathogenic fungi, plant pathogenic fungi and non-pathogenic fungi are black, red, green and blue, respectively.