

PART TWO**Table SMO. Dataset collection for the genome projects of 461 eukaryotic species**

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Genome-wide features of introns are evolutionary decoupled among themselves and from genome size throughout Eukarya.

<https://www.biorxiv.org/content/early/2018/03/18/283549>

Relative taxonomic order	Species name	Abbreviation	Kingdom	Estimated genome size (published)	Assembled genome size (available file)	Genome sequence status (published)	Number of protein-coding genes (published)	Number of protein-coding genes (available file)	Database collection	Reference for genome publication	Download sequence link
274	1 <i>Trypanosoma brucei</i>	tbr	Protist	35.00	25.79	chromosomes	9,068	8747	sanger	Berriman M., et al. (2005). The genome of the African trypanosome <i>Trypanosoma brucei</i> . Science, 309:416-22.	http://tritrypdb.org/common/downloads/Current_Release/Tbrucei/ ; ftp://ftp.ensemblgenomes.org/pub/protists/release-16/fasta/trypanosoma_brucel/
275	2 <i>Trypanosoma vivax</i>	tvi	Protist	47.50	47.5	chromosomes	11,870	11885	tritrypdb	Jackson A.P., et al. (2012). Antigenic diversity is generated by distinct evolutionary mechanisms in African trypanosome species. Proc Natl Acad Sci U S A., 109:3416-3421.	https://tritrypdb.org/tritrypdb/app/#downloads
276	3 <i>Leishmania major</i>	lma	Protist	32.82	33.15	chromosomes	8272	8308	tritrypdb	Ivens A.C., et al. (2005). The genome of the kinetoplastid parasite, <i>Leishmania major</i> . Science, 309:436-42.	http://tritrypdb.org/common/downloads/Current_Release/Lmajor/ ; ftp://ftp.sanger.ac.uk/pub/pathogens/Leishmania/major/ ; ftp://ftp.ensemblgenomes.org/pub/protists/release-16/fasta/leishmania_major/
277	4 <i>Naegleria gruberi</i>	ngr	Protist	41.00	40.96	assembly	15,727	15709	jgi	Fritz-Laylin L.K., et al. (2010). The Genome of <i>Naegleria gruberi</i> Illuminates Early Eukaryotic Versatility. Cell, 140: 631–642.	http://genome.jgi-psf.org/Naegr1/Naegr1.download.ftp.html
278	5 <i>Trichomonas vaginalis</i>	tva	Protist	160.00	176.41	assembly	59,681	59681	trichdb	Carlton J.M., et al. (2007). Draft genome sequence of the sexually transmitted pathogen <i>Trichomonas vaginalis</i> . Science, 315:207-12.	http://trichdb.org/common/downloads/Current_Release/Tvaginalis/
279	6 <i>Giardia intestinalis</i>	gin	Protist	11.70	11	assembly	5,012	6098	ensembl	Franzen O., et al. (2009). Draft Genome Sequencing of Giardia intestinalis Assemblage B Isolate GS: Is Human Giardiasis Caused by Two Different Species? PLoS Pathog, 5(8):e1000560; Adam ED, et al. (2013). Genome sequencing of <i>Giardia lamblia</i> genotypes A2 and E (WB and Pig). Genomic Biol Evol, 5(12):2498-511.	http://protists.ensembl.org/Giardia_lamblia/info/Index ; http://giardiadb.org/giardiadb/
280	7 <i>Spironucleus salmonicida</i>	sal	Protist	12.60	12.95	assembly	8,067	8333	ensembl	Xu F., et al. (2014). The Genome of <i>Spironucleus salmonicida</i> Highlights a Fish Pathogen Adapted to Fluctuating Environments. The Genome of <i>Spironucleus salmonicida</i> Highlights a Fish Pathogen Adapted to Fluctuating Environments. PLoS Genet 10(2): e1004053	http://protists.ensembl.org/Spironucleus_salmonicida/info/Index
281	8 <i>Acanthamoeba castellanii</i>	aca	Protist	45.10	42.02	assembly	15,455	15688	amoebadb	Clarke M., et al. (2013). Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. Genome Biology, 14:R11.	https://genomebiology.biomedcentral.com/articles/10.1186/gb-2013-14-2-r11
282	9 <i>Polysphondylium pallidum</i>	pp	Protist	33.00	32.94	assembly	12,373	12356	coge	Heidel A.J., et al. (2011). Phylogeny-wide analysis of social amoeba genomes highlights ancient origins for complex intercellular communication. Genome Res., 21(11):1882-91.	http://genomes.dictybase.org/pallidum/current
283	10 <i>Dictyostelium fasciculatum</i>	dfa	Protist	31.00	31.02	assembly	12,173	12165	coge	Heidel A.J., et al. (2011). Phylogeny-wide analysis of social amoeba genomes highlights ancient origins for complex intercellular communication. Genome Res., 21(11):1882-91.	http://genomewevolution.org/CoGe/OrganismView.pl?org_desc=Amoebozoa
284	11 <i>Dictyostelium purpureum</i>	dpu	Protist	33.00	32.97	assembly	12,410	12399	jgi	Sugang R., et al. (2011). Comparative genomics of the social amoeba <i>Dictyostelium discoideum</i> and <i>Dictyostelium purpureum</i> . Genome biology, 12(2):R20.	http://genome.jgi.doe.gov/Dicp1/Dicp1.download.ftp.html
285	12 <i>Dictyostelium discoideum</i>	ddi	Protist	34.00	33.94	chromosomes	13,541	13212	dictybase	Eichinger L., et al. (2005). The genome of the social amoeba <i>Dictyostelium discoideum</i> . Nature, 435(7038): 43-57.	http://dictybase.org/db/cgi-bin/dictyBase/download/blast_databases.pl
286	13 <i>Entamoeba dispar</i>	edi	Protist	24.00	22.96	assembly	8,811	8748	amoebadb	J. Craig Venter Institute: Weiland G.D. and Hall N. (2011). Evolutionary genomics of Entamoeba. Res Microbiol., 162(6):637-45.	http://amoebadb.org/common/downloads/Current_Release/EdisparSAW760/ ; http://www.sanger.ac.uk/resources/downloads/protozoa/entamoeba.html ; http://genome.jgi-psf.org/Entamoeba_dispar_saw760/info/Index ; http://www.sanger.ac.uk/resources/downloads/protozoa/entamoeba.html ; http://genome.jgi-psf.org/pages/dynamicOrganismDownload.jsf?organism=Guith1
287	14 <i>Entamoeba invadens</i>	ein	Protist	40.89	40.89	assembly	11,549	11549	amoebadb	Ehrenkaufer G.M., et al. (2013). The genome and transcriptome of the enteric parasite <i>Entamoeba invadens</i> , a model for encystation. Genome Biol, 14(7):R77.	http://amoebadb.org/common/downloads/Current_Release/EdisparSAW760/ ; http://www.sanger.ac.uk/resources/downloads/protozoa/entamoeba.html ; http://genome.jgi-psf.org/Entamoeba_invadens_saw760/info/Index ; http://www.sanger.ac.uk/resources/downloads/protozoa/entamoeba.html ; <a href="http://genome

Dataset_461_genomes_eukaryotes													
298	25	<i>Symbiodinium minutum</i>	sym	Protist	1,500.00	609.48	assembly	41,925	41925	oistjp	Shoguchi E., et al. (2013). Draft Assembly of the Symbiodinium minutum Nuclear Genome Reveals Dinoflagellate Gene Structure. <i>Curr Biol.</i> , 23(15):1399-1408.	https://marinegenomics.oist.jp/symb/viewer/info?project_id=21	
299	26	<i>Perkinsus marinus</i>	pkm	Protist	86.61	86.61	assembly	23,474	23474	ensembl	The Institute for Genomic Research (TIGR) and the Center for Marine Biotechnology (COMB): El-Sayed N., et al. (2007). Perkinsus marinus ATCC 50983 strain: PmcV4CB52B3D4. BioProject ID: PRJNA2737.	http://protists.ensembl.org/Perkinsus_marinus_atcc_50983/info/Index	
300	27	<i>Vitrella brassicaformis</i>	vbr	Protist	72.70	72.7	assembly	22,817	23034	ensembl	Woo Y., et al. (2015). Chromerid genomes reveal the evolutionary path from photosynthetic algae to obligate intracellular parasites. <i>Elife</i> , 4:e06974.	http://protists.ensembl.org/Vitrella_brassicaformis_ccmp3155/info/Index	
301	28	<i>Cryptosporidium muris</i>	cmu	Protist	9.25	9.25	assembly	3,934	3937	cryptodb	Feng Y., et al. (2011). Development of a multilocus sequence tool for typing Cryptosporidium muris and Cryptosporidium andersoni. <i>J Clin Microbiol.</i> , 49: 34-41.	https://cryptodb.org/cryptodb/app	
302	29	<i>Cryptosporidium parvum</i>	cpv	Protist	9.10	9.1	chromosomes	3,807	3805	cryptodb	Abrahamsen M.S., et al. (2004). Complete genome sequence of the apicomplexan, Cryptosporidium parvum. <i>Science</i> , 304:441-5.	http://cryptodb.org/common/downloads/	
303	30	<i>Neospora caninum</i>	nca	Protist	61.00	59.1	chromosomes	7,121	7122	toxodb	Reid A.J., et al. (2012). Comparative Genomics of the Apicomplexan Parasites Toxoplasma gondii and Neospora caninum: Coccidia Differing in Host Range and Transmission Strategy. <i>PLoS Pathog.</i> , 8(3): e1002567.	http://toxodb.org/common/downloads/Current_Release/NcaninumLIV/	
304	31	<i>Toxoplasma gondii</i>	tgo	Protist	80.00	63.71	chromosomes	7993	8320	toxodb	Reid A.J., et al. (2012). Comparative Genomics of the Apicomplexan Parasites Toxoplasma gondii and Neospora caninum: Coccidia Differing in Host Range and Transmission Strategy. <i>PLoS Pathog.</i> , 8(3): e1002567. Bonelli L.L., et al. (2009). Whole genome sequencing of a natural recombinant Toxoplasma gondii strain reveals chromosome sorting and local allelic variants. <i>Genome Biol.</i> , 10:R53.	ftp://ftp.ensemblgenomes.org/pub/protists/release-16/fasta/toxoplasma_gondii/ ; http://toxodb.org/common/downloads/Current_Release/TgondiiME49/	
305	32	<i>Gregarina niphandrodes</i>	gni	Protist	14.01	14.01	assembly	6,375	6375	genbank	Unpublished, but available at CryptoDB and https://www.ncbi.nlm.nih.gov/genome/3294?genome_assembly_id=56219 ; Walzer K.A., et al. (2013). Hammondiella hammondi, an avirulent relative of Toxoplasma gondii, has functional orthologs of known T. gondii virulence genes. <i>Proc Natl Acad Sci U S A.</i> , 110(18):7446-51.	https://www.ncbi.nlm.nih.gov/assembly/GCA_000223845.4	
306	33	<i>Hammondia hammondi</i>	hha	Protist	67.67	67.67	assembly	8,176	8003	ensembl	Walzer K.A., et al. (2013). Hammondiella hammondi, an avirulent relative of Toxoplasma gondii, has functional orthologs of known T. gondii virulence genes. <i>Proc Natl Acad Sci U S A.</i> , 110(18):7446-51.	http://protists.ensembl.org/Hammondia_hammondi/info/Index	
307	34	<i>Babesia bovis</i>	bbo	Protist	8.20	8.14	assembly	3,671	3703	piroplasmadb	Brayton K.A., et al. (2007). Genome sequence of Babesia bovis and comparative analysis of apicomplexan hemoprotozoa. <i>PLoS Pathogen.</i> , 3: 1401-1413.	http://piroplasmadb.org/common/downloads/Current_Release/Bbovis12B0/	
308	35	<i>Theileria annulata</i>	tan	Protist	8.35	8.36	chromosomes	3,792	3795	piroplasmadb	Pain A., et al. (2005). Title Genome of the host-cell transforming parasite Theileria annulata compared with T. parva. <i>Science</i> , 309:131-3.	ftp://ftp.ncbi.nlm.nih.gov/genomes/Protozoa/Theileria_annulata/	
309	36	<i>Theileria parva</i>	tpv	Protist	8.30	8.31	assembly	4,035	4079	piroplasmadb	Gardner M.J., et al. (2005). Genome sequence of Theileria parva, a bovine pathogen that transforms lymphocytes. <i>Science</i> , 309:134-7.	http://piroplasmadb.org/pipe/app/downloads/Current_Release/TparvaMuguga/	
310	37	<i>Plasmodium vivax</i>	pvx	Protist	26.90	27.01	chromosomes	5,433	5050	plasmodb	Carlton J.M., et al. (2008). Comparative genomics of the neglected human malaria parasite Plasmodium vivax. <i>Nature</i> , 455:757-83.	http://plasmodb.org/common/downloads/Current_Release/PvivaxSal1/ ; http://ftp.ensemblgenomes.org/pub/protists/release-16/fasta/plasmodium_vivax/	
311	38	<i>Plasmodium berghei</i>	pbe	Protist	20.00	18.52	chromosomes	5,864	4881	plasmodb	Hall N., et al. (2005). A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic and proteomic analyses. <i>Science</i> , 307:82-6.	http://plasmodb.org/annotation/genome/Plasmodium_berghei/ ; http://ftp.sanger.ac.uk/pub/pathogens/P_berghei/ ; http://plasmodb.org/common/downloads/Current_Release/PbergheiANKA/	
312	39	<i>Plasmodium falciparum</i>	pfa	Protist	22.90	23.26	chromosomes	5,268	5429	broadi	Gardner M.J., et al. (2002). Genome sequence of the human malaria parasite Plasmodium falciparum. <i>Nature</i> , 419:498-511.	http://broadinstitute.org/annotation/genome/Plasmodium_falciparum_ssp/MultiDownloads.html ; http://plasmodb.org/common/downloads/Current_Release/Pfalciparum3D7/ ; http://ftp.ensemblgenomes.org/pub/protists/release-16/fasta/plasmodium_falciparum/	
313	40	<i>Aurantiochytrium limacinum</i> (<i>Schizochytrium limacinum</i>)	ali	Protist	60.93	60.93	assembly	14,859	14859	jgi	Liang L., et al. (2020). Genome and Transcriptome Analyses Provide Insight Into the Omega-3 Long-Chain Polyunsaturated Fatty Acids Biosynthesis of Schizochytrium limacinum SR21. <i>Front Microbiol.</i> , 11:687.	http://genome.jgi.doe.gov/pages/dynamicOrganismDownload.jsf?organism=Aurli1	
314	41	<i>Blastocystis hominis</i>	bho	Protist	18.82	18.82	assembly	6,020	6020	coge	Denoedou F., et al. (2011). Genome sequence of the stramenopile Blastocysts, a human anaerobic parasite. <i>Genome Biol.</i> , 12(3): R29.	http://www.genoscope.cns.fr/externe/GenomeBrowser/Blastocysts/ ; http://protists.ensembl.org/Blastocysts_hominis/info/Index	
315	42	<i>Saprolegnia parasitica</i>	sap	Protist	62.80	53.09	assembly	20,113	20212	ensembl	Jiang R., et al. (2013). Distinctive Expansion of Potential Virulence Genes in the Genome of the Oomycete Fish Pathogen Saprolegnia parasitica. <i>PLoS Genet.</i> , 9(6): e1003272.	http://protists.ensembl.org/Saprolegnia_parasitica_cbs_223_65/info/Index	
316	43	<i>Albugo laibachii</i>	ala	Protist	37.00	32.77	assembly	13,032	13804	ensembl	Kemen E., et al. (2011). Gene Gain and Loss during Evolution of Obligate Parasitism in the White Rust Pathogen of Arabidopsis thaliana. <i>PLoS Biol.</i> , 9(7): e1001094.	http://protists.ensembl.org/Albugo_laibachii/info/Index	
317	44	<i>Pythium ultimum</i>	pul	Protist	42.80	44.91	assembly	15,291	15290	pythiumpdb	Lévesque C.A., et al. (2010). Genome sequence of the necrotrophic plant pathogen, Pythium ultimum, reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 11(7):R75.	http://pythiumpdb.plantbiology.msu.edu/download.html ; http://ftp.ensemblgenomes.org/pub/protists/release-16/fasta/pythium_ultimum/	
318	45	<i>Hyaloperonospora arabidopsis</i>	hpa	Protist	100.00	78.9	assembly	14,543	14321	ensembl	Baxter L., et al. (2010). Signatures of Adaptation to Obligate Biotrophy in the Hyaloperonospora arabidopsis Genome. <i>Science</i> , 330 (6010): 1549-1551.	http://protists.ensembl.org/Hyaloperonospora_arabidopsis/info/Index	
319	46	<i>Phytophthora infestans</i>	pif	Protist	240.00	228.54	assembly	17,797	17785	broadi	Haas B.J., et al. (2009). Genome sequence and analysis of the Irish potato famine pathogen Phytophthora infestans. <i>Nature</i> , 461:493-8.	http://plasmodb.org/annotation/genome/Phytophthora_infestans/ ; http://www.broadinstitute.org/annotation/genome/phytophthora_infestans/ ; http://ftp.ensemblgenomes.org/pub/protists/release-16/fasta/phytophthora_infestans/	
320	47	<i>Phytophthora ramorum</i>	pra	Protist	65.00	66.65	assembly	15,743	15605	jgi	Tyler B.M., et al. (2006). Phytophthora Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 313(5791): 1261-1266.	http://plasmodb.org/annotation/genome/Phytophthora_ramorum/ ; http://genome.jgi-psf.org/Phyta1_1/Phyta1_1_download.ftp.html	
321	48	<i>Phytophthora sojae</i>	pso	Protist	95.00	86.03	assembly	19,027	18969	jgi	Tyler B.M., et al. (2006). Phytophthora Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. <i>Science</i> , 313(5791): 1261-1266.	http://plasmodb.org/annotation/genome/Phytophthora_sojae/ ; http://genome.jgi-psf.org/pages/dynamicOrganismDownload.jsf?organism=Physo3	
322	49	<i>Nannochloropsis gaditana</i>	nga	Protist	29.00	34.13	assembly	9,053	10496	gps	Radakovits R., et al. (2012). Draft genome sequence and genetic transformation of the oleaginous alga Nannochloropsis gaditana. <i>Nature Communications</i> , 3, Article number: 686.	http://nannochloropsis.genomeprojects-databases.com/	
323	50	<i>Ectocarpus siliculosus</i>	esi	Protist	214.00	195.78	assembly	16,256	16276	beg	Cock M., et al. (2010). The Ectocarpus genome and the independent evolution of multicellularity in brown algae. <i>Nature</i> , 465: 617-621.	https://bioinformatics.psb.ugent.be/gdb/ectocarpus/	
324	51	<i>Aureococcus anophagefferens</i>	aan	Protist	56.00	56.66	assembly	11,501	11520	jgi	Goble C.J., et al. (2011). Niche of harmful alga Aureococcus anophagefferens revealed through ecogenomics. <i>Proc Natl Acad Sci U S A.</i> , 108 (11): 4352-4357.	http://genome.jgi.doe.gov/Auran1/Auran1.download.ftp.html	
325	52	<i>Thalassiosira oceanica</i>	toc	Protist	81.60	92.04	chromosomes	37,921	34500	ensembl	Lommer M., et al. (2012). Genome and low-iron response of an oceanic diatom adapted to chronic iron limitation. <i>Genome Biology</i> , 13:R66.	http://protists.ensembl.org/Thalassiosira_oceanica/info/Index	
326	53	<i>Thalassiosira pseudonana</i>	tps	Protist	32.40	32.44	chromosomes	11,242	11674	jgi	Armbrust E.V., et al. (2004). The Genome of the Diatom Thalassiosira Pseudonana: Ecology, Evolution, and Metabolism. <i>Science</i> , 306(5693): 79-86.	http://genome.jgi-psf.org/Thaps3/Thaps3.download.ftp.html ; http://ftp.ensemblgenomes.org/pub/protists/release-16/fasta/thalassiosira_pseudonana/	
327	54	<i>Phaeodactylum tricornutum</i>	pti	Protist	27.40	27.45	chromosomes	10,402	12178	jgi	Bowler C., et al. (2008). The Phaeodactylum genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 456(7219):239-44.	http://genome.jgi-psf.org/Phat2/Phat2.download.ftp.html	

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328	55	<i>Fragilariopsis cylindrus</i>	fcy	Protist	80.54	80.54	assembly	18,082	27137	jgi	Mock T., et al. (2017). Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 541:536-540.	http://genome.jgi-psf.org/Fracy1/Fracy1.download.ftp.html	
329	56	<i>Pseudonitzschia multiseries</i>	psm	Protist	218.73	218.73	assembly	19,703	19703	jgi	Unpublished, but available at JGI and Ensembl: https://protists.ensembl.org/Pseudonitzschia_multistriata/Info/Annotation/ ; https://genome.jgi.doe.gov/portal/PSemu1/PSemu1.download.html	http://genome.jgi.doe.gov/portal/PSemu1/PSemu1.download.html	
330	1	<i>Fonticula alba</i>	fal	Protist	31.22	31.22	assembly	5,901	5881	broadi	The Broad Institute: https://protists.ensembl.org/Fonticula_alba_gca_000388065/Info/Annotation/ ; Katinka M.D., et al. (2001). Genome sequence and gene compaction of the eukaryote parasite <i>Encephalitozoon cuniculi</i> . <i>Nature</i> , 414(6862):450-453.	http://protists.ensembl.org/Fonticula_alba/Info/Index	
331	2	<i>Encephalitozoon cuniculi</i>	ecu	Fungi	2.90	2.5	chromosomes	1,997	1996	coge	Haijema C.H., et al. (2017). A parts list for fungal celluloses revealed by comparative genomics. <i>Nat Microbiol.</i> , 2:1078.	http://www.broadinstitute.org/annotation/genome/microsporidia_comparativeGenomesIndex.html	
332	3	<i>Piromyces sp</i>	pyr	Fungi	71.02	71.02	assembly	10,992	14648	jgi	Mondo S.J., et al. (2017). Widespread adenine N6-methylation of active genes in fungi. <i>Nat Genet.</i> , 49(6):964-968.	http://genome.jgi-psf.org/PirE2_1/PirE2_1.info.html	
333	4	<i>Catenaria anguillulae</i>	can	Fungi	36.22	36.22	assembly	12,804	14188	jgi	The Broad Institute: https://www.ncbi.nlm.nih.gov/bioproject/20563 ; https://www.broadinstitute.org/scientific-community/science/programs/genome-sequencing-and-analysis/update-our-microbial-eukaryotes ; Chang Y., et al. (2015). Phylogenomic Analyses Indicate that Early Fungi Evolved Digesting Cell Walls of Algal Ancestors of Land Plants. <i>Genome Biol Evol</i> , 7(6):1590-1601.	http://www.broadinstitute.org/annotation/genome/multicellularity_project/GenomesIndex.html	
334	5	<i>Allomyces macrogyrus</i>	amg	Fungi	57.06	57.06	assembly	19,446	17386	broadi	Russ C., et al. (2016). Genome Sequence of <i>Spizellomyces punctatus</i> . <i>Genome Announc.</i> 4(4). James et al., 2006. <i>Mycologia</i> , 98:860-871. James et al., 2006. <i>Nature</i> , 443:818-822. Hibbett D.S., et al. (2007). <i>Mycological Research</i> , 111:509-547.	http://www.broadinstitute.org/annotation/genome/multicellularity_project/GenomesIndex.html	
335	6	<i>Gonapodya prolifera</i>	gpr	Fungi	48.79	48.79	assembly	13,902	13902	jgi	Rosenblum E.B., et al. (2013). Complex history of the amphibian-killing chytrid fungus revealed with genome resequencing data. <i>Proc Natl Acad Sci U S A.</i> , 110(323):9385-9390.	http://genome.jgi-psf.org/Ganpr1/Ganpr1.info.html	
336	7	<i>Spizellomyces punctatus</i>	spt	Fungi	24.13	24.13	assembly	9,424	8779	broadi	Ma L.J., et al. (2009). Genomic analysis of the basal lineage fungus <i>Rhizopus oryzae</i> reveals a whole-genome duplication. <i>PLoS Genet.</i> , 5(7):e1000549.	http://www.broadinstitute.org/annotation/genome/rhizopus_oryzae/MultiHome.html	
337	8	<i>Batrachochytrium dendrobatidis</i>	bde	Fungi	24.30	24.32	assembly	10,138	8732	jgi	Tang X., et al. (2015). Complete Genome Sequence of a High Lipid-Producing Strain of <i>Mucor circinelloides</i> WJ11 and Comparative Genome Analysis with a Low Lipid-Producing Strain CBS 277.49. <i>PLoS One</i> , 10(9):e0137543.	http://genome.jgi-psf.org/Mucci1/Mucci1.home.html	
338	9	<i>Rhizopus oryzae</i>	ror	Fungi	45.30	46.09	assembly	17,467	17413	broadi	Chaudhary S., et al. (2013). A New Genetic Linkage Map of the Zygomycete Fungus <i>Phycomyces blakesleeana</i> . <i>PLoS ONE</i> , 8(3):e58931.	http://genome.jgi-psf.org/Phyb1/Phyb1.home.html	
339	10	<i>Mucor circinelloides</i>	mci	Fungi	36.59	36.59	assembly	10,930	11719	jgi	Chang Y., et al. (2015). Phylogenomic Analyses Indicate that Early Fungi Evolved Digesting Cell Walls of Algal Ancestors of Land Plants. <i>Genome Biol Evol</i> , 7(6):1590-1601.	http://mycocosm.jgi.doe.gov/Coere1/Coere1.home.html	
340	11	<i>Phycomyces blakesleeana</i>	pbl	Fungi	53.94	53.94	assembly	16,528	16528	jgi	Nishida H., et al. (2011). Draft genome sequencing of the enigmatic basidiomycete <i>Mixia osmundae</i> . <i>J Gen Appl Microbiol.</i> , 57(1):63-67. Toome M., et al. (2014). Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Mixia osmundae</i> . <i>New Phytol.</i> , 202(2):554-564.	http://genome.jgi-psf.org/Mixos1/Mixos1.home.html	
341	12	<i>Coemansia reversa</i>	cor	Fungi	21.84	21.84	assembly	7,347	7347	jgi	Li C., et al. (2021). High-Quality Genome Assembly of Oleaginous Red Yeast <i>Sporobolomyces roseus</i> CGMCC 2.4355. <i>Genome Biology and Evolution</i> , 13(12): evab258.	http://genome.jgi-psf.org/Sporo1/Sporo1.home.html	
342	13	<i>Conidiobolus coronatus</i>	cco	Fungi	39.90	39.9	assembly	10,635	10635	jgi	Firminiel A., et al. (2015). Genome sequence of the plant growth promoting endophytic yeast <i>Rhodotorula graminis</i> WP1. <i>Front Microbiol.</i> , 6: 978.	http://genome.jgi-psf.org/Rhoba1_1/Rhoba1_1.home.html	
343	14	<i>Mixia osmundae</i>	mox	Fungi	13.63	13.63	assembly	6,903	6903	jgi	Duplesses S., et al. (2011). Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proc Natl Acad Sci U S A.</i> , 108(22):9166-9171.	http://www.broadinstitute.org/annotation/genome/puccinia_group/GenomesIndex.html	
344	15	<i>Sporobolomyces roseus</i>	spr	Fungi	21.17	21.17	assembly	5,536	5536	jgi	Duplesses S., et al. (2011). Obligate biotrophy features unraveled by the genomic analysis of rust fungi. <i>Proc Natl Acad Sci U S A.</i> , 108(22):9166-9171.	http://mycocosm.jgi.doe.gov/Mellp1/Mellp1.home.html	
345	16	<i>Rhodotorula graminis</i>	rgr	Fungi	21.01	21.01	assembly	7,283	7283	jgi	Pendleton A.L., et al. (2014). Duplications and losses in gene families of rust pathogens highlight putative effectors. <i>Front Plant Sci.</i> , 5:299.	http://genome.jgi-psf.org/Croqu1/Croqu1.home.html	
346	17	<i>Puccinia graminis</i> (Puccinia graminis f. sp. <i>Triticum</i>)	pgr	Fungi	88.64	88.64	assembly	20,534	15800	ensembl	Xu J., et al. (2007). Dandru-associated <i>Malassezia</i> genomes reveal convergent and divergent virulence traits shared with plant and human fungal pathogens. <i>Proc Natl Acad Sci U S A.</i> , 104(47):18730-18735.	http://genome.jgi-psf.org/Malgl1/Malgl1.home.html	
347	18	<i>Melampsora laricis</i> (Melampsora larici-populin)	mlp	Fungi	101.00	101.13	assembly	16,694	9969	coge	Kamper J., et al. (2006). Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 444: 97-101.	http://www.broadinstitute.org/annotation/genome/ustilago_maydis/2/Home.html	
348	19	<i>Cronartium quercuum</i>	cqu	Fungi	90.00	76.57	assembly	13,903	13903	jgi	Schirawski J., et al. (2010). Pathogenicity determinants in Smut fungi revealed by genome comparison. <i>Science</i> , 330(6010):1546-1548.	http://mips.helmholtz-muenchen.de/genre/proj/sporisorium/	
349	20	<i>Malassezia globosa</i>	mgl	Fungi	8.96	8.96	assembly	4,286	4286	jgi	Lofthus B.J., et al. (2005). The genome of the basidiomycetous yeast and human pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 307(5713):1321-1324.	http://www.broadinstitute.org/annotation/genome/cryptococcus_neoformans/MultiHome.html	
350	21	<i>Ustilago maydis</i>	uma	Fungi	19.80	19.74	assembly	6,522	6522	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi.doe.gov/Dacsp1/Dacsp1.home.html	
351	22	<i>Sporisorium reilianum</i>	sre	Fungi	18.33	18.33	chromosomes	6,648	6673	ensembl	Zuccaro A., et al. (2011). Endophytic life strategies decoded by genome and transcriptome analyses of the mutualistic root symbiont <i>Piriformospora indica</i> . <i>PLoS Pathog.</i> , 7(10):e1002290.	http://genome.jgi-psf.org/Pirin1/Pirin1.home.html	
352	23	<i>Cryptococcus neoformans</i>	cne	Fungi	19.00	19.05	chromosomes	6,572	6273	ensembl	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47: 410-415.	http://genome.jgi-psf.org/Sebve1/Sebve1.home.html	
353	24	<i>Dacryopinax sp</i> (<i>Dacryopinax primogenitus</i>)	dac	Fungi	27.60	29.5	assembly	10,242	10242	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi.doe.gov/Botbo1/Botbo1.home.html	
354	25	<i>Piriformospora indica</i>	pin	Fungi	24.98	24.98	assembly	11,769	11767	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47, 410-415.	http://genome.jgi-psf.org/Tulca1/Tulca1.home.html	
355	26	<i>Sebacina vermifera</i>	sve	Fungi	38.09	38.09	assembly	15,312	15312	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi-psf.org/Sphst1/Sphst1.home.html	
356	27	<i>Botryobasidium botryosum</i>	bob	Fungi	46.67	46.67	assembly	16,526	16526	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47, 410-415.	http://genome.jgi.doe.gov/Phibr1/Phibr1.home.html	
357	28	<i>Tulasnella calospora</i>	tuc	Fungi	62.39	62.39	assembly	19,659	19659	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47, 410-415.	http://genome.jgi.doe.gov/Aurde1/Aurde1.home.html	
358	29	<i>Auricularia delicata</i> (Auricularia subglabra)	ade	Fungi	69.05	74.92	assembly	20,614	23577	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi-psf.org/Firin1/Firin1.home.html	
359	30	<i>Sphaerobolus stellatus</i>	sst	Fungi	176.37	176.37	assembly	35,274	35274	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47, 410-415.	http://genome.jgi-psf.org/Fomme1/Fomme1.home.html	
360	31	<i>Fomitiporia mediterranea</i>	fme	Fungi	56.77	63.35	assembly	11,333	11333	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi.doe.gov/Phaca1/Phaca1.home.html	
361	32	<i>Phanerochaete carnosa</i>	pca	Fungi	46.29	46.29	assembly	13,937	13937	jgi	Suzuki H., et al. (2012). Comparative genomics of the white-rot fungi, <i>Phanerochaete carnosa</i> and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. <i>BMC Genomics</i> , 13:444.	http://genome.jgi-psf.org/Sebve1/Sebve1.home.html	
362	33	<i>Phlebia brevispora</i>	pbr	Fungi	49.96	49.96	assembly	16,170	16170	jgi	Binder M., et al. (2013). Phylogenetic and phylogenomic overview of the Polyporales. <i>Mycologia</i> , 105(6):1350-73.	http://genome.jgi-psf.org/Phibr1/Phibr1.home.html	

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363	34	<i>Punctularia strigosozonata</i>	pst	Fungi	33.07	34.17	assembly	11,538	11538	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi-psf.org/Punst1/Punst1.home.html	
364	35	<i>Gloeophyllum trabeum</i>	gtr	Fungi	34.43	37.18	assembly	11,846	11846	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi-psf.org/Glotr1_1/Glotr1_1.home.html	
365	36	<i>Phlebiopsis gigantea</i>	pgi	Fungi	30.00	30.14	assembly	11,891	11891	jgi	Hori C., et al. (2014). Analysis of the Phlebiopsis gigantea Genome, Transcriptome and Secretome Provides Insight into Its Pioneer Colonization Strategies of Wood. <i>PLoS Genet</i> , 10(12):e1004759.	http://genome.jgi-psf.org/Phlgi1/Phlgi1.home.html ; http://genome.jgi-psf.org/Pirin1/Pirin1.home.html	
366	37	<i>Bjerkandera adusta</i>	bad	Fungi	42.73	42.73	assembly	15,473	15473	jgi	Binder M., et al. (2013). Phylogenetic and phylogenomic overview of the Polyporales. <i>Mycologia</i> , 105(6):1350-73.	http://genome.jgi-psf.org/Bjead1_1/Bjead1_1.home.html	
367	38	<i>Ceriporiopsis subvermispora</i>	ces	Fungi	39.00	38.97	assembly	12,125	12125	jgi	Fernandez-Fueyo E., et al. (2012). Comparative genomics of Ceriporiopsis subvermispora and Phanerochaete chrysosporium provide insight into selective ligninolysis. <i>Proc Natl Acad Sci U S A</i> , 109(14):5458-63.	http://genome.jgi.doe.gov/Cersu1/Cersu1.home.html	
368	39	<i>Postia placenta</i>	ppl	Fungi	90.90	90.93	assembly	17,137	17173	jgi	Martinez D., et al. (2009). Genome, transcriptome, and secretome analysis of wood decay fungus Postia placenta supports unique mechanisms of lignocellulose conversion. <i>Proc. Natl. Acad. Sci. U.S.A.</i> , 106(6):1954-1959.	http://genome.jgi-psf.org/Pospl1/Pospl1.home.html	
369	40	<i>Wolfiporia cocos</i>	wco	Fungi	48.24	50.48	assembly	12,746	12746	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719. Luo H., et al. (2020). The Wolfiporia cocos Genome and Transcriptome Shed Light on the Formation of Its Edible and Medicinal Sclerotinia. <i>Genomics, Proteomics & Bioinformatics</i> , 18(4): 455-467.	http://genome.jgi-psf.org/Wolco1/Wolco1.home.html	
370	41	<i>Fomitopsis pinicola</i>	fpi	Fungi	42.06	41.61	assembly	14,724	13885	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi-psf.org/Fompi1/Fompi1.home.html	
371	42	<i>Trametes versicolor</i>	tve	Fungi	44.79	44.79	assembly	14,296	14296	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi-psf.org/Trave1/Trave1.home.html	
372	43	<i>Ganoderma sp</i>	gan	Fungi	39.52	39.52	assembly	12,910	12910	jgi	Binder M., et al. (2013). Phylogenetic and phylogenomic overview of the Polyporales. <i>Mycologia</i> , 105(6):1350-73.	http://genome.jgi-psf.org/Gansp1/Gansp1.home.html	
373	44	<i>Dichomitus squalens</i>	dsq	Fungi	39.45	42.75	assembly	12,290	12290	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi.doe.gov/Dicsq1/Dicsq1.home.html	
374	45	<i>Heterobasidion annosum</i>	han	Fungi	33.60	33.65	assembly	11,453	13405	jgi	Olson A., et al. (2012). Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytol</i> , 194(4):1001-13.	http://genome.jgi-psf.org/Hetan2/Hetan2.home.html	
375	46	<i>Stereum hirsutum</i>	shi	Fungi	45.64	46.51	assembly	14,072	14072	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi-psf.org/Stehi1/Stehi1.home.html	
376	47	<i>Piloderma croceum</i> (<i>Piloderma olivaceum</i> , syn. <i>Piloderma fallax</i>)	pcr	Fungi	59.33	59.33	assembly	21,583	21583	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nat Genet</i> , 47(4):410-5.	http://genome.jgi-psf.org/Pilcr1/Pilcr1.info.html	
377	48	<i>Japia argillacea</i>	jar	Fungi	45.05	45.05	assembly	16,419	16419	jgi	Riley R., et al. (2014). Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proc Natl Acad Sci U S A</i> , 111(27):9923-8.	http://genome.jgi-psf.org/Jaaar1/Jaaar1.home.html	
378	49	<i>Plicaturopsis crispa</i>	pic	Fungi	34.50	34.5	assembly	13,626	13626	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nat Genet</i> , 47(4):410-5.	http://genome.jgi.doe.gov/Plicr1/Plicr1.home.html	
379	50	<i>Amanita muscaria</i>	amu	Fungi	40.70	40.7	assembly	18,153	18153	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nat Genet</i> , 47(4):410-5.	http://genome.jgi.doe.gov/Plicr1/Plicr1.home.html	
380	51	<i>Pleurotus ostreatus</i>	pos	Fungi	30.00	34.34	assembly	12,330	12330	jgi	Riley R., et al. (2014). Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proc Natl Acad Sci U S A</i> , 111(27):9923-8.	http://genome.jgi-psf.org/PleosPC15_2/PleosPC15_2.home.html	
381	52	<i>Schizophyllum commune</i>	scm	Fungi	38.50	38.48	assembly	13,210	13181	jgi	Ohm R.A., et al. (2010). Genome sequence of the model mushroom Schizophyllum commune. <i>Nat Biotechnol</i> , 28(9):957-63.	http://genome.jgi-psf.org/Schco1/Schco1.info.html	
382	53	<i>Gymnopus luxurians</i>	glu	Fungi	66.28	66.28	assembly	22,057	22057	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nat Genet</i> , 47(4):410-5.	http://genome.jgi.doe.gov/Gymlu1/Gymlu1.home.html	
383	54	<i>Agaricus bisporus</i>	abb	Fungi	30.39	30.23	assembly	10,438	10438	jgi	Morin E., et al. (2012). Genome sequence of the button mushroom Agaricus bisporus reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proc Natl Acad Sci U S A</i> , 109(43):17501-6.	http://genome.jgi.doe.gov/Agabi_varbis97_2/Agabi_varbis97_2.home.html	
384	55	<i>Laccaria bicolor</i>	lbc	Fungi	60.00	64.88	assembly	20,614	20614	jgi	Martin F., et al. (2008). The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. <i>Nature</i> , 452(183):88-92.	http://genome.jgi-psf.org/Lacbi2/Lacbi2.home.html	
385	56	<i>Coprinopsis cinerea</i>	cci	Fungi	37.00	36.15	assembly	13,342	13342	broadi	Jason E., et al. (2010). Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom Coprinopsis cinerea (Coprinus cinereus). <i>Proc Natl Acad Sci U S A</i> , 107(26):11889-11894.	http://www.broadinstitute.org/annotation/genome/coprinus_cinereus/Info.html	
386	57	<i>Hebeloma cylindrosporum</i>	hcy	Fungi	37.61	37.61	assembly	15,382	16841	jgi	Marmisse R., (2004). Hebeloma cylindrosporum: A Model Species to Study Ecotomycorrhizal Symbiosis. <i>From Gene to Ecosystem</i> . New Phytologist, 163(3):491-498.	http://genome.jgi-psf.org/Hebcy1/Hebcy1.home.html	
387	58	<i>Galerina marginata</i>	gam	Fungi	59.42	59.42	assembly	21,461	21461	jgi	Riley R., et al. (2014). Extensive sampling of basidiomycete genomes demonstrates inadequacy of the white-rot/brown-rot paradigm for wood decay fungi. <i>Proc Natl Acad Sci U S A</i> , 111(27):9923-8.	http://genome.jgi.doe.gov/Galma1/Galma1.home.html	
388	59	<i>Hypoloma sublateritium</i>	hsu	Fungi	48.03	48.03	assembly	17,911	17911	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nat Genet</i> , 47(4):410-5.	http://genome.jgi-psf.org/Hyps1/1/hyps1.home.html	
389	60	<i>Coniophora puteana</i>	cpu	Fungi	41.86	42.97	assembly	13,761	13761	jgi	Floudas D., et al. (2012). The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 336(6089):1715-1719.	http://genome.jgi-psf.org/Conpu1/Conpu1.home.html	
390	61	<i>Serpula lacrymans</i>	sla	Fungi	43.00	42.73	assembly	14,072	12789	jgi	Eastwood D.C., et al. (2011). The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. <i>Science</i> , 333(6043):762-765.	http://genome.jgi-psf.org/SerlaS7_9_2/SerlaS7_9_2.home.html	
391	62	<i>Hydnomerulius pinastri</i>	hpi	Fungi	38.28	38.28	assembly	13,270	13270	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47: 410-415.	http://genome.jgi.doe.gov/Hydp1/2/hydp1.home.html	
392	63	<i>Paxillus rubicundulus</i> (<i>Paxillus adelphus</i>)	pru	Fungi	53.01	53.01	assembly	22,065	22065	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47: 410-415.	http://genome.jgi.doe.gov/Paxru1/Paxru1.home.html	
393	64	<i>Scleroderma citrinum</i>	sci	Fungi	56.14	56.14	assembly	21,012	21012	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47: 410-415.	http://genome.jgi-psf.org/Sclic1/Sclic1.home.html	
394	65	<i>Pisolithus microcarpus</i>	pmi	Fungi	53.03	53.03	assembly	21,064	21064	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47: 410-415.	http://genome.jgi-psf.org/Pism1/1/Pism1.home.html	
395	66	<i>Pisolithus tinctorius</i>	pit	Fungi	71.01	71.01	assembly	22,701	22701	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 47: 410-415.	http://genome.jgi-psf.org/Pist1/1/Pist1.home.html	
396	67	<i>Saitoella complicata</i>	sco	Fungi	14.10	14.14	assembly	7,034	7034	jgi	Nishida H., et al. (2011). Draft genome sequencing of the enigmatic yeast Saitoella complicata. <i>J Gen Appl Microbiol</i> , 57(4):243-6.	http://genome.jgi-psf.org/Saico1/Saico1.home.html	
397	68	<i>Schizosaccharomyces pombe</i>	spo	Fungi	12.61	12.61	chromosomes	4,929	5143	ensembl	Wood V., et al. (2002). The genome sequence of Schizosaccharomyces pombe. <i>Nature</i> , 415(6874):871-80.	http://old.genedb.org/genedb/pombe/	
398	69	<i>Lipomyces starkeyi</i>	lst	Fungi	15.00	21.27	assembly	8,192	8192	jgi	Riley R., et al. (2016). Comparative genomics of biotechnologically important yeasts. <i>Proc Natl Acad Sci U S A</i> , 113(35):9882-7.	http://genome.jgi-psf.org/Lipst1_1/Lipst1_1.home.html	
399	70	<i>Yarrowia lipolytica</i>	yli	Fungi	20.50	20.5	chromosomes	6,703	6448	ensembl	Dujon B., et al. (2004). Genome evolution in yeasts. <i>Nature</i> , 430(6995):35-44.	http://genolevures.org/yali.html#info	

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400	71	<i>Nadsonia fulvescens</i>	nfu	Fungi	13.75	13.75	assembly	5,657	5657	jgi	Riley R., et al. (2016). Comparative genomics of biotechnologically important yeasts. Proc Natl Acad Sci U S A., 113(35):9882-7.	http://genome.jgi.doe.gov/Nadfu1/Nadfu1.home.html	
401	72	<i>Wickerhamomyces anomalus</i>	wan	Fungi	25.47	14.15	assembly	11,512	6423	jgi	Schneider J., et al. (2012). Genome sequence of <i>Wickerhamomyces anomalus</i> DSM 6766 reveals genetic basis of biotechnologically important antimicrobial activities. FEMS Yeast Res., 12(3):382-6.	http://genome.jgi-psf.org/Wican1/Wican1.home.html	
402	73	<i>Hansenula polymorpha</i>	hpo	Fungi	9.50	8.97	assembly	5,933	5177	jgi	Ramezani-Rad M., et al. (2003). The Hansenula polymorpha (strain CBS4732) genome sequencing and analysis. FEMS Yeast Res., 4(2):207-15.	http://genome.jgi-psf.org/Hanpo2/Hanpo2.home.html	
403	74	<i>Dekkera bruxellensis</i>	dbr	Fungi	13.00	13.39	assembly	5,600	5636	jgi	Piškár J., et al. (2012). The genome of wine yeast <i>Dekkera bruxellensis</i> provides a tool to explore its food-related properties. Int J Food Microbiol., 157(2):202-9.	http://genome.jgi.doe.gov/Dekbr2/Dekbr2.home.html	
404	75	<i>Pachysolen tannophilus</i>	pta	Fungi	13.60	12.6	assembly	4,463	5675	jgi	Liu X., et al. (2012). Draft Genome Sequence of the Yeast <i>Pachysolen tannophilus</i> CBS 4044/NRRL Y-2460. Eukaryotic Cell., 11(6):827.	http://genome.jgi-psf.org/Pacta1_2/Pacta1_2.home.html	
405	76	<i>Pichia pastoris</i>	pip	Fungi	9.22	9.22	chromosomes	5,313	5040	coge	De Schutter K., et al. (2009). Genome sequence of the recombinant protein production host <i>Pichia pastoris</i> . Nat Biotechnol., 27(6):561-7.	https://mycocosm.jgi.doe.gov/Picpa1/Picpa1.home.html	
406	77	<i>Pichia stipitis</i>	pic	Fungi	15.40	15.44	chromosomes	5,841	5816	coge	Jeffries T.W., et al. (2007). Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast <i>Pichia stipitis</i> . Nat Biotechnol., 25:319-326.	http://genome.jgi-psf.org/Picst3/Picst3.home.html	
407	78	<i>Candida albicans</i>	cal	Fungi	15.85	14.42	assembly	6,040	6059	broadi	Jones T., et al. (2004). The diploid genome sequence of <i>Candida albicans</i> . Proc Natl Acad Sci., 101(19):7329-7334.	http://www.candidagenome.org/ ; http://www.broadinstitute.org/annotation/genome/candida_group/MultiHome.html	
408	79	<i>Babjeviella inositovora</i>	bin	Fungi	15.22	15.22	assembly	6,403	6403	jgi	Riley R., et al. (2016). Comparative genomics of biotechnologically important yeasts. Proc Natl Acad Sci U S A., 113(35):9882-7.	http://genome.jgi-psf.org/Babin1/Babin1.home.html	
409	80	<i>Debaryomyces hansenii</i>	dha	Fungi	12.20	12.22	chromosomes	6,906	6088	coge	Dujon B., et al. (2004). Genome evolution in yeasts. Nature., 430(6995):35-44.	http://genolevures.org/deha.html#info	
410	81	<i>Spathaspora passalidarum</i>	spa	Fungi	13.20	13.18	assembly	5,983	5983	jgi	Wohlbach D.J., et al. (2011). Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. Proc Natl Acad Sci., 108(32):13212-13217.	http://genome.jgi.doe.gov/Spapa3/Spapa3.home.html	
411	82	<i>Hyphopichia burtonii</i>	hbu	Fungi	12.40	12.4	assembly	6,002	6005	jgi	Riley R., et al. (2016). Comparative genomics of biotechnologically important yeasts. Proc Natl Acad Sci U S A., 113(35):9882-7.	http://genome.jgi-psf.org/Hypbu1/Hypbu1.home.html	
412	83	<i>Metschnikowia bicuspidata</i>	mbi	Fungi	16.06	16.06	assembly	5,851	5851	jgi	Ahrendt S.R., et al. (2018). Leveraging single-cell genomics to expand the fungal tree of life. Nat Microbiol., 3(12):1417-1428.	http://genome.jgi-psf.org/Metbi1/Metbi1.home.html	
413	84	<i>Ascoidea rubescens</i>	aru	Fungi	17.50	17.5	assembly	6,802	6802	jgi	Riley R., et al. (2016). Comparative genomics of biotechnologically important yeasts. Proc Natl Acad Sci U S A., 113(35):9882-7.	http://genome.jgi-psf.org/Ascru1/Ascru1.home.html	
414	85	<i>Hanseniaspora valbyensis</i>	hva	Fungi	11.40	11.46	assembly	4,800	4800	jgi	Riley R., et al. (2016). Comparative genomics of biotechnologically important yeasts. Proc Natl Acad Sci U S A., 113(35):9882-7.	http://genome.jgi-psf.org/Hanva1_1/Hanva1_1.home.html	
415	86	<i>Ashbya gossypii</i> (<i>Eremothecium gossypii</i>)	ago	Fungi	8.70	9.1	chromosomes	4,718	4776	ensembl	Dietrich F.S., et al. (2004). The <i>Ashbya gossypii</i> genome as a tool for mapping the ancient Saccharomycetes cerevisiae genome. Science., 304(5668):304-307.	https://fungi.ensembl.org/Ashbya_gossypii/info/Index	
416	87	<i>Kluyveromyces lactis</i>	kla	Fungi	10.70	10.69	chromosomes	5,329	5076	coge	Dujon B., et al. (2004). Genome evolution in yeasts. Nature., 430(6995):35-44.	http://genolevures.org/klla.html	
417	88	<i>Lachancea thermotolerans</i>	lth	Fungi	10.39	10.39	chromosomes	5,094	5092	coge	Souza J.L., et al. (2009). Comparative genomics of protoploid <i>Saccharomycetaceae</i> . Genome Res., 19:1696-709.	https://www.ncbi.nlm.nih.gov/genome/69	
418	89	<i>Saccharomyces cerevisiae</i>	sce	Fungi	12.16	12.07	chromosomes	5,885	6692	ensembl	Goffeau A., et al. (1996). Life with 6000 genes. Science., 274(5287):546, 563-567. Engel S.R., et al. (2014). The Reference Genome Sequence of <i>Saccharomyces cerevisiae</i> : Then and Now. <i>Nat. Rev. Genet.</i> , 15:1696-709.	http://www.ensembl.org/Saccharomyces_cerevisiae/info/Index	
419	90	<i>Zygosaccharomyces rouxii</i>	zro	Fungi	9.76	9.76	chromosomes	4,992	4991	coge	Dietrich F.S., et al. (2004). The <i>Ashbya gossypii</i> genome as a tool for mapping the ancient Saccharomycetes cerevisiae genome. Science., 304(5668):304-307.	http://genolevures.org/zyro.html	
420	91	<i>Tuber melanosporum</i>	tme	Fungi	125.53	124.95	assembly	7,496	7496	jgi	Martin F., et al. (2010). Perigord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. Nature., 464:1033-8.	http://mycor.nancy.inra.fr/IMGC/TuberGenome/ ; http://genome.jgi-doe.org/Tuberme1/Tuberme1.home.html	
421	92	<i>Aureobasidium pullulans</i>	apu	Fungi	26.72	25.8	assembly	10809	10809	jgi	Gostinčar C., et al. (2014). Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. BMC Genomics., 15:549.	http://genome.jgi-doe.gov/Aurpu_var_sub1/Aurpu_var_sub1.home.html	
422	93	<i>Acidomyces richmondensis</i>	ari	Fungi	29.88	29.88	assembly	11,202	11202	jgi	Mosier AC, et al. (2016). Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. Front Microbiol., 7:238.	http://genome.jgi-psf.org/Acir1_iso/Acir1_iso.home.html	
423	94	<i>Baudoinia compniacensis</i>	bco	Fungi	21.88	21.88	assembly	10,513	10513	jgi	Ohm R.A., et al. (2012). Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. PLoS Pathog., 8(12):e1003037.	http://genome.jgi.doe.gov/Bauco1/Bauco1.home.html	
424	95	<i>Mycosphaerella graminicola</i>	mgr	Fungi	39.67	39.69	chromosomes	10,933	10931	ensembl	Goodwin S.B., et al. (2011). Finished genome of the fungal wheat pathogen <i>Mycosphaerella graminicola</i> reveals dispensome structure, chromosome plasticity, and stealth pathogenesis. PLoS Genet., 7(6):e1002070.	http://genomeportal.jgi-psf.org/Mycgr3/Mycgr3.home.html	
425	96	<i>Septoria musiva</i>	smu	Fungi	29.35	29.35	assembly	10,233	10233	jgi	Ohm R.A., et al. (2012). Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. PLoS Pathog., 8(12):e1003037.	http://genome.jgi-psf.org/Sepmu1/Sepmu1.home.html	
426	97	<i>Cladosporium fulvum</i>	cfu	Fungi	61.10	61.11	assembly	14,127	14127	jgi	de Wit P.J., et al. (2012). The genomes of the fungal plant pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> reveal adaptation to different hosts and lifestyles but also signatures of common ancestry. PLoS Genet., 8(11):e1003088.	http://genome.jgi-psf.org/Clafu1/Clafu1.home.html	
427	98	<i>Cercospora zeae</i>	cze	Fungi	46.61	46.61	assembly	12,020	12020	jgi	Haridas S., et al. (2020). 101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. Stud Mycol., 96:141-153.	http://genome.jgi-psf.org/Cerzm1/Cerzm1.home.html	
428	99	<i>Zasmidium cellare</i>	zce	Fungi	38.25	38.25	assembly	16,015	16015	jgi	Haridas S., et al. (2020). 101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. Stud Mycol., 96:141-153.	http://genome.jgi.doe.gov/Zasce1/Zasce1.home.html	
429	100	<i>Dothistroma septosporum</i>	dse	Fungi	30.20	30.21	assembly	12,580	12580	jgi	de Wit P.J., et al. (2012). The genomes of the fungal plant pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> reveal adaptation to different hosts and lifestyles but also signatures of common ancestry. PLoS Genet., 8(11):e1003088. Ohn R.A., et al. (2012). Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. PLoS Pathog., 8(12):e1003037.	http://genome.jgi.doe.gov/Dotse1/Dotse1.home.html	
430	101	<i>Hysterium pulicare</i>	hpu	Fungi	38.43	38.43	assembly	12,352	12352	jgi	Ohm R.A., et al. (2012). Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. PLoS Pathog., 8(12):e1003037.	http://genome.jgi-psf.org/Hyps1/Hyps1.home.html	
431	102	<i>Rhytidhysteron rufulum</i>	rft	Fungi	40.18	40.18	assembly	12,117	12117	jgi	Ohm R.A., et al. (2012). Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. PLoS Pathog., 8(12):e1003037.	http://genome.jgi-psf.org/Rhyru1/Rhyru1.home.html	
432	103	<i>Leptosphaeria maculans</i>	lpm	Fungi	45.10	44.89	assembly	12,469	12469	jgi	Rouxel T., et al. (2011). Effector diversification within compartments of the <i>Leptosphaeria maculans</i> genome affected by Repeat-Induced Point mutations. Nat Commun., 2:202.	http://urgi.versailles.inra.fr/species/Leptosphaeria	
433	104	<i>Didymella exigua</i>	dex	Fungi	34.39	34.39	assembly	12,394	12394	jgi	Haridas S., et al. (2020). 101 Dothideomycetes genomes: A test case for predicting lifestyles and emergence of pathogens. Stud Mycol., 96:141-153.	http://genome.jgi.doe.gov/Didex1/Didex1.home.html	
434	105	<i>Phaeosphaerella nodorum</i> (<i>Parastagonospora nodorum</i>)	pno	Fungi	37.10	37.24	assembly	12,380	12391	ensembl	Hane JK., et al. (2007). Dothideomycete plant interactions illuminated by genome sequencing and EST analysis of the wheat pathogen <i>Stagonospora nodorum</i> . Plant Cell., 19:3347-68.	http://www.broadinstitute.org/annotation/genome/stagonospora_nodorum/GenomesIndex.html	
435	106	<i>Setosphaeria turcica</i>	set	Fungi	43.01	43.01	assembly	11,702	11702	jgi	Ohm R.A., et al. (2012). Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. PLoS Pathog., 8(12):e1003037. Condón B.J., et al. (2013). Comparative genome structure, secondary metabolite, and effector coding capacity across Cochliobolus pathogens. PLoS Genet., 9(1):e1003233.	http://genome.jgi-psf.org/Settu1/Settu1.home.html	

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436	107	<i>Cochliobolus heterostrophus</i>	che	Fungi	36.46	36.46	assembly	13,336	13336	jgi	Ohm R.A., et al. (2012). Diverse lifestyles and strategies of plant pathogenesis encoded in the genomes of eighteen Dothideomycetes fungi. <i>PLoS Pathog.</i> , 8(12):e1003037. Condon B.J., et al. (2013). Comparative genome structure, secondary metabolite, and effector coding capacity across <i>Cochliobolus</i> pathogens. <i>PLoS Genet.</i> , 9(1):e1003233.	http://genomeportal.jgi-psf.org/CocheC5_3/CocheC5_3.home.html	
437	108	<i>Pyrenophora teres</i>	pte	Fungi	35.50	33.58	assembly	11,799	11799	jgi	Pyrenophora teres f. teres. <i>Genome Biol.</i> , 11:R109.	http://genome.jgi-psf.org/Pyrt1/Pyrt1.home.html	
438	109	<i>Cladonia grayi</i>	cig	Fungi	39.61	39.61	assembly	11389	11415	jgi	Arnaoae D., et al. (2019). The lichen symbiosis re-reviewed through the genomes of <i>Cladonia</i> grayi and its algal partner <i>Asterochloris</i> glomerata. <i>BMC Genomics</i> , 20(1):605.	http://genome.jgi.doe.gov/Claqr2/Claqr2.home.html	
439	110	<i>Xanthoria parietina</i>	xpa	Fungi	31.90	31.9	assembly	11,065	10818	jgi	https://genome.jgi.doe.gov/Xanpa2/Xanpa2.info.html	http://genome.jgi-psf.org/Xanpa1/Xanpa1.home.html	
440	111	<i>Aspergillus nidulans</i>	ani	Fungi	30.06	29.83	chromosomes	9,541	10534	ensembl	Galagan J., et al. (2005). Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . <i>Nature</i> , 438:1105-1115.	https://fungi.ensembl.org/Aspergillus_nidulans/info/Index	
441	112	<i>Aspergillus niger</i>	ang	Fungi	34.85	34.41	chromosomes	14,165	14068	ensembl	Pel J., et al. (2007). Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.80. <i>Nature Biotechnology</i> , 25:221-231.	https://fungi.ensembl.org/Aspergillus_niger/info/Index	
442	113	<i>Eurotium rubrum</i> (<i>Aspergillus rubrum</i> , <i>Aspergillus ruber</i> , <i>Aspergillus rubrobrunneus</i>)	ehe	Fungi	26.21	26.21	assembly	10,076	10076	jgi	Kis-Papo T., et al. (2014). Genomic adaptations of the halophilic Dead Sea filamentous fungus <i>Eurotium rubrum</i> . <i>Nat Commun.</i> , 5:3745.	http://genome.jgi.doe.gov/Eurhe1/Eurhe1.home.html	
443	114	<i>Penicillium chrysogenum</i>	pec	Fungi	32.19	31.34	assembly	12,943	11396	jgi	an den Berg M.A., et al. (2008). Genome sequencing and analysis of the filamentous fungus <i>Penicillium chrysogenum</i> . <i>Nat Biotechnol.</i> , 26:1161-8.	http://genome.jgi.doe.gov/Pench1/Pench1.home.html	
444	115	<i>Amorphotheca resinae</i>	are	Fungi	28.63	28.63	assembly	9,642	9642	jgi	Martino E., et al. (2018). Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytol.</i> , 217(3):1213-1229.	http://genome.jgi-psf.org/Amore1/Amore1.home.html	
445	116	<i>Oidiodendron maius</i>	oma	Fungi	46.43	46.43	assembly	16,703	16703	jgi	Kohler A., et al. (2015). Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nat Genet.</i> , 47(4):410-5. Martino E., et al. (2018). Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytol.</i> , 217(3):1213-1229.	http://genome.jgi.doe.gov/Oidma1/Oidma1.home.html	
446	117	<i>Botrytis cinerea</i>	bci	Fungi	42.30	42.66	assembly	16,360	16447	jgi	Amselem J., et al. (2011). Genomic analysis of the necrotrophic fungal pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genet.</i> , 7(8):e1002230.	https://mycocosm.jgi.doe.gov/Botci1/Botci1.home.html	
447	118	<i>Sclerotinia sclerotiorum</i>	scs	Fungi	38.30	27.27	assembly	14,522	10175	broadi	Amselem J., et al. (2011). Genomic analysis of the necrotrophic fungal pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genet.</i> , 7(8):e1002230.	http://genome.jgi-psf.org/Scls1/Scls1.home.html ; http://www.broadinstitute.org/annotation/genome/sclerotinia_sclerotiorumGenomesIndex.html	
448	119	<i>Daldinia eschscholzii</i>	des	Fungi	35.49	37.55	assembly	11445	11173	jgi	Ng K.P., et al. (2012). Draft Genome Sequence of <i>Daldinia eschscholzii</i> Isolated from Blood Culture. <i>Eukaryotic Cell</i> , 11(5):703-704.	http://genome.jgi-psf.org/DalEC12_1/DalEC12_1.home.html	
449	120	<i>Hypoxyylon sp</i>	hyp	Fungi	47.30	47.3	assembly	11,712	12261	jgi	Wu W., et al. (2017). Characterization of four endophytic fungi as potential consolidated bioprocessing hosts for conversion of lignocellulose into advanced biofuels. <i>Appl Microbiol Biotechnol.</i> , 101(6):2603-2618.	http://genome.jgi-psf.org/HypCO275_1/HypCO275_1.home.html	
450	121	<i>Acremonium alcalophilum</i>	aal	Fungi	54.42	54.42	assembly	9,521	9521	jgi	Klosterman S.J., et al. (2011). Comparative genomics yields insights into niche adaptation of plant vascular wilt pathogens. <i>PLoS Pathog.</i> , 7(7):e1002137.	http://genome.jgi-psf.org/Acral2/Acral2.home.html	
451	122	<i>Verticillium dahliae</i>	vda	Fungi	33.83	33.83	assembly	10,353	10535	jgi	Druzhinina I.S., et al. (2018). Massive lateral transfer of genes encoding plant cell wall-degrading enzymes by the mycoparasitic fungus <i>Trichoderma</i> from its plant-associated hosts. <i>PLoS Genet.</i> , 14(4):e1007322.	http://genome.jgi.doe.gov/Verda1/Verda1.home.html	
452	123	<i>Trichoderma citrinoviride</i>	tci	Fungi	33.48	33.48	assembly	9,737	9397	jgi	Ma L.J., et al. (2010). Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 464: 367-373.	http://www.broadinstitute.org/annotation/genome/fusarium_graminearum/GenomeDescriptions.html#FO_FOSC_3_a_V1	
453	124	<i>Fusarium oxysporum</i>	fox	Fungi	59.90	57.72	chromosomes	17,735	17696	broadi	Ma L.J., et al. (2010). Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 464: 367-373.	https://fungi.ensembl.org/Fusarium_verticillioides/info/Index	
454	125	<i>Gibberella moniliformis</i> (<i>Fusarium verticillioides</i>)	gmf	Fungi	41.10	41.1	chromosomes	14179	14166	ensembl	Coleman J.J., et al. (2009). The genome of <i>Nectria haematococca</i> : contribution of supernumerary chromosomes to gene expansion. <i>PLoS Genet.</i> , 5(8):e1000618.	http://genome.jgi-psf.org/Nech2/Nech2.home.html	
455	126	<i>Nectria haematococca</i>	nha	Fungi	54.43	47.33	chromosomes	15,707	15705	ensembl	Okagaki L., et al. (2015). Genome Sequences of Three Phytopathogenic Species of the Magnaportheaceae Family of Fungi. <i>G3</i> , 5(12):2539-2545.	http://www.broadinstitute.org/annotation/genome/magnaporthe_comparativeGenomesIndex.html ; http://fungi.ensembl.org/Magnaporthe_poae/info/Index	
456	127	<i>Magnaporthe poae</i>	mpo	Fungi	40.30	39.5	assembly	12,169	11209	broadi	Crouch J.A., et al. (2020). Genome Sequence of the Chestnut Blight Fungus <i>Cryphonectria parasitica</i> EP155: A Fundamental Resource for an Archetypical Invasive Plant Pathogen. <i>Phytopathology</i> , 110(6):1180-1188.	http://genomeportal.jgi-psf.org/Crypa2/Crypa2.home.html	
457	128	<i>Cryphonectria parasitica</i>	crp	Fungi	43.87	43.87	assembly	11,609	11604	jgi	Cuomo C., et al. (2015). Draft Genome Sequence of the Cellulolytic Fungus <i>Chaetomium globosum</i> . <i>Genome Announc.</i> , 3(1):e00021-15.	http://genome.jgi-psf.org/Chagl_1/Chagl_1.home.html	
458	129	<i>Chaetomium globosum</i>	cgl	Fungi	34.89	34.89	assembly	11,124	11124	jgi	Berka R.M., et al. (2011). Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Mycelopithora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nat Biotechnol.</i> , 29(10):922-7.	http://genome.jgi-psf.org/Spoth2/Spoth2.home.html	
459	130	<i>Mycelopithora thermophila</i> (<i>Sporotrichum thermophile</i>)	mth	Fungi	38.70	38.74	chromosomes	9,110	9108	coge	Berka R.M., et al. (2011). Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Mycelopithora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nat Biotechnol.</i> , 29(10):922-7.	http://genome.jgi-psf.org/Thite2/Thite2.home.html	
460	131	<i>Thielavia terrestris</i> (<i>Thermothielavioidea terrestris</i>)	tte	Fungi	36.90	36.91	chromosomes	9,813	9813	coge	Galagan J.E., et al. (2003). The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , 422(6934):859-868.	http://www.broadinstitute.org/annotation/genome/neurospora/MultiHome.html	
461	132	<i>Neurospora crassa</i>	ncr	Fungi	38.64	39.23	assembly	10,082	9820	broadi			