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ARTICLE

A plant pathology perspective of fungal genome sequencing

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Abstract: The majority of plant pathogens are fungi and many of these adversely affect food security. This mini-review aims to provide an analysis of the plant pathogenic fungi for which genome sequences are publically available, to assess their general genome characteristics, and to consider how genomics has impacted plant pathology. A list of sequenced fungal species was assembled, the taxonomy of all species verified, and the potential reason for sequencing each of the species considered. The genomes of 1090 fungal species are currently (October 2016) in the public domain and this number is rapidly rising. Pathogenic species comprised the largest category (35.5 %) and, amongst these, plant pathogens are predominant. Of the 191 plant pathogenic fungal species with available genomes, 61.3 % cause diseases on food crops, more than half of which are staple crops. The genomes of plant pathogens are slightly larger than those of other fungal species sequenced to date and they contain fewer coding sequences in relation to their genome size. Both of these factors can be attributed to the expansion of repeat elements. Sequenced genomes of plant pathogens provide blueprints from which potential virulence factors were identified and from which genes associated with different pathogenic strategies could be predicted. Genome sequences have also made it possible to evaluate adaptability of pathogen genomes and genomic regions that experience selection pressures. Some genomic patterns, however, remain poorly understood and plant pathogen genomes alone are not sufficient to unravel complex pathogen-host interactions. Genomes, therefore, cannot replace experimental studies that can be complex and tedious. Ultimately, the most promising application lies in using fungal plant pathogen genomics to inform disease management and risk assessment strategies. This will ultimately minimize the risks of future disease outbreaks and assist in preparation for emerging pathogen outbreaks.

Key words:
genome size
pathogen evolution
pathogen lifestyle
plant pathology

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INTRODUCTION

Sequencing of fungal genomes is being driven by various groups of scientists having different interests and needs from genomic data. Mycologists desire genome data to understand how fungi live and evolve, while industries require information on how to improve metabolic pathways or how to find new sources of natural products. The medical and plant pathology sectors need this information to understand diseases, improve diagnoses, understand how they function, and ultimately prevent or at least manage disease outbreaks (Kelman 1985). By 2007, the genomes of 42 eukaryotes were available (Cornell *et al.* 2007) and by 2008 the number of fungal genomes exceeded 90 (Park *et al.* 2008). Today, more than 3000 fungi are in completed or ongoing genome projects and the genomes of more than 900 fungal species have been released. The substantial and growing investment in determining genome sequences reflects the positive impact that this field is having on research. Our question here is what the impact has been for plant pathogenic fungi.

This mini-review aims to summarise the number of available fungal plant pathogen genomes, determine their general characteristics, and consider the impact that the availability of these genomes is having on the study of plant pathology. In order to determine which fungal plant pathogens have been sequenced, we surveyed fungal species (including *Microsporidia*, but excluding *Oomycota*) listed in 11 online genome repositories (Table 1), including MycoCosm (Grigoriev *et al.* 2012, 2013), NCBI Genome (www.ncbi.nlm.nih.gov/genome), the Broad Institute (www.broadinstitute.org), and the universal cataloguing database, Genomes OnLine Database (GOLD; Reddy *et al.* 2014). Fungal species that were found in more than one database were clustered and the current classification of all species was verified up to ordinal level using MycoBank (Robert *et al.* 2013) and Index Fungorum (www.IndexFungorum.org). The most recent scientific literature was consulted where the two online reference databases were not in agreement. Synonymous names associated with each species were noted by consulting MycoBank. We used this non-redundant list to accurately determine the number of fungal species with

Table 1. Fungal genome resources used to populate the genome species list.

Name	Abbreviation	Number of fungal genome projects	URL
Aspergillus Genome Database	AspGD	4	www.aspgd.org
Candida Genome Database	CGD	4	www.candidagenome.org
EnsemblFungi		53	fungi.ensembl.org
Fungal Genome Resource		4	gene.genetics.uga.edu
Genomes OnLine Database	GOLD	3362	genomesonline.org
JGI Genome Portal: MycoCosm		>1200	genome.jgi.doe.gov/fungi
NCBI Genome		>1000	www.ncbi.nlm.nih.gov/genome
PomBase		1	www.pombase.org
Saccharomyces Genome Database	SGD	>50	www.yeastgenome.org
The Broad Institute		>100	www.broadinstitute.org/science/projects/fungal-genome-initiative
The Institute of Bioinformatics and Systems Biology	IBIS	20	www.helmholtz-muenchen.de/en/ibis/institute/groups/fungal-microbial-genomics/resources/index.html
University of Kentucky		29	www.endophyte.uky.edu/

available genome sequences and, specifically, the extent to which fungal plant pathogens have been sequenced.

BEYOND THE 1000 MARK

The lower cost of genome sequencing, due to high-throughput technologies, has encouraged large scale genome initiatives. These include the 5000 Insect Genome Project (i5k; Robinson *et al.* 2011), Genome 10K (Genome 10K, Community of Scientists 2009) and 1000 Plants (www.onekp.com). These projects aim to sample species diversity by sequencing, respectively, whole genomes of insects and vertebrates and the transcriptomes of plant species. Similarly, fungal genome sequencing programmes such as the Fungal Genome Initiative (Fungal Research Community 2002, The Fungal Genome Initiative Steering Committee 2003), the Fungal Genomics Program (Grigoriev *et al.* 2011, Martin *et al.* 2011), and its extension, the 1000 Fungal Genomes (1KFG) Project (Spatafora 2011), have contributed significantly to the number of fungal genomes currently available and continue to do so.

The prevalence of fungi as study organisms is evident when considering the on-going and completed genome sequencing projects. A catalogue of genome projects, GOLD (Reddy *et al.* 2014), began in 1997 with six genome entries (Bernal *et al.* 2001) and in October 2016 included 7422 eukaryote whole genome sequencing projects, of which 3515 (47.4 %) are fungal. Although the respective genome databases (Table 1) list numerous completed and on-going fungal projects, many entries do not represent different species. Of the 1459 completed fungal genome projects in GOLD, slightly more than half (*ca.* 775) are different species, whilst the remainder comprise additional strains of already-sequenced species. To illustrate the extent and prevalence of sequenced genomes in the fungal kingdom, we mapped species with publically available genomes onto ordinal consensus trees (Fig. 1A–C).

The most recent of the fungal genome sequencing initiatives, the five-year international collaborative 1KFG Project, aims to sequence and annotate two species from each of the more than 500 known fungal families (Spatafora 2011). In three years, there has been a shift from obtaining representative genomes for all the fungal phyla (Buckley 2008) to targeting genome sequencing at the family level. By October 2016, the genomes of 1090 different fungal species were publically available (Supplementary File 1). Of this number, the 1KFG Project has released approximately 60 % of the fungal species genomes available.

Although the target of 1000 sequenced fungal species has been reached, the goal of two genomes from each family is a bigger task than the number 1000 (Fig. 1). The goal of having the genome sequences for two representatives have only been achieved in 85 families in the *Ascomycota*, 66 in the *Basidiomycota*, and 11 in the remainder of the fungi. Not surprisingly, some economically and medically important families (e.g. *Aspergillaceae, Clavicipitaceae, Mucoraceae, Mycosphaerellaceae, Saccharomycetaceae, Tremella-ceae, Ustilaginaceae*) have many more than two representatives. Additionally, taxonomic revision and species descriptions continue to generate new fungal families and orders. In the almost ten years since the publication of the Hibbett *et al.* (2007) consensus tree, more than 50 fungal orders have been described, somewhat increasing the workload of the 1KFG Project. Additionally, less than 10 % of the conservative estimate of 1.5 million total fungal species are known (Hawksworth 2012) and new species descriptions continuously emerge. Therefore, the combined goals of sampling fungal biodiversity and sequencing the genomes of representative species are a continuous process.

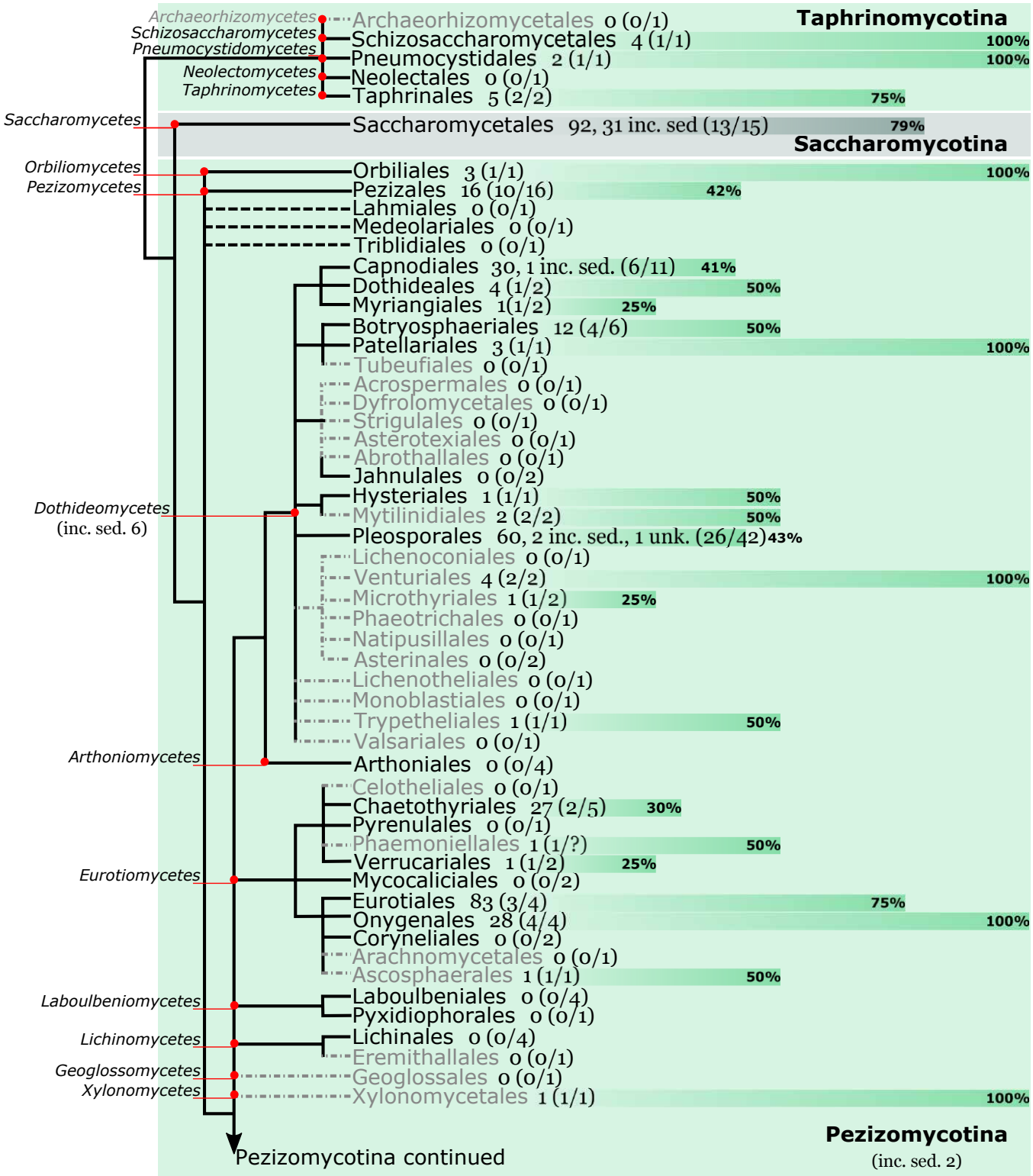

Fig. 1. Ordinal consensus trees depicting the taxonomic (subphylum, class and order) distribution of publically available genomes for the *Ascomycota* (**A**), *Basidiomycota* (**B**) and early-diverging fungi (**C**). The number of sequenced genomes from each order is indicated after the order name. Where sequenced species are not classified into a family or have not been described, these are indicated as *incertae sedis* (inc. sed.) or unknown (unk.), respectively. The number of families with sequenced representatives out of the total number of described families is indicated in brackets. For each order, horizontal bars show the current progress of sequencing two genomes per family, indicated according to the scale bar below the figure. *Dikarya* consensus trees are according to Hibbett *et al.* (2007), while the classification of Spatafora *et al.* (2016) was included in the tree of early-diverging fungi. Orders described after Hibbett *et al.* (2007) have been added in grey (see Supplementary File 3 for references). The figures do not include unclassified fungi that have not been sequenced.

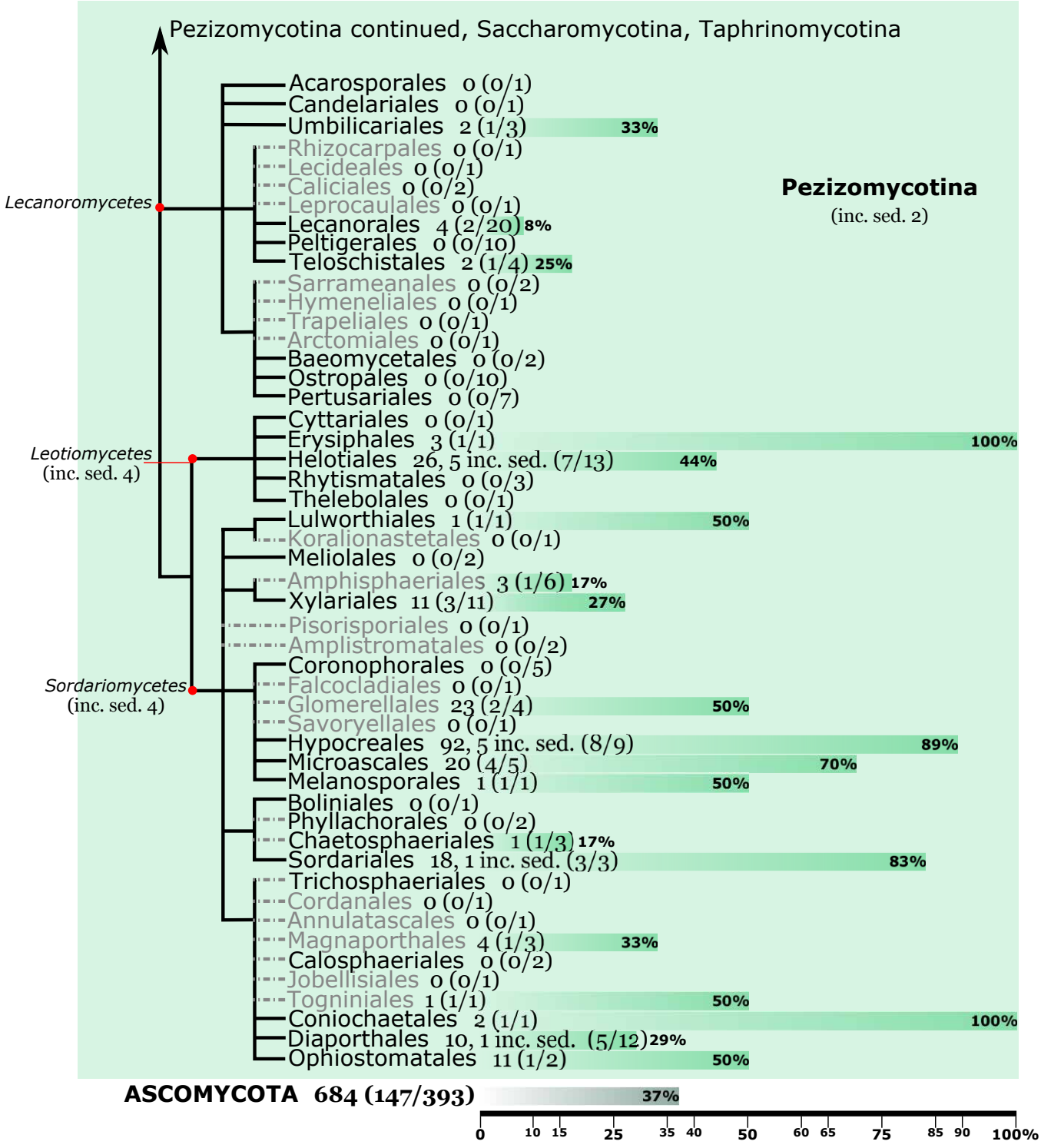

Fig. 1A. (Continued).

ARE PATHOGENS PREFERENTIALLY SEQUENCED?

More than 90 % of known fungal species reside in the subkingdom *Dikarya* (Kirk *et al.* 2008) comprised of the two largest phyla, *Ascomycota* and *Basidiomycota*. The large number of ascomycete and basidiomycete species for which genome sequences have been determined (Table 2) is, therefore, not an over-emphasis of these common phyla, but rather reflects the size and diversity of the *Dikarya* (Fig. 2). In the majority of cases, the proportion of sequenced species in the phyla of early-diverging fungi is congruent with the known species, suggesting that genome projects have not neglected them (Fig. 2). *Mucoromycota* has a larger proportion of sequenced species than known species due to the sequencing of several *Mucoraceae* species that cause human mucoromycosis. One phylum (*Olpidiomycota*) and one subphylum (*Zoopagomycotina*) of early-diverging fungi,

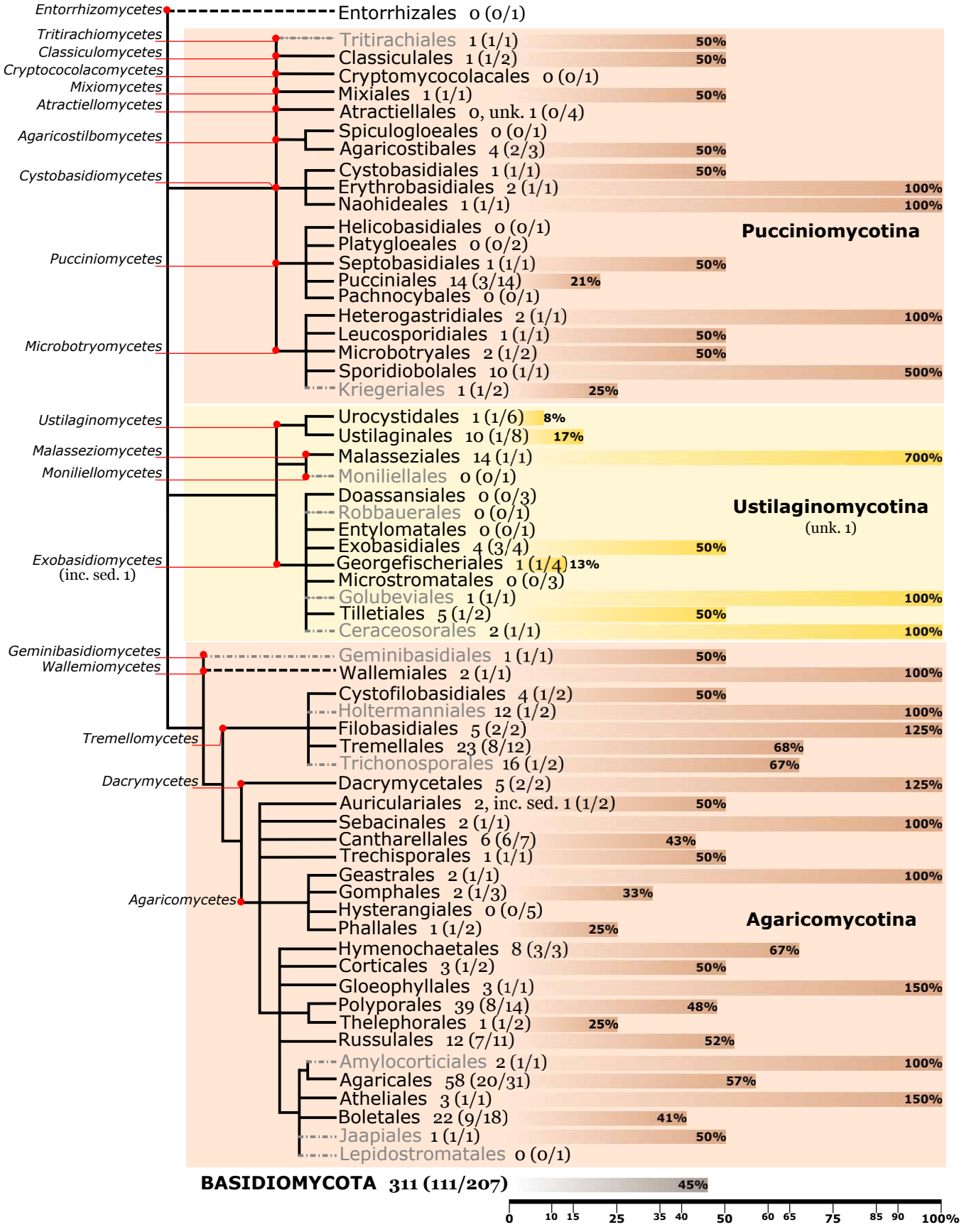

Fig. 1B. (Continued).

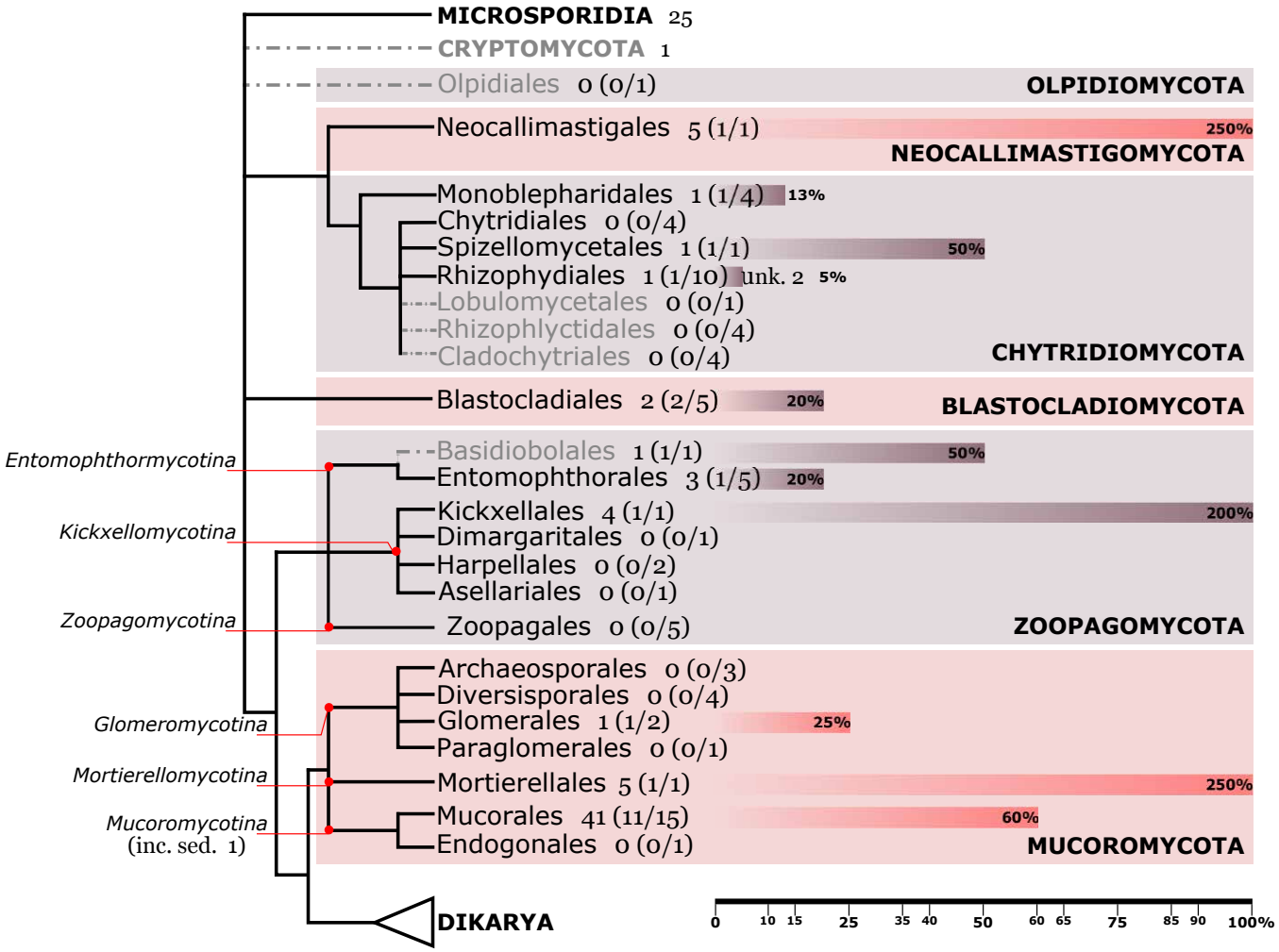

Fig. 1C. (Continued).

however, do not have any sequenced representatives and do not have "targeted" or "in progress" projects listed on GOLD. *Olpidiomycota* was only described recently (Doweld 2013) and its members appear to be poorly known. The lack of *Zoopagomycotina* sequences can likely be ascribed to very few available pure cultures of this predominantly parasitic group of fungi (Spatafora *et al.* 2016).

Within the subphyla of *Ascomycota* and *Basidio-mycota*, the proportion of sequenced species also largely corresponds to the number of known species (Fig. 3), with the major exception being *Saccharomycotina* (budding yeasts; Fig. 3A). The emphasis placed on this subphylum is even more pronounced when considering not only the number of species, but also the number of strains that have been sequenced. Although *Pezizomycotina* (filamentous fungi) is by far the most species-rich subphylum on the genome list (547 spp.), most sequenced strains are in *Saccharomycotina* (416), maintaining its previous status as the most sequenced subphylum in the kingdom (Cuomo & Birren 2010). Other than members of *Saccharomycotina*, seven highly sequenced (≥ 10 strains) species are listed in GOLD (Table 3). One is of industrial importance (*Rhodotorula toruloides*), whereas the remainder influence food security (*Aspergillus flavus*, *Fusarium oxysporum*, and *Magnaporthe oryzae*) or human health (*Cryptococcus gattii*, *Coccidioides posadasii*, and *Trichophyton rubrum*).

A 2008 report by the American Academy of Microbiology (Buckley 2008) stated that fungal genome sequencing is "heavily" skewed in the favour of human pathogens. At that time whole-genome sequencing of eukaryotes, especially fungi, was in its infancy and the statement was based on "100-150 fungal representatives". The initial high cost of genome sequencing would have favoured fungi of medical importance, but as the number of sequenced fungi grew and the cost decreased, this pattern was bound to change. We assessed whether pathogens are highly sequenced by consulting recent scientific literature (where available) on each fungal species on the genome list and categorising them according to their significance and reason for being sequenced. The largest (41.4 %) category consisted of pathogenic fungi and fungi of medical importance (Fig. 4), of which plant pathogens were the most prevalent group (49.4 %). Currently, 191 plant pathogenic species have publically available genomes (Supplementary File 2) and all belong to *Dikarya*. Of these, 117 are pathogens of at least one food crop and 43 affect gymnosperms, the majority of which are commercially important (Table 4). The 117 food crop species include pathogens of cereals, fruit, vegetables, and legumes. At least 60 of these species are responsible for diseases on 10 of the 15 global staple food crops (FAO 1995).

Table 2. Number of fungal species from each phylum and subphylum with at least one available genome.

Phylum and subphylum	Sequenced species	Known species[a]
ASCOMYCOTA	**684**	**> 64 000**
Pezizomycotina	*547*	
Saccharomycotina	*123*	
Taphrinomycotina	*11*	
Incertae sedis	*3*	
BASIDIOMYCOTA	**311**	**> 31 000**
Agaricomycotina	*227*	
Pucciniomycotina	*43*	
Ustilaginomycotina	*41*	
BLASTOCLADIOMYCOTA	**2**	**> 175**
CHYTRIDIOMYCOTA	**5**	**> 700**
CRYPTOMYCOTA	**1**	**?**
MICROSPORIDIA	**25**	**> 1 300**
MUCOROMYCOTA	**47**	
Glomeromycotina	*1*	> 165
Mortierellomycotina	*5*	
Mucoromycotina	*41*	> 325
NEOCALLIMASTIGOMYCOTA	**5**	**> 20**
ZOOPAGOMYCOTA	**8**	
Entomophthoromycotina	*4*	> 275
Kickxellomycotina	*4*	> 260
UNKNOWN	**2**	
Total sequenced	***1090***	

[a] According to Kirk *et al.* (2008).

Table 3. Fungal species on the Genomes OnLine Database (Bernal *et al.* 2001) with 10 or more completed whole-genome sequencing projects.

Species	Strains	Phylum	Subphylum
Saccharomyces cerevisiae	166	*Ascomycota*	*Saccharomycotina*
Magnaporthe oryzae	48	*Ascomycota*	*Pezizomycotina*
Candida albicans	35	*Ascomycota*	*Saccharomycotina*
Komagataella pastoris	32	*Ascomycota*	*Saccharomycotina*
Saccharomyces kudriavzevii	20	*Ascomycota*	*Saccharomycotina*
Cryptococcus gattii	18	*Basidiomycota*	*Agaricomycotina*
Fusarium oxysporum	17	*Ascomycota*	*Pezizomycotina*
Trichophyton rubrum	12	*Ascomycota*	*Pezizomycotina*
Aspergillus flavus	10	*Ascomycota*	*Pezizomycotina*
Coccidioides posadasii	10	*Ascomycota*	*Pezizomycotina*
Rhodotorula toruloides	10	*Basidiomycota*	*Pucciniomycotina*
Saccharomyces pastorianus	10	*Ascomycota*	*Saccharomycotina*

Clearly, genome sequencing projects have placed an emphasis on plant pathogenic species, specifically those affecting food security or commercial forestry. In general, fungal pathogens are highly represented in the genome list. Furthermore, as the number of available genomes has increased, plant pathogens have replaced human pathogens as the predominantly sequenced category of species. Since most plant pathogens are fungi (Carris *et al.* 2012), the emphasis placed on fungal genome sequencing may (at least partly) be attributed to food security. For example, *M. oryzae*, a plant pathogen for which numerous strains have been sequenced (Table 3), is predicted to increase its distribution range and impact due to increased temperature and carbon dioxide levels (Gautam *et al.* 2013). The sheer number of plant species and their associated disease-causing fungi makes this change in the focus of genome sequencing understandable. Sequencing a large number of plant pathogens that affect a range of plant species is, after all, less of a bias than sequencing many pathogenic species associated with a single species (humans).

GENOME SIZE AND GENE NUMBERS IN PLANT PATHOGENIC FUNGAL GENOMES

As far as we are aware, this review includes the first comprehensive list of plant pathogenic fungal genomes that have been sequenced to date. We, therefore, briefly present an overview of the genome characteristics of these species in comparison to other sequenced fungal species. We specifically looked at genome size and the numbers of genes encoded, because previous studies have revealed a link between plant pathogenicity and genome size and gene content (Duplessis *et al.* 2011, Ohm *et al.* 2012, Spanu *et al.* 2010).

The 1090 fungal species with publically available genome sequences have haploid genome sizes ranging between two and 336 million base pairs (Mbp; Fig. 5A). The majority of these genomes fall within the 30–40 Mbp range (average = 37.2, median = 33.6), consistent with the size distribution of the 1940 entries in the Fungal Genome Size Database (Kullman *et al.* 2005). The genome sizes of sequenced plant pathogens are only slightly, but significantly, larger compared to this “norm”. This difference was most apparent in the pathogenic ascomycetes for which Mann-Whitney U tests indicated the highest level of significance (Median = 38.0; $U = 48131$, $P < 0.01$). The average genome size of plant pathogenic basidiomycetes (57.3 Mb) was much larger than that of the plant pathogenic ascomycetes (39.4 Mb) and the remainder of the fungal genomes (34.8 Mb), owing to several pathogenic pucciniomycete (rust) species with genomes larger than 100 Mb.

Somewhat larger genome sizes in plant pathogens are congruent with the hypothesis that they often contain more repeated elements than other species (discussed below) (Castanera *et al.* 2016, Ma *et al.* 2010). Sequenced plant pathogens also have larger genomes than human, animal and opportunistic fungal pathogens (Fig. 5B). Although sequencing has thus far sampled the genome size distribution of the majority of the fungal kingdom, species with excessively large genome sizes have been omitted. This is not necessarily

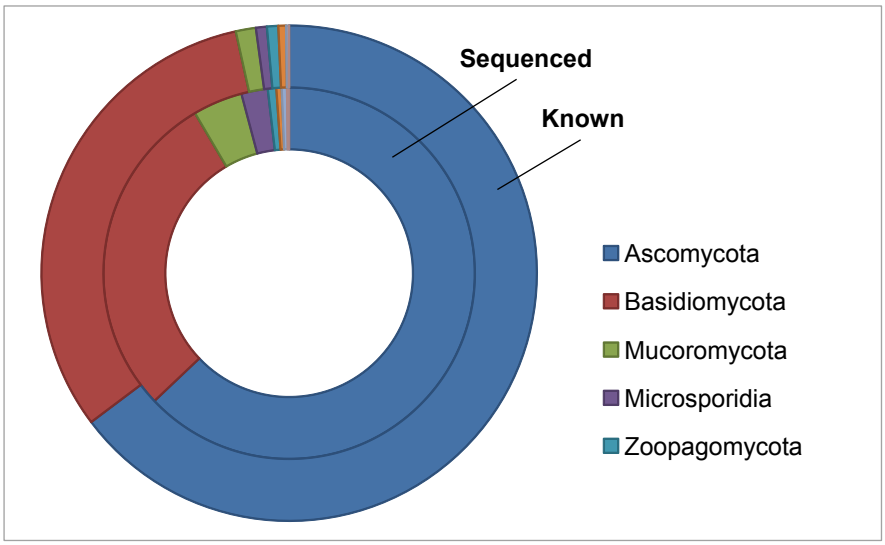

Fig. 2. Comparison between the proportion of known and sequenced fungal species in the major fungal taxonomic groups. The number of known species were obtained from Kirk *et al.* (2008).

only due to the higher cost of sequencing large genomes, but probably also the complexity of obtaining sufficient biomaterial from a single obligately parasitic individual cultured on a live host (Barnes & Szabo 2008). Since the majority of species in *Pucciniomycotina* reside in the order *Pucciniales* of obligate plant pathogens (Kirk *et al.* 2008), the latter may also explain why the proportion of sequenced species in this group is slightly less than the known species (Fig. 3B). Therefore, genome-sequencing efforts so far, most likely underestimate the maximum size of plant pathogen genomes.

Considering the number of predicted open reading frames (ORFs), 714 of the available genomes have publically accessible gene annotations. The sequenced fungi have, on average, 11 256 ± 3 873 total predicted ORFs at a density of 351.8 ± 104.0 ORFs per Mbp (Fig. 5C). In comparison to the other genomes, plant pathogenic fungi do not differ in the number of predicted ORFs, but they do have significantly fewer ORFs when accounting for genome size ($U = 35647$; $P < 0.01$). This trend was also observed in the animal pathogenic fungi (including entomopathogens; $U = 8847$; $P < 0.01$). Previous whole-genome studies suggest that the number of coding genes does not necessarily increase with genome size, since transposable elements and repetitive sequences proliferate in large genomes (Kidwell 2002).

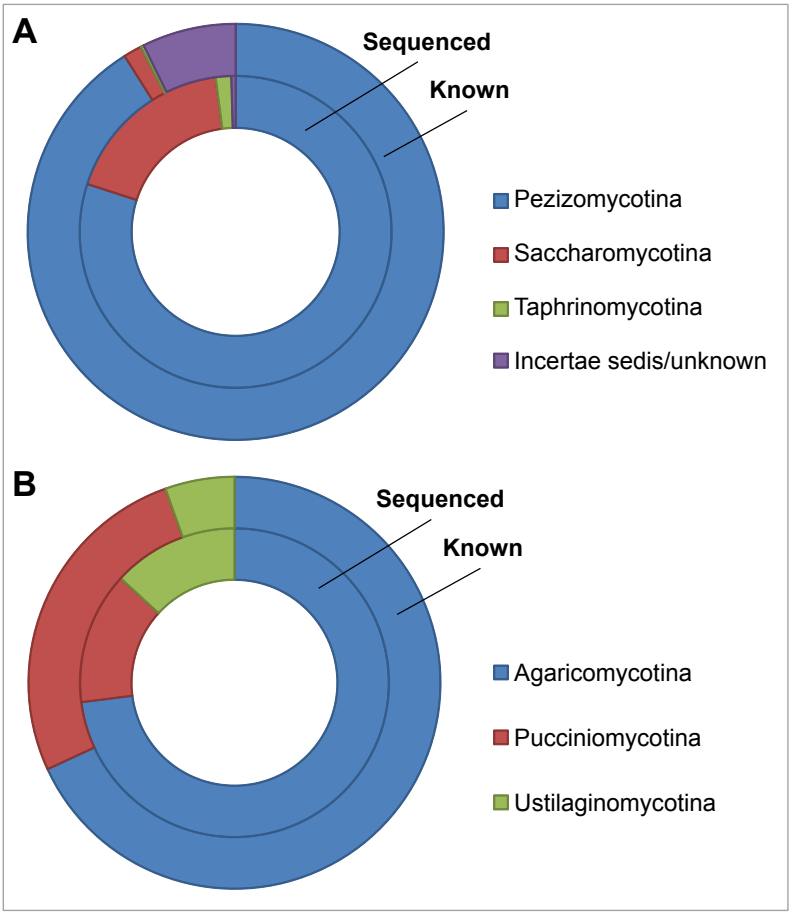

Fig. 3. Comparison between the proportion of known and sequenced fungal species in the subphyla of *Ascomycota* (A) and *Basidiomycota* (B). The number of known species were obtained from Kirk *et al.* (2008).

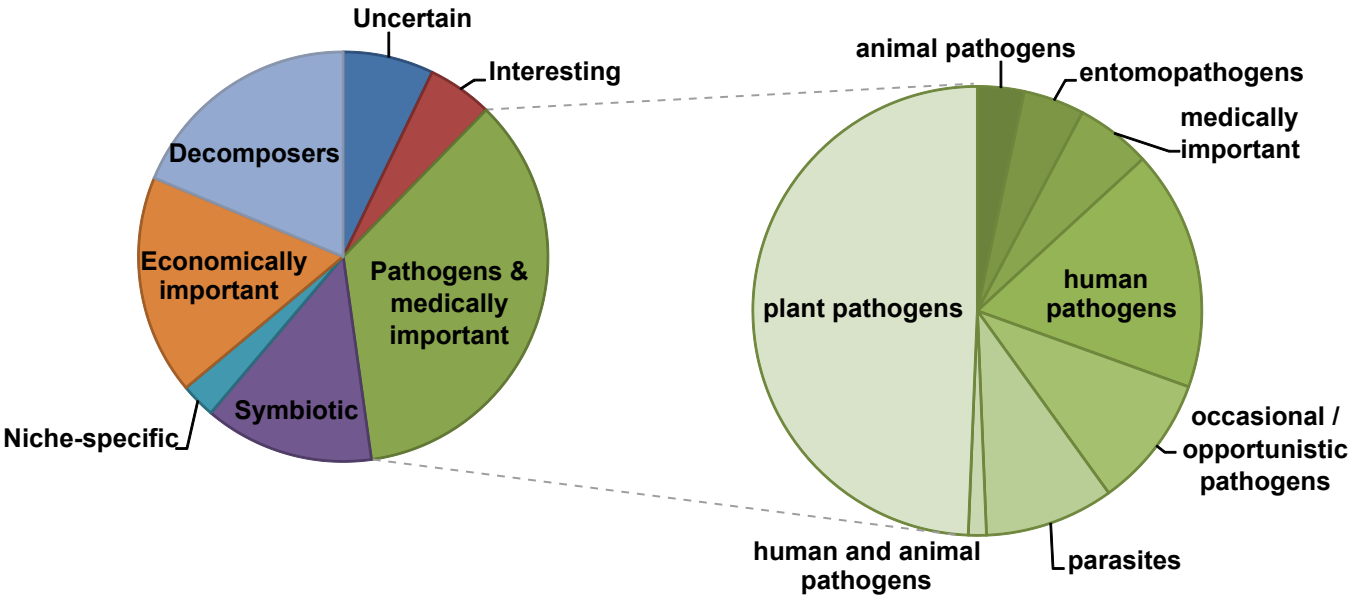

Fig. 4. Categories of significance identified in the 1090 sequenced fungal species. Pathogens comprise the largest category within which plant pathogens are predominant. "Medically important" species represent fungi that are not directly pathogenic, but cause food or environmental contamination. "Interesting" species are studied for their development or metabolism. "Niche-specific" refers to species occupying abiotic niches, whereas "symbiotic" species are associated with other organisms. "Economically important" species have a use in the economy, (e.g. culinary, biocontrol or pharmaceutical industries). Most of the parasites belong to *Microsporidia*.

Table 4. Categories of plants affected by the 191 sequenced fungal plant pathogens.

Plant pathogen categories	Genomes available	%
Cash Crop Pathogens	8	4.2
Food Crop Pathogens	117	61.3
Grains	*48*	*25.2*
Fruit	*37*	*19.4*
Vegetables	*10*	*5.2*
Legumes	*11*	*5.8*
Multiple crop types	*11*	*5.8*
Gymnosperm Pathogens	43	22.5
Other[a]	23	12.0
TOTAL	*171*	*100*

[a] Non-gymnosperms not cultivated for food.

The lower number of ORFs/Mb in the genome of plant pathogenic Ascomycetes is, therefore, consistent with their larger genome size possibly being due to repetitive elements. Additionally, some pathogens have lost genes redundant in their lifecycles (Spanu *et al.* 2010), which may also decrease their ORFs/Mb. This trend could, however, not be detected in the genomes of human and opportunistic pathogens (Fig. 5D).

IMPACT OF GENOMES ON PLANT PATHOLOGY

Ever since the advent of plant pathology, researchers have been interested in the biology of plant pathogens and how this can be translated into means for disease control. In this regard, genome data are not used in isolation, but provide context for observational and experimental data, thereby accelerating the pace of traditional research methods. For emerging pathogens, a disease may be known, but the mechanisms relating to infection biology and virulence are not necessarily understood. In these cases, a genome can provide the first glimpse of the potential effectors and toxins that are present (e.g. Ellwood *et al.* 2010). In some plant pathogens, genomes have resulted in a shift of conventional paradigms. Here a classic example is the discovery of entire horizontally transferrable chromosomes related to pathogenicity in *Fusarium oxysporum* f. sp. *lycopersici* (Ma *et al.* 2010). The primary impacts of genome sequences on plant pathology have been a better understanding of the pathogenicity, life-style and genome evolution of pathogens. Furthermore, genomes are also resources from which genetic tools can be used to mine information.

Pathogenicity and life-style

Secreted and cell surface proteins mediate the interaction between pathogen and host and are often the first to be characterised from plant pathogen genomes. Genome sequences enable *in silico* predictions of secreted virulence proteins (effectors), bypassing traditional enzyme assays or chromatography/spectrometry techniques that were ineffective at detecting less abundant effectors. For the corn smut fungus, *Mycosarcosoma maydis* (syn. *Ustilago maydis*), previous experimental studies were not able to identify the virulence factors that were eventually highlighted by interrogating the genome sequence (Kamper *et al.* 2006). The proteins identified *in silico* could then be used to experimentally determine the function of specific effectors in the infection process (Liu *et al.* 2015). This genome-based effector identification

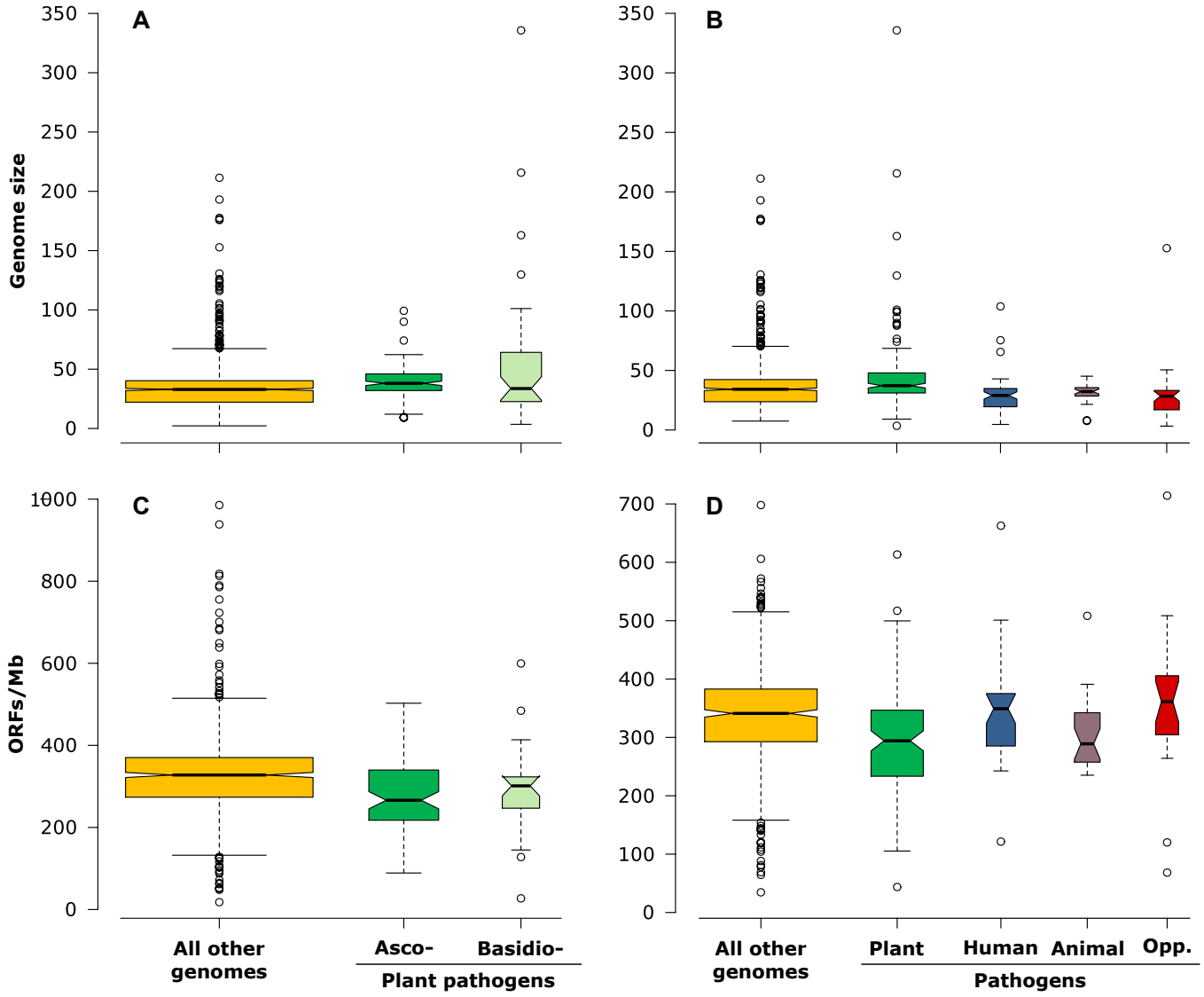

Fig. 5. Genome size (**A** and **B**) and number of open reading frames (ORFs) per million base pairs (Mbp; **C** and **D**) in the plant pathogen genomes compared to the remainder of the genome list and other pathogens. Boxplots were drawn in BoxplotR (Spitzer *et al.* 2014) using the Tukey whisker extent. Width of the boxes is proportional to the square root of the sample size; notches show the 95 % confidence interval of the median. Opp. = opportunistic pathogens. In B and D, animal pathogens include entomopathogenic fungi and *Microsporidia* are excluded from "other" genomes, since they have small genomes with many ORFs/Mb.

and subsequent phenotype determination has contributed significantly to the online Pathogen Host Interactions Database (Urban *et al.* 2015). Similarly, genomic prediction of fungal product biosynthesis genes have been well established (Keller *et al.* 2005) and gene deletion systems could subsequently be used to determine the phenotypes that they confer (Lee *et al.* 2005). Gene inventories of plant pathogens have also revealed proteins not previously known to be involved in pathogenicity, for example the high diversity of membrane transporters in the *F. oxysporum* and *Pyrenochaeta lycopersici* genomes strongly implicates them in the pathogenicity of these fungi (Aragona *et al.* 2014).

Intuitively, cell wall degrading enzymes can be expected to be important in plant pathogenesis and the presence of these enzymes in plant pathogens was well established before the genomic era (Jones *et al.* 1972, Schneider & Collmer 2010). Genome sequences have confirmed that most plant pathogens encode an array of cell wall degrading enzymes, specifically pectinolytic enzymes in dicot pathogens (Klosterman *et al.* 2011, Olson *et al.* 2012). The diversity of cell wall degrading enzymes in a genome appears to increase with host range, as exemplified by the massive number of carbohydrate degrading enzymes in *Macrophomina phaseolina* that infects over 500 plant species (Islam *et al.* 2012). Exceptions to this perceived norm typically occur in specialised modes of pathogenesis. For example, cell wall degrading enzymes are absent from the genome of the anther smut fungus *Microbotryum lychnidis-dioicae* (Perlin *et al.* 2015). Rather than attacking plant cells, this pathogen has an array of enzymes to influence host development, enabling fungal spores to be substituted for pollen. In contrast, gene inventories suggest that necrotrophic pathogens induce apoptosis in host cells rather than breaking down their cell walls (McDonald *et al.* 2015). Metabolism-related enzymes in fungal genomes, therefore, have great potential to predict infection strategies and lifestyle.

Beyond the analysis of single genome sequences, comparing the genomes of ecologically different strains and species has substantial value. For example, analysis of the *Rhizoctonia solani* AG2-2IIIB genome would have revealed only an abundance of cell wall degrading enzymes. However, comparisons with less aggressive *R. solani* strains revealed that its virulence can be linked to a significant expansion of polysaccharide lyase enzymes (Wibberg *et al.* 2016). Similarly, comparisons of resistant and non-resistant *Penicillium digitatum* strains has enabled identification of mutations conferring tolerance to antifungal compounds (Marcet-Houben *et al.* 2012).

Comparisons between the genomes of 18 dothideo-mycete species has suggested that the number of effectors encoded by these fungi are linked to the pathogenic lifestyle (Ohm *et al.* 2012). The greatest number of effectors was identified from necrotrophic pathogens, whereas hemibiotrophs have apparently reduced their effector arsenal to evade plant defences before they switch to necrotrophy (Ohm *et al.* 2012). Furthermore, multiple genome comparisons have been used to highlight specific genes under diversifying selection, revealing that evolutionary pressure on plant pathogen effector proteins drive their adaptation (Schirawski *et al.* 2010, Stukenbrock *et al.* 2011). Comparison between plant and fungal genomes have also become essential tools to tease apart pathogen and plant RNA sequences when analysing *in planta* transcript data (McDonald *et al.* 2015). The value of multiple genome comparisons has prompted projects such as the Fungal Genome Initiative and the 1KFP to focus not on sequencing single species, but groups of species useful in a comparative context (Grigoriev *et al.* 2013, The Fungal Genome Initiative Steering Committee 2004).

The evolution of different fungal lifestyles is a fascinating topic considered by many comparative genomics studies. Some plant pathogenic fungi with different lifestyles have surprisingly similar gene contents (De Wit *et al.* 2012), yet unique genes mediate their host interactions. The large proportion of unique secreted effector proteins and host-specific hydrolytic enzymes in plant pathogenic fungi implies that host association drives their adaptation and, therefore, evolution (De Wit *et al.* 2012, Duplessis *et al.* 2011, O'Connell *et al.* 2012, Spanu *et al.* 2010). The effect of host association is further emphasised by the diversification of both effectors and hydrolytic enzymes in broad host range pathogens such as *Colletotrichum higginsianum* (O'Connell *et al.* 2012). In contrast, host association cannot explain the loss of primary metabolism genes that led to obligate biotrophy in powdery mildew fungi (Spanu *et al.* 2010). Similarly, selective pressures that mediate the evolution of a hemibiotrophic strategy, where the pathogen transitions between a biotrophic and necrotrophic lifestyle, are poorly understood.

Genome evolution of plant pathogens

The arms race between pathogen and host (Stahl & Bishop 2000) makes pathogen adaptability, or evolu-tionary potential, particularly interesting (McDonald & Linde 2002). Reproduction and gene diversity are two of the factors that influence evolutionary potential (McDonald & Linde 2002) and these can be estimated from genome sequences. For example, an analysis of the mating type genes that govern sexual reproduction can provide insights into the mating strategy of a fungus. Heterothallic ascomycete fungi are identified by the occurrence of a single mating type in a genome (Kronstad & Staben 1997), whereas homothallic fungi contain both mating types, either in the same genome or in a dikaryotic cellular state (Wilson *et al.* 2015). Many fungi propagate only vegetatively or sexual reproduction is difficult to observe. In such cases, genomic analyses have been able to reveal the presence of mating type genes (e.g. Bihon *et al.* 2014, Marcet-Houben *et al.* 2012), suggesting that these species could have a cryptic sexual cycle (Bihon *et al.* 2014). The mating type sequence information can subsequently be used to determine the distribution of different mating types in a population (Aylward *et al.* 2016, Haasbroek *et al.* 2014). In contrast, genomes can also reveal the importance of mitotic recombination for generating new allelic combinations. For example, a whole genome survey concluded that mating type genes are completely absent from the tomato pathogen *P. lycopersici* and that it has an expansion of gene modules associated with heterokaryon incompatibility (Aragona *et al.* 2014).

Adaptability to a changing environment or a resistant host can also be mediated by genome plasticity. Transposons are repetitive elements in DNA known to contribute to genome plasticity and evolution (Wöstemeyer & Kreibich 2002). The expansion of repeats in many plant pathogen genomes points to their role in diversification and adaptation (Raffaele & Kamoun 2012, Spanu *et al.* 2010, Thon *et al.* 2006) and has been directly implicated in the pathogenicity of the wheat necrotroph *Pyrenophora tritici-repentis* (Manning *et al.* 2013). Surveys of transposons across plant pathogen genomes have revealed differences in their number and activity between the essential core and dispensable supernumerary chromosomes (Ohm *et al.* 2012, Vanheule *et al.* 2016). In *Fusarium poae*, repeat expansion in the core chromosomes is contained, while the non-essential supernumerary chromosomes have many active transposons that invade the core chromosomes (Vanheule *et al.* 2016). The supernumerary chromosomes also provide opportunity for duplication and diversification of core genes, thereby facilitating adaptation. An example of such diversification and adaptation in the post-harvest spoilage fungus *Penicillium digitatum* is the association of DNA transposons and ABC transporters in drug resistant strains (Sun *et al*. 2013b).

Horizontal gene transfer (HGT) may add novel ecological capabilities to the genomes of recipient species. Although not historically considered relevant to eukaryotic evolution, genome level investigations have revealed multiple HGT events in fungi, often from other kingdoms (e.g. Marcet-Houben & Gabaldón 2010, Sun *et al*. 2013a). Such phylogenomic studies have reported, amongst others, horizontal acquisition of genes that mediate pathogenicity (Friesen *et al*. 2006, Kroken *et al*. 2003, Slot & Rokas 2011, Thynne *et al*. 2015), tolerance to host defences (Marcet-Houben & Gabaldón 2010, Sun *et al*. 2013a), and nutrient uptake and metabolism (Soanes & Richards 2014, Sun *et al*. 2013a). Moreover, a comparative genomics study found evidence of HGT at chromosome level in *F. oxysporum* f. sp. *lycopersici*, as entire pathogenicity-related chromosomes could be transferred between strains (Ma *et al.* 2010).

Acquiring new ecological capabilities through HGT has previously played a causal role in the emergence of new pathogens and will likely do so again in future (Friesen *et al*. 2006, Soanes & Richards 2014, Thynne *et al*. 2015).

Resources for genetic tools

Other than facilitating whole-genome related studies, genome sequences have become ideal resources for mining genetic tools. Previously, species-specific population genetic tools such as microsatellites had to be developed painstakingly by cloning and genome walking (Barnes *et al.* 2001, Burgess *et al.* 2001). Now, any genome sequence enables rapid identification of such genetic markers (e.g. Haasbroek *et al.* 2014). This holds true for diagnostic markers: genome regions that unambiguously and rapidly identify a pathogen and/or differentiate between pathogens can be designed by inspecting whole genome sequences. Although development of such markers in fungi is lagging behind viral and bacterial pathogens, some examples have recently become available. A pathotype specific marker has been developed from the genome of *M. oryzae* f.sp. *triticum* (Pieck *et al.* 2016) and comparative genomics has detected diagnostic regions in two *Calonectria* species (Malapi-Wight *et al.* 2016) and in *Pseudoperonospora cubensis* (Withers *et al.* 2016). Continued application of fungal genomes to generate identification tools is bound to increase the efficiency of quarantine procedures (McTaggart *et al.* 2016).

CHALLENGES

Although the availability of fungal genomes has dramatically increased our knowledge and understan-ding of infection processes and genome evolution, there remains much to learn. For example, the regulatory elements in most genomes remain poorly annotated and require complex experimental methodologies for accurate identification (e.g. Shen *et al.* 2012). In a recent review, Schatz (2015) commented that sequencing human genomes has been one of the greatest accomplishments of the past two decades but “one of the greatest pursuits for the next twenty years will be trying to understand what it all means”. The same can be said for fungal genomes. The information that can be gleaned from a genome sequence is bound to increase as our understanding of these sequences grows.

Genome sequences should not be seen to provide “silver bullets”, although they are often sold this way. They provide the blueprint of potential cellular activities, but are not sufficient to unravel the complexity of pathogen-host interactions. For example, in *Fusarium oxysporum*, the cell wall degrading enzymes secreted during infection of tomato displayed a clear succession (Jones *et al.* 1972), an ecologically relevant process that could not be deduced from a gene inventory. In combination with transcriptome data, however, genomic data has revealed how pathogens tolerate host defences (DiGuistini *et al.* 2011) and how hosts can resist pathogen infection (Zhu *et al.* 2012). Experimental work, both *in vitro* and *in plantae*, will remain essential components in studying fungal plant pathogens.

The end goal of studying any host-pathogen relationship is clearly to inform disease management and control. Thus far, identifying specific molecular targets has had little impact on developing new antifungal inhibitors (Odds 2005) and integrative management strategies must, therefore, be a priority. Ultimately, the elucidated effector proteins, host targets, and the overall insights gained into the biology of pathogens must inform disease management strategies (Maloy 2005). It is also crucial that they inform risk assessment protocols governing biosecurity (McTaggart *et al.* 2016). It is, therefore, essential that the ecological significance of genome patterns is studied to ensure that this knowledge can be extrapolated to emerging pathogen threats.

As revealed by comparative genomics, deciphering plant pathogen evolution is in many cases dependent on being able to do comparisons with species having other lifestyles. A large scale example of this is the revised classification of species previously known as *Zygomycetes* (Spatafora *et al.* 2016); an endeavour possible because of the availability of multiple genome sequences for this group. In this regard, filling in the gaps in the list of sequenced species is crucial to our understanding of relationships and pathogenesis. The challenge is, therefore, to continue sequencing apparently uninteresting or unimportant taxonomic groups along with the economically important in order to ultimately gain a holistic view.

CONCLUSIONS

The activities of independent research groups and several fungal sequencing initiatives (Fungal Research Community 2002, Grigoriev *et al.* 2011, Martin *et al.* 2011, Spatafora 2011, The Fungal Genome Initiative Steering Commitee 2003), have resulted in the number of publically available fungal genomes growing exponentially since 1996 when the first genome was sequenced (Goffeau *et al.* 1996). The taxonomic distribution of sequenced fungal genomes is currently roughly congruent with the number of species known from each phylum and subphylum. This is an important and impressive achievement in the goal of sampling biodiversity and representing the phylogenetic groups of the fungal kingdom (Fungal Research Community 2002, The Fungal Genome Initiative Steering Commitee 2003). Many of the genomes have been sequenced to sample environmental and ecological diversity. However, investment continues to be primarily focused on projects that have direct human importance. The emphasis on genomes of plant pathogenic fungi has specifically increased subsequent to the Buckley (2008) overview of sequenced fungal species.

The genomes of more than 1 000 fungal species are already publically available and this number is growing steadily. Fungal genomics has enabled rapid characterization of plant pathogen genomes and revealed features that allow better understanding of the biology of these species. It has also made it possible to rapidly develop tools to study pathogen biology and genetics. In a field where delayed action has profound consequences for livelihoods and food security, genome sequences provide us with essential tools to prepare for the emergence of new plant pathogens and future disease outbreaks. In this regard, the medical example provided by Bill Gates (Gates 2015) that the application of available technologies could significantly have reduced the impact of the recent Ebola epidemic also holds for plant

pathology. Particularly in the era of genomics, we have significant tools to deal with the plant disease arms race and we must apply them more actively and aggressively.

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Supplementary File 1: Ascomycota, Basidiomycota, and Early-diverging

Sequenced Ascomycota species

	Classification											Genome statistics						
SPECIES	**PHYLUM**	**SUBPHYLUM**	**CLASS**	**SUBCLASS**	**ORDER**	**FAMILY**	**Strain**	**GOLD Accession**	**GENOME Accession**	**NCBI Project ID**	**Significance**	**Size (Mb)**	**coverage**	**# of contigs**	**# of scaffolds**	**# genes**	**GC**	**Technology**
Cerataphis brasiliensis yeast-like sy	Ascomycota	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	not specified	Gp0039293	AOFP01	169168	arthropod associated (aphid symbiont)	25,5	39,00	11971	1181		56	Illumina HiSeq
Endocalyx cinctus	Ascomycota	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	JCM 7946	Gp0143759	BCKC01	313891	uncertain saprotroph	44,77	252,00	178	17		45,4	HiSeq 2500
Nilaparvata lugens yeast-like symbi	Ascomycota	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	not specified	Gp0076238	JRMI01	177649	uncertain	26,809	193,00	2794	578		55	454; Illumina
Aplosporella prunicola	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Aplosporellaceae	CBS 121167	Gp0019419	JGI	196034	probable tree pathogen	32,82	194	763	334	12579		
Aplosporella prunicola	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Aplosporellaceae	CBS 121167	Gp0019419	JGI	196034	probable tree pathogen	32,82	194,00	763	334	12579		
Botryosphaeria dothidea	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	CBS 115476	Gp0038455	AYEP01	81801	plant pathogen (broad host range of trees and shrubs)	43,5		3301	1711	14998		
Botryosphaeria dothidea	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	CBS 115476	Gp0038455	AYEP01	81801	plant pathogen (broad host range of trees and shrubs)	43,5		3301	1711	14998		
Diplodia pinea	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	CMW39103	Gp0093398	JHUM01	242796	plant pathogen (pines)	36,0534	10,00	2367			56,9	Illumina MiSeq
Diplodia pinea	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	CMW39103	Gp0093398	JHUM01	242796	plant pathogen (pines)	36,0534	10,00	2367			56,9	Illumina MiSeq
Diplodia scrobiculata	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	CMW30223	Gp0143864	LAEG01	278001	plant pathogen (conifer spp.)	34,93	15	4037	3772		57	Illumina MiSeq
Diplodia scrobiculata	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	CMW30223	Gp0143864	LAEG01	278001	plant pathogen (conifer spp.)	34,93	15,00	4037	3772		57	Illumina MiSeq
Diplodia seriata	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	DS831	Gp0117696	LAQI01	261773	plant pathogen (grapevine bot canker)	37,12	78,93	1522	694	9343	56,7	Illumina HiSeq
Diplodia seriata	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	DS831	Gp0117696	LAQI01	261773	plant pathogen (grapevine bot canker)	37,12	78,93	1522	694	9343	56,7	Illumina HiSeq
Guignardia citricarpa	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	CGMCC3.14348	Gp0041977	AOTE01	188924	plant pathogen (citrus)	32,007	300,00	6716			52,6	454; Illumina
Guignardia citricarpa	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	CGMCC3.14348	Gp0041977	AOTE01	188924	plant pathogen (citrus)	32,007	300,00	6716			52,6	454; Illumina
Macrophomina phaseolina	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	MS6	Gp0044758	AHHD01	78845	plant pathogen (broad host range)	48,882	66,00	1506		14712	52,3	454; Illumina
Macrophomina phaseolina	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	MS6	Gp0044758	AHHD01	78845	plant pathogen (broad host range)	48,882	66,00	1506		14712	52,3	454; Illumina
Neofusicoccum parvum	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	UCRNP2	Gp0039200	AORE01	187491	plant pathogen (grapevines)	42,59	100	1728	1297	10366	56,8	Illumina HiSeq
Neofusicoccum parvum	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Botryosphaeriaceae	UCRNP2	Gp0039200	AORE01	187491	plant pathogen (grapevines)	42,59	100,00	1728	1297	10366	56,8	Illumina HiSeq
Phyllosticta capitalensis	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Phyllostictaceae	Gm33		LOEO01	301361	endophyte; weak plant pathogen	32,45	70	1341			54,6	IonTorrent
Phyllosticta capitalensis	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Phyllostictaceae	Gm33		LOEO01	301361	endophyte; weak plant pathogen	32,45	70,00	1341			54,6	IonTorrent
Phyllosticta citricarpa	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Phyllostictaceae	Gc12	Gp0144687	LOEN01	301361	plant pathogen (citrus black spot)	31,13	75	5748			53,1	IonTorrent
Phyllosticta citricarpa	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Phyllostictaceae	Gc12	Gp0144687	LOEN01	301361	plant pathogen (citrus black spot)	31,13	75,00	5748			53,1	IonTorrent
Phyllosticta citriasiana	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Phyllostictaceae	CBS 120486	Gp0032376	1011300	243943	plant pathogen (citrus tan spot)	32,7	88,60	741	133	11368		Illumina
Saccharata proteae	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Saccharataceae	CBS 121410	Gp0033051	JGI	196072	endophyte; occasional *plant* pathogen	31,43	98,8	727	245	9234		Illumina HiSeq
Saccharata proteae	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Botryosphaeriales	Saccharataceae	CBS 121410	Gp0033051	JGI	196072	endophyte; occasional plant pathogen	31,43	98,80	727	245	9234		Illumina HiSeq
Polychaeton citri	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Capnodiaceae	CBS 116435	Gp0033215	JGI	196013	uncertain; mold (non-pathogenic sooty)	27,21	145,2	451	416	10582		Illumina HiSeq
Polychaeton citri	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Capnodiaceae	CBS 116435	Gp0033215	JGI	196013	uncertain; mold (non-pathogenic sooty)	27,21	145,2	451	416	10582		Illumina HiSeq
Cladosporium fulvum	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Cladosporiaceae	not specified		JGI		plant pathogen (leaf mold of tomato)	61,11		5382	4865	14127		
Cladosporium fulvum	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Cladosporiaceae	not specified		JGI		plant pathogen (leaf mold of tomato)	61,11		5382	4865	14127		
Cladosporium sphaerospermum	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Cladosporiaceae	UM 843	Gp0021025	AIIA02	85131	human allergen; dermatiaceous	26,89	98,00	877	155		56,6	Illumina
Cladosporium sphaerospermum	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Cladosporiaceae	UM 843	Gp0021025	AIIA02	85131	human allergen; dermatiaceous	26,89	98,00	877	155		56,6	Illumina
Dissoconium aciculare	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Dissoconiaceae	CBS 342.82	Gp0033050	JGI	196071	mycoparasitic (Erysiphaceae)	26,54	97,7	232	54	10299		Illumina
Dissoconium aciculare	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Dissoconiaceae	CBS 342.82	Gp0033050	JGI	196071	mycoparasitic (Erysiphaceae)	26,54	97,70	232	54	10299		Illumina
Pseudovirgaria hyperparasitica	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Incertae sedis	CBS 121739	Gp0072276	JGI	245627	biocontrol (mycoparasite of rust)	35,44	86,3	408	122	11232		Illumina
Pseudovirgaria hyperparasitica	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Incertae sedis	CBS 121739	Gp0072276	JGI	245627	biocontrol (mycoparasite of rust)	35,44	86,30	408	122	11232		Illumina
Cercospora canescens	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	BHU	Gp0037543	ANSM01	183604	plant pathogen (leaf spot of various bean crops and tomato)	33,96	12,00	8239			52	Illumina
Cercospora canescens	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	BHU	Gp0037543	ANSM01	183604	plant pathogen (leaf spot of various bean crops and tomato)	33,96	12,00	8239			52	Illumina
Cercospora zeae-maydis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	SC01	Gp0002172	JGI	68833	plant pathogen (maize); toxin-producing	46,61	39,29	2555	917	12020		
Cercospora zeae-maydis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	SC01	Gp0002172	JGI	68833	plant pathogen (maize); toxin-producing	46,61	39,29	2555	917	12020		
Lecanosticta acicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 871.95	Gp0047147	AWYC01	212329	plant pathogen (pine)	34,873	295,00	4114	2052		48,7	Illumina HiSeq
Lecanosticta acicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 871.95	Gp0047147	AWYC01	212329	plant pathogen (pine)	34,873	295,00	4114	2052		48,7	Illumina HiSeq
Mycosphaerella arachidis (Cercosp	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CALF-13A	Gp0150604	LIHB01	291633	plant pathogen (leaf spot on peanuts)	33,24	100,00	796	491		52,4	
Mycosphaerella eumusae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 114824	Gp0143045	LFZN01	289096	plant pathogen (banana)	47,12	165	2944	2626	12632	47,9	Illumina HiSeq
Mycosphaerella eumusae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 114824	Gp0143045	LFZN01	289096	plant pathogen (banana)	47,12	165,00	2944	2626	12632	47,9	Illumina HiSeq
Mycosphaerella fijiensis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CIRAD86	Gp0002650	JGI	19049	plant pathogen (leaf spot of banana)	74,14	7,11	778	56	13107	45,2	Sanger
Mycosphaerella fijiensis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CIRAD86	Gp0002650	JGI	19049	plant pathogen (leaf spot of banana)	74,14	7,11	778	56	13107	45,2	Sanger
Mycosphaerella laricina	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 326.52	Gp0047149	AWYE01	212505	plant pathogen (larch)	25,598	527,00	1307	642		52,5	Illumina HiSeq
Mycosphaerella laricina	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 326.52	Gp0047149	AWYE01	212505	plant pathogen (larch)	25,598	527,00	1307	642		52,5	Illumina HiSeq
Mycosphaerella pini	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	NZE10	Gp0017021	AIEN01	74753	plant pathogen (pine)	30,21	34,28	264	20	12580	53,1	Sanger; 454; Illumina
Mycosphaerella pini	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	NZE10	Gp0017021	AIEN01	74753	plant pathogen (pine)	30,21	34,28	264	20	12580	53,1	Sanger; 454; Illumina
Mycosphaerella sp. Ston1	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	STON1	Gp0045163	AWYF01	212506	poplar-associated	27,509	491,00	3346	1929		51,2	Illumina HiSeq
Mycosphaerella sp. Ston1	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	STON1	Gp0045163	AWYF01	212506	poplar-associated	27,509	491,00	3346	1929		51,2	Illumina HiSeq
Passalora (Cladosporium) fulva	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 131901	Gp0039398	AMRR01	86753	plant pathogen (tomato)	61,1	21,00	5714	4864		48,8	454
Pseudocercospora musae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 116634	Gp0143044	LFZO01	289098	plant pathogen (banana)	60,44	112	3640	3331	13129	44	Illumina HiSeq
Pseudocercospora musae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 116634	Gp0143044	LFZO01	289098	plant pathogen (banana)	60,44	112	3640	3331	13129	44	Illumina HiSeq
Pseudocercospora pini-densiflorae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 125139	Gp0047148	AWYD01	212512	animal pathogen (bats)	45,171	304,00	7359	5537		48,5	Illumina HiSeq
Pseudocercospora pini-densiflorae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	CBS 125139	Gp0047148	AWYD01	212512	animal pathogen (bats)	45,171	304,00	7359	5537		48,5	Illumina HiSeq
Sphaerulina musiva	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	SO2202	Gp0008704	AEFD01	51781	plant pathogen (poplar)	29,35	35,00	706	72	10233	51,1	454; Illumina
Sphaerulina musiva	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	SO2202	Gp0008704	AEFD01	51781	plant pathogen (poplar)	29,35	35	706	72	10233	51,1	454; Illumina
Sphaerulina populicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	P02.02b	Gp0048413	AIDU01	214559	plant pathogen (poplar)	33,188		2873	502		50,2	
Sphaerulina populicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	P02.02b	Gp0048413	AIDU01	214559	plant pathogen (poplar)	33,188		2873	502		50,2	
Zasmidium cellare	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	ATCC 36951	Gp0007071	JGI	207845	mold (wine cellar); uses volatile carbon sources (alcohol)	38,25	143,7	365	267	16015		
Zasmidium cellare	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	ATCC 36951	Gp0007071	JGI	207845	mold (wine cellar); uses volatile carbon sources (alcohol)	38,25	143,7	365	267	16015		
Zymoseptoria ardabiliae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	STIR04 1.1.2	Gp0010424	AFIV01	63043	plant pathogen (grasses); hemibiotroph	31,136	45,00	705			53,8	Illumina
Zymoseptoria ardabiliae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	STIR04 1.1.2	Gp0010424	AFIV01	63043	plant pathogen (grasses); hemibiotroph	31,136	45	705			53,8	Illumina
Zymoseptoria brevis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	ZB163	Gp0144861	JYJE01	274679	plant pathogen (bunchgrass)	36,1	88	11113	6895		51,2	Illumina HiSeq; MiSeq
Zymoseptoria brevis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	ZB163	Gp0144861	JYJE01	274679	plant pathogen (bunchgrass)	36,1	88	11113	6895		51,2	Illumina HiSeq; MiSeq
Zymoseptoria passerinii	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	P63	Gp0010309	AFIY01	63049	plant pathogen (barley leaf blotch)	28,786	45,00	1517			53,6	Illumina
Zymoseptoria passerinii	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	P63	Gp0010309	AFIY01	63049	plant pathogen (barley leaf blotch)	28,786	45	1517			53,6	Illumina
Zymoseptoria pseudotritici	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	STIR04 3.11.1	Gp0008224	AFIO01	46489	plant pathogen (grasses)	33,456	45,00	2408			53,4	Illumina
Zymoseptoria pseudotritici	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	STIR04 3.11.1	Gp0008224	AFIO01	46489	plant pathogen (grasses)	33,456	45	2408			53,4	Illumina
Zymoseptoria tritici	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	STIR04 A26b	Gp0010420	AFIP01	62705	plant pathogen (wheat leaf blotch)	32,641	45,00	1154		10964	52,1	Illumina
Zymoseptoria tritici	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Mycosphaerellaceae	STIR04 A26b	Gp0010420	AFIP01	62705	plant pathogen (wheat leaf blotch)	32,641	45	1154		10964	52,1	Illumina
Piedraia hortae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Piedraiaceae	CBS 480.64	Gp0024398	JGI	196052	opportunistic dermatophyte; keratinolytic	16,95	78,7	214	132	7572		Illumina
Piedraia hortae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Piedraiaceae	CBS 480.64	Gp0024398	JGI	196052	opportunistic dermatophyte; keratinolytic	16,95	78,7	214	132	7572		Illumina not publically available
Acidomyces richmondensis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Teratosphaeriaceae	BFW	Gp0017632	JGI	207869	acidophile	29,88	17,1	3164	3164	11202		
Acidomyces richmondensis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Teratosphaeriaceae	BFW	Gp0017632	JGI	207869	acidophile	29,88	17,1	3164	3164	11202		
Baudoinia compniacensis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Teratosphaeriaceae	UAMH 10762	Gp0016926	JGI	53579	extremophile	21,88	43,53	35	19	10513	54,8	454; Sanger; Illumina
Baudoinia compniacensis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Teratosphaeriaceae	UAMH 10762	Gp0016926	JGI	53579	extremophile	21,88	43,53	35	19	10513	54,8	454; Sanger; Illumina
Hortaea acidophila	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Teratosphaeriaceae	CBS 113389 v1.0		1040525		industrial importance (acid-tolerant black yeast)	20,43	100,7	59	39	9831		Illumina
Hortaea werneckii	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Teratosphaeriaceae	EXF-2000	Gp0039001	AIJO01	87027	halotolerant	51,647	70,00	12770	11193			Illumina GAIIx
Hortaea werneckii	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Teratosphaeriaceae	EXF-2000	Gp0039001	AIJO01	87027	halotolerant	51,647	70,00	12770	11193			Illumina GAIIx
Teratosphaeria nubilosa	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Teratosphaeriaceae	CBS 116005	Gp0036290	1019765	245625	plant pathogen (leaf spot of Eucalyptus)	28,44	146,3	320	273	10998		Illumina HiSeq
Aureobasidium melanogenum	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Dothideales	Dothideaceae	CBS 110374		JGI	207873	industrial importance	26,2	140,2	174	150	10594		Illumina
Aureobasidium melanogenum	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Dothideales	Dothideaceae	CBS 110374		JGI	207873	industrial importance	26,2	140,20	174	150	10594		Illumina
Aureobasidium namibiae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Dothideales	Dothideaceae	CBS 147.97		JGI	207872	uncertain	25,43	138,7	55	47	10266		Illumina
Aureobasidium namibiae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Dothideales	Dothideaceae	CBS 147.97		JGI	207872	uncertain	25,43	138,70	55	47	10266		Illumina
Aureobasidium pullulans	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Dothideales	Dothideaceae	AY4	Gp0039262	AMCU01	171022	industrial importance; opportunistic pathogen; endophyte	26,7	46,00	515		11844	50	Illumina GAIIx
Aureobasidium pullulans	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Dothideales	Dothideaceae	AY4	Gp0039262	AMCU01	171022	industrial importance; opportunistic pathogen; endophyte	26,7	46	515		11844	50	Illumina GAIIx
Aureobasidium subglaciale	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Dothideales	Dothideaceae	EXF-2481		AYYB01	161477	uncertain	25,79	814,00	85	75	10792	50,8	Illumina
Aureobasidium subglaciale	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Dothideales	Dothideaceae	EXF-2481		AYYB01	161477	uncertain	25,79	814	85	75	10792	50,8	Illumina
Hysterium pulicare	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Hysteriales	Hysteriaceae	CBS 123377	Gp0038492	AJFK01	81797	saprotroph	37,8	75	5425	2010	10200	48,8	Illumina GAII
Hysterium pulicare	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Hysteriales	Hysteriaceae	CBS 123377	Gp0038492	AJFK01	81797	saprotroph	37,8	75,00	5425	2010	10200	48,8	Illumina GAII
Lepidopterella palustris	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Incertae sedis	Argynnaceae	CBS 459.81	Gp0033495	JGI	196014	saprotroph (freshwater)	45,67	133,8	3529	3371	13870		Illumina HiSeq
Lepidopterella palustris	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Incertae sedis	Argynnaceae	CBS 459.81	Gp0033495	JGI	196014	saprotroph (freshwater)	45,67	133,80	3529	3371	13870		Illumina HiSeq
Aulographum hederae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Incertae sedis	Aulographaceae	CBS 113979	Gp0019269	JGI	195869	saprotroph (plant)	31,98	116	613	173	12127		Illumina HiSeq
Aulographum hederae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Incertae sedis	Aulographaceae	CBS 113979	Gp0019269	JGI	195869	saprotroph (plant)	31,98	116,00	613	173	12127		Illumina HiSeq

Eremomyces bilateralis	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Incertae sedis	Eremomycetaceae	CBS 781.70	Gp0033623	1011349	217190	uncertain	26,86	91,10	321	95	9881		Illumina HiSeq	
Cryomyces antarcticus	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Incertae sedis	Incertae sedis	CCFEE 534	Gp0076232	AYQD01	222806	rock-inhabiting; stress-tolerant	24,32	108,00	12491			53,9	Ion Torrent	
Cryomyces antarcticus	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Incertae sedis	Incertae sedis	CCFEE 534	Gp0076232	AYQD01	222806	rock-inhabiting; stress-tolerant	24,32	108,00	12491			53,9	Ion Torrent	
Peltaster fructicola	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Incertae sedis	Incertae sedis	LNHT1506	Gp0143846	LJAO01	293964	plant pathogen (apples)	19,02	253	16	14		51,9		
Peltaster fructicola	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Incertae sedis	Incertae sedis	LNHT1506	Gp0143846	LJAO01	293964	plant pathogen (apples)	19,02	253	16	14		51,9		
Lizonia empirigonia	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Incertae sedis	Pseudoperisporiaceae	CBS 542.76 v1.0	Gp0036392	1019757	245629	uncertain	51,52	21,6	423	423	12467		PacBio	
Lizonia empirigonia	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Incertae sedis	Pseudoperisporiaceae	CBS 542.76 v1.0	Gp0036392	1019757	245629	uncertain	51,52	21,6	423	423	12467		PacBio	
Microthyrium microscopicum	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Microthyriales	Microthyriaceae	CBS 115976	Gp0033175	1011369	234668	saprotroph	37,12	72,9	265	58	12494		Illumina HiSeq	
Microthyrium microscopicum	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Microthyriales	Microthyriaceae	CBS 115976	Gp0033175	1011369	234668	saprotroph	37,12	72,90	265	58	12494		Illumina HiSeq	
Myriangium duriaei	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Myriangiales	Myriangiaceae	CBS 260.36	Gp0019337	JGI	196043	parasite (insect)	25,69	97,70	32	16	10685		Illumina HiSeq	
Myriangium duriaei	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Myriangiales	Myriangiaceae	CBS 260.36	Gp0019337	JGI	196043	parasite (insect)	25,69	97,70	32	16	10685		Illumina HiSeq	
Cenococcum geophilum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Mytilinidiales	Gloniaceae		1,58	Gp0006117	JGI	196023	ectomycorrhizal	177,57	75	2893	268	27529		Illumina HiSeq	
Cenococcum geophilum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Mytilinidiales	Gloniaceae		1,58	Gp0006117	JGI	196023	ectomycorrhizal	177,57	75,00	2893	268	27529		Illumina HiSeq	
Lophium mytilinum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Mytilinidiales	Mytilinidiaceae	CBS 269.34	Gp0036355	JGI	234407	uncertain	43,41	74,4	286	49	15153		Illumina HiSeq	
Lophium mytilinum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Mytilinidiales	Mytilinidiaceae	CBS 269.34	Gp0036355	JGI	234407	uncertain	43,41	74,40	286	49	15153		Illumina HiSeq	
Patellaria atrata	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Patellariales	Patellariaceae	CBS 101060	Gp0019408	JGI	208393	saprotroph	28,69	192,4	501	127	9794		Illumina HiSeq	
Patellaria atrata	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Patellariales	Patellariaceae	CBS 101060	Gp0019408	JGI	208393	saprotroph	28,69	192,4	501	127	9794		Illumina HiSeq	
Rhizodiscina lignyota	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Patellariales	Patellariaceae	CBS 133067	Gp0036565	1019729	263052	mycobiont (lichen-forming)	33,43	95,90	43	33	12801		Illumina HiSeq	
Rhytidhysteron rufulum	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Patellariales	Patellariaceae	CBS 306.38	Gp0038493	AJFL01	81799	saprotroph (mainly); occasionaly plant pathogen	40,18	109,00	4455	3308	12117	47,9	Illumina GAII	
Rhytidhysteron rufulum	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Patellariales	Patellariaceae	CBS 306.38	Gp0038493	AJFL01	81799	saprotroph (mainly); occasionaly plant pathogen	40,18	109	4455	3308	12117	47,9	Illumina GAII	
Amniculicola lignicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Amniculicolaceae	CBS 123094	Gp0033118	JGI	217192	saprotroph	49,58	99	1274	510	15590		Illumina HiSeq	
Amniculicola lignicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Amniculicolaceae	CBS 123094	Gp0033118	JGI	217192	saprotroph	49,58	99,00	1274	510	15590		Illumina HiSeq	
Nigrograna mackinnonii	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Biatriosporaceae	E5202H	Gp0039092	JGVQ01	187080	endophyte (root)	51,71	272	425			47,9	Illumina HiSeq	
Corynespora cassicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Corynesporascaceae	UM 591	Gp0086748	JAQF01	250634	plant pathogen (broad host range)	41,385	118,00	1941		17166	52,5	Illumina HiSeq	
Corynespora cassicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Corynesporascaceae	UM 591	Gp0086748	JAQF01	250634	plant pathogen (broad host range)	41,385	118	1941		17166	52,5	Illumina HiSeq	
Cucurbitaria berberidis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Cucurbitariaceae	CBS 394.84	Gp0019330	JGI	196042	saprotroph	32,91	145,7	184	42	12439		Illumina HiSeq	
Cucurbitaria berberidis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Cucurbitariaceae	CBS 394.84	Gp0019330	JGI	196042	saprotroph	32,91	145,7	184	42	12439		Illumina HiSeq	
Delitschia confertaspora	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Delitschiaceae	ATCC 74209	Gp0039185	JGI	251766	coprophilous	31,16	74,9	822	764	10171		Illumina HiSeq	
Delitschia confertaspora	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Delitschiaceae	ATCC 74209	Gp0039185	JGI	251766	coprophilous	31,16	74,9	822	764	10171		Illumina HiSeq	
Clathrospora elynae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Diademaceae	CBS 161.51	Gp0036331	JGI	245624	uncertain	37,39	80,8	1994	617	13617		Illumina HiSeq	
Clathrospora elynae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Diademaceae	CBS 161.51	Gp0036331	JGI	245624	uncertain	37,39	80,8	1994	617	13617		Illumina HiSeq	
Ascochyta rabiei	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Didymellaceae	ArDII	Gp0150874	JYNV01	272665	plant pathogen (blight on chickpea)	34,66	178	932	338	10596	50,7	Illumina	
Didymella exigua	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymellaceae	CBS 183.55	Gp0019438	JGI	207857	saprotroph	34,39	82,1	1010	176	12394		Illumina	
Didymella exigua	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymellaceae	CBS 183.55	Gp0019438	JGI	207857	saprotroph	34,39	82,1	1010	176	12394		Illumina	
Macroventuria anomochaeta	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymellaceae	CBS 525.71	Gp0036390	JGI	234398	saprotroph	33,34	116,6	346	75	12954		Illumina HiSeq	
Macroventuria anomochaeta	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymellaceae	CBS 525.71	Gp0036390	JGI	234398	saprotroph	33,34	116,6	346	75	12954		Illumina HiSeq	
Phoma herbarum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymellaceae	JCM 15942	Gp0144010	BCGR01	313796	plant pathogen (hop & hemp)	39,26	462				51,7	HiSeq 2500	
Phoma herbarum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymellaceae	JCM 15942	Gp0144010	BCGR01	313796	plant pathogen (hop & hemp)	39,26	462				51,7	HiSeq 2500	
Stagonosporopsis tanaceti	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymellaceae	Pooled DNA	Gp0146030	JUDZ01	268685	plant pathogen (Asteraceae)	40,1	140	9716			52,3	Illumina	
Stagonosporopsis tanaceti	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymellaceae	Pooled DNA	Gp0146030	JUDZ01	268685	plant pathogen (Asteraceae)	40,1	140	9716			52,3	Illumina	
Karstenula rhodostoma	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymosphaeriaceae	CBS 690.94	Gp0036420	JGI	217209	saprotroph	45,07	121	498	139	15043		Illumina HiSeq	
Karstenula rhodostoma	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymosphaeriaceae	CBS 690.94	Gp0036420	JGI	217209	saprotroph	45,07	121,00	498	139	15043		Illumina HiSeq	
Verruculina enalia	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymosphaeriaceae	CBS 304.66	Gp0036357	JGI	239483	marine fungus; mangrove-associated	61,21	81,2	1600	611	13748		Illumina HiSeq	
Verruculina enalia	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Didymosphaeriaceae	CBS 304.66	Gp0036357	JGI	239483	marine fungus; mangrove-associated	61,21	81,20	1600	611	13748		Illumina HiSeq	
Dothidotthia symphoricarpi	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Dothidotthiaceae	CBS 119687	Gp0033174	JGI	217191	saprotroph	34,43	93,4	268	59	11790		Illumina HiSeq	
Dothidotthia symphoricarpi	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Dothidotthiaceae	CBS 119687	Gp0033174	JGI	217191	saprotroph	34,43	93,40	268	59	11790		Illumina HiSeq	
Lineolata rhizophorae	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Fenestellaceae	ATCC 16933 v1.0		1051209		marine fungus	31,14	97,8	426	68	10230		Illumina	
Aaosphaeria arxii	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Incertae sedis	CBS 175.79	Gp0036559	JGI	234399	uncertain	38,9	86,5	176	55	14203		Illumina HiSeq	
Aaosphaeria arxii	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Incertae sedis	CBS 175.79	Gp0036559	JGI	234399	uncertain	38,9	86,50	176	55	14203		Illumina HiSeq	
Periconia macrospinosa	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Incertae sedis	DSE2036	Gp0046570	1025594	243955	endophyte (root)	54,99	139,40	2470	1566	18750			
Trinosporium guianense	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Incertae sedis	CBS132537	Gp0095856	1040180	255619	uncertain; environmental contaminant	24,23	140,90	298	23600,00%	8062		Illumina HiSeq	
Lentithecium fluviatile	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Lentitheciaceae	CBS 122367	Gp0019312	JGI	196040	saprotroph (freshwater)	54,69	85,4	2078	195	16742		Illumina HiSeq	
Lentithecium fluviatile	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Lentitheciaceae	CBS 122367	Gp0019312	JGI	196040	saprotroph (freshwater)	54,69	85,40	2078	195	16742		Illumina HiSeq	
Leptosphaeria maculans	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Leptosphaeriaceae	JN3	Gp0010336	ASM23037	63129	plant pathogen (Brassica crops)	45,124		76		12469	45,3		
Leptosphaeria maculans	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Leptosphaeriaceae	JN3	Gp0010336	ASM23037	63129	plant pathogen (Brassica crops)	45,124		76		12469	45,3		
Ophiobolus disseminans	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Leptosphaeriaceae	CBS 113818	Gp0036265	JGI	239491	uncertain; isolated from poisonous Mercurialis perennis	41,68	97,1	408	72	16027		Illumina HiSeq	
Ophiobolus disseminans	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Leptosphaeriaceae	CBS 113818	Gp0036265	JGI	239491	uncertain; isolated from poisonous Mercurialis perennis	41,68	97,10	408	72	16027		Illumina HiSeq	
Plenodomus tracheiphilus	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Leptosphaeriaceae	IPT5	Gp0039845	JGI	223133	plant pathogen (citrus)	34,24	98,6	431	273	13209		Illumina HiSeq	
Plenodomus tracheiphilus	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Leptosphaeriaceae	IPT5	Gp0039845	JGI	223133	plant pathogen (citrus)	34,24	98,6	431	273	13209		Illumina HiSeq	
Lophiostoma macrostomum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Lophiostomataceae	CBS 122681	Gp0033112	JGI	196073	saprotroph	42,58	140,3	1294	1282	16160		Illumina HiSeq	
Lophiostoma macrostomum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Lophiostomataceae	CBS 122681	Gp0033112	JGI	196073	saprotroph	42,58	140,30	1294	1282	16160		Illumina HiSeq	
Lophiotrema nucula	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Lophiostomataceae	CBS 627.86	Go0036416	1019701	333967	uncertain	48,64	138,80	251	187	18117		Illumina	
Byssothecium circinans	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Massarinaceae	CBS 675.92	Gp0036418	JGI	239485	saprotroph	49,29	96,3	1506	160	15785		Illumina HiSeq	
Byssothecium circinans	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Massarinaceae	CBS 675.92	Gp0036418	JGI	239485	saprotroph	49,29	96,3	1506	160	15785		Illumina HiSeq	
Helminthosporium solani	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Massarinaceae	B-AC-16A	Gp0047673	AWWW01	219149	plant pathogen (potato)	34,513	50,00	5686			49,1	454; Illumina HiSeq	
Helminthosporium solani	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Massarinaceae	B-AC-16A	Gp0047673	AWWW01	219149	plant pathogen (potato)	34,513	50,00	5686			49,1	454; Illumina HiSeq	
Massarina eburnea	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Massarinaceae	CBS 473.64	Gp0033455	1011361	217519	uncertain	38,24	56,80	1105	233	12935		Illumina HiSeq	
Beverwykella pulmonaria	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Melanommataceae	JCM 9230	Gp0144040	BCHH01	313810	saprotroph	45,97	111	666	50		48,2	HiSeq 2500	
Beverwykella pulmonaria	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Melanommataceae	JCM 9230	Gp0144040	BCHH01	313810	saprotroph	45,97	111,00	666	50		48,2	HiSeq 2500	
Melanomma pulvis-pyrius	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Melanommataceae	CBS 109.77	Gp0032998	JGI	196087	saprotroph	42,09	119,3	1771	1754	15881		Illumina HiSeq	
Melanomma pulvis-pyrius	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Melanommataceae	CBS 109.77	Gp0032998	JGI	196087	saprotroph	42,09	119,30	1771	1754	15881		Illumina HiSeq	
Bimuria novae-zelandiae	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Montagnulaceae	CBS 107.79 v1.0	Gp0036259	1019717	234400	parasite; lichenicolous	78,18	62,30	1338	321	16681		Illumina	
Paraconiothyrium sporulosum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Montagnulaceae	AP3s5-JAC2a	Gp0050663	1029422	239489	manganese(II)-oxidizing; saprotroph (soil)	38,46	118,90	339	61	14745		Illumina HiSeq	
Parastagonospora nodorum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Phaeosphaeriaceae	SN15	Gp0002465	AAGI01	13754	plant pathogen (wheat)	37,21	10,00	494	108	12380	50	Sanger	
Parastagonospora nodorum	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Phaeosphaeriaceae	SN15	Gp0002465	AAGI01	13754	plant pathogen (wheat)	37,21	10,00	494	108	12380	50	Sanger	
Phaeosphaeriaceae sp.	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Phaeosphaeriaceae	PMI808	Gp0039952	1021562	251767	uncertain	56,37	148,72	591	591	15864			
Setomelanomma holmii	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Phaeosphaeriaceae	CBS 110217 v1.0	Gp0036261	1019737	245746	plant pathogen (spruce needle drop)	39,18	109,5	651	557	14389		Illumina	
Setomelanomma holmii	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Phaeosphaeriaceae	CBS 110217 v1.0	Gp0036261	1019737	245746	plant pathogen (spruce needle drop)	39,18	109,50	651	557	14389		Illumina	
Stagonospora sp. SRC1lsM3a	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Phaeosphaeriaceae	SRC1lsM3a	Gp0050685	1029438	255590	Mn(II)-oxidizing; mineral cycling	36,08	87,50	120	44	14430			
Trichodelitschia bisporula	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Phaeotrichaceae	CBS 262.69	Gp0036337	1019741	245628	coprophilous	25,79	85,50	253	44	10181		Illumina HiSeq	
Pleomassaria siparia	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleomassariaceae	CBS 279.74	Gp0032996	JGI	196086	saprotroph	43,18	87,3	1023	193	13486		Illumina HiSeq	
Pleomassaria siparia	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleomassariaceae	CBS 279.74	Gp0032996	JGI	196086	saprotroph	43,18	87,30	1023	193	13486		Illumina HiSeq	
Alternaria alternata	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	SRC1lrK2f	Gp0047507	1029429	239482	plant pathogen (leaf spot; broad host range)	32,99	147,10	86	79	13469		Illumina HiSeq	
Alternaria arborescens	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	EGS 39-128	Gp0038059	AIIC01	78243	plant pathogen (tomato)	33,9	90	820				Illumina GA II	
Alternaria arborescens	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	EGS 39-128	Gp0038059	AIIC01	78243	plant pathogen (tomato)	33,9	90,00	820				Illumina GA II	
Alternaria brassicicola	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	ATCC 96866	Gp0002466	ACIW01	34523	plant pathogen (Brassica dark leaf spot)	29,5	6,4	3280					
Alternaria brassicicola	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	ATCC 96866	Gp0002466	ACIW01	34523	plant pathogen (Brassica dark leaf spot)	29,5	6,40	3280					
Bipolaris maydis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	C5	Gp0003183	AIHU01	83117	plant pathogen (wheat)	36,46	67,50	88	68	13456	49,8	Illumina	not publically released
Bipolaris maydis	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	C5	Gp0003183	AIHU01	83117	plant pathogen (wheat)	36,46	67,5	88	68	13456	49,8	Illumina	
Bipolaris oryzae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	WK-1C, ATCC 44560	Gp0010035	AMCO01	160935	plant pathogen (rice)	31,36	191,00	667	619	12007	50,5	Illumina	
Bipolaris oryzae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	WK-1C, ATCC 44560	Gp0010035	AMCO01	160935	plant pathogen (rice)	31,36	191	667	619	12007	50,5	Illumina	
Bipolaris sorokiniana	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	ND90Pr	Gp0004797	AEIN01	87041	plant pathogen (cereals)	34,41	42,43	478	157	12250	49,8	454; Sanger; Illumina	
Bipolaris sorokiniana	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	ND90Pr	Gp0004797	AEIN01	87041	plant pathogen (cereals)	34,41	42,43	478	157	12250	49,8	454; Sanger; Illumina	
Bipolaris victoriae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	FI3	Gp0010034	AMCY01	160941	plant pathogen (blight of oats)	32,8	304	709	676	12882	50,1	Illumina	
Bipolaris victoriae	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	FI3	Gp0010034	AMCY01	160941	plant pathogen (blight of oats)	32,8	304	709	676	12882	50,1	Illumina	
Bipolaris zeicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	26-R-13	Gp0010036	AMCN01	160939	plant pathogen (sorghum, maize and apple)	31,27	200	882	844	12857	50,8	Illumina	
Bipolaris zeicola	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	26-R-13	Gp0010036	AMCN01	160939	plant pathogen (sorghum, maize and apple)	31,27	200,00	882	844	12857	50,8	Illumina	
Cochliobolus lunatus	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	CX-3	Gp0039341	JGI	182303	plant pathogen (sorghum); pharmaceutical importance	31,17	129,5	240	171	12131		Illumina HiSeq	
Cochliobolus lunatus	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	CX-3	Gp0039341	JGI	182303	plant pathogen (sorghum); pharmaceutical importance	31,17	129,50	240	171	12131		Illumina HiSeq	
Curvularia papendorfii	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	UM 226	Gp0117671	JXCC01	271317	opportunistic human pathogen; rare	33,38	121	374			50,6	Illumina HiSeq; PacBio	
Curvularia papendorfii	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	UM 226	Gp0117671	JXCC01	271317	opportunistic human pathogen; rare	33,38	121,00	374			50,6	Illumina HiSeq; PacBio	

Decorospora gaudefroyi	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	CBS 332.63		1032355		marine saprotroph	30,56	152,6	879	699	11835		Illumina		
Decorospora gaudefroyi	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Pleosporales	Pleosporaceae	CBS 332.63		1032355		marine saprotroph	30,56	152,60	879	699	11835		Illumina		
Pyrenochaeta lycopersici	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	CRA-PAV_ER 1211	Gp0090025	ASRS01	202288	plant pathogen (tomato)	50,489	300,00	12392	7018		47,7	Illumina GAIIx		
Pyrenochaeta lycopersici	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	CRA-PAV_ER 1211	Gp0090025	ASRS01	202288	plant pathogen (tomato)	50,489	300,00	12392	7018		47,7	Illumina GAIIx		
Pyrenochaeta sp. DS3sAY3a	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	DS3sAY3a	Gp0050683	JGI	255591	Mn(II)-oxidizing; mineral cycling	38,5	86,7	209	69	14995		Illumina HiSeq		
Pyrenochaeta sp. DS3sAY3a	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	DS3sAY3a	Gp0050683	JGI	255591	Mn(II)-oxidizing; mineral cycling	38,5	86,70	209	69	14995		Illumina HiSeq		
Pyrenochaeta sp. UM 256	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	UM 256	Gp0039028	AOUM01	189754	human pathogen	35,484	27,00	286	254		50,4		454	
Pyrenochaeta sp. UM 256	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	UM 256	Gp0039028	AOUM01	189754	human pathogen	35,484	27,00	286	254		50,4		454	
Pyrenophora seminiperda	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	CCB06	Gp0037221	ATLS01	192591	plant pathogen (necrotrophic; seeds of grasses/cereals)	32,539	17,00	660	54		49,8		454	
Pyrenophora seminiperda	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	CCB06	Gp0037221	ATLS01	192591	plant pathogen (necrotrophic; seeds of grasses/cereals)	32,539	17,00	660	54		49,8		454	
Pyrenophora teres	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	0-1	Gp0008318	AEEY01	50389	plant pathogen (barley and some other crops)	33,583	20,00	6684	6412	11799	50,9	Illumina		
Pyrenophora teres	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	0-1	Gp0008318	AEEY01	50389	plant pathogen (barley and some other crops)	33,583	20,00	6684	6412	11799	50,9	Illumina		
Pyrenophora tritici-repentis	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	Pt-1C-BFP	Gp0003140	AAXI01	18815	plant pathogen (cereals and grasses; necrotrophic)	37,997	6,93	48		12300	51	Sanger		
Pyrenophora tritici-repentis	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	Pt-1C-BFP	Gp0003140	AAXI01	18815	plant pathogen (cereals and grasses; necrotrophic)	37,997	6,93	48		12300	51	Sanger		
Setosphaeria turcica	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	Et28A	Gp0008856	AIHT01	82947	plant pathogen (maize)	43,01	58,10	1959	407	11702	51,4	454; Sanger; Illumina		
Setosphaeria turcica	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	Et28A	Gp0008856	AIHT01	82947	plant pathogen (maize)	43,01	58,10	1959	407	11702	51,4	454; Sanger; Illumina		
Stemphylium lycopersici	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	CIDEFI 216	Gp0118324	LGLR01	274742	plant pathogen (fruits)	35,17	77,39	5130	414	8997	50,7	Illumina HiSeq		
Stemphylium lycopersici	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Pleosporaceae	CIDEFI 216	Gp0118324	LGLR01	274742	plant pathogen (fruits)	35,17	77,39	5130	414	8997	50,7	Illumina HiSeq		
Shiraia sp. slf14	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Shiraiaceae	Slf14	Gp0071001	AXZN01	222884	endophyte	32,067	55,00	288			48	Illumina HiSeq		
Shiraia sp. slf14	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Shiraiaceae	Slf14	Gp0071001	AXZN01	222884	endophyte	32,067	55,00	288			48	Illumina HiSeq		
Sporormia fimetaria	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Sporormiaceae	CBS 119925	Gp0033217	JGI	205956	coprophilous	25,89	104	293	140	10783		Illumina HiSeq		
Sporormia fimetaria	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Sporormiaceae	CBS 119925	Gp0033217	JGI	205956	coprophilous	25,89	104	293	140	10783		Illumina HiSeq		
Westerdykella ornata	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Sporormiaceae	CBS 379.55	Gp0036361	JGI	245619	pharmaceutical importance (antibiotic-producing)	26,98	162,1	180	94	10410		Illumina HiSeq		
Westerdykella ornata	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Sporormiaceae	CBS 379.55	Gp0036361	JGI	245619	pharmaceutical importance (antibiotic-producing)	26,98	162,1	180	94	10410		Illumina HiSeq		
Polyplosphaeria fusca	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Tetraplosphaeriaceae	CBS 125425	Gp0036310	JGI	245626	bambusicolous	37,01	151	593	468	15194		Illumina HiSeq		
Polyplosphaeria fusca	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Tetraplosphaeriaceae	CBS 125425	Gp0036310	JGI	245626	bambusicolous	37,01	151	593	468	15194		Illumina HiSeq		
Trematosphaeria pertusa	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Trematosphaeriaceae	CBS 122368	Gp0036292	JGI	234397	saprotroph (freshwater)	47,75	96,4	675	101	17306		Illumina HiSeq		
Trematosphaeria pertusa	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Trematosphaeriaceae	CBS 122368	Gp0036292	JGI	234397	saprotroph (freshwater)	47,75	96,4	675	101	17306		Illumina HiSeq		
Pleosporales sp. UM 1110 2012	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	unknown	UM 1110	Gp0039009	AJMS01	89471	uncertain	36,919	100,00	11436			51,4	Illumina GAIIx		
Pleosporales sp. UM 1110 2012	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	unknown	UM 1110	Gp0039009	AJMS01	89471	uncertain	36,919	100	11436			51,4	Illumina GAIIx		
Zopfia rhizophila	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Zopfiaceae	CBS 207.26	Gp0024306	JGI	196051	opportunistic root rot	152,78	95,5	1349	864	21730		Illumina HiSeq; PacBio		
Zopfia rhizophila	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Zopfiaceae	CBS 207.26	Gp0024306	JGI	196051	opportunistic root rot	152,78	95,5	1349	864	21730		Illumina HiSeq; PacBio		
Lineolata rhizophorae	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Fenestellaceae	ATCC 16933 v1.0		1051209		marine fungus	31,14	97,8	426	68	10230		Illumina		
Trypethelium eluteriae	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Trypetheliales	Trypetheliaceae	not specified		JGI		mycobiont (lichen-forming)	32,16	142,1	747	730	11858		Illumina		
Trypethelium eluteriae	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Trypetheliales	Trypetheliaceae	not specified		JGI		mycobiont (lichen-forming)	32,16	142,10	747	730	11858		Illumina		
Ochroconis constricta	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Venturiales	Sympoventuriaceae	UM 578	Gp0076216	AZYM01	232808	animal pathogen; opportunistic human pathogen	34,434	87,00	544			52,1	Illumina HiSeq		
Ochroconis constricta	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Venturiales	Sympoventuriaceae	UM 578	Gp0076216	AZYM01	232808	animal pathogen; opportunistic human pathogen	34,434	87	544			52,1	Illumina HiSeq		
Verruconis gallopava	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Venturiales	Sympoventuriaceae	CBS 43764		JYBX01	325802	medical importance (black yeast)	31,78	145	565	367	11357		Illumina		
Tothia fuscella	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Venturiales	Venturiaceae	CBS 130266	Gp0036563		245630	uncertain	36,78	146,8	687	363	13685		Illumina HiSeq		
Tothia fuscella	Ascomycota	Pezizomycotina	Dothideomycetes	Incertae sedis	Venturiales	Venturiaceae	CBS 130266	Gp0036563		245630	uncertain	36,78	146,8	687	363	13685		Illumina HiSeq		
Venturia pyrina	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Venturiales	Venturiaceae	ICMP 11032	Gp0095335	JEMP01	232087	plant pathogen (hemibiotrophic; pear)	41,177	40,00	2308			47,6	Illumina GAIIx		
Venturia pyrina	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Venturiales	Venturiaceae	ICMP 11032	Gp0095335	JEMP01	232087	plant pathogen (hemibiotrophic; pear)	41,177	40	2308			47,6	Illumina GAIIx		
Hortaea acidophila	Ascomycota	Pezizomycotina	Dothideomycetes	Dothideomycetidae	Capnodiales	Teratosphaeriaceae	CBS 113389 v1.0		1040525		industrial importance (acid-tolerant black yeast)	20,43	100,7	59	39	9831		Illumina		
Bimuria novae-zelandiae	Ascomycota	Pezizomycotina	Dothideomycetes	Pleosporomycetidae	Pleosporales	Montagnulaceae	CBS 107.79 v1.0		1019717		parasite; lichenicolous	78,18	62,3	1338	321	16681		Illumina		
Rhizodiscina lignyota	Ascomycota	Pezizomycotina	Dothidiomycetes	Incertae sedis	Patellariales	Patellariaceae	CBS 133067	Gp0036565	1019729	263052	mycobiont (lichen-forming)	33,43	95,9	43	33	12801		Illumina HiSeq		
Ascosphaera apis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Ascosphaerales	Ascosphaeraceae	USDA-ARSEF 7405	Gp0002467	AARE01	17285	animal pathogen (honey bees)	21,5	4	6559	1667			Sanger		
Ascosphaera apis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Ascosphaerales	Ascosphaeraceae	USDA-ARSEF 7405	Gp0002467	AARE01	17285	animal pathogen (honey bees)	21,5	4,00	6559	1667			Sanger		
Cyphellophora europaea	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Cyphellophoraceae	CBS 101466		AOBU01	172438	human pathogen (superficial infection); dermatiaceous	28,7813	132,00	106	19	11153	54	Illumina		
Cyphellophora europaea	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Cyphellophoraceae	CBS 101466		AOBU01	172438	human pathogen (superficial infection); dermatiaceous	28,7813	132	106	19	11153	54	Illumina		
Capronia coronata	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 617.96	Gp0037646	AMWN01	164585; Broad	saprotroph; possible beetle associate; black yeast	25,8	90,00	52		9231	52,8			
Capronia coronata	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 617.96	Gp0037646	AMWN01	164585; Broad	saprotroph; possible beetle associate; black yeast	25,8	90	52		9231	52,8			
Capronia epimyces	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 606.96	Gp0037042; Broad	AMGY01	164587	uncertain; yeast (black)	28,9	83,00	231		10469	53,4			
Capronia epimyces	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 606.96	Gp0037042; Broad	AMGY01	164587	uncertain; yeast (black)	28,9	83	231		10469	53,4			
Capronia semiimmersa	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS27337	Go0076064	JYCC01	325795	medical importance (black yeast)	31,62	87	73	13	11909		Illumina		
Cladophialophora bantiana	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 173.52	Go0076062	JYBT01	233316	medical importance (black yeast)	36,72	122	140	60	12762		Illumina		
Cladophialophora carrionii	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 160.54	Gp0037643	AOFF01	185784	human pathogen (chromoblastomycosis); dermatiaceous	28,99	80,00	102	19	10428	54,3	Illumina		
Cladophialophora carrionii	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 160.54	Gp0037643	AOFF01	185784	human pathogen (chromoblastomycosis); dermatiaceous	28,99	80,00	102	19	10428	54,3	Illumina		
Cladophialophora immunda	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 110551	Gp0117567	JSEJ01	264781	industrial importance (black yeast; bioremediation; degrades polyaromatic	41,58	318	464		12879	52,8	IonTorrent		
Cladophialophora immunda	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 110551	Gp0117567	JSEJ01	264781	industrial importance (black yeast; bioremediation; degrades polyaromatic h	41,58	318,00	464		12879	52,8	IonTorrent		
Cladophialophora psammophila	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 110553	Gp0037823	AMGX01	164589	industrial importance (bioremediation)	39,42	133,00	317		13421	50,6	Illumina		
Cladophialophora psammophila	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 110553	Gp0037823	AMGX01	164589	industrial importance (bioremediation)	39,42	133,00	317		13421	50,6	Illumina		
Cladophialophora yegresii	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 114405	Gp0037865	AMGW01	164591	endophyte (cactus); dermatiaceous; potential human pathogen	27,89	132,00	63		10118	54	Illumina		
Cladophialophora yegresii	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 114405	Gp0037865	AMGW01	164591	endophyte (cactus); dermatiaceous; potential human pathogen	27,89	132,00	63		10118	54	Illumina		
Coniosporium apollinis	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 352.97	Gp0037641	AJKL01	157061	rock-inhabiting black yeast	28,64	128,00	241	169	9367	52,1	Illumina		
Coniosporium apollinis	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 352.97	Gp0037641	AJKL01	157061	rock-inhabiting black yeast	28,64	128	241	169	9367	52,1	Illumina		
Exophiala alcalophila	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	JCM 1751	Gp0144016	BCHY01	313825	black yeast; soil-associated	29,85	209	85	12		54,1	HiSeq 2500		
Exophiala alcalophila	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	JCM 1751	Gp0144016	BCHY01	313825	black yeast; soil-associated	29,85	209	85	12		54,1	HiSeq 2500		
Exophiala aquamarina	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 119918	Gp0037642	AMGV01	164593	animal pathogen (marine)	41,566	79,00	687	151	13118	49	Illumina		
Exophiala aquamarina	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 119918	Gp0037642	AMGV01	164593	animal pathogen (marine)	41,566	79	687	151	13118	49	Illumina		
Exophiala calicioides	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	JCM 6030	Gp0144033	BCHZ01	313826	insect-associated (bark beetles)	36,37	153	124	37		52,8	HiSeq 2500		
Exophiala calicioides	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	JCM 6030	Gp0144033	BCHZ01	313826	insect-associated (bark beetles)	36,37	153,00	124	37		52,8	HiSeq 2500		
Exophiala dermatitidis	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	NIH 8656	Gp0010413	AFPA01	64935	human pathogen (rare); thermophilic	26,37	151,60	239	11	9356	51,5	Illumina		not publically released
Exophiala dermatitidis	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	NIH 8656	Gp0010413	AFPA01	64935	human pathogen (rare); thermophilic	26,37	151,60	239	11	9356	51,5	Illumina		
Exophiala mesophila	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 120910	Gp0117764	JSEI01	264779	industrual importance (bioremediation; black yeast)	30,38	393	507		10347	50,4	IonTorrent		
Exophiala mesophila	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 120910	Gp0117764	JSEI01	264779	industrual importance (bioremediation; black yeast)	30,38	393,00	507		10347	50,4	IonTorrent		
Exophiala oligosperma	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS72588		JYCA01	325798	medical importance (black yeast)	38,22	240	287	143	13234		Illumina		
Exophiala sideris	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS121828		JYBR01	325799	medical importance (black yeast)	29,51	271	69	5	11120		Illumina		
Exophiala spinifera	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	JCM 15939	Gp0144009	BCHD01	313807	human pathogen (cutaneous)	32,7	156	107	38	12110	51,7	HiSeq 2500		
Exophiala spinifera	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	JCM 15939	Gp0144009	BCHD01	313807	human pathogen (cutaneous)	32,7	156	107	38	12110	51,7	HiSeq 2500		
Exophiala xenobiotica	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 102455	Gp0117765	JTCI01	265165	opportunistic human pathogen; bioremdiation	32,27	354	2050		12077	51,5	IonTorrent		
Exophiala xenobiotica	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 102455	Gp0117765	JTCI01	265165	opportunistic human pathogen; bioremdiation	32,27	354,00	2050		12077	51,5	IonTorrent		
Fonsecaea erecta	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 125763	Gp0150370	LVYI01	312449	medical importance (black yeast)	34,75	60	94	57	12120		Illumina; Ion Torrent		
Fonsecaea monophora	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 269.37	Gp0150371	LVKK01	312449	medical importance (black yeast)	35,23	90,00	324		12021	52,2	Illumina; Ion Torrent		
Fonsecaea multimorphosa	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 102226	Go0076063	JYBV01	233317	medical importance (black yeast)	33,45	176	133	67	12369		Illumina		
Fonsecaea nubica	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 269.64	Gp0150372	LVCJ01	312449	medical importance (black yeast)	33,79	85	259	258	11717	52,5	Illumina; Ion Torrent		
Fonsecaea pedrosoi	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 271.37	Go0076060	JYBS01	233314	medical importance (black yeast)	34,69	115	98	11	12527		Illumina		
Herpotrichiellaceae sp. UM238	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	UM238	Gp0039008	AMYF01	176958	opportunistic human pathogen	28,364	100,00	217			49,8	Illumina GaII		
Herpotrichiellaceae sp. UM238	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	UM238	Gp0039008	AMYF01	176958	opportunistic human pathogen	28,364	100	217			49,8	Illumina GaII		
Phialophora attae	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 131958	Gp0124601	LFJN01	286118	insect-associated (ants)	30,36	58	131		11848	53,6	IonTorrent		
Phialophora attae	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 131958	Gp0124601	LFJN01	286118	insect-associated (ants)	30,36	58	131		11848	53,6	IonTorrent		
Rhinocladiella mackenziei	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Chaetothyriales	Herpotrichiellaceae	CBS 650.93	Gp0076061	JYBU01	233315	human pathogen (neurotropic; cerebral phaeohyphomycosis)	32,47	260	130	17	11418				
Aspergillus acidus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 16872	Gp0009655	JGI	207686	saprotroph	37,47	65,70	318	107	13530		454 GS-FLX		
Aspergillus acidus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 16872	Gp0009655	JGI	207686	saprotroph	37,47	65,70	318	107	13530		454 GS-FLX		
Aspergillus aculeatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 16872	Gp0003551	JGI	82765	industrial importance	35,4		851	660	10845	50	454; Sanger		
Aspergillus aculeatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 16872	Gp0003551	JGI	82765	industrial importance	35,4		851	660	10845	50	454; Sanger		
Aspergillus awamori	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	JCM 22320	Gp0144020	BCGT01	313798	industrial importance (fermentation; starch degradation)	36,06	209,00	102	35		48,8	Illumina		
Aspergillus brasiliensis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 101740	Gp0009965	JGI	207691	industrial importance	35,81	156,80	290	105	13000		454; Illumina		
Aspergillus brasiliensis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 101740	Gp0009965	JGI	207691	industrial importance	35,81	156,80	290	105	13000		454; Illumina		
Aspergillus calidoustus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ACAL_DNA_1	Gp0143643	CDMC01	307674	human pathogen	41,1		220	78	15139	51,1			
Aspergillus calidoustus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ACAL_DNA_1	Gp0143643	CDMC01	307674	human pathogen	41,1		220	78	15139	51,1			
Aspergillus carbonarius	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ITEM 5010	Gp0003596	JGI	34741	industrial importance	36,3	17,78	1346	963	11624	51	454; Sanger		

Aspergillus carbonarius	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ITEM 5010	Gp0003596	JGI	34741	industrial importance	36,3	17,78	1346	963	11624	51	454; Sanger	
Aspergillus chevalieri	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	JCM 23047	Gp0144024	BCIE01	313830	opportunistic human pathogen	28,01	313	342	75		48	HiSeq 2500	
Aspergillus chevalieri	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	JCM 23047	Gp0144024	BCIE01	313830	opportunistic human pathogen	28,01	313,00	342	75		48	HiSeq 2500	
Aspergillus clavatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 1	Gp0002493	AAKD03	15664	soil- and manure-associated; occasional pathogen	27,9	11,4	231	143		49	Sanger	
Aspergillus clavatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 1	Gp0002493	AAKD03	15664	soil- and manure-associated; occasional pathogen	27,9	11,40	231	143		49	Sanger	
Aspergillus flavus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 3357	Gp0002470	AAIH02	13284	post-harvest decay	36,9	5		331		48	Sanger	Originally submitted as *A. delicata*
Aspergillus flavus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 3357	Gp0002470	AAIH02	13284	post-harvest decay	36,9	5,00		331		48	Sanger	
Aspergillus fumigatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	A1163 (CEA10)	Gp0002472	ABDB01	18733	opportunistic human pathogen; saprotroph	29,2	10,00		55			Sanger	
Aspergillus fumigatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	A1163 (CEA10)	Gp0002472	ABDB01	18733	opportunistic human pathogen; saprotroph	29,2	10,00		55			Sanger	
Aspergillus glaucus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 516.65	Gp0010048	JGI	169684	saprotroph	27,99	175,90	433	82	11277		454 GS-FLX	
Aspergillus glaucus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 516.65	Gp0010048	JGI	169684	saprotroph	27,99	175,90	433	82	11277		454 GS-FLX	
Aspergillus kawachii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	IFO 4308	Gp0039000	BACL01	66971	industrial importance	37,1	17,00		1163	11472	49	454 GS-FLX	
Aspergillus kawachii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	IFO 4308	Gp0039000	BACL01	66971	industrial importance	37,1	17,00		1163	11472	49	454 GS-FLX	
Aspergillus lentulus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	IFM 54703	Gp0144501	BCLY01	300219	opportunistic human pathogen	30,96		19		9986	49,5	PacBio RSII	
Aspergillus lentulus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	IFM 54703	Gp0144501	BCLY01	300219	opportunistic human pathogen	30,96		19		9986	49,5	PacBio RSII	
Aspergillus luchuensis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	RIB 2604	Gp0143306	BCWF01	314070	industrial importance	34,18		44		12920	49,9	ABI 3730	
Aspergillus luchuensis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	RIB 2604	Gp0143306	BCWF01	314070	industrial importance	34,18		44		12920	49,9	ABI 3730	
Aspergillus nidulans	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FGSC A4	Gp0000218; Gp000	JGI	130	human pathogen	30,48	1,00	82	8	10680	51	Sanger	
Aspergillus nidulans	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FGSC A4	Gp0000218; Gp000	JGI	130	human pathogen	30,48	1,00	82	8	10680	51	Sanger	
Aspergillus niger	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 513.88	Gp0000211; Gp001	JGI	19275	industrial importance	34,85	8,90		21	11197	50		
Aspergillus niger	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 513.88	Gp0000211; Gp001	JGI	19275	industrial importance	34,85	8,90		21	11197	50		
Aspergillus nomius	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL13137	Gp0120416	JNOM01	246595	human pathogen (aspergillosis)	36,14	42	1118		11914	48,9	IonTorrent	
Aspergillus nomius	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL13137	Gp0120416	JNOM01	246595	human pathogen (aspergillosis)	36,14	42,00	1118		11914	48,9	IonTorrent	
Aspergillus ochraceoroseus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	SRRC1432	Gp0117374	JYKN01	275128	medical importance (mycotoxin-producing)	24,27	39	3590		7829	48,2	IonTorrent	
Aspergillus ochraceoroseus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	SRRC1432	Gp0117374	JYKN01	275128	medical importance (mycotoxin-producing)	24,27	39,00	3590		7829	48,2	IonTorrent	
Aspergillus oryzae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	AS 3.951	Gp0038983	AKXN01	89727	industrial importance	36,3	7,00	969				Illumina GAII	
Aspergillus oryzae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	AS 3.951	Gp0038983	AKXN01	89727	industrial importance	36,3	7,00	969				Illumina GAII	
Aspergillus parasiticus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	SU-1	Gp0094495	JMUG01	246303	medical importance (aflatoxin-producing)	40	50,00	4409				Illumina HiSeq	
Aspergillus parasiticus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	SU-1	Gp0094495	JMUG01	246303	medical importance (aflatoxin-producing)	40	50,00	4409				Illumina HiSeq	
Aspergillus rambellii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	SRRC1468	Gp0117376	JZBS01	275129	medical importance (mycotoxin-producing)	26,44	89	4177		7761	45,8	IonTorrent	
Aspergillus rambellii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	SRRC1468	Gp0117376	JZBS01	275129	medical importance (mycotoxin-producing)	26,44	89,00	4177		7761	45,8	IonTorrent	
Aspergillus ruber	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 135680	Gp0010009	JGI	215335	halotolerant	26,21	91,70	371	110	10076		454; Illumina	
Aspergillus ruber	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 135680	Gp0010009	JGI	215335	halotolerant	26,21	91,70	371	110	10076		454; Illumina	
Aspergillus sojae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NBRC 4239	Gp0038873	BACA01	60265	traditional use	39,7	14,00		542				454
Aspergillus sojae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NBRC 4239	Gp0038873	BACA01	60265	traditional use	39,7	14,00		542				454
Aspergillus sp. Z5	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	Z5	Gp0120939	LDZW01	285783	marine fungus; secondary metabolite biosynthesis	33,81	100	956			50,5	Illumina HiSeq	
Aspergillus sp. Z5	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	Z5	Gp0120939	LDZW01	285783	marine fungus; secondary metabolite biosynthesis	33,81	100,00	956			50,5	Illumina HiSeq	
Aspergillus sydowii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 593.65	Gp0009566	JGI	207689	animal pathogen (sea fan corals)	34,38	95,10	133	97	13620		454 GS-FLX	
Aspergillus sydowii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 593.65	Gp0009566	JGI	207689	animal pathogen (sea fan corals)	34,38	95,10	133	97	13620		454 GS-FLX	
Aspergillus terreus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NIH2624	Gp0002492	JGI	15631	soil-associated; cosmopolitan	29,33	11,50	267	26	10406	53	Sanger	
Aspergillus terreus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NIH2624	Gp0002492	JGI	15631	soil-associated; cosmopolitan	29,33	11,50	267	26	10406	53	Sanger	
Aspergillus tubingensis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 134.48	Gp0010145	JGI	207690	industrial importance	35,15	125,70	87	33	12322		454; Illumina	
Aspergillus tubingensis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 134.48	Gp0010145	JGI	207690	industrial importance	35,15	125,70	87	33	12322		454; Illumina	
Aspergillus udagawae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	IFM 46973	Gp0122201	BBXM01	288122	animal pathogen; aspergillosis	32,19		1029		10214	49,6	HiSeq 1500	
Aspergillus udagawae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	IFM 46973	Gp0122201	BBXM01	288122	animal pathogen; aspergillosis	32,19		1029		10214	49,6	HiSeq 1500	
Aspergillus ustus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	3.3904	Gp0117377	JOMC01	253260	opportunistic human pathogen	38,35	100	1502	770		51	Illumina HiSeq	
Aspergillus ustus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	3.3904	Gp0117377	JOMC01	253260	opportunistic human pathogen	38,35	100,00	1502	770		51	Illumina HiSeq	
Aspergillus versicolor	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 583.65	Gp0010019	JGI	207687	industrial importance	33,13	178,10	58	51	13228		454 GS-FLX	
Aspergillus versicolor	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 583.65	Gp0010019	JGI	207687	industrial importance	33,13	178,10	58	51	13228		454 GS-FLX	
Aspergillus wentii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	DTO 134E9	Gp0009565	JGI	170886	industrial importance	31,35	95,00	118	27	12442		Illumina	
Aspergillus wentii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	DTO 134E9	Gp0009565	JGI	170886	industrial importance	31,35	95,00	118	27	12442		Illumina	
Aspergillus westerdijkiae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 112803	Gp0124190	LKBE01	296723	medical importance (mycotoxin-producing)	36,07	142	3022	239		50,2	Illumina MiSeq	
Aspergillus westerdijkiae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 112803	Gp0124190	LKBE01	296723	medical importance (mycotoxin-producing)	36,07	142,00	3022	239		50,2	Illumina MiSeq	
Aspergillus zonatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 506.65	Gp0009569	JGI	207688	industrial importance	28,92	84,80	460	260	9886		Illumina	
Aspergillus zonatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 506.65	Gp0009569	JGI	207688	industrial importance	28,92	84,80	460	260	9886		Illumina	
Basipetospora chlamydospora	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	JCM 23157	Gp0144025	BCHP01	313817	uncertain	33,49	162	342	17		55,7	HiSeq 2500	
Basipetospora chlamydospora	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	JCM 23157	Gp0144025	BCHP01	313817	uncertain	33,49	162,00	342	17		55,7	HiSeq 2500	
Monascus purpureus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 1596	Gp0019248	JGI	204098	industrial importance (toxin producing)	23,44	102,00	319	296	8918		Illumina HiSeq	
Monascus purpureus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 1596	Gp0019248	JGI	204098	industrial importance (toxin producing)	23,44	102,00	319	296	8918		Illumina HiSeq	
Monascus ruber	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 1597	Gp0019414	JGI	196033	industrial importance	24,8	123,40	362	320	9650		Illumina HiSeq	
Monascus ruber	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 1597	Gp0019414	JGI	196033	industrial importance	24,8	123,40	362	320	9650		Illumina HiSeq	
Penicillium aurantiogriseum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 62431	Gp0038385	ALJY01	170336	endophyte	31,5475	50,00	4775			48,5	Illumina GAIIx	
Penicillium aurantiogriseum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	NRRL 62431	Gp0038385	ALJY01	170336	endophyte	31,5475	50,00	4775			48,5	Illumina GAIIx	
Penicillium biforme	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM169	Gp0101004	CBXO01	238635	pharmaceutical importance (rugulovasine production)	34,87		692	582		48,1		
Penicillium biforme	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM169	Gp0101004	CBXO01	238635	pharmaceutical importance (rugulovasine production)	34,87		692	582		48,1		
Penicillium bilaiae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 20851	Gp0035113	JGI	196077	P-solubilizing	37,54	101	319	132	13606		Illumina HiSeq	
Penicillium bilaiae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 20851	Gp0035113	JGI	196077	P-solubilizing	37,54	101,00	319	132	13606		Illumina HiSeq	
Penicillium brasilianum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	PMG11	Gp0143650	CDHK01	284459	endophyte	35,89		244	87	11943	49,5		
Penicillium brasilianum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	PMG11	Gp0143650	CDHK01	284459	endophyte	35,89		244	87	11943	49,5		
Penicillium brevicompactum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	AgRF18	Gp0039189	JGI	217207	industrial importance (metabolite production); water-damage contaminan	31,68	98,40	154	73	12343		Illumina	
Penicillium brevicompactum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	AgRF18	Gp0039189	JGI	217207	industrial importance (metabolite production); water-damage contaminan	31,68	98,40	154	73	12343		Illumina	
Penicillium camemberti	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM 013	Gp0101005	CBVV01	230337	industrial importance (cheese-making)	35,012		936	180	14418	48,2		
Penicillium camemberti	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM 013	Gp0101005	CBVV01	230337	industrial importance (cheese-making)	35,012		936	180	14418	48,2		
Penicillium canescens	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 10419	Gp0035119	JGI	196079	calcium phosphate solubilizer	33,26	97	248	62	12374		Illumina	
Penicillium canescens	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 10419	Gp0035119	JGI	196079	calcium phosphate solubilizer	33,26	97,00	248	62	12374		Illumina	
Penicillium capsulatum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 134186	Gp0101007	JPLR01	255347	industrial importance (paper production); opportunitsic human pathogen	34,34	231	62			49,1	Illumina; PacBio	
Penicillium capsulatum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	CBS 134186	Gp0101007	JPLR01	255347	industrial importance (paper production); opportunitsic human pathogen	34,34	231,00	62			49,1	Illumina; PacBio	
Penicillium carneum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	LCP05634	Gp0101008	CBXS01	238633	saprotroph; medical importance (mycotoxin-producing)	25,94		7894	2090		49,1		
Penicillium carneum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	LCP05634	Gp0101008	CBXS01	238633	saprotroph; medical importance (mycotoxin-producing)	25,94		7894	2090		49,1		
Penicillium chrysogenum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	IB 08/921	Gp0122307	JPDR01	253579	saprotroph	31,4		2353	1151	11198	48,9	Illumina HiSeq	
Penicillium chrysogenum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	IB 08/921	Gp0122307	JPDR01	253579	saprotroph	31,4		2353	1151	11198	48,9	Illumina HiSeq	
Penicillium citrinum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	DSM 1997	Gp0124599	LKUP01	298119	saprotroph; medical importance (mycotoxin-producing)	31,53	64	976			46,9	Illumina MiSeq	
Penicillium citrinum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	DSM 1997	Gp0124599	LKUP01	298119	saprotroph; medical importance (mycotoxin-producing)	31,53	64,00	976			46,9	Illumina MiSeq	
Penicillium digitatum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	Pd1	Gp0038329	AKCU01	157543	post-harvest decay	26,082	24,00	562	54	8961	48,9		454
Penicillium digitatum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	Pd1	Gp0038329	AKCU01	157543	post-harvest decay	26,082	24,00	562	54	8961	48,9		454
Penicillium expansum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	d1	Gp0118132	JQFY01	255745	post-harvest decay	32,1	605	270		11060	47,5	Illumina HiSeq	
Penicillium expansum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	d1	Gp0118132	JQFY01	255745	post-harvest decay	32,1	605,00	270		11060	47,5	Illumina HiSeq	
Penicillium fellutanum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 48694	Gp0035121	JGI	196080	calcium phosphate solubilizer	30,2	121	50	20	11300		Illumina HiSeq	
Penicillium fellutanum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 48694	Gp0035121	JGI	196080	calcium phosphate solubilizer	30,2	121,00	50	20	11300		Illumina HiSeq	
Penicillium freii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	DAOM 242723	Gp0143842	LLXE01	277835	psychrophile	33,55	79	1925	1923	11739	47,4	Illumina HiSeq	
Penicillium freii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	DAOM 242723	Gp0143842	LLXE01	277835	psychrophile	33,55	79,00	1925	1923	11739	47,4	Illumina HiSeq	
Penicillium fuscoglaucum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM041	Gp0101009	CBXP01	238636	contaminant (cheese)	36,0855		1131	953		47,7		
Penicillium fuscoglaucum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM041	Gp0101009	CBXP01	238636	contaminant (cheese)	36,0855		1131	953		47,7		
Penicillium glabrum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	DAOM 239074	Gp0035115	JGI	196078	post-harvest decay	33,16	96	189	117	12328		Illumina HiSeq	
Penicillium glabrum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	DAOM 239074	Gp0035115	JGI	196078	post-harvest decay	33,16	96,00	189	117	12328		Illumina HiSeq	
Penicillium griseofulvum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	PG3	Gp0145454	LHQR01	289974	post-harvest decay	29,14	270	92		9630	47,3	Illumina MiSeq	
Penicillium griseofulvum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	PG3	Gp0145454	LHQR01	289974	post-harvest decay	29,14	270,00	92		9630	47,3	Illumina MiSeq	
Penicillium italicum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	PHI-1	Gp0118134	JQGA01	255746	post-harvest decay	30,16	421	1632			47,2	Illumina HiSeq	
Penicillium italicum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	PHI-1	Gp0118134	JQGA01	255746	post-harvest decay	30,16	421,00	1632			47,2	Illumina HiSeq	
Penicillium janthinellum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 10455	Gp0039214	JGI	218033	endophyte	35,15	99,00	273	94	12098			
Penicillium janthinellum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 10455	Gp0039214	JGI	218033	endophyte	35,15	99,00	273	94	12098			

Penicillium lanosocoeruleum v1.0	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 48919	Gp0035117	JGI	208390	pharmaceutical importance (antibiotic- and mycotoxin-producing)	29,05	113	148	13	10698		Illumina	
Penicillium lanosocoeruleum v1.0	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 48919	Gp0035117	JGI	208390	pharmaceutical importance (antibiotic- and mycotoxin-producing)	29,05	113,00	148	13	10698		Illumina	
Penicillium nalgiovense	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM193	Gp0101010	CBXQ01	238637	industrial importance (fermentation; metabolite production)	31,9375		975	896		48,5		
Penicillium nalgiovense	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM193	Gp0101010	CBXQ01	238637	industrial importance (fermentation; metabolite production)	31,9375		975	896		48,5		
Penicillium nordicum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	BFE487	Gp0090030	JNNR01	239658	contaminant (food; toxigenic)	30,421	20,00	915			47,7	Illumina HiSeq	
Penicillium nordicum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	BFE487	Gp0090030	JNNR01	239658	contaminant (food; toxigenic)	30,421	20,00	915			47,7	Illumina HiSeq	
Penicillium oxalicum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	114-2		AGIH01	60877	lignocellulolytic	30,18	28	345	9	9979			
Penicillium oxalicum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	114-2		AGIH01	60877	lignocellulolytic	30,18	28,00	345	9	9979			
Penicillium paneum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM227	Gp0101011	CBXN01	238634	contaminant (cereal; toxigenic)	26,5793		397	224		49		
Penicillium paneum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM227	Gp0101011	CBXN01	238634	contaminant (cereal; toxigenic)	26,5793		397	224		49		
Penicillium paxilli	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 26601	Gp0038413	AOTG01	189173	pharmaceutical importance (production of paxelline and antimicrobial com	34,8	150,00	635	420		47,9	Illumina MiSeq	
Penicillium paxilli	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 26601	Gp0038413	AOTG01	189173	pharmaceutical importance (production of paxelline and antimicrobial com	34,8	150,00	635	420		47,9	Illumina MiSeq	
Penicillium raistrickii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 10490	Gp0039212	JGI	217210	calcium phosphate solubilizer	31,44	95,10	104	76	11368			
Penicillium raistrickii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	ATCC 10490	Gp0039212	JGI	217210	calcium phosphate solubilizer	31,44	95,10	104	76	11368			
Penicillium roqueforti	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM164	Gp0101012	CBMR01	214067	industrial importance (cheese-making)	29,01		157	48	12425	48,7		
Penicillium roqueforti	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FM164	Gp0101012	CBMR01	214067	industrial importance (cheese-making)	29,01		157	48	12425	48,7		
Penicillium rubens	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	Wisconsin 54-1255	Gp0003458	JGI	27927	industrial importance (penicillin production)	32,22	9,8	242	49	13671			
Penicillium rubens	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	Wisconsin 54-1255	Gp0003458	JGI	27927	industrial importance (penicillin production)	32,22	9,80	242	49	13671			
Penicillium solitum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae		Gp0093017	JYNM02	225689	post-harvest decay	35,23	7,00				47,1		
Penicillium verrucosum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	BFE808	Gp0121007	LAKW01	276626	medical importance (ochratoxin-producing)	31,15	60	4207			48,1	Illumina MiSeq	
Penicillium verrucosum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	BFE808	Gp0121007	LAKW01	276626	medical importance (ochratoxin-producing)	31,15	60,00	4207			48,1	Illumina MiSeq	
Xeromyces bisporus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FRR 0525	Gp0144500	CCCX01	271389	xerophile	22,03		1479	572		29,4		
Xeromyces bisporus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Aspergillaceae	FRR 0525	Gp0144500	CCCX01	271389	xerophile	22,03		1479	572		29,4		
Byssochlamys spectabilis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Thermoascaceae	No. 5	Gp0070862	BAUL01	227278	industrial importance (formaldehyde resistant)	29,76	53,5	1053		8877	48,6	Illumina	
Byssochlamys spectabilis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Thermoascaceae	No. 5	Gp0070862	BAUL01	227278	industrial importance (formaldehyde resistant)	29,76	53,50	1053		8877	48,6	Illumina	
Thermoascus aurantiacus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Thermoascaceae	ATCC 26904	Gp0017900	JGI	207868	industrial importance (thermophile)	28,49	95,90	196	48	8798		Illumina	
Thermoascus aurantiacus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Thermoascaceae	ATCC 26904	Gp0017900	JGI	207868	industrial importance (thermophile)	28,49	95,90	196	48	8798		Illumina	
Thermoascus crustaceus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Thermoascaceae	JCM 12817	Gp0144001	BCIC01	313828	thermophile	31,64	195	258	33		49,2	HiSeq 2500	
Thermoascus crustaceus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Thermoascaceae	JCM 12817	Gp0144001	BCIC01	313828	thermophile	31,64	195,00	258	33		49,2	HiSeq 2500	
Neosartorya fischeri	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	NRRL 181	Gp0006742	AAKE03	15672	opportunistic human pathogen	32,55	1,00	976	976	10406	49	Sanger	
Neosartorya fischeri	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	NRRL 181	Gp0006742	AAKE03	15672	opportunistic human pathogen	32,55	1,00	976	976	10406	49	Sanger	
Rasamsonia emersonii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	CBS393.64	Gp0021159	LASV01	222976	thermophile	28,25	14,50		862	9843	50,6	Sanger; 454	
Rasamsonia emersonii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	CBS393.64	Gp0021159	LASV01	222976	thermophile	28,25	14,50		862	9843	50,6	Sanger; 454	
Talaromyces aculeatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	ATCC 10409	Gp0039191	JGI	217211	iron phosphate solubilizer	37,27	91,80	165	49	13793		Illumina	
Talaromyces aculeatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	ATCC 10409	Gp0039191	JGI	217211	iron phosphate solubilizer	37,27	91,80	165	49	13793		Illumina	
Talaromyces cellulolyticus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	Y-94	Gp0122238	BBPS01	271761	industrial importance (cellulase production)	36,4	19	1723	60	10910	46,6		454
Talaromyces cellulolyticus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	Y-94	Gp0122238	BBPS01	271761	industrial importance (cellulase production)	36,4	19,00	1723	60	10910	46,6		454
Talaromyces islandicus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	PIS	Gp0143952	CVMT01	282635	industrial importance (biopolymer degradation, mycotoxins)	34,72		1345	116	9927	46,3		
Talaromyces islandicus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	PIS	Gp0143952	CVMT01	282635	industrial importance (biopolymer degradation, mycotoxins)	34,72		1345	116	9927	46,3		
Talaromyces leycettanus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	CBS 398.68	Gp0107549	JSYV01	261108	industrial importance (thermophilic enzzymes)	25,95	180	991			49,7	Illumina HiSeq	
Talaromyces leycettanus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	CBS 398.68	Gp0107549	JSYV01	261108	industrial importance (thermophilic enzzymes)	25,95	180,00	991			49,7	Illumina HiSeq	
Talaromyces marneffei	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	ATCC 18224	Gp0002656	ABAR01	19555	opportunistic pathogen (dimorphic; penicilliosis)	28,64	8,8	524	452	10638	47	Sanger	
Talaromyces marneffei	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	ATCC 18224	Gp0002656	ABAR01	19555	opportunistic pathogen (dimorphic; penicilliosis)	28,64	8,80	524	452	10638	47	Sanger	
Talaromyces pinophilus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	1-95	Gp0144166	LSFK01	310372	industrial importance (enzyme production)	36,41	150	265	131		46,8	Illumina HiSeq	
Talaromyces pinophilus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	1-95	Gp0144166	LSFK01	310372	industrial importance (enzyme production)	36,41	150,00	265	131		46,8	Illumina HiSeq	
Talaromyces purpureogenus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	MYA-38	Gp0122196	LIAB01	276974	medical importance (mycotoxin-producing)	38,85	213	1150	1010		48,7	Illumina HiSeq; PacBio	
Talaromyces purpureogenus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	MYA-38	Gp0122196	LIAB01	276974	medical importance (mycotoxin-producing)	38,85	213,00	1150	1010		48,7	Illumina HiSeq; PacBio	
Talaromyces stipitatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	ATCC 10500	Gp0002704	ABAS01	19557	saprotroph	35,69	8,1	896	820	13252	46	Sanger	
Talaromyces stipitatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	ATCC 10500	Gp0002704	ABAS01	19557	saprotroph	35,69	8,10	896	820	13252	46	Sanger	
Talaromyces verruculosus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	TS63-9	Gp0124670	LHCL01	291496	industrial importance (cellulase production)	37,63	100	719	540	11326	46,2	Illumina HiSeq	
Talaromyces verruculosus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	TS63-9	Gp0124670	LHCL01	291496	industrial importance (cellulase production)	37,63	100,00	719	540	11326	46,2	Illumina HiSeq	
Thermomyces lanuginosus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	SSBP	Gp0038902	ANHP01	88097	industrial importance (thermophile; xylanase producer)	19,156	48,00	311			52,2	454; Illumina GAII	
Thermomyces lanuginosus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Eurotiales	Trichocomaceae	SSBP	Gp0038902	ANHP01	88097	industrial importance (thermophile; xylanase producer)	19,156	48,00	311			52,2	454; Illumina GAII	
Ajellomyces dermatitidis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Ajellomycetaceae	SLH14081	Gp0002636	ACBU01	29173	human pathogen (blastomycosis)	75,4	8,45		103		36	Sanger	
Ajellomyces dermatitidis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Ajellomycetaceae	SLH14081	Gp0002636	ACBU01	29173	human pathogen (blastomycosis)	75,4	8,45		103		36	Sanger	
Emmonsia crescens	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Ajellomycetaceae	UAMH 3008	Gp0037041	LCZI01	178252	occasional human pathogen (dimorphic)	30,7	163,00	2489	1734	9558	45,2		
Emmonsia parva	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Ajellomycetaceae	UAMH 139	Gp0037822	LDEV01	178178	occasional animal pathogen (dimorphic)	31	116,00	4890	3706	8706	44,4		
Histoplasma capsulatum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Ajellomycetaceae	NAm1	Gp0002625	AMXR01	12654	human pathogen (histoplasmosis)	32,99	7	2867	275	9251	46,1	Illumina HiSeq	
Histoplasma capsulatum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Ajellomycetaceae	NAm1	Gp0002625	AMXR01	12654	human pathogen (histoplasmosis)	32,99	7,00	2867	275	9251	46,1	Illumina HiSeq	
Paracoccidioides brasiliensis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Ajellomycetaceae	Pb03	Gp0002633	ABHV01	27779	human pathogen (paracoccidioidomycosis)	29,06	8,9	552	65	7876	44,3		
Paracoccidioides brasiliensis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Ajellomycetaceae	Pb03	Gp0002633	ABHV01	27779	human pathogen (paracoccidioidomycosis)	29,06	8,90	552	65	7876	44,3		
Paracoccidioides lutzii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Ajellomycetaceae		Gp0002632	ABKH02	28731	human pathogen (paracoccidioidomycosis)	32,93	148,00	372	110	8953	42,8	Illumina	
Arthroderma benhamiae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 112371	Gp0004096	ABSU01	30573	human pathogen (dermatophytosis)	22,2	8	68			49		454
Arthroderma benhamiae	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 112371	Gp0004096	ABSU01	30573	human pathogen (dermatophytosis)	22,2	8,00	68			49		454
Microsporum canis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 113480	Gp0002508	ABVF01	30939	human pathogen	23,24	7,78	309	16	8915	47	Sanger	
Microsporum canis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 113480	Gp0002508	ABVF01	30939	human pathogen	23,24	7,78	309	16	8915	47	Sanger	
Microsporum gypseum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 118893	Gp0002509	ABQE01	61175	occasional human pathogen; dermatophyte	23,2682	9,06	318	19	9015	48,5	Sanger	
Microsporum gypseum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 118893	Gp0002509	ABQE01	61175	occasional human pathogen; dermatophyte	23,2682	9,06	318	19	9015	48,5	Sanger	
Trichophyton equinum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 127.97	Gp0002504	ABWI01	20577	animal pathogen (horse); dermatophyte	24,158	4,88	1716	125	8785	47,4	Sanger	
Trichophyton equinum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 127.97	Gp0002504	ABWI01	20577	animal pathogen (horse); dermatophyte	24,158	4,88	1716	125	8785	47,4	Sanger	
Trichophyton interdigitale	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	MR816	Gp0037045	AOKY01	186835	human pathogen (dermatophyte)	22,469	56,00	956		8083	48	Illumina	
Trichophyton interdigitale	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	MR816	Gp0037045	AOKY01	186835	human pathogen (dermatophyte)	22,469	56,00	956		8083	48	Illumina	
Trichophyton rubrum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 118892	Gp0002506	ACPH01	38221	human pathogen (dermatophyte)	22,5	8,19	622	35	8707	48,3	Sanger	
Trichophyton rubrum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 118892	Gp0002506	ACPH01	38221	human pathogen (dermatophyte)	22,5	8,19	622	35	8707	48,3	Sanger	
Trichophyton soudanense	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 452.61	Gp0037864	AOKW01	186831	human pathogen (tinea capitis)	22,85	75,00	421	420	9016	47,5	Illumina	
Trichophyton tonsurans	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 112817	Gp0002507	ACPI01	38223	human pathogen (dermatophyte; ringworm of scalp)	22,988	5,00	1164	111	8625	48,1	Sanger	
Trichophyton tonsurans	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CBS 112817	Gp0002507	ACPI01	38223	human pathogen (dermatophyte; ringworm of scalp)	22,988	5,00	1164	111	8625	48,1	Sanger	
Trichophyton verrucosum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	HKI 0517	Gp0006822	ACYE01	39693	animal pathogen (cattle, hoerse); dermatophyte	22,54	3	523	523	8024	48	454; Sanger	
Trichophyton verrucosum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	HKI 0517	Gp0006822	ACYE01	39693	animal pathogen (cattle, hoerse); dermatophyte	22,54	3,00	523	523	8024	48	454; Sanger	
Trichophyton violaceum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CMCC(F)T3l	Gp0122011	LHPN01	291786	human pathogen (dermatophyte)	23,37	250	938	261	7037	47	Illumina HiSeq; PacBio	
Trichophyton violaceum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Arthrodermataceae	CMCC(F)T3l	Gp0122011	LHPN01	291786	human pathogen (dermatophyte)	23,37	250,00	938	261	7037	47	Illumina HiSeq; PacBio	
Gymnascella aurantiaca	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Gymnoascaceae	NRRL 5967	Gp0019261	JGI	196037	saprotroph	25,35	143,9	356	347	9106		Illumina HiSeq	
Gymnascella aurantiaca	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Gymnoascaceae	NRRL 5967	Gp0019261	JGI	196037	saprotroph	25,35	143,90	356	347	9106		Illumina HiSeq	
Gymnascella citrina	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Gymnoascaceae	NRRL 5970	Gp0019431	JGI	205958	saprotroph	25,16	146,5	305	272	9779		Illumina HiSeq	
Gymnascella citrina	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Gymnoascaceae	NRRL 5970	Gp0019431	JGI	205958	saprotroph	25,16	146,50	305	272	9779		Illumina HiSeq	
Lacazia loboi	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Incertae sedis	LDI48194	Gp0117927	LBNG01	282657	human pathogen (blastomycosis)	14	80	367			33	IonTorrent	
Lacazia loboi	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Incertae sedis	LDI48194	Gp0117927	LBNG01	282657	human pathogen (blastomycosis)	14	80,00	367			33	IonTorrent	
Amauroascus mutatus	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	UAMH 3576	Gp0150598	LJPJ01	284880	uncertain; comparsion with patogenic Onygenales	30,38	50,00	12189	3075		48,9	Illumina	
Amauroascus niger	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	UAMH 3544	Gp0150597	LJPK01	284880	uncertain; comparsion with patogenic Onygenales	36,72	50,00	11245	3481		49,7	Illumina	
Byssoonygena ceratinophila	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	UAMH 5669	Gp0150599	LJPH01	284880	keratinophilic	27,45	50,00	10645	4851		48,2	Illumina	
Chrysosporium lucknowense	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	VKM F-3500-D	Gp0002587			industrial importance	38,5	12,60			9499	48,6	454; Sanger	
Chrysosporium lucknowense	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	VKM F-3500-D	Gp0002587			industrial importance	38,5	12,60			9499	48,6	454; Sanger	
Chrysosporium queenslandicum	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	CBS 280.77	Gp0150596	LJPI01	284880	industrial importance (antimicorbial compunds); comparsion with pathoge	32,34	50,00	9187	2724		52,6	Illumina	
Coccidioides immitis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	RMSCC 2394	Gp0002591	AATX01	17713	human pathogen (Coccidiomycosis)	28,9	8,22	527	31	10560	46	Sanger	
Coccidioides immitis	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	RMSCC 2394	Gp0002591	AATX01	17713	human pathogen (Coccidiomycosis)	28,9	8,22	527	31	10560	46	Sanger	
Coccidioides posadasii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	RMSCC 2133	Gp0002602	ABFM01	17763	human pathogen (Coccidiomycosis/valley fever)	27,9	6,70	1052	55	7255	46,6	Sanger	
Coccidioides posadasii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	RMSCC 2133	Gp0002602	ABFM01	17763	human pathogen (Coccidiomycosis/valley fever)	27,9	6,70	1052	55	7255	46,6	Sanger	
Onygena corvina	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	CBS 281.48	Gp0118086	JWPT01	270018	saprotroph	21,71	370	521			48,2	Illumina	
Onygena corvina	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	CBS 281.48	Gp0118086	JWPT01	270018	saprotroph	21,71	370,00	521			48,2	Illumina	
Uncinocarpus reesii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	UAMH 1704	Gp0002710	JGI	15634	saprotroph (soil); closely related to Coccidioides	22,33	5,00	582	44	7798	49	Sanger	
Uncinocarpus reesii	Ascomycota	Pezizomycotina	Eurotiomycetes	Eurotiomycetidae	Onygenales	Onygenaceae	UAMH 1704	Gp0002710	JGI	15634	saprotroph (soil); closely related to Coccidioides	22,33	5,00	582	44	7798	49	Sanger	

Phaeomoniella chlamydospora	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Phaeomoniellales	Incertae sedis	UCRPC4	Gp0118145	LCWF01	261774	plant pathogen (grapevine trunk disease)	27,51	107,28	917	702	6907	47	Illumina HiSeq	
Phaeomoniella chlamydospora	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Phaeomoniellales	Incertae sedis	UCRPC4	Gp0118145	LCWF01	261774	plant pathogen (grapevine trunk disease)	27,51	107,28	917	702	6907	47	Illumina HiSeq	
Endocarpon pusillum	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Verrucariales	Verrucariaceae	Z07020	Gp0048200	APWS01	181958	mycobiont (lichen-forming)	37,5	78,00	1731	908	9285	46	454; Illumina GAIIx	
Endocarpon pusillum	Ascomycota	Pezizomycotina	Eurotiomycetes	Chaetothyriomycetidae	Verrucariales	Verrucariaceae	Z07020	Gp0048200	APWS01	181958	mycobiont (lichen-forming)	37,5	78,00	1731	908	9285	46	454; Illumina GAIIx	
Symbiotaphrina buchneri	Ascomycota	Pezizomycotina	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	JCM 9740	Gp0144048	BCIG01	313832	insect-associated (beetle endosymbiont)	23,71	251	211	169		51,6	HiSeq 2500	
Symbiotaphrina buchneri	Ascomycota	Pezizomycotina	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	JCM 9740	Gp0144048	BCIG01	313832	insect-associated (beetle endosymbiont)	23,71	251,00	211	169		51,6	HiSeq 2500	
Symbiotaphrina kochii	Ascomycota	Pezizomycotina	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	CBS 250.77	Gp0010144		207854	insect-associated (beetle endosymbiont)	24,83	69	59	54	10482		454; Illumina	
Symbiotaphrina kochii	Ascomycota	Pezizomycotina	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	CBS 250.77	Gp0010144		207854	insect-associated (beetle endosymbiont)	24,83	69,00	59	54	10482		454; Illumina	
Cladonia grayi	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Lecanorales	Cladoniaceae	Cgr/DA2myc/ss		JGI		mycobiont (lichen-forming)	39,6		5214	1506	11415		454; Illumina	
Cladonia grayi	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Lecanorales	Cladoniaceae	Cgr/DA2myc/ss		JGI		mycobiont (lichen-forming)	39,6		5214	1506	11415		454; Illumina	
Cladonia macilenta	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Lecanorales	Cladoniaceae	KoLRI003786	Gp0042523	AUPP01	210603	mycobiont (lichen-forming)	37,12	540,00	1310	240		44,8	Illumina	
Cladonia macilenta	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Lecanorales	Cladoniaceae	KoLRI003786	Gp0042523	AUPP01	210603	mycobiont (lichen-forming)	37,12	540,00	1310	240		44,8	Illumina	
Cladonia metacorallifera	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Lecanorales	Cladoniaceae	KoLRI002260	Gp0049795	AXCT02	219240	mycobiont (lichen-forming)	36,68	1023,00	625	30		45	Illumina	
Cladonia metacorallifera	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Lecanorales	Cladoniaceae	KoLRI002260	Gp0049795	AXCT02	219240	mycobiont (lichen-forming)	36,68	1023,00	625	30		45	Illumina	
Usnea florida	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Lecanorales	Parmeliaceae	ATCC18376 v1.0		1051215		mycobiont (lichen-forming)	44,32	87,6	1774	274	12649		Illumina	
Usnea florida	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Lecanorales	Parmeliaceae	ATCC18376 v1.0		1051215		mycobiont (lichen-forming)	44,32	87,60	1774	274	12649		Illumina	
Gyalolechia flavorubescens	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Teloschistales	Teloschistaceae	KoLRI002931	Gp0047051	AUPK01	210248	mycobiont (lichen-forming)	34,468	541,00	189	36		42	Illumina HiSeq	
Gyalolechia flavorubescens	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Teloschistales	Teloschistaceae	KoLRI002931	Gp0047051	AUPK01	210248	mycobiont (lichen-forming)	34,468	541,00	189	36		42	Illumina HiSeq	
Xanthoria parietina	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Teloschistales	Teloschistaceae	46-1	Gp0017906	JGI	62697	mycobiont (lichen-forming)	31,9	43,84	302	39	10818			454
Xanthoria parietina	Ascomycota	Pezizomycotina	Lecanoromycetes	Lecanoromycetidae	Teloschistales	Teloschistaceae	46-1	Gp0017906	JGI	62697	mycobiont (lichen-forming)	31,9	43,84	302	39	10818			454
Lasallia pustulata	Ascomycota	Pezizomycotina	Lecanoromycetes	Incertae sedis	Umbilicariales	Umbilicariaceae	Sardinia_28052013	Gp0138618	JYIL01	275184	mycobiont (lichen-forming)	39,23	90	5331	3891		51,2	PacBio; Illumina HiSeq	
Lasallia pustulata	Ascomycota	Pezizomycotina	Lecanoromycetes	Incertae sedis	Umbilicariales	Umbilicariaceae	Sardinia_28052013	Gp0138618	JYIL01	275184	mycobiont (lichen-forming)	39,23	90,00	5331	3891		51,2	PacBio; Illumina HiSeq	
Umbilicaria muehlenbergii	Ascomycota	Pezizomycotina	Lecanoromycetes	Incertae sedis	Umbilicariales	Umbilicariaceae		Gp0090033	JFDN01	239196	mycobiont (lichen-forming); genetically tractable	34,812	663,00	297	7		47,1	Illumina HiSeq	
Umbilicaria muehlenbergii	Ascomycota	Pezizomycotina	Lecanoromycetes	Incertae sedis	Umbilicariales	Umbilicariaceae		Gp0090033	JFDN01	239196	mycobiont (lichen-forming); genetically tractable	34,812	663,00	297	7		47,1	Illumina HiSeq	
Blumeria graminis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Erysiphales	Erysiphaceae	A6	Gp0038457	AOLT01	186717	plant pathogen (mildew on grasses and cereals)	47,46	70,00	21305		7088	46,4	454; Illumina HiSeq	
Blumeria graminis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Erysiphales	Erysiphaceae	A6	Gp0038457	AOLT01	186717	plant pathogen (mildew on grasses and cereals)	47,46	70,00	21305		7088	46,4	454; Illumina HiSeq	
Erysiphe necator	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Erysiphales	Erysiphaceae	branching	Gp0117742	JNUS01	248900	plant pathogen (powdery mildew of grape)	50,66	29	11631	6224	6484	39	Illumina HiSeq	
Erysiphe necator	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Erysiphales	Erysiphaceae	branching	Gp0117742	JNUS01	248900	plant pathogen (powdery mildew of grape)	50,66	29,00	11631	6224	6484	39	Illumina HiSeq	
Erysiphe pisi	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Erysiphales	Erysiphaceae	not specified	Gp0008359	CACN01	50315	plant pathogen (powdery mildew of pea)	41	8,30	26142			39,2		454
Erysiphe pisi	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Erysiphales	Erysiphaceae	not specified	Gp0008359	CACN01	50315	plant pathogen (powdery mildew of pea)	41	8,30	26142			39,2		454
Marssonina brunnea	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Dermateaceae	MB_m1	Gp0038386	AFXC01	66127	plant pathogen (poplar leaf spot)	51,949	34,00	2415	89	10027	42,9	454; Sanger	
Marssonina brunnea	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Dermateaceae	MB_m1	Gp0038386	AFXC01	66127	plant pathogen (poplar leaf spot)	51,949	34,00	2415	89	10027	42,9	454; Sanger	
Ascocoryne sarcoides	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	NRRL 50072	Gp0039091	AIAA01	71021	pharmaceutical importance (antibiotic-producing); saprotroph	34,2	250	219	13				454
Ascocoryne sarcoides	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	NRRL 50072	Gp0039091	AIAA01	71021	pharmaceutical importance (antibiotic-producing); saprotroph	34,2	250,00	219	13				454
Glarea lozoyensis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	74030	Gp0020666	AGUE01	74639	pharmaceutical importance (produces antifugal compounds)	38,718	34,40	880	581	13083	46	Illumina HiSeq	
Glarea lozoyensis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	74030	Gp0020666	AGUE01	74639	pharmaceutical importance (produces antifugal compounds)	38,718	34,40	880	581	13083	46	Illumina HiSeq	
Hymenoscyphus fraxineus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 133217	Gp0124450	LLCC01	297734	plant pathogen (ash dieback)	51,52	90	4749			43,7	Illumina HiSeq	
Hymenoscyphus fraxineus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 133217	Gp0124450	LLCC01	297734	plant pathogen (ash dieback)	51,52	90,00	4749			43,7	Illumina HiSeq	
Hymenoscyphus fructigenus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 650.92	Gp0124451	LKUV01	298282	saprotroph	61,12	400	504			43,1	Illumina HiSeq	
Hymenoscyphus fructigenus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 650.92	Gp0124451	LKUV01	298282	saprotroph	61,12	400,00	504			43,1	Illumina HiSeq	
Hymenoscyphus infarciens	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 122016	Gp0124452	LLCB01	297733	saprotroph	68,15	250	1714			37,6	Illumina HiSeq	
Hymenoscyphus infarciens	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 122016	Gp0124452	LLCB01	297733	saprotroph	68,15	250,00	1714			37,6	Illumina HiSeq	
Hymenoscyphus laetus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 340.76	Gp0124448	LLCA01	297728	saprotroph	36,47	140				51,9	Illumina HiSeq	not publically available
Hymenoscyphus laetus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 340.76	Gp0124448	LLCA01	297728	saprotroph	36,47	140,00				51,9	Illumina HiSeq	
Hymenoscyphus repandus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 341.76	Gp0124456	LLCE01	297738	saprotroph	42,81	50	925			46,6	Illumina HiSeq	
Hymenoscyphus repandus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 341.76	Gp0124456	LLCE01	297738	saprotroph	42,81	50,00	925			46,6	Illumina HiSeq	
Hymenoscyphus salicellus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 111550	Gp0124453	LLCD01	297737	saprotroph	57,95	30				44,4	Illumina HiSeq	
Hymenoscyphus salicellus	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 111550	Gp0124453	LLCD01	297737	saprotroph	57,95	30,00				44,4	Illumina HiSeq	
Hymenoscyphus scutula	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 480.97	Gp0124454	LKTO01	297978	saprotroph	62,23	100	2591			41,1	Illumina HiSeq	
Hymenoscyphus scutula	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	CBS 480.97	Gp0124454	LKTO01	297978	saprotroph	62,23	100,00	2591			41,1	Illumina HiSeq	
Meliniomyces bicolor	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	E	Gp0009599	JGI	196026	mycorrhizal	82,38	190,6	301	206	18619		Illumina HiSeq	
Meliniomyces bicolor	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	E	Gp0009599	JGI	196026	mycorrhizal	82,38	190,60	301	206	18619		Illumina HiSeq	
Meliniomyces variabilis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	F	Gp0019251	JGI	200595	mycorrhizal	55,86	108,4	272	93	20389		Illumina HiSeq	
Meliniomyces variabilis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	F	Gp0019251	JGI	200595	mycorrhizal	55,86	108,40	272	93	20389		Illumina HiSeq	
Rhizoscyphus ericae	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Helotiaceae	UAMH 7357	Gp0019396	1006265	263050	mycorrhizal (ericoid)	57,41	120,90	1025	267	16784		Illumina HiSeq	
Calycina herbarum	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Hyaloscyphaceae	CBS 466.73	Gp0124449	LLEY01	298390	uncertain saprotroph	69,31	300	529			41,7	Illumina HiSeq	
Calycina herbarum	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Hyaloscyphaceae	CBS 466.73	Gp0124449	LLEY01	298390	uncertain saprotroph	69,31	300,00	529			41,7	Illumina HiSeq	
Acephala macrosclerotiorum	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Incertae sedis	EW76-UTF0540 v1.0		1034881		ectomycorrhizal	73,68	141,3	1901	1695	21024		Illumina	
Acephala macrosclerotiorum	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Incertae sedis	EW76-UTF0540 v1.0		1034881		ectomycorrhizal	73,68	141,30	1901	1695	21024		Illumina	
Cadophora sp. DSE1049	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Incertae sedis	DSE1049	Gp0046557	JGI	243951	endophyte (grasslands)	70,46	79,2	1294	1193	22766		Illumina HiSeq	
Cadophora sp. DSE1049	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Incertae sedis	DSE1049	Gp0046557	JGI	243951	endophyte (grasslands)	70,46	79,20	1294	1193	22766		Illumina HiSeq	
Cairneyiella heathii	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Incertae sedis	VPRI 42388	Gp0067908	AYLM01	225634	mycorrhizal	50,69	20,00	3371			50,69		
Chalara longipes	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Incertae sedis	BDJ	Gp0019347	JGI	213334	saprotroph	52,43	104,7	175	54	19765		Illumina	
Chalara longipes	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Incertae sedis	BDJ	Gp0019347	JGI	213334	saprotroph	52,43	104,70	175	54	19765		Illumina	
Leptodontium sp.	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Incertae sedis	PMI_412 v1.0	Gp0040004	1021550	243948	endophyte; root	73,78	140,9	966	815	22064		Illumina HiSeq	
Leptodontium sp.	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Incertae sedis	PMI_412 v1.0	Gp0040004	1021550	243948	endophyte; root	73,78	140,90	966	815	22064		Illumina HiSeq	
Loramyces juncicola	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Loramycetaceae	46458 v1.0		1045303		saprotroph; marine	42,68	86,5	240	58	14372		Illumina	
Loramyces juncicola	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Loramycetaceae	46458 v1.0		1045303		saprotroph; marine	42,68	86,50	240	58	14372		Illumina	
Oidiodendron maius	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Myxotrichaceae	Zn	Gp0009005	JGI	74727	endomycorrhizal; metal-tolerant	46,43	28,7	387	100	16703		454; Illumina	
Oidiodendron maius	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Myxotrichaceae	Zn	Gp0009005	JGI	74727	endomycorrhizal; metal-tolerant	46,43	28,70	387	100	16703		454; Illumina	
Rutstroemia firma	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Rutstroemiaceae	CBS 115.86 v1.0		1042909		saprotroph	44,27	81,90	367	48	13359		Illumina	
Rutstroemia sydowiana	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Rutstroemiaceae	CBS 115975	Gp0106337	JWJB01	254410	saprotroph	51,99	101	11777			43,1	Illumina MiSeq	
Rutstroemia sydowiana	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Rutstroemiaceae	CBS 115975	Gp0106337	JWJB01	254410	saprotroph	51,99	101,00	11777			43,1	Illumina MiSeq	
Botrytis cinerea (Botryotinia fuckel	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	B05.10	Gp0002499	AAID02	15632	plant pathogen (grapevines)	41,2	65	902	82	16584	43	Sanger	
Botrytis cinerea (Botryotinia fuckel	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	B05.10	Gp0002499	AAID02	15632	plant pathogen (grapevines)	41,2	65,00	902	82	16584	43	Sanger	
Botrytis paeoniae	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	AR05	Gp0117480	LBGX01	281662	plant pathogen (peony; Botrytis blight)	44,24	236	11700			41,1	IonTorrent	
Botrytis paeoniae	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	AR05	Gp0117480	LBGX01	281662	plant pathogen (peony; Botrytis blight)	44,24	236,00	11700			41,1	IonTorrent	
Ciborinia camelliae	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	ICMP 19812	Gp0124232	LGKQ01	289037	plant pathogen (ornamental camellia cultivars)	40,73	142	3291	2604		42,5	Illumina MiSeq	
Ciborinia camelliae	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	ICMP 19812	Gp0124232	LGKQ01	289037	plant pathogen (ornamental camellia cultivars)	40,73	142,00	3291	2604		42,5	Illumina MiSeq	
Rutstroemia (Sclerotinia) echinoph	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	CBS 111548		JWJA00000000		saprotroph	40,3			7.348	12555	43,1		
Rutstroemia (Sclerotinia) echinoph	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	CBS 111548		JWJA00000000		saprotroph	40,3			7348	12555	43,1		
Sclerotinia borealis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	F-4157	Gp0070994	AYSA01	227173	plant pathogen (cereals; sychrophilic)	39,45	23,00	1741	1241	10347	41,9		454
Sclerotinia borealis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	F-4157	Gp0070994	AYSA01	227173	plant pathogen (cereals; sychrophilic)	39,45	23,00	1741	1241	10347	41,9		454
Sclerotinia homoeocarpa	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	ShHRS10	Gp0142968	LNGN01	302176	plant pathogen (turfgrass)	42,27	50	560	231		43,9	Illumina HiSeq; PacBio	
Sclerotinia homoeocarpa	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	ShHRS10	Gp0142968	LNGN01	302176	plant pathogen (turfgrass)	42,27	50,00	560	231		43,9	Illumina HiSeq; PacBio	
Sclerotinia sclerotiorum	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	ATCC 18683	Gp0002703	AAGT01	15530	plant pathogen (broadest host range known)	38,532	8,00	682	39	14637	41,8	Sanger	
Sclerotinia sclerotiorum	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Sclerotiniaceae	ATCC 18683	Gp0002703	AAGT01	15530	plant pathogen (broadest host range known)	38,532	8,00	682	39	14637	41,8	Sanger	
Phialocephala scopiformis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Vibrisseaceae	CBS 120377	Gp0046824	LKNI01	262390	endophyte	48,88		345	71	18567	47,6	Illumina HiSeq	
Phialocephala scopiformis	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Vibrisseaceae	CBS 120377	Gp0046824	LKNI01	262390	endophyte	48,88		345	71	18567	47,6	Illumina HiSeq	
Amorphotheca resinae	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Incertae sedis	Amorphothecaceae	DAOM 194228	Gp0020936	JGI	207866	industrial importance	28,63	42,94	261	32	9642		454-GS-FLX-Titanium; Illumina HiSeq	
Amorphotheca resinae	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Incertae sedis	Amorphothecaceae	DAOM 194228	Gp0020936	JGI	207866	industrial importance	28,63	42,94	261	32	9642		454-GS-FLX-Titanium; Illumina HiSeq	
Pseudogymnoascus destructans	Ascomycota	Pezizomycotina	Leotiomycetes	Incertae sedis	Incertae sedis	Pseudeurotiaceae	M1379	Gp0070898	AYKP01	225231	animal pathogen (white nose syndrome in bats); psychrophile	30,282	150,00	5304		9225	50,1	Illumina HiSeq	
Pseudogymnoascus destructans	Ascomycota	Pezizomycotina	Leotiomycetes	Incertae sedis	Incertae sedis	Pseudeurotiaceae	M1379	Gp0070898	AYKP01	225231	animal pathogen (white nose syndrome in bats); psychrophile	30,282	150,00	5304		9225	50,1	Illumina HiSeq	
Pseudogymnoascus pannorum	Ascomycota	Pezizomycotina	Leotiomycetes	Incertae sedis	Incertae sedis	Pseudeurotiaceae	M1372	Gp0068134	AYKR01	225336	human pathogen (geomycosis); soil-dwelling psychrophile	29,455	100,00	971			50,5	Illumina HiSeq	
Pseudogymnoascus pannorum	Ascomycota	Pezizomycotina	Leotiomycetes	Incertae sedis	Incertae sedis	Pseudeurotiaceae	M1372	Gp0068134	AYKR01	225336	human pathogen (geomycosis); soil-dwelling psychrophile	29,455	100,00	971			50,5	Illumina HiSeq	
Pseudogymnoascus sp. BL549	Ascomycota	Pezizomycotina	Leotiomycetes	Incertae sedis	Incertae sedis	Pseudeurotiaceae	BL549	Gp0150255	LNAR01	299331	soil-associated	25,86	26,00	2455	2106		51,1	Illumina	
Rutstroemia firma	Ascomycota	Pezizomycotina	Leotiomycetes	Leotiomycetidae	Helotiales	Rutstroemiaceae	CBS 115.86 v1.0		1042909		saprotroph	44,27	81,9	367	48	13359		Illumina	
Arthrobotrys oligospora	Ascomycota	Pezizomycotina	Orbiliomycetes	Orbiliomycetidae	Orbiliales	Orbiliaceae	ATCC 24927	Gp0005961	ADOT01	41495	biocontrol (nematophagous)	40,1	33	323	215			Sanger; 454	
Arthrobotrys oligospora	Ascomycota	Pezizomycotina	Orbiliomycetes	Orbiliomycetidae	Orbiliales	Orbiliaceae	ATCC 24927	Gp0005961	ADOT01	41495	biocontrol (nematophagous)	40,1	33,00	323	215			Sanger; 454	
Dactylellina haptotyla	Ascomycota	Pezizomycotina	Orbiliomycetes	Orbiliomycetidae	Orbiliales	Orbiliaceae	CBS 200.50	Gp0047799	AQGS01	186729	biocontrol (nematophagous)	39,531	28,00	1343	1279	10959	45,3		454
Dactylellina haptotyla	Ascomycota	Pezizomycotina	Orbiliomycetes	Orbiliomycetidae	Orbiliales	Orbiliaceae	CBS 200.50	Gp0047799	AQGS01	186729	biocontrol (nematophagous)	39,531	28,00	1343	1279	10959	45,3		454

Drechslerella stenobrocha	Ascomycota	Pezizomycotina	Orbiliomycetes	Orbiliomycetidae	Orbiliales	Orbiliaceae	YNWS02-9-1	Gp0005661			biocontrol (nematophagous)	29,02	80,00		142	7781		Illumina	
Drechslerella stenobrocha	Ascomycota	Pezizomycotina	Orbiliomycetes	Orbiliomycetidae	Orbiliales	Orbiliaceae	YNWS02-9-1	Gp0005661			biocontrol (nematophagous)	29,02	80,00		142	7781		Illumina	
Ascobolus immersus	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Ascobolaceae	RN42	Gp0017640	JGI	250965	coprophilous	59,53	86,3	1225	706	17877		Illumina HiSeq	
Ascobolus immersus	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Ascobolaceae	RN42	Gp0017640	JGI	250965	coprophilous	59,53	86,30	1225	706	17877		Illumina HiSeq	
Ascodesmis nigricans	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Ascodesmidaceae	CBS 389.68	Gp0090695	1034820	247594	coprophilous	27,39	96,90	407	176	9622		Illumina	
Caloscypha fulgens	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Caloscyphaceae	ATCC 42695 v1.0		1052670		plant pathogen (seed rot of conifers)	44,84		405	405	9203		Illumina	
Caloscypha fulgens	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Caloscyphaceae	ATCC 42695 v1.0		1052670		plant pathogen (seed rot of conifers)	44,84		405	405	9203		Illumina	
Gyromitra esculenta	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Discinaceae	CBS101906 v1.0		1051239		saprotroph	45,05	83,6	774	271	11202		Illumina	
Gyromitra esculenta	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Discinaceae	CBS101906 v1.0		1051239		saprotroph	45,05	83,60	774	271	11202		Illumina	
Morchella conica	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Morchellaceae	CCBAS932	Gp0044465	JGI	217205	mycorrhizal; saprotroph	48,21	67,80	1793	540	11600		Illumina HiSeq	
Morchella conica	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Morchellaceae	CCBAS932	Gp0044465	JGI	217205	mycorrhizal; saprotroph	48,21	67,80	1793	540	11600		Illumina HiSeq	
Morchella importuna	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Morchellaceae	SCYDJ1-A1 v1.0		1047733		saprotroph; edible	48,8	83,9	1509	338	11971		Illumina	
Morchella importuna	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Morchellaceae	SCYDJ1-A1 v1.0		1047733		saprotroph; edible	48,8	83,90	1509	338	11971		Illumina	
Kalaharituber pfeilii	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pezizaceae	F3 v1.0		1060175		mycorrhizal; edible desert truffle	78,99		595	595	15190		PacBio	
Kalaharituber pfeilii	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pezizaceae	F3 v1.0		1060175		mycorrhizal; edible desert truffle	78,99		595	595	15190		PacBio	
Terfezia boudieri	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pezizaceae	S1	Gp0009600	JGI	200599	mycorrhizal	63,23	104,4	2078	516	10200		454; Illumina; PacBio	
Terfezia boudieri	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pezizaceae	S1	Gp0009600	JGI	200599	mycorrhizal	63,23	104,40	2078	516	10200		454; Illumina; PacBio	
Pyronema confluens	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pyronemataceae	CBS 100304	Gp0035318	CATG00000000	65573	saprotroph (soil)	50,03		1865	1588	13367	48	454; Illumina HiSeq	
Pyronema confluens	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pyronemataceae	CBS 100304	Gp0035318	CATG00000000	65573	saprotroph (soil)	50,03		1865	1588	13367	48	454; Illumina HiSeq	
Ramularia collo-cygni	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pyronemataceae		Gs0120586	CZLF01	306455	plant pathogen (barley)	30,3	90,00	832	576	11617	51,4		
Ramularia collo-cygni	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pyronemataceae		Gs0120586	CZLF01	306455	plant pathogen (barley)	30,3	90,00	832	576	11617	51,4		
Wilcoxina mikolae	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pyronemataceae	CBS 423.85	Gp0035338	JGI	196022	ectomycorrhizal	117,29	95	5591	1604	13093		Illumina HiSeq; PacBio	
Wilcoxina mikolae	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Pyronemataceae	CBS 423.85	Gp0035338	JGI	196022	ectomycorrhizal	117,29	95,00	5591	1604	13093		Illumina HiSeq; PacBio	
Sarcoscypha coccinea	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Sarcoscyphaceae	ATCC 58028 v1.0		1042915		saprotroph	39,09	95,9	1481	461	13738		Illumina	
Sarcoscypha coccinea	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Sarcoscyphaceae	ATCC 58028 v1.0		1042915		saprotroph	39,09	95,90	1481	461	13738		Illumina	
Plectania melastoma	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Sarcosomataceae	CBS 918.72 v1.0		1040543		saprotroph	92,51	72,3	504	175	16180		Illumina	
Plectania melastoma	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Sarcosomataceae	CBS 918.72 v1.0		1040543		saprotroph	92,51	72,30	504	175	16180		Illumina	
Choiromyces venosus	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Tuberaceae	120613-1	Gp0035337	JGI	204096	ectomycorrhizal	126,04	89,5	3183	1176	17986		Illumina; PacBio	
Choiromyces venosus	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Tuberaceae	120613-1	Gp0035337	JGI	204096	ectomycorrhizal	126,04	89,50	3183	1176	17986		Illumina; PacBio	
Tuber borchii	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Tuberaceae	Tbo3840	Go0002708	1034997		ectomycorrhizal	97,18	97,00	969	969	12346		PacBio	
Tuber melanosporum	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Tuberaceae	Mel28	Gp0002709	CABJ01	38847	ectomycorrhizal (edible delicacy)	124,945	10,00	4440	398	7496	45	Sanger	
Tuber melanosporum	Ascomycota	Pezizomycotina	Pezizomycetes	Pezizomycetidae	Pezizales	Tuberaceae	Mel28	Gp0002709	CABJ01	38847	ectomycorrhizal (edible delicacy)	124,945	10,00	4440	398	7496	45	Sanger	
Microdochium bolleyi	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Amphisphaeriales	Incertae sedis	J235TASD1	Gp0113784	LSSP01	308023	endophyte	38,84	136,20	262	173	13165	57,1	HiSeq 2500	
Pestalotiopsis fici	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Amphisphaeriales	Pestalotiopsidaceae	W106-1	Gp0038703	ARNU01	174299	endophyte	51,91	80,00	518	39	15413	52	454; Illumina HiSeq	
Pestalotiopsis sp. JCM 9685	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Amphisphaeriales	Pestalotiopsidaceae	JCM 9685	Gp0149822	BCGF01	313890	endophyte (Taxus brevifolia)	48,23	235,00	130	13		51,6	Illumina	
Thozetella sp. PMI_491	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Chaetosphaeriales	Chaetosphaeriaceae	PMI_491	Gp0039995	JGI	251777	endophyte	72,86	112,6	627	194	23281		Illumina HiSeq	
Thozetella sp. PMI_491	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Chaetosphaeriales	Chaetosphaeriaceae	PMI_491	Gp0039995	JGI	251777	endophyte	72,86	112,60	627	194	23281		Illumina HiSeq	
Coniochaeta ligniaria	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Coniochaetales	Coniochaetaceae	NRRL 30616	Gp0036825	JGI	223108	industrial importance	42,38	94,40	230	135	13657		Illumina HiSeq	
Coniochaeta ligniaria	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Coniochaetales	Coniochaetaceae	NRRL 30616	Gp0036825	JGI	223108	industrial importance	42,38	94,40	230	135	13657		Illumina HiSeq	
Coniochaeta sp. PMI_546	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Coniochaetales	Coniochaetaceae	PMI_546	Gp0039950	JGI	234867	endophyte (root); saproptroph	33,51	102	68	37	11346		Illumina HiSeq	
Coniochaeta sp. PMI_546	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Coniochaetales	Coniochaetaceae	PMI_546	Gp0039950	JGI	234867	endophyte (root); saproptroph	33,51	102,00	68	37	11346		Illumina HiSeq	
Chrysoporthe austroafricana	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Cryphonectriaceae	CMW 2113	Gp0146002	JYIP01	263707	plant pathogen (eucalyptus, Tibouchina, Syzygium)	44,66	40	6415			54,3	Illumina MiSeq; IonTorrent	
Chrysoporthe austroafricana	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Cryphonectriaceae	CMW 2113	Gp0146002	JYIP01	263707	plant pathogen (eucalyptus, Tibouchina, Syzygium)	44,66	40,00	6415			54,3	Illumina MiSeq; IonTorrent	
Chrysoporthe cubensis	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Cryphonectriaceae	CMW 10028	Gp0117564	LJCY01	264999	plant pathogen (eucalyptus, Tibouchina, Syzygium)	42,62	40	1257	954		55,1	Illumina MiSeq	
Chrysoporthe cubensis	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Cryphonectriaceae	CMW 10028	Gp0117564	LJCY01	264999	plant pathogen (eucalyptus, Tibouchina, Syzygium)	42,62	40,00	1257	954		55,1	Illumina MiSeq	
Chrysoporthe deuterocubensis	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Cryphonectriaceae	CMW 8650	Gp0117565	LJDD01	265023	plant pathogen (eucalyptus, Tibouchina, Syzygium)	43,97	45	3126	2574		55,3	Illumina MiSeq	
Chrysoporthe deuterocubensis	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Cryphonectriaceae	CMW 8650	Gp0117565	LJDD01	265023	plant pathogen (eucalyptus, Tibouchina, Syzygium)	43,97	45,00	3126	2574		55,3	Illumina MiSeq	
Cryphonectria parasitica	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Cryphonectriaceae	EP155	Gp0002604	JGI	207842	plant pathogen (chestnut blight)	43,9	8,54	33	26	11184			
Cryphonectria parasitica	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Cryphonectriaceae	EP155	Gp0002604	JGI	207842	plant pathogen (chestnut blight)	43,9	8,54	33	26	11184			
Diaporthe ampelina	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Diaporthaceae	UCDDA912	Gp0117694	LCUC01	261766	endophyte	47,33	50	3116	2383		59,5	Illumina HiSeq	
Diaporthe ampelina	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Diaporthaceae	UCDDA912	Gp0117694	LCUC01	261766	endophyte	47,33	50,00	3116	2383		59,5	Illumina HiSeq	
Diaporthe aspalathi	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Diaporthaceae	DPM001935	Gp0144055	LJJS01	295230	plant pathogen (soybean stem canker)	55,03	100	5371	1871		51,6	Illumina HiSeq	
Diaporthe aspalathi	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Diaporthaceae	DPM001935	Gp0144055	LJJS01	295230	plant pathogen (soybean stem canker)	55,03	100,00	5371	1871		51,6	Illumina HiSeq	
Diaporthe longicolla	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Diaporthaceae	MS10-6	Gp0038530	AYRD01	174445	plant pathogen (soybean)	62,26	97,00	8023	5943			Illumina HiSeq	
Diaporthe longicolla	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Diaporthaceae	MS10-6	Gp0038530	AYRD01	174445	plant pathogen (soybean)	62,26	97,00	8023	5943			Illumina HiSeq	
Ophiognomonia clavigignenti-jugla	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Gnomoniaceae	pooled sample	Gp0008964	AEGN01	52061	plant pathogen (butternut)	15,906	2,13	28868			48,8		454
Ophiognomonia clavigignenti-jugla	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Gnomoniaceae	pooled sample	Gp0008964	AEGN01	52061	plant pathogen (butternut)	15,906	2,13	28868			48,8		454
Lollipopaia minuta	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Incertae sedis	CBS 116597 v1.0		1032359		saprotroph tropical	37,42	138	427	380	11996		Illumina	
Lollipopaia minuta	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Incertae sedis	CBS 116597 v1.0		1032359		saprotroph tropical	37,42	138,00	427	380	11996		Illumina	
Melanconium sp. 1 NRRL 54901	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Melanconidaceae	NRRL 54901	Gp0019267	JGI	207856	plant pathogen (probable maize pathogen)	58,52	92,80	465	100	16656		Illumina	
Melanconium sp. 1 NRRL 54901	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Melanconidaceae	NRRL 54901	Gp0019267	JGI	207856	plant pathogen (probable maize pathogen)	58,52	92,80	465	100	16656		Illumina	
Valsa mali	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Valsaceae	SXYL134	Gp0118828	JUIZ01	268128	plant pathogen (apple & pear)	35,73	180	2917	475	11165	49,3	Illumina GAIIx	
Valsa mali	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Diaporthales	Valsaceae	SXYL134	Gp0118828	JUIZ01	268128	plant pathogen (apple & pear)	35,73	180,00	2917	475	11165	49,3	Illumina GAIIx	
Acremonium chrysogenum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Plectosphaerellaceae	ATCC 11550	Gp0095146	JPKY00000000.1	248608	industrial importance; pharamceutical importance	28,5	137		543	8901		Illumina HiSeq	
Acremonium furcatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Plectosphaerellaceae	JCM 9210	Gp0144039	BCIA01	313827	biocontrol (mycoparasite)	40,32	281	94	9		57,7	HiSeq 2500	
Colletotrichum godetiae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	CBS 193.32 v1.0		1060998		insect-associated	51,65	235	194	194	16071		PacBio	
Colletotrichum lupini	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	CBS 109225 v1.0		1061002		plant pathogen (Lupinus flowering plants)	58,76	97	116	116	15365		PacBio	
Colletotrichum caudatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	CBS131602 v1.0		1006149		plant pathogen (warm-season grasses)	44,2	143	1381	1257	15294		Illumina	
Colletotrichum caudatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	CBS131602 v1.0		1006149		plant pathogen (warm-season grasses)	44,2	143,00	1381	1257	15294		Illumina	
Colletotrichum falcatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	Cf671	Gp0124244	LPVI01	272959	plant pathogen (sugar-cane red rot)	48,19	150	6400	4358		51,6		
Colletotrichum falcatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	Cf671	Gp0124244	LPVI01	272959	plant pathogen (sugar-cane red rot)	48,19	150,00	6400	4358		51,6		
Colletotrichum fioriniae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	MH 18	Gp0019317	JGI	196041	plant pathogen (anthracnose in various fruit)	49		3756	1096	13759	52,5	Illumina HiSeq	
Colletotrichum fioriniae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	MH 18	Gp0019317	JGI	196041	plant pathogen (anthracnose in various fruit)	49		3756	1096	13759	52,5	Illumina HiSeq	
Colletotrichum gloeosporioides	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	Nara gc5	Gp0038653	ANPB01	171218	plant pathogen (disease and anthracnose on a range of fuit and vegetables	55,6	37,00	5335	1241	15469	53,6	Illumina HiSeq	
Colletotrichum gloeosporioides	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	Nara gc5	Gp0038653	ANPB01	171218	plant pathogen (disease and anthracnose on a range of fuit and vegetables	55,6	37,00	5335	1241	15469	53,6	Illumina HiSeq	
Colletotrichum godetiae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	CBS 193.32 v1.0		1060998		insect-associated	51,65	235,00	194	194	16071		PacBio	
Colletotrichum graminicola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	M1.001	Gp0004788	ACOD01	37879	plant pathogen (anthracnose in cereals)	51,64	9,00	1152	654	12400	49,1	454; Sanger	
Colletotrichum graminicola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	M1.001	Gp0004788	ACOD01	37879	plant pathogen (anthracnose in cereals)	51,64	9,00	1152	654	12400	49,1	454; Sanger	
Colletotrichum higginsianum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	IMI 349063	Gp0008317	CACQ02	47061	plant pathogen (anthracnose in Brassicaceae)	44,11		10235		16596	55,1		
Colletotrichum higginsianum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerallales	Glomerellaceae	IMI 349063	Gp0008317	CACQ02	47061	plant pathogen (anthracnose in Brassicaceae)	44,11		10235		16596	55,1		
Colletotrichum incanum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	MAFF 238704	Gp0150230	LFIW01	286717	plant pathogen (broad host range; including soybean)	53,6	230,00	2908	2896	12809			
Colletotrichum lupini	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	CBS 109225 v1.0		1061002		plant pathogen (Lupinus flowering plants)	58,76	97,00	116	116	15365		PacBio	
Colletotrichum orbiculare	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	MAFF 240422	Gp0038654	AMCV01	171217	plant pathogen (melons and cucumber)	90	55,00	8092	3370	13393	37,6	454; Illumina GAIIx	
Colletotrichum orbiculare	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	MAFF 240422	Gp0038654	AMCV01	171217	plant pathogen (melons and cucumber)	90	55,00	8092	3370	13393	37,6	454; Illumina GAIIx	
Colletotrichum phormii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	CBS102054	Go0111565	1060996	333354	plant pathogen (anthracnose on flax)	51,67	97,00	71	71	15209		PacBio	
Colletotrichum salicis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	CBS 607.94	Gp0090026	JFFI01	238477	plant pathogen (black canker of willow)	48,37	40,40	5121	2776	13783	52,8		
Colletotrichum simmondsii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	CBS122122	Gp0122385	JFBX01	239224	plant pathogen (safflower oil crop)	50,47	39,38	3860	929	13884	51,7	Illumina	
Colletotrichum simmondsii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	CBS122122	Gp0122385	JFBX01	239224	plant pathogen (safflower oil crop)	50,47	39,38	3860	929	13884	51,7	Illumina	
Colletotrichum sublineola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	TX430BB	Gp0094476	JMSE01	246670	plant pathogen (anthracnose in wild rice and sorghum)	46,75	92,00	13516		12699	53,3	Illumina GAII	
Colletotrichum sublineola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	TX430BB	Gp0094476	JMSE01	246670	plant pathogen (anthracnose in wild rice and sorghum)	46,75	92,00	13516		12699	53,3	Illumina GAII	
Colletotrichum tofieldiae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	CBS 168.49	Gp0150227	LFHQ01	286723	endophyte (root)	52,96	300,00	1303	1300			Illumina	
Colletotrichum zoysiae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Glomerellaceae	MAFF235873		1043139	262217	plant pathogen (warm-season grasses)	46,53	102,80	722	617	15326		Illumina	
Acremonium chrysogenum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	ATCC 11550	Gp0095146	JPKY00000000.1	248608	industrial importance; pharamceutical importance	28,5	137,00		543	8901		Illumina HiSeq	
Acremonium furcatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	JCM 9210	Gp0144039	BCIA01	313827	biocontrol (mycoparasite)	40,32	281,00	94	9		57,7	HiSeq 2500	
Sodiomyces alkalinus	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	F11	Gp0022516	JGI	196044	alkaliphile	43,45	113,5	290	29	9411		Illumina	
Sodiomyces alkalinus	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	F11	Gp0022516	JGI	196044	alkaliphile	43,45	113,50	290	29	9411		Illumina	
Verticillium alfalfae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	VaMs.102	Gp0005850	ABPE01	29511	plant pathogen (broad host range); wilt disease	32,83	4,08	4147	26	10221	56	Sanger	
Verticillium alfalfae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	VaMs.102	Gp0005850	ABPE01	29511	plant pathogen (broad host range); wilt disease	32,83	4,08	4147	26	10221	56	Sanger	
Verticillium dahliae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	VdLs.17	Gp0003474	ABJE01	28529	plant pathogen (broad host range); wilt disease	33,9	7,40	1565	55	10811	56		
Verticillium dahliae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	VdLs.17	Gp0003474	ABJE01	28529	plant pathogen (broad host range); wilt disease	33,9	7,40	1565	55	10811	56		
Verticillium longisporum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	VL1	Gp0143280	CVQH01	285310	plant pathogen (canola)	99,19		38029	28081	20793	53,9		

Verticillium longisporum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	VL1	Gp0143280	CVQH01	285310	plant pathogen (canola)	99,19		38029	28081	20793	53,9	
Verticillium tricorpus	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	MUCL9297	Gp0076233	JPET01	229139	opportunistic plant pathogen (lettuce); saprotroph	36,06	65,00	251			57,3	Illumina HiSeq; PacBio
Verticillium tricorpus	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Glomerellales	Plectosphaerellaceae	MUCL9297	Gp0076233	JPET01	229139	opportunistic plant pathogen (lettuce); saprotroph	36,06	65,00	251			57,3	Illumina HiSeq; PacBio
Clonostachys rosea	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Bionectriaceae	CBS 125111	Gp0072263	JGI	247918	endophyte; saprotroph; parasite; biocontrol	52,44	59	774	74	18639		Illumina HiSeq
Clonostachys rosea	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Bionectriaceae	CBS 125111	Gp0072263	JGI	247918	endophyte; saprotroph; parasite; biocontrol	52,44	59,00	774	74	18639		Illumina HiSeq
Gliomastix tumulicola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Bionectriaceae	JCM 17184	Gp0144014	BCHX01	313824	uncertain	42,39	295	194	72		54,8	HiSeq 2500
Gliomastix tumulicola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Bionectriaceae	JCM 17184	Gp0144014	BCHX01	313824	uncertain	42,39	295,00	194	72		54,8	HiSeq 2500
Stanjemonium grisellum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Bionectriaceae	CBS 655.79	Gp0050687	1029499	239486	soil-associated	33	103,00	831	151	11832		Illumina
Aciculosporium take	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	MAFF-241224	Gp0038974	University of Kentucky	67241	plant pathogen (bamboo parasite)	58,836	18,5	3298			40,1	454 GS FLX Titanium
Aciculosporium take	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	MAFF-241224	Gp0038974	University of Kentucky	67241	plant pathogen (bamboo parasite)	58,836	18,50	3298			40,1	454 GS FLX Titanium
Aschersonia aleyrodis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	RCEF 2490	Gp0039338	AZGY01	72735	entomopathogen	30,87	76,00	604	97	8461	30,87	Illumina HiSeq
Atkinsonella hypoxylon	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	B4728	Gp0067879	JFHB01	221544	parasite (systemic grass)	35,6	31,60	688				454
Atkinsonella hypoxylon	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	B4728	Gp0067879	JFHB01	221544	parasite (systemic grass)	35,6	31,60	688				454
Atkinsonella texensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	B6155	Gp0120993	LBNC01	274998	epiphyte	29,37	63,7	3966	2630		49,8	Illumina MiSeq
Atkinsonella texensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	B6155	Gp0120993	LBNC01	274998	epiphyte	29,37	63,70	3966	2630		49,8	Illumina MiSeq
Balansia obtecta	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	B249	Gp0047672	JFZS01	221345	parasite (systemic grass)	30,1	21,6	1552			48,5	
Balansia obtecta	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	B249	Gp0047672	JFZS01	221345	parasite (systemic grass)	30,1	21,60	1552			48,5	
Claviceps fusiformis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	PRL 1980	Gp0038970	AFRA01	67243	plant pathogen (pearl millet)	52,585	34,90	6930			36,9	454
Claviceps fusiformis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	PRL 1980	Gp0038970	AFRA01	67243	plant pathogen (pearl millet)	52,585	34,90	6930			36,9	454
Claviceps paspali	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	7990	Gp0008743	AFRC01	51623	medical importance (ergot fungus; mycotoxin-producing)	28,97	54,40	2304			47,5	454
Claviceps paspali	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	7990	Gp0008743	AFRC01	51623	medical importance (ergot fungus; mycotoxin-producing)	28,97	54,40	2304			47,5	454
Claviceps purpurea	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	20,1	Gp0038662	CAGA01	76493	plant pathogen (cereals)	32,09		191		8979	51,6	
Claviceps purpurea	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	20,1	Gp0038662	CAGA01	76493	plant pathogen (cereals)	32,09		191		8979	51,6	
Epichloe (Neotyphodium) gansuens	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E7080		AFRE01	174039	endophyte (grass)	39,62	41,50	1621			44,4	454
Epichloe amarillans	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E57	Gp0038968	AFRF01	67301	endophyte; plant pathogen	38,06	27,70	2180	2180		44,3	454
Epichloe amarillans	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E57	Gp0038968	AFRF01	67301	endophyte; plant pathogen	38,06	27,70	2180	2180		44,3	454
Epichloe baconii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ATCC 200745	Gp0068053	JFGY01	221976	endophyte; plant pathogen	38,08	18,40	3603			41,6	454
Epichloe baconii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ATCC 200745	Gp0068053	JFGY01	221976	endophyte; plant pathogen	38,08	18,40	3603			41,6	454
Epichloe brachyelytri	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E4804	Gp0038969	AFRB01	67245	endophyte; plant pathogen	44,23	24,60	5136			40,2	454
Epichloe brachyelytri	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E4804	Gp0038969	AFRB01	67245	endophyte; plant pathogen	44,23	24,60	5136			40,2	454
Epichloe bromicola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ATCC 200750	Gp0047721	JFHA01	221343	endophyte; plant pathogen	28,57	6,70	16548			45,3	454
Epichloe bromicola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ATCC 200750	Gp0047721	JFHA01	221343	endophyte; plant pathogen	28,57	6,70	16548			45,3	454
Epichloe elymi	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E56	Gp0039395	AMDJ01	173776	endophyte	32,335	31,80	6988			46,6	454; Ion Torrent
Epichloe elymi	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E56	Gp0039395	AMDJ01	173776	endophyte	32,335	31,80	6988			46,6	454; Ion Torrent
Epichloe festucae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	FI1	Gp0008744	AFRX01	51625	endophyte	35,105	27,80	1722	799		44,1	454; Sanger
Epichloe festucae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	FI1	Gp0008744	AFRX01	51625	endophyte	35,105	27,80	1722	799		44,1	454; Sanger
Epichloe glyceriae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E277	Gp0038972	AFRG01	67247	endophyte; plant pathogen	46,72	27,70	3076			45	454
Epichloe glyceriae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E277	Gp0038972	AFRG01	67247	endophyte; plant pathogen	46,72	27,70	3076			45	454
Epichloe mollis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	AL9924	Gp0047723	JFGW01	215230	endophyte; plant pathogen	36,169	28,00	1068			44	454
Epichloe mollis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	AL9924	Gp0047723	JFGW01	215230	endophyte; plant pathogen	36,169	28,00	1068			44	454
Epichloe sylvatica	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	GR10156	Gp0120997	LCTT01	275112	endophyte; plant pathogen (woodland grass sp.)	36,1	160	36463			44,8	Illumina MiSeq
Epichloe sylvatica	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	GR10156	Gp0120997	LCTT01	275112	endophyte; plant pathogen (woodland grass sp.)	36,1	160,00	36463			44,8	Illumina MiSeq
Epichloe typhina	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E5819	Gp0038966	AFSE01	68441	plant pathogen (Poaceae)	34,185	18,50	2556			41,5	454
Epichloe typhina	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E5819	Gp0038966	AFSE01	68441	plant pathogen (Poaceae)	34,185	18,50	2556			41,5	454
Epichloe uncinata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	e167	Gp0120998	LELE01	275109	endophyte (grasses)	53,34	131,4	23517	23102		49,6	Illumina MiSeq
Epichloe uncinata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	e167	Gp0120998	LELE01	275109	endophyte (grasses)	53,34	131,40	23517	23102		49,6	Illumina MiSeq
Hypocrella siamensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	MTCC 10142	Gp0091946	JMQE01	242986	entomopathogenic	28,856	90,00	2034			53,1	Illumina HiSeq
Hypocrella siamensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	MTCC 10142	Gp0091946	JMQE01	242986	entomopathogen	28,856	90,00	2034			53,1	Illumina HiSeq
Metacordyceps chlamydosporia	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	123	Gp0038416	AOSW01	68669	biocontrol (nematophagous)	42,462	136,00	8574	956		49,7	Illumina HiSeq
Metacordyceps chlamydosporia	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	123	Gp0038416	AOSW01	68669	biocontrol (nematophagous)	42,462	136,00	8574	956		49,7	Illumina HiSeq
Metarhizium acridum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	CQMa102	Gp0006357	ADNI01	38715	entomopathogenic ; biocontrol	39,422	113,00	1608	241	9974	49,9	Illumina
Metarhizium album	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ARSEF 1941	Gp0039284	AZHE01	72731	entomopathogen	30,45	117,07	731	257	8472	30,45	Illumina HiSeq
Metarhizium anisopliae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ARSEF 23	Gp0006292	ADNJ01	38717	entomopathogenic ; biocontrol	39,145	100,00	1265	176	10726	51,5	Illumina
Metarhizium anisopliae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ARSEF 23	Gp0006292	ADNJ01	38717	entomopathogen ; biocontrol	39,145	100,00	1265	176	10726	51,5	Illumina
Metarhizium brunneum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ARSEF 3297	Gp0039279	AZNG01	184756	biocontrol (entomopathogen)	37,07	80,13	180	92	10689	51,5	Illumina HiSeq
Metarhizium guizhouense	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ARSEF 977	Gp0039280	AZNH01	184755	biocontrol (entomopathogen)	43,47	95,42	1111	563	11787	49,6	Illumina HiSeq
Metarhizium majus	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ARSEF 297	Gp0039281	AZNE01	184757	biocontrol (entomopathogen)	42,02	71,17	1847	1134	11535	51	Illumina HiSeq
Metarhizium rileyi	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	RCEF 4871	Gp0039340	AZHC01	72739	entomopathogen	32,01	107,34	1000	389	8764	49,3	Illumina HiSeq
Metarhizium robertsii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ARSEF 2575	Gp0076192	ELW01	230500	parasite (arthropod)	40,317	25,00	464		12479	50,8	454
Metarhizium robertsii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ARSEF 2575	Gp0076192	ELW01	230500	parasite (arthropod)	40,317	25,00	464		12479	50,8	454
Neotyphodium aotearoae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ATCC MYA-1229	Gp0070855	JFGX01	221524	endophyte (grass)	34,423	26,30	2094			43,6	454
Neotyphodium aotearoae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	ATCC MYA-1229	Gp0070855	JFGX01	221524	endophyte (grass)	34,423	26,30	2094			43,6	454
Neotyphodium gansuense	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E7080	Gp0038971	AFRE01	67299	endophyte (grass); medical importance (mycotoxin-producing)	39,616	41,50	1621			44,4	454
Neotyphodium gansuense	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	E7080	Gp0038971	AFRE01	67299	endophyte (grass); medical importance (mycotoxin-producing)	39,616	41,50	1621			44,4	454
Paecilomyces hepiali	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	FENG	Gp0143068	LNDK02	301665	pharmaceutical importance (anticancer properties)	34,68	100	287	129		53,9	Illumina HiSeq
Paecilomyces hepiali	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	FENG	Gp0143068	LNDK02	301665	pharmaceutical importance (anticancer properties)	34,68	100,00	287	129		53,9	Illumina HiSeq
Periglandula ipomoeae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	IasaF13	Gp0038973	AFRD01	67303	pharmaceutical importance (ergoline-alkaloid-producing)	35,3		864			50,6	454
Periglandula ipomoeae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	IasaF13	Gp0038973	AFRD01	67303	pharmaceutical importance (ergoline-alkaloid-producing)	35,3		864			50,6	454
Tolypocladium inflatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	NRRL 8044	Gp0038458	AOHE01	73163	entomopathogen	30,217	82,00	194			58	454; Illumina
Tolypocladium inflatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	NRRL 8044	Gp0038458	AOHE01	73163	entomopathogen	30,217	82,00	194			58	454; Illumina
Torrubiella hemipterigena	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	BCC 1449	Gp0122800	CDHN01	268463	entomopathogen	28,48		56	26	11471	50,6	
Torrubiella hemipterigena	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	BCC 1449	Gp0122800	CDHN01	268463	entomopathogen	28,48		56	26	11471	50,6	
Villosiclava virens	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	UV-8b	Gp0094980	JHTR01	240653	plant pathogen; (false smut of rice)	39,397	142,00	3155		8426	49,9	454; Illumina HiSeq
Villosiclava virens	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Clavicipitaceae	UV-8b	Gp0094980	JHTR01	240653	plant pathogen; (false smut of rice)	39,397	142,00	3155		8426	49,9	454; Illumina HiSeq
Beauveria bassiana	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	ARSEF 2860	Gp0005962	ADAH01	38719	entomopathogenic	33,69	28,00	1229	237	10364	51,5	454
Beauveria bassiana	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	ARSEF 2860	Gp0005962	ADAH01	38719	entomopathogen	33,69	28,00	1229	237	10364	51,5	454
Beauveria sp. YA-2014	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	YA-2014 MTCC8017	Gp0093215	JMNB01	242988	insect-associated	36,58	66,00	4708			50,1	Illumina HiSeq
Beauveria sp. YA-2014	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	YA-2014 MTCC8017	Gp0093215	JMNB01	242988	insect-associated	36,58	66,00	4708			50,1	Illumina HiSeq
Cordyceps brongniartii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	RCEF 3172	Gp0039312	AZHA01	72729	entomopathogen	32,52	73,46	967	241	9595	51,5	Illumina HiSeq
Cordyceps cicadae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	BA-001	Gp0008555	AEIW01	53245	pharmaceutical importance; traditional use	32,52	28,00	2934			52,7	454
Cordyceps confragosa	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	RCEF 1005	Gp0039339	AZHF01	72733	entomopathogen	35,59	35,59	197	130	11030	53,1	Illumina HiSeq
Cordyceps militaris	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	CM01	Gp0005960	AEVU01	41129	entomopathogenic	32,26	100,00	597	32	9651	51,4	454; Illumina
Cordyceps militaris	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	CM01	Gp0005960	AEVU01	41129	entomopathogen	32,26	100,00	597	32	9651	51,4	454; Illumina
Isaria farinosa	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	MTCC 4114	Gp0093214	JMNC01	242987	entomopathogenic	34,157	60,00	1314			53,2	Illumina HiSeq
Isaria farinosa	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	MTCC 4114	Gp0093214	JMNC01	242987	entomopathogen	34,157	60,00	1314			53,2	Illumina HiSeq
Isaria fumosorosea	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Cordycipitaceae	ARSEF 2679	Gp0039313	AZHB01	72737	entomopathogen	33,49	86,99	685	430	10061	53,5	Illumina HiSeq
Trichoderma asperellum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	CBS 433.97	Gp0009681	JGI	207877	biocontrol (mycoparasite); saprotroph to biotroph	37,46	130	456	419	12586		454; Illumina
Trichoderma asperellum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	CBS 433.97	Gp0009681	JGI	207877	biocontrol (mycoparasite); saprotroph to biotroph	37,46	130,00	456	419	12586		454; Illumina
Trichoderma atroviride	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	IMI 206040	Gp0003182	ABDG02	19867	biocontrol (mycoparasite)	36,1	8,30	29	29	11863	49,7	Sanger
Trichoderma atroviride	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	IMI 206040	Gp0003182	ABDG02	19867	biocontrol (mycoparasite)	36,1	8,30	29	29	11863	49,7	Sanger
Trichoderma citrinoviride	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	TUCIM 6016		1013721		opportunistic human pathogen	33,22	63,1	699	533	9737		Illumina
Trichoderma citrinoviride	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	TUCIM 6016		1013721		opportunistic human pathogen	33,22	63,10	699	533	9737		Illumina
Trichoderma hamatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	GD12	Gp0039327	ANCB01	178391	biocontrol (mycoparasite)	38,176	40,00	14797	2770		48,5	Illumina HiSeq
Trichoderma hamatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	GD12	Gp0039327	ANCB01	178391	biocontrol (mycoparasite)	38,176	40,00	14797	2770		48,5	Illumina HiSeq
Trichoderma harzianum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	CBS 226.95	Gp0009680	JGI	207867	biocontrol (mycoparasite)	40,98	120	576	532	14095	47	Illumina
Trichoderma harzianum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	CBS 226.95	Gp0009680	JGI	207867	biocontrol (mycoparasite)	40,98	120,00	576	532	14095	47	Illumina
Trichoderma longibrachiatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	ATCC 18648	Gp0009711	JGI	207876	biocontrol (plant pathogenic soil nematodes)	32,24	104,2	1460	130	10938	54	Illumina
Trichoderma longibrachiatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	ATCC 18648	Gp0009711	JGI	207876	biocontrol (plant pathogenic soil nematodes)	32,24	104,20	1460	130	10938	54	Illumina
Trichoderma parareesei	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	CBS 125925	Gp0120464	LFMI01	287603	biocontrol (mycoparasite)	32,1	28	3910	885		53,7	Illumina
Trichoderma parareesei	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	CBS 125925	Gp0120464	LFMI01	287603	biocontrol (mycoparasite)	32,1	28,00	3910	885		53,7	Illumina

Trichoderma pseudokoningii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	SMF2	Gp0039277	ANBJ01	175761	biocontrol (nematode parasite)	31,743	69,00	316	194		54	454; Illumina HiSeq
Trichoderma pseudokoningii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	SMF2	Gp0039277	ANBJ01	175761	biocontrol (nematode parasite)	31,743	69,00	316	194		54	454; Illumina HiSeq
Trichoderma reesei	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	QM6a	Gp0017902	AAIL02	15571	industrial importance (cellulases; hemicellulases)	33,3	9,00	128	77	9129	52,8	Sanger
Trichoderma reesei	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	QM6a	Gp0017902	AAIL02	15571	industrial importance (cellulases; hemicellulases)	33,3	9,00	128	77	9129	52,8	Sanger
Trichoderma virens	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	Gv29-8	Gp0002706	ABDF02	19983	biocontrol	39	8,05	93	93	12427	49,2	Sanger
Trichoderma virens	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Hypocreaceae	Gv29-8	Gp0002706	ABDF02	19983	biocontrol	39	8,05	93	93	12427	49,2	Sanger
Acremonium (Sarocladium) strictur	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Incertae sedis	DS1bioAY4a	Gp0047505	1029426	239484	endophyte (grasses); mycoparasite	35,79	120,00	81	13	13158		Illumina
Sarocladium oryzae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Incertae sedis	Saro-13		LOPT01	305454	plant pathogen (rice sheath rot)	32,78	82,00	5856			53,5	Illumina
Stachybotrys chartarum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Incertae sedis	IBT 40293	Gp0039336	ASEQ01	185808	medical importance (stachybotryotoxicosis; mycotoxin-producing-satratox	36,48	192,00	4267	2342	11453	53,3	Illumina HiSeq
Stachybotrys chartarum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Incertae sedis	IBT 40293	Gp0039336	ASEQ01	185808	medical importance (stachybotryotoxicosis; mycotoxin-producing-satratox	36,48	192,00	4267	2342	11453	53,3	Illumina HiSeq
Stachybotrys chlorohalonata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Incertae sedis	IBT 40285	Gp0039361	APWP01	185807	medical importance (atranone-producing)	34,39	196,00	5591	2802	10706	53,4	Illumina HiSeq
Stachybotrys chlorohalonata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Incertae sedis	IBT 40285	Gp0039361	APWP01	185807	medical importance (atranone-producing)	34,39	196,00	5591	2802	10706	53,4	Illumina HiSeq
Ustilaginoidea virens	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Incertae sedis	IPU010	Gp0115332	BBTG02	279060	plant pathogen (rice)	33,57		139		8426	49,9	Illumina MiSeq; PacBio
Ustilaginoidea virens	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Incertae sedis	IPU010	Gp0115332	BBTG02	279060	plant pathogen (rice)	33,57		139		8426	49,9	Illumina MiSeq; PacBio
Dactylonectria macrodidyma	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	JAC 15-24	Gp0117674	JYGD01	274176	plant pathogen (grapevine, avocado, and olive)	58	74	1466	911		50	Illumina MiSeq
Dactylonectria macrodidyma	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	JAC 15-24	Gp0117674	JYGD01	274176	plant pathogen (grapevine, avocado, and olive)	58	74,00	1466	911		50	Illumina MiSeq
Fusarium acuminatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	CS5907	Gp0043378	CBMG000000000.1	206959	plant pathogen (cereals)	43,98		3907	758			Illumina HiSeq
Fusarium acuminatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	CS5907	Gp0043378	CBMG000000000.1	206959	plant pathogen (cereals)	43,98		3907	758			Illumina HiSeq
Fusarium avenaceum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	FaLH03	Gp0143156	JQGD01	253730	plant pathogen (generalist, including grain crops)	43,17	459	115	105		48	Illumina HiSeq
Fusarium avenaceum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	FaLH03	Gp0143156	JQGD01	253730	plant pathogen (generalist, including grain crops)	43,17	459,00	115	105		48	Illumina HiSeq
Fusarium circinatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	FSP 34	Gp0005151	AYJV01	41113	plant pathogen (pitch canker of pines)	44,138	11,00	4145			47,3	454
Fusarium circinatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	FSP 34	Gp0005151	AYJV01	41113	plant pathogen (pitch canker of pines)	44,138	11,00	4145			47,3	454
Fusarium equiseti	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	CS3069	Gp0044229	CBMI000000000.1	209001	plant pathogen (members of the Leguminoseae and some cereals)	38,06		5111				Illumina HiSeq
Fusarium equiseti	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	CS3069	Gp0044229	CBMI000000000.1	209001	plant pathogen (members of the Leguminoseae and some cereals)	38,06		5111				Illumina HiSeq
Fusarium fujikuroi	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	B14	Gp0039409	ANFV01	171493	plant pathogen (rice)	43,81	75,80	455	333		48,3	Illumina HiSeq
Fusarium fujikuroi	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	B14	Gp0039409	ANFV01	171493	plant pathogen (rice)	43,81	75,80	455	333		48,3	Illumina HiSeq
Fusarium graminearum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	CS3005	Gp0086804	JATU01	235346	plant pathogen (wheat and barley)	36,66	50,00	1205	199	11578	48,3	Illumina HiSeq
Fusarium graminearum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	CS3005	Gp0086804	JATU01	235346	plant pathogen (wheat and barley)	36,66	50,00	1205	199	11578	48,3	Illumina HiSeq
Fusarium langsethiae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	Fl201059	Gp0121990	JXCE01	271560	medical importance (mycotoxin-producing)	37,54	500	2538	1586	12232	48,3	Illumina GAIIx; 454
Fusarium langsethiae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	Fl201059	Gp0121990	JXCE01	271560	medical importance (mycotoxin-producing)	37,54	500,00	2538	1586	12232	48,3	Illumina GAIIx; 454
Fusarium nygamai	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	MRC8546	Gp0124341	LBNR01	281294	plant pathogen (rice)	51,62	333	743	409		47,5	Illumina HiSeq
Fusarium nygamai	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	MRC8546	Gp0124341	LBNR01	281294	plant pathogen (rice)	51,62	333,00	743	409		47,5	Illumina HiSeq
Fusarium oxysporum f. sp. congluti	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	NRRL 54008	Gp0037083	AGNF01	73543	plant pathogen (broad host range)	53,57	124,00	3350	2552	20232	48,4	Illumina
Fusarium oxysporum f. sp. congluti	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	NRRL 54008	Gp0037083	AGNF01	73543	plant pathogen (broad host range)	53,57	124,00	3350	2552	20232	48,4	Illumina
Fusarium pseudograminearum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	CS3427	Gp0043380	CBMD000000000.1	206566	plant pathogen (wheat)	36,93		685	685	12447	47,8	Illumina HiSeq
Fusarium pseudograminearum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	CS3427	Gp0043380	CBMD000000000.1	206566	plant pathogen (wheat)	36,93		685	685	12447	47,8	Illumina HiSeq
Fusarium sambucinum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	F-4	Gp0144734	LSRD01	274729	plant pathogen (potato dry rot); mycotoxin-producing	37,78	18	961			47,8	454
Fusarium sambucinum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	F-4	Gp0144734	LSRD01	274729	plant pathogen (potato dry rot); mycotoxin-producing	37,78	18,00	961			47,8	454
Fusarium sp. JS1030	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	JS1030	Gp0119197	JWIW01	269535	uncertain	53,75	1244	310	107		51,7	Illumina HiSeq; MiSeq
Fusarium sp. JS1030	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	JS1030	Gp0119197	JWIW01	269535	uncertain	53,75	1244,00	310	107		51,7	Illumina HiSeq; MiSeq
Fusarium sp. JS626	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	JS626	Gp0119196	JWIV01	269534	uncertain	42,87	1966	216	63		48,2	Illumina HiSeq; MiSeq
Fusarium sp. JS626	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	JS626	Gp0119196	JWIV01	269534	uncertain	42,87	1966,00	216	63		48,2	Illumina HiSeq; MiSeq
Fusarium temperatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	CMWF389	Gp0093049	LJGR01	242703	plant pathogen (maize); opportunistic human pathogen	45,46	414,00	244	43		47	Illumina HiSeq
Fusarium verticillioides	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	FGSC 7600	Gp0002615	AAIM02	15553	plant pathogen (maize)	41,8851	8,00	210	39	15935	48,7	Sanger
Fusarium verticillioides	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	FGSC 7600	Gp0002615	AAIM02	15553	plant pathogen (maize)	41,8851	8,00	210	39	15935	48,7	Sanger
Fusarium virguliforme	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	Mont-1	Gp0038801	AEYB01	63281	plant pathogen (soybean)	50,448	20,00	3098			49,4	454
Fusarium virguliforme	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	Mont-1	Gp0038801	AEYB01	63281	plant pathogen (soybean)	50,448	20,00	3098			49,4	454
Ilyonectria europaea	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	PMI-82	Gp0019433	JGI	196035	root-associated	63,66	153,5	950	325	22250		Illumina HiSeq
Ilyonectria europaea	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	PMI-82	Gp0019433	JGI	196035	root-associated	63,66	153,50	950	325	22250		Illumina HiSeq
Nectria haematococca	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	MPVI 77-13-4	Gp0017718	JGI	16586	plant pathogen (broad host range)	51			72	15707	50,8	
Nectria haematococca	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	MPVI 77-13-4	Gp0017718	JGI	16586	plant pathogen (broad host range)	51			72	15707	50,8	
Neonectria ditissima	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	RS324p	Gp0144542	LDPL01	285413	plant pathogen (apple canker)	44,95	200	189	172		51,8	Illumina HiSeq
Neonectria ditissima	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Nectriaceae	RS324p	Gp0144542	LDPL01	285413	plant pathogen (apple canker)	44,95	200,00	189	172		51,8	Illumina HiSeq
Niesslia exilis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Niessliaceae	CBS 358.70	Gp0036359	1019485	239481	saprotroph	35,38	85,00	74	34	13499		Illumina HiSeq
Valetoniellopsis laxa	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Niessliaceae	CBS 191.97	Gp0036333	1019489	239487	uncertain; monotypic genus	22,13	95,00	213	83	8026		Illumina HiSeq
Drechmeria coniospora	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	ATCC 96282	Gp0120732	JYHR01	269584	biocontrol (nematode endoparasite)	31,89	100	1012	75	8216	53,9	Illumina MiSeq; SOLiD
Drechmeria coniospora	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	ATCC 96282	Gp0120732	JYHR01	269584	biocontrol (nematode endoparasite)	31,89	100,00	1012	75	8216	53,9	Illumina MiSeq; SOLiD
Hirsutella minnesotensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	3608	Gp0038705	JPUM01	67943	biocontrol (nematode pathogen)	51,11	128,00	2109	736	12700	52,1	Illumina HiSeq
Hirsutella thompsonii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	MTCC3556	Gp0038699	APKB01	192877	arthropod pathogen (acarine)	34,557	180,00	621			52,6	Illumina HiSeq
Hirsutella thompsonii	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	MTCC3556	Gp0038699	APKB01	192877	arthropod pathogen (acarine)	34,557	180,00	621			52,6	Illumina HiSeq
Ophiocordyceps polyrhachis-furcat	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	BCC 54312	Gp0042014	LKCN01	200756	uncertain	43,16	37,00	4013	418		42,8	454; Illumina
Ophiocordyceps sinensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	CO18	Gp0008980	ANOV01	59569	traditional use	78,515	241,00	25873	10603	6972	46,2	454; Illumina HiSeq
Ophiocordyceps sinensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	CO18	Gp0008980	ANOV01	59569	traditional use	78,515	241,00	25873	10603	6972	46,2	454; Illumina HiSeq
Ophiocordyceps unilateralis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	SC16a	Gp0122527	LAZP01	280567	entomopathogen	25,49	120	8182	6790	7821	55	Illumina MiSeq
Ophiocordyceps unilateralis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	SC16a	Gp0122527	LAZP01	280567	entomopathogen	25,49	120,00	8182	6790	7821	55	Illumina MiSeq
Purpureocillium lilacinum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	TERIBC 1	Gp0145585	LOFA01	284314	saprotroph	38,82	200	300		11773	57,9	Illumina HiSeq
Purpureocillium lilacinum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	TERIBC 1	Gp0145585	LOFA01	284314	saprotroph	38,82	200,00	300		11773	57,9	Illumina HiSeq
Tolypocladium (Elaphocordyceps) c	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	CBS 100239	Gp0038496	LFRF01	91059	parasite	31,25	76,00	1244	172	9158	57	Illumina HiSeq
Tolypocladium sp. Salcha MEA-2	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	MEA-2	Gp0133497	JPIJ02	254396	uncertain	30,83	42	44			57,9	PacBio
Tolypocladium sp. Salcha MEA-2	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	MEA-2	Gp0133497	JPIJ02	254396	uncertain	30,83	42,00	44			57,9	PacBio
Tolypocladium sp. Sup5 PDA-1	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	PDA-1	Gp0133211	JPHH03	254396	uncertain	37,87	469	464			56	PacBio; Illumina HiSeq; Oxford Nanopore
Tolypocladium sp. Sup5 PDA-1	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Ophiocordycipitaceae	PDA-1	Gp0133211	JPHH03	254396	uncertain	37,87	469,00	464			56	PacBio; Illumina HiSeq; Oxford Nanopore
Myrothecium inundatum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Stachybotriaceae	CBS 120646	Gp0036288	1019493	239488	saprotroph; biocontrol; industrial importance	39,21	95,00	352	62	13553		Illumina HiSeq
Stachybotrys echinata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Stachybotriaceae	JCM 22618	Gp0143986	BCHF01	313808	medical importance (mycotoxin-producing)	43,68	215	550	106		49,8	HiSeq 2500
Stachybotrys echinata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Hypocreales	Stachybotriaceae	JCM 22618	Gp0143986	BCHF01	313808	medical importance (mycotoxin-producing)	43,68	215,00	550	106		49,8	HiSeq 2500
Albophoma yamanashiensis	Ascomycota	Pezizomycotina	Sordariomycetes		Incertae sedis	Incertae sedis	JCM 11844	Gp0143836	BCKH01	313424	uncertain	31,39	325	215	66		56,7	HiSeq 2500
Albophoma yamanashiensis	Ascomycota	Pezizomycotina	Sordariomycetes	Incertae sedis	Incertae sedis	Incertae sedis	JCM 11844	Gp0143836	BCKH01	313424	uncertain	31,39	325,00	215	66		56,7	HiSeq 2500
Didymobotryum rigidum	Ascomycota	Pezizomycotina	Sordariomycetes		Incertae sedis	Incertae sedis	JCM 8837	Gp0143835	BCKI01	313898	uncertain	41,73	204	178	31		54,7	HiSeq 2500
Didymobotryum rigidum	Ascomycota	Pezizomycotina	Sordariomycetes	Incertae sedis	Incertae sedis	Incertae sedis	JCM 8837	Gp0143835	BCKI01	313898	uncertain	41,73	204,00	178	31		54,7	HiSeq 2500
Plectosphaerella cucumerina	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Incertae sedis	Plectosphaerellaceae	DS2psM2a2 v1.0		1029418		plant pathogen (blight of cucurbits); nematophagous	36,84	86,9	124	26	14254		Illumina
Plectosphaerella cucumerina	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Incertae sedis	Plectosphaerellaceae	DS2psM2a2 v1.0		1029418		plant pathogen (blight of cucurbits); nematophagous	36,84	86,90	124	26	14254		Illumina
Torpedospora radiata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Incertae sedis	Torpedosporaceae	JK5252C	Gp0036318	1019473	255593	marine fungus	33,2	93,7	682	96	11634		Illumina HiSeq
Torpedospora radiata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Incertae sedis	Torpedosporaceae	JK5252C	Gp0036318	1019473	255593	marine fungus	33,2	93,70	682	96	11634		Illumina HiSeq
Lindra thalassiae	Ascomycota	Pezizomycotina	Sordariomycetes	Lulworthiomycetidae	Lulworthiales	Lulworthiaceae	JK4322	Gp0036541	1019501	255592	probable plant pathogen (turtle grass)	31,92	145,00	173	149	8029		Illumina HiSeq
Gaeumannomyces graminis	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Magnaporthales	Magnaporthaceae	R3-111a-1	Gp0005124	ADBI01	37931	plant pathogen (root rot of cereals)	43,76	25,00	1860	517	14749	56,8	454
Gaeumannomyces graminis	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Magnaporthales	Magnaporthaceae	R3-111a-1	Gp0005124	ADBI01	37931	plant pathogen (root rot of cereals)	43,76	25,00	1860	517	14749	56,8	454
Harpophora oryzae	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Magnaporthales	Magnaporthaceae	R5-6-1	Gp0101971	JNVV01	252809	endophyte	50,7794	120,00	1540	247		56,5	Illumina HiSeq
Harpophora oryzae	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Magnaporthales	Magnaporthaceae	R5-6-1	Gp0101971	JNVV01	252809	endophyte	50,7794	120,00	1540	247		56,5	Illumina HiSeq
Magnaporthe oryzae	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Magnaporthales	Magnaporthaceae	KJ201	Gp0039276	ANSL02	179498	plant pathogen (rice)	45,096	199,00	3188	123	13032	51,6	Illumina GAIIx
Magnaporthe oryzae	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Magnaporthales	Magnaporthaceae	KJ201	Gp0039276	ANSL02	179498	plant pathogen (rice)	45,096	199,00	3188	123	13032	51,6	Illumina GAIIx
Magnaporthiopsis poae	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Magnaporthales	Magnaporthaceae	ATCC 64411	Gp0005728	ADBL01	37933	plant pathogen (turfgrass)	39,6418	40,00	3118	206		56	454
Magnaporthiopsis poae	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Magnaporthales	Magnaporthaceae	ATCC 64411	Gp0005728	ADBL01	37933	plant pathogen (turfgrass)	39,6418	40,00	3118	206		56	454
Melanospora tiffanyae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Melanosporales	Ceratostomataceae	F1KG0001 v1.0		1019477		biocontrol (mycoparasite)	28,36	136,7	510	420	8994		Illumina
Melanospora tiffanyae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Melanosporales	Ceratostomataceae	F1KG0001 v1.0		1019477		biocontrol (mycoparasite)	28,36	136,70	510	420	8994		Illumina
Ceratocystis adiposa	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CBS136.34	Gp0149937	LXGU01	319432	plant pathogen (black root in sugar cane)	28,34	93,00	757	644		47	Illumina
Ceratocystis albifundus	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW17620	Gp0109102	JSSU01	263706	plant pathogen (woody & herbaceaous)	26,88	24	2894	1405		48,6	Illumina GAIIx
Ceratocystis albifundus	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW17620	Gp0109102	JSSU01	263706	plant pathogen (woody & herbaceaous)	26,88	24,00	2894	1405		48,6	Illumina GAIIx
Ceratocystis eucalypticola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW9998	Gp0121626	LJOA01	294286	probable plant pathogen (eucalyptus)	30,72	80	1307	959		48,1	Illumina HiSeq 2000
Ceratocystis eucalypticola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW9998	Gp0121626	LJOA01	294286	probable plant pathogen (eucalyptus)	30,72	80,00	1307	959		48,1	Illumina HiSeq 2000
Ceratocystis fimbriata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	C1421	Gp0006908	APWK02	67151	plant pathogen (sweet potato)	29,4	27,00	1185		7266	48,06	454
Ceratocystis fimbriata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	C1421	Gp0006908	APWK02	67151	plant pathogen (sweet potato)	29,4	27,00	1185		7266	48,06	454

Ceratocystis manginecans	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW17570	Gp0097242	JJRZ01	243355	plant pathogen (mango)	31,7	22,00	2295		7494	48	Illumina	
Ceratocystis manginecans	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW17570	Gp0097242	JJRZ01	243355	plant pathogen (mango)	31,7	22,00	2295		7494	48	Illumina	
Ceratocystis platani	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CFO	Gp0117548	LBBL01	278456	plant pathogen (trees)	29,18	655	1213		5963	48,2	Illumina HiSeq	
Ceratocystis platani	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CFO	Gp0117548	LBBL01	278456	plant pathogen (trees)	29,18	655,00	1213		5963	48,2	Illumina HiSeq	
Chalaropsis thielavioides	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	JCM 1933	Gp0143985	BCGU01	313799	plant pathogen (Fabaceae sp.)	29,33	387	252	12		52,1	HiSeq 2500	
Chalaropsis thielavioides	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	JCM 1933	Gp0143985	BCGU01	313799	plant pathogen (Fabaceae sp.)	29,33	387,00	252	12		52,1	HiSeq 2500	
Endoconidiophora laricicola	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CBS100207	Gp0149935	LXGT01	319433	insect-associated	32,69	93,00	898	879		45,4	Illumina	
Huntiella moniliformis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CBS118127	Gp0094242	JMSH01	246136	saprotroph	25,4	38,00	600		6832	47,9	Illumina GAIIx	
Huntiella moniliformis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CBS118127	Gp0094242	JMSH01	246136	saprotroph	25,4	38,00	600		6832	47,9	Illumina GAIIx	
Huntiella omanensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW 11056	Gp0121623	JSUI01	263445	plant pathogen (weak mango pathogen)	31,13	9	6763	6542		47,7	Illumina	
Huntiella omanensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW 11056	Gp0121623	JSUI01	263445	plant pathogen (weak mango pathogen)	31,13	9,00	6763	6542		47,7	Illumina	
Huntiella savannae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CBS 121151	Gp0143126	LCZG01	283473	saproptroph	28,54	22	1617	361		48,3	Illumina HiSeq	
Huntiella savannae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CBS 121151	Gp0143126	LCZG01	283473	saproptroph	28,54	22,00	1617	361		48,3	Illumina HiSeq	
Thielaviopsis musarum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW1546	Gp0145653	LKBB01	296851	post harvest pathogen (banana)	28,42	95	1849	541		49,2	Illumina GAIIx	
Thielaviopsis musarum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CMW1546	Gp0145653	LKBB01	296851	post harvest pathogen (banana)	28,42	95,00	1849	541		49,2	Illumina GAIIx	
Thielaviopsis paradoxa	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	JCM 6020	Gp0144032	BCHJ01	313811	plant pathogen (palm)	29,63	345	282	30		49	HiSeq 2500	
Thielaviopsis paradoxa	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	JCM 6020	Gp0144032	BCHJ01	313811	plant pathogen (palm)	29,63	345,00	282	30		49	HiSeq 2500	
Thielaviopsis punctulata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CR-DP1	Gp0118396	LAEV01	273322	plant pathogen (date palm)	28,12	75	3751	2315	5296	48,3		
Thielaviopsis punctulata	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Ceratocystidaceae	CR-DP1	Gp0118396	LAEV01	273322	plant pathogen (date palm)	28,12	75,00	3751	2315	5296	48,3		
Knoxdaviesia capensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Gondwanamycetaceae		Gs0110866	LNGK01	246171	saprotroph (plant-associated)	35,54	188,00		29	7940	52,8	HiSeq 2500	
Knoxdaviesia capensis	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Gondwanamycetaceae		Gs0110866	LNGK01	246171	saprotroph (plant-associated)	35,54	188,00		29	7940	52,8	HiSeq 2500	
Knoxdaviesia proteae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Gondwanamycetaceae	SB2.3	Gp0110284	LNGL01	275563	saprotroph (plant-associated)	35,489	271	1379	133	8173	52,7	HiSeq 2500	
Knoxdaviesia proteae	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Gondwanamycetaceae	SB2.3	Gp0110284	LNGL01	275563	saprotroph (plant-associated)	35,489	271,00	1379	133	8173	52,7	HiSeq 2500	
Corollospora maritima	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Halosphaeriaceae	CBS 119819 v2.0		1060067		marine saprotroph	36,97	144,8	983	866	12991		Illumina	
Corollospora maritima	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Halosphaeriaceae	CBS 119819 v2.0		1060067		marine saprotroph	36,97	144,80	983	866	12991		Illumina	
Microascus trigonosporus	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Microascaceae	CBS 218.31	Gp0033164	JGI	196081	human pathogen	36,1	104	143	13	13087		Illumina	
Microascus trigonosporus	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Microascaceae	CBS 218.31	Gp0033164	JGI	196081	human pathogen	36,1	104,00	143	13	13087		Illumina	
Scedosporium apiospermum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Microascaceae	IHEM 14462	Gp0092899	JOWA01	244532	human pathogen (infects lungs, especially in cystic fibrosis patients)	41,437	280,00	333		10919	50,4	Illumina HiSeq; PacBio	
Scedosporium apiospermum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Microascaceae	IHEM 14462	Gp0092899	JOWA01	244532	human pathogen (infects lungs, especially in cystic fibrosis patients)	41,437	280,00	333		10919	50,4	Illumina HiSeq; PacBio	
Scedosporium aurantiacum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Microascaceae	WM 09.24	Gp0118269	JUDQ01	261653	human pathogen	39,89	162	2285	1584		49,2	Illumina HiSeq	
Scedosporium aurantiacum	Ascomycota	Pezizomycotina	Sordariomycetes	Hypocreomycetidae	Microascales	Microascaceae	WM 09.24	Gp0118269	JUDQ01	261653	human pathogen	39,89	162,00	2285	1584		49,2	Illumina HiSeq	
Graphilbum fragrans	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	CBS 138720	Gp0124538	LLKO01	298958	insect-associated (conifer-infesting beetles)	34,27	64	393	80		55,7	Illumina HiSeq	
Graphilbum fragrans	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	CBS 138720	Gp0124538	LLKO01	298958	insect-associated (conifer-infesting beetles)	34,27	64,00	393	80		55,7	Illumina HiSeq	
Grosmannia clavigera	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	kw1407	Gp0002583	ACXQ02	39837	plant pathogen; blue stain	29,79	50,00	333	289	8312	51,4	Sanger; 454; Illumina	
Grosmannia clavigera	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	kw1407	Gp0002583	ACXQ02	39837	plant pathogen; blue stain	29,79	50,00	333	289	8312	51,4	Sanger; 454; Illumina	
Leptographium lundbergii	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	CBS 138716	Gp0145151	LDEF01	284246	insect-associated (beetles)	26,54	70	735	411		56,9	Illumina HiSeq	
Leptographium lundbergii	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	CBS 138716	Gp0145151	LDEF01	284246	insect-associated (beetles)	26,54	70,00	735	411		56,9	Illumina HiSeq	
Leptographium procerum	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	CMW34542	Gp0107386	JRUC01	262457	plant pathogen (pine)	28,57	32	2747	2687		54,8	Illumina MiSeq	
Leptographium procerum	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	CMW34542	Gp0107386	JRUC01	262457	plant pathogen (pine)	28,57	32,00	2747	2687		54,8	Illumina MiSeq	
Ophiostoma novo-ulmi	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	H327	Gp0038489	AMZD01	173023	plant pathogen (Dutch Elm Disease)	31,855	61,00	161	10		50,1		454
Ophiostoma novo-ulmi	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	H327	Gp0038489	AMZD01	173023	plant pathogen (Dutch Elm Disease)	31,855	61,00	161	10		50,1		454
Ophiostoma piceae	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	UAMH 11346	Gp0048401	AQHS01	182071	saprotroph; wood-staining	32,84	735	343	45	8884	53,4	454; Illumina HiSeq	
Ophiostoma piceae	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	UAMH 11346	Gp0048401	AQHS01	182071	saprotroph; wood-staining	32,84	735,00	343	45	8884	53,4	454; Illumina HiSeq	
Sporothrix brasiliensis	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	5110	Gp0047830	AWTV01	218075	human and animal pathogen (sporotrichosis)	33,21	20,00	13		9231			454
Sporothrix globosa	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	CBS 120340	Gp0149694	LVYW01	315855	human and animal pathogen (sporotrichosis)	33,47	146,00	222	24		54,3	Illumina	
Sporothrix insectorum	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	RCEF 264	Gp0039314	AZHD01	72727	entomopathogen	34,72	7037,00	819	78	9496		Illumina HiSeq	
Sporothrix pallida	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	SPA8	Gp0095173	JNEX01	248334	saprotroph (environmental)	39,881	20,00	3392			53	Ion Torrent	
Sporothrix pallida	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	SPA8	Gp0095173	JNEX01	248334	saprotroph (environmental)	39,881	20,00	3392			53	Ion Torrent	
Sporothrix schenckii	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	ATCC 58251	Gp0034023	AWEQ01	217088	human and animal pathogen (sporotrichosis)	32,228	56,00	125	29	8805	55,1	Illumina	
Sporothrix schenckii	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Ophiostomatales	Ophiostomataceae	ATCC 58251	Gp0034023	AWEQ01	217088	human and animal pathogen (sporotrichosis)	32,228	56,00	125	29	8805	55,1	Illumina	
Chaetomium globosum	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 148.51	Gp0002586	AAFU01	12795	human pathogen and allergen (mycosis; mycotoxin-producing)	34,88	7,00	1245	37	11232	55,6	Sanger	
Chaetomium thermophilum	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	DSM 1495	Gp0007119	ADUW01	47065	thermophile	28,32	24,00	112	21	7475	52,6		454
Chaetomium thermophilum	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	DSM 1495	Gp0007119	ADUW01	47065	thermophile	28,32	24,00	112	21	7475	52,6		454
Myceliophthora heterothallica	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 203.75 v1.0	Gp0017713	1006350	219689	thermophile	35,36	132,8	547	37	10061		Illumina HiSeq	
Myceliophthora heterothallica	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 203.75 v1.0	Gp0017713	1006350	219689	thermophile	35,36	132,80	547	37	10061		Illumina HiSeq	
Myceliophthora thermophila	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	ATCC 42464	Gp0004720	GCA_000226095.1	32775	thermophile	38,74		7	7	9110	51		
Myceliophthora thermophila	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	ATCC 42464	Gp0004720	GCA_000226095.1	32775	thermophile	38,74		7	7	9110	51		
Thielavia antarctica	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 123565	Gp0036308	JGI	234663	industrial importance	40,66	88,1	1650	153	9204		Illumina	
Thielavia antarctica	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 123565	Gp0036308	JGI	234663	industrial importance	40,66	88,10	1650	153	9204		Illumina	
Thielavia appendiculata	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 731.68	Gp0036422	JGI	214269	industrial importance	32,74	95,3	501	109	11942		Illumina HiSeq	
Thielavia appendiculata	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 731.68	Gp0036422	JGI	214269	industrial importance	32,74	95,30	501	109	11942		Illumina HiSeq	
Thielavia arenaria	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 508.74	Gp0036388	JGI	214268	industrial importance	30,99	95,8	354	69	10954		Illumina HiSeq	
Thielavia arenaria	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 508.74	Gp0036388	JGI	214268	industrial importance	30,99	95,80	354	69	10954		Illumina HiSeq	
Thielavia hyrcaniae	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 757.83	Gp0036446	JGI	214270	industrial importance	31,18	88,9	972	251	11338		Illumina	
Thielavia hyrcaniae	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	CBS 757.83	Gp0036446	JGI	214270	industrial importance	31,18	88,90	972	251	11338		Illumina	
Thielavia terrestris	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	NRRL 8126	Gp0003189	GCA_000226115.1	32847	industrial importance (thermophile, acidophile)	36,91		6	6	9813	55	Sanger	
Thielavia terrestris	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Chaetomiaceae	NRRL 8126	Gp0003189	GCA_000226115.1	32847	industrial importance (thermophile, acidophile)	36,91		6	6	9813	55	Sanger	
Madurella mycetomatis	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Incertae sedis	mm55	Gp0118004	LCTW02	267680	human pathogen (eumycetoma)	36,7	43,50	829	804	10707	54,8	PacBio; Illumina; 454	
Podospora anserina	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Lasiosphaeriaceae	S mat+	Gp0002675	GCA_000226545.1	12954	saprotroph (dung-inhabiting)	35,01	10,00	7	7	10588	52	Sanger	
Neurospora africana	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Sordariaceae	FGSC 1740	Gp0080990	CAPO02	232141	model organism	36,078		13167	1978		51,9		
Neurospora crassa	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Sordariaceae	OR74A	Gp0000645	AABX03	13841	model organism	41,102	20,25	411	20	10785	50	Sanger; 454	
Neurospora discreta	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Sordariaceae	FGSC 8579	Gp0002652		207861	model organism	37,3	8,59		176	9948		Illumina	
Neurospora pannonica	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Sordariaceae	FGSC 7221	Gp0080992	CAPQ02	232144	model organism	38,595		30909	3551		51,8	Illumina	
Neurospora sublineolata	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Sordariaceae	FGSC 5508	Gp0080989	CAPP02	232140	model organism	35,701		22228	2917		52,3	Illumina	
Neurospora terricola	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Sordariaceae	FGSC 1889	Gp0080991	CAPR02	232142	model organism	39,33		40841	6008		51,2	Illumina	
Neurospora tetrasperma	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Sordariaceae	FGSC 2509	Gp0017721	AFCY01	65453	model organism	39,123	47,60	856	303	10380	49,4	454; Sanger	
Sordaria macrospora	Ascomycota	Pezizomycotina	Sordariomycetes	Sordariomycetidae	Sordariales	Sordariaceae	k-hell	Gp0007787	CABT02	39253	model organism	38,391		1583		11315	52,5		
Phaeoacremonium aleophilum	Ascomycota	Pezizomycotina	Sordariomycetes	Diaportheomycetidae	Togniniales	Togniniaceae	UCRPA7	Gp0039199	AORD01	188116	plant pathogen (grapevine trunk disease)	47,47	100,00	1083	624	8834	49,7	Illumina HiSeq	
Apiospora montagnei	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Apiosporaceae	NRRL 25634	Gp0019297	JGI		cellulolytic	47,67	95,70	706	686	16992		Illumina	
Anthostoma avocetta	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Diatrypaceae	NRRL 3190	Gp0019416	JGI	221352	pharmaceutical importance (antibiotic producing-heptelidic acid)	56,23	117,70	1038	786	15755		Ilumina	
Eutypa lata	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Diatrypaceae	UCREL1	Gp0039198	AORF01	187490	plant pathogen; grapevine dieback	54	100,00	3322	2334	11685	46,6	Illumina HiSeq	
Daldinia eschscholtzii	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Xylariaceae	UM1020	Gp0039007	AIID01	82955	saproptroph	35,8424	100,00	11382			46,8	Illumina GAIIx	
Hypoxylon sp. CI-4A	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Xylariaceae	CI-4A	Gp0017031	JGI	207862	endophyte	37,7	114,60	944	899	11712		Illumina	
Hypoxylon sp. CO27-5	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Xylariaceae	CO27-5	Gp0012686	JGI	207870	endophyte	46,59	138,10	580	505	12256		454; Illumina	
Hypoxylon sp. E7406B	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Xylariaceae	E7406B	Gp0093682	JYCQ01	244689	uncertain	39,9	450,00	745			46,5	Illumina HiSeq	
Hypoxylon sp. EC38	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Xylariaceae	EC38	Gp0017032	1056738	333390	endophyte	47,72	116,10	582	288	12534		Illumina; PacBio	
Rosellinia necatrix	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Xylariaceae	W97	Gp0146048	BBSO01	298873	plant pathogen (fruits)	45,03	20,00	6503	4176	11171	49,9		454
Xylaria hypoxylon	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Xylariaceae	OSC100004	Go0112340	1050987	332938	saprotroph (white rot)	42,85	148,60	1015	990	13084		Illumina	
Xylaria sp. JS573	Ascomycota	Pezizomycotina	Sordariomycetes	Xylariomycetidae	Xylariales	Xylariaceae	JS573	Gp0118505	JWIU01	269533	saprotroph	40,89	1974,00	398	100		52,6	Illumina HiSeq; MiSeq	
Xylona heveae	Ascomycota	Pezizomycotina	Xylonomycetes	Incertae sedis	Xylonomycetales	Xylonomycetaceae	TC161	Gp0036344	JGI	200619	endophyte (sapwood)	24,34	124,50	56	27	8205		Illumina HiSeq	
Alloascoidea hylecoeti	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Alloascoideaceae	JCM 7604	Gp0143990	BCKZ01	313885	insect-associated	24,82	139,00	346	136		31,1	HiSeq 2500	
Ascoidea asiatica	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Ascoideaceae	JCM 7603	Gp0150862	BCKQ01	313877	insect-associated	20,31	184,00	264	71		24,8	Illumina	
Ascoidea rubescens	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Ascoideaceae	DSM 1968	Gp0017641	JGI	207865	insect-vectored	17,5	140,00	101	63	6802		Illumina HiSeq	
Babjeviella inositovora	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	NRRL Y-12698	Gp0009549	JGI	207852	grows on myo-inositol	15,22	80,00	210	49	6403		454; Illumina	
Candida sojae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	GF41	Gp0150634	LMTL01	299010	insect-associated	11,75	48,00	511			32,4	Illumina	
Debaryomyces fabryi	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	CBS 789	Gp0121009	LMYN01	288902	probable human pathogen	11,7	1000,00	540		6027	35,6	IonTorrent	
Debaryomyces hansenii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	CBS767	Gp0000565	GCA_000006445.2	13832	industrial importance	12,18	9,70	15		6642	36,4	Sanger	
Meyerozyma caribbica	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	MG20W	Gp0107407	BADS01	73189	biocontrol (mycoparasite)	10,61	21,00	9			43,8		454
Meyerozyma guilliermondii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	ATCC 6260	Gp0002582	AAFM01	12729	uncertain; yeast (nonpathogenic)	10,609	12,00	71	9	6062	44		
Millerozyma acaciae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	JCM 10732	Gp0150861	BCKO01	313876	metabolically interesting (toxin immunity)	11,07	248,00	29	10		41,4	Illumina	

Millerozyma farinosa	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	CBS 7064	Gp0038456	GCA_000315895.1	73835	halotolerant; osmotolerant	21,459	9,80	17		11662	41,33	Sanger	
Priceomyces haplophilus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	JCM 1635	Gp0144012	BCIF01	313831	insect-associated (bark beetles)	10,52	273,00	29	9	41	HiSeq 2500		
Scheffersomyces lignosus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	JCM 9837	Gp0144050	BCGS01	313797	fermentation (xylose)	16,59	171,00	73	19	41,2	HiSeq 2500		
Scheffersomyces stipitis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	CBS 6054	Gp0017786	AAVQ01	16843	fermentation	15,4			9	5841	41		
Spathaspora arborariae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	UFMG-19.1A	Gp0043415	AYLH01	207280	industrial importance	12,87	23,00	381	41		31,9		454
Spathaspora passalidarum	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	NRRL Y-27907	Gp0017849	AEIK01	53891	industrial importance (biofuel production-xylose fermentation)	13,2		26	8	5983	42	454; Sanger	
Wickerhamia fluorescens	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Debaryomycetaceae	JCM 1821	Gp0144017	BCGE01	313784	saprotroph	13,18	239,00	109	20		37,3	HiSeq 2500	
Geotrichum candidum	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Dipodascaceae	3C	Gp0106203	JMRO01	243259	plant pathogen (citrus)	41,38	31,25	560			41,38		454
Saprochaete clavata	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Dipodascaceae	CNRMA 12.647	Gp0145559	CBXB01	221847	human pathogen	17,72		3170	339		33,8		
Sporopachydermia quercuum	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Dipodascaceae	JCM 9486	Gp0144045	BCGN01	313792	endophyte	16,41	182,00	37	15		36,2	Illumina HiSeq	
Yarrowia deformans	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Dipodascaceae	JCM 1694	Gp0144013	BCIW01	313845	industrial importance (Alkane-using)	20,88	131,00	174	44		50	HiSeq 2500	
Yarrowia keelungensis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Dipodascaceae	JCM 14894	Gp0144005	BCJD01	313892	Industrial importance; oil-degrading	21,82	203,00	180	41		48	HiSeq 2500	
Yarrowia lipolytica	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Dipodascaceae	CLIB122	Gp0000567	GCA_000002525.1	13837	industrial importance (Alkane-using)	20,5	10,00	6	6	6447	49	Sanger	
Yarrowia sp. JCM 30694	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Dipodascaceae	JCM 30694	Gp0143753	BCKF01	313895	uncertain	21,76	217,00	244	19		46	HiSeq 2500	
Yarrowia sp. JCM 30695	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Dipodascaceae	JCM 30695	Gp0150865	BCLX01	313897	uncertain	21,9	251,00	189	41		47,8	Illumina	
Yarrowia sp. JCM 30696	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Dipodascaceae	JCM 30696	Gp0143755	BCKG01	313896	uncertain	21,75	230,00	206	39		47,9	HiSeq 2500	
Ashbya aceri	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Eremotheciaceae	FD-2008	Gp0006845	GCA_000412225.2	39551	insect-associated	8,9			7	3887	51	Sanger	
Eremothecium (Ashbya) gossypii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Eremotheciaceae	ATCC 10895	Gp0000589	GCA_000091025.4	13834	plant pathogen (insect-associated; cotton)	9,1	4,20	7	7	4768	19	Sanger	
Eremothecium coryli	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Eremotheciaceae	CBS 5749	Gp0097267	AZAH01	229863	plant pathogen (soybean)	9,09	18,00	63	19		41,6	Illumina HiSeq	
Eremothecium cymbalariae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Eremotheciaceae	DBVPG#7215	Gp0008918	GCA_000235365.1	60715	plant pathogen (stigmatomycosis; fruit rot; crops)	9,66	40,00	9	8	4853	40,3		
Ambrosiozyma kashinagacola	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	JCM 15019	Gp0144006	BCGA01	313780	insect-associated	12,32	227,00	59	23		36,1	HiSeq 2500	
Ambrosiozyma monospora	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	JCM 7599	Gp0144035	BCIP01	313840	industrial importance; ethanol production	24,98	116,00	304	118		37,2	HiSeq 2500	
Candida albicans	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	SC5314	Gp0000024	AACQ01	10701	opportunistic human pathogen	27,56		413		14217	33,4		
Candida apicola	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	NRRL Y-50540	Gp0120946	LBNK01	278776	industrial importance (sophorolipid producing)	9,77	211,00	135	40		45,2	Illumina GAIIx	
Candida arabinofermentans	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	NRRL YB-2248	Gp0009551	JGI	207879	industrial importance	13,23	74,00	244	62	5861		454; Illumina	
Candida auris	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	6684	Gp0144502	LGST01	267757	human pathogen (multridrug healthcare infections)	12,5	179,00	759	99	8301	45,1	Illumina HiSeq; MiSeq	
Candida boidinii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	GF002	Gp0143128	LMZO01	299882	industrial importance (methylotrophic)	19,11	144,00	43	428		30,4	Illumina HiSeq	
Candida bracarensis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	CBS 10154	Gp0041972	CAPU00000000.1	202296	opportunistic human pathogen	12,2		51					
Candida carpophila	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	JCM 9396	Gp0144041	BCGK01	313789	probable human pathogen	10,24	273,00	26	10		47,4	HiSeq 2500	
Candida caseinolytica	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	NRRL Y-17796	Gp0005936	JGI	76687	plant pathogen (possible; associated with rot in cacti)	9,18	47,89	49	6	4657		454; Illumina	
Candida castellii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	CBS 4332	Gp0041973	CAPW00000000.1	202297	uncertain	10,2		101					
Candida dubliniensis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	CD36	Gp0002579	ASM2694v1	34697	opportunistic human pathogen	14,62	11,00		8	6095	33	Sanger	
Candida ethanolica	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	M2	Gp0039259	ANNA01	171020	industrial importance	23,58	85,00	2647			26,4	Illumina HiSeq	
Candida glabrata	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	CBS 138	Gp0000563	ASM254v2	13831	human pathogen	12,3	8,00		13	5462	39	Sanger	
Candida homilentoma	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	JCM 1507	Gp0144054	BCGB01	313781	insect-associated (Bostrychid beetles)	12,18	223,00	32	8		49,4	HiSeq 2500	
Candida intermedia	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	JCM 1607	Gp0144011	BCGD01	313783	opportunistic human pathogen (candidiasis)	13,03	218,00	54	12		43,2	HiSeq 2500	
Candida maltosa	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	Xu316	Gp0039144	AOGT01	184737	industrial importance	12,8	130,00	2947		5986	34,2	Illumina HiSeq	
Candida nivariensis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	CBS 9983	Gp0041974	CAPV00000000.1	202298	human pathogen; drug-resistant	11,56		123					
Candida orthopsilosis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	AY2	Gp0039261	AMDC01	171019	human pathogen	12,65	67,00	4152	8	3296	37,6	Illumina GAIIx	
Candida parapsilosis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	CDC317	Gp0002580	CABE01	32889	human pathogen (sepsis)	13,08	9,20	24			38,7	Sanger	
Candida sorboxylosa	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	JCM 1536	Gp0144008	BCGC01	313782	industrial importance (fermentative yeast)	10,71	247,00	277	37		38,2	HiSeq 2500	
Candida succiphila	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	JCM 9445	Gp0144043	BCGL01	313790	industrial importance (methanol-assimilating)	12,15	234,00	64	22		40,9	HiSeq 2500	
Candida tanzawaensis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	NRRL Y-17324	Gp0009552	JGI	207878	insect-associated	13,14	74,00	52	16	5895		454; Illumina	
Candida tenuis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	ATCC 10573	Gp0016931	JGI	33673	industrial importance	10,7	26,90	668	25	5533	42	454; Sanger	
Candida tropicalis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	MYA-3404	Gp0006759	AAFN02	13675	human pathogen (candidiasis); industrial importance (biodiesel production	14,6	10,00	128	24	6441	33	Sanger	
Candida versatilis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	JCM 5958	Gp0144031	BCJV01	313866	industrial importance (salt-tolerant)	9,31	441,00	52	19		44,9	HiSeq 2500	
Lodderomyces elongisporus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	NRRL YB-4239	Gp0002646	AAPO01	12899	possible human pathogen	15,547	8,70	145	28	5908	37		
Nadsonia fulvescens	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	DSM 6958	Gp0009966	JGI	207853	uncertain; yeast (bipolar budding)	13,75	72,50	64	20	5657	39	454; Illumina	
Pachysolen tannophilus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	NRRL Y-2460	Gp0038525	CAHV01	85615	Fermentation; osmotolerant	12,6	90,65	583	198	5675	29,8	454; Illumina; Sanger	
Starmerella bombicola	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	JCM 9596	Gp0144046	BCGO01	313793	industrial importance (Sophorolipids, Glycolipid Biosurfactant production)	9,56	299,00	63	16		47,6	HiSeq 2500	
Zygoascus hellenicus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Incertae sedis	Y-7136 v1.0		1040573		human pathogen (fungemia)	12,17	98,40	48	11	5430		Illumina	
Clavispora lusitaniae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Metschnikowiaceae	ATCC 42720	Gp0002581	AAFT01	12753	human pathogen	12,1	9,00	88	9	6153	44,5	Sanger	
Metschnikowia bicuspidata	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Metschnikowiaceae	Baker2002	Gp0072273	JGI	246206	parasite (brine shrimp); hypersaline	16,06	16,08	421	48	1497		454; Illumina MiSeq	
Metschnikowia fructicola	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Metschnikowiaceae	277	Gp0037508		179032	biocontrol (spoilage control)	24,482	700,00	8430			45,5	Illumina HiSeq	
Cyberlindnera fabianii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Phaffomycetaceae	JCM 3601	Gp0144028	BCGI01	313787	industrial importance (waste water treatment; alcoholic fermentation)	12,3	223,00	53	12		44,2	HiSeq 2500	
Cyberlindnera jadinii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Phaffomycetaceae	NBRC 0988	Gp0038874	BAEL01	167219	industrial importance	14,27	20,00	1163			46	454; Sanger	
Brettanomyces (Dekkera) bruxeller	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Pichiaceae	CBS 2499	Gp0005465	AHMD01	76499	industrial importance	13,37	127,50	1374	84	5600	40,3	454; Illumina	
Brettanomyces anomalus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Pichiaceae	YV396	Gp0120591	LCTY01	281311	industrial importance (fermentative yeast)	12,88	100,00	280	30		39,9	Illumina HiSeq	
Hyphopichia burtonii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Pichiaceae	NRRL Y-1933	Gp0009550		207851	spoilage yeast	12,4	50,40	105	27	6002		454; Illumina	
Nakazawaea peltata	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Pichiaceae	JCM 9829	Gp0144049	BCGQ01	313795	fermentation	11,65	239,00	34	11		40,5	HiSeq 2500	
Ogataea methanolica	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Pichiaceae	JCM 10240	Gp0143979	BCKW01	313882	industrial importance (methylotrophic)	15,1	248,00	168	32		36,2	HiSeq 2500	
Ogataea polymorpha	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Pichiaceae	BY4329	Gp0109098	BBNV01	263660	industrial importance (methylotrophic)	8,89	20,00	66			47,7	454 GS FLX; GAIIx	
Pichia kudriavzevii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Pichiaceae	NBRC1279	Gp0107454	BBOI01	260583	spoilage yeast	10,18	45,00	669		7107	38,5		454
Pichia membranifaciens	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Pichiaceae	NRRL Y-2026	Gp0007246	JGI	52937	spoilage yeast; contaminant	11,58	38,95	279	11	5560			
Eremothecium sinecaudum	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	ATCC 58844	Gp0150734		310026	industrial importance (oxylipin synthesis)	8,92		7	7	4536	40,13		
Kazachstania africana	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 2517	Gp0038942	GCA_000304475.1	70967	uncertain	11,13		34	12	5649	36,4		
Kazachstania naganishii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 8797	Gp0038944	GCA_000348985.1	70969	saprotroph (soil)	10,845		95	13	5488	46,1		
Kluyveromyces aestuarii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	ATCC 18862	Gp0008229	AEAS01	49737	marine yeast	9,91	14,00	336			38,3		454
Kluyveromyces dobzhanskii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 2104	Gp0122802	CCBQ01	271459	insect-associated (Drosophila)	10,74		86		4957	41,3	PacBio RS II; Ion Torrent	
Kluyveromyces lactis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	NRRL Y-1140	Gp0000566	GCA_000002515.1	13835	industrial importance	10,729	11,40		6	5379	39	Sanger	
Kluyveromyces marxianus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	DMKU3-1042	Gp0005866	AKFM00000000.1	65233	industrial importance (thermotolerant)	10,851		346	116	4998	40,1	Illumina	
Kluyveromyces wickerhamii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	UCD 54-210	Gp0008298	AEAV01	50387	gut associate (Drosophila)	9,8	12,00	510			40,9		454
Kuraishia capsulata	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 1993	Gp0100965	CBUD02	236987	nitrate assimilating	11,3712		73	7	6029	45,6		
Lachancea kluyveri	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	NRRL Y-12651	Gp0002690	AACE03	176298	uncertain; yeast (budding)	11,37	0,20	36	8		41,6	Sanger	
Lachancea lanzarotensis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 12615	Gp0122660	CDLU01	270482	industrial importance (grape fermentation)	11,1		34	24	5058	44,3	Illumina MiSeq	
Lachancea thermotolerans	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 6340	Gp0002639	ASM14280	12499	industrial importance	10,392	12,30	10	8	5498	47	Sanger	
Lachancea waltii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	NCYC 2644	Gp0000028	AADM01	10734	uncertain; yeast (budding)	10,912	8,00	713			44,3	Sanger	
Nakaseomyces bacillisporus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 7720	Gp0041979	CAPX00000000	202300	fermentation	10,839		186					
Nakaseomyces delphensis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 2170	Gp0041980	CAPT00000000	202299	fermentation	10,867		179					
Naumovozyma castellii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	NRRL Y-12630	Gp0002683	AACF01	1444	uncertain; yeast (budding)	11,242	3,90	57		5870	36,86	Sanger	
Naumovozyma dairenensis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 421	Gp0022846		70961	uncertain; yeast (budding)	13,527		279	11	5816	34		
Ogataea angusta	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	ATCC MYA-335	Gp0017030	JGI	50737	industrial importance (thermotolerant)	8,97		9	7	5177		454; Sanger	
Ogataea parapolymorpha	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	DL-1	Gp0008917	AEOI02	60503	industrial importance	8,874	49,00	10	7	5408	47,9		454
Pichia pastoris (Komagataella phaff	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	GS115	Gp0004868	ASM2700	37871	industrial importance (methylotroph); model organism	9,216	20,00	15		5040	41		454
Saccharomyces arboricola	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	H-6	Gp0045176	ALIE01	88533	uncertain; yeast (budding); closely related to S. cerevisae	11,619	50,00	219	35	3732	38,7	454; SOLiD	
Saccharomyces bayanus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	MCYC 623	Gp0002682	AACA01	1441	fermentation (wine- and cider-making)	11,477	6,40	1098			40,2	Sanger	
Saccharomyces boulardii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	EDRL	Gp0043133	ATCS01	207020	pharmaceutical importance (probiotic)	11,482	50,00	194			38,2		454
Saccharomyces cerevisiae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	S288c	Gp0000787	GCA_000091065.1	13838	fermentation	12,07		16	16	6575	38	Sanger	
Saccharomyces eubayanus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS12357	Gp0038986	BBYU01	307492	industrial importance (fermentation; brewing)	11,65	360,00		47	5379	40	Illumina	
Saccharomyces kudriavzevii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	IFO 1802	Gp0002692	AACI03	1442	uncertain; yeast (budding)	11,189	3,40	2055	2054		44,4	Sanger	
Saccharomyces mikatae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	IFO 1815	Gp0002694	AABZ01	374	uncertain; yeast (budding)	11,47	5,90	1648			38	Sanger	
Saccharomyces paradoxus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	NRRL Y-17217	Gp0002695	AABY01	1440	fermentation (wine-making)	11,872	7,70	832			38,7	Sanger	
Saccharomyces pastorianus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 1513	Gp0038325	AZCJ01	71341	fermentation (lager beer)	19,367	18,00	282	77		39,3		454
Saccharomyces uvarum	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	A9	Gp0095594	JNVO01	251664	Fermentation (Bottom-fermenting wine yeast)	11,595	30,00	3985			40,1	ion Torrent	
Tetrapisispora blattae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 6284	Gp0038943	GCA_000315915.1	70963	gut symbiont (cockroach)	14,048		82	10	5725	31,79		
Tetrapisispora phaffii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 4417	Gp0018177	GCA_000236905	70965	biocontrol (spoilage control); killer yeast	12,115		105	17	5460	34		
Torulaspora delbrueckii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 1146	Gp0023773	GCA_000243375.1	70971	industrial importance (biotechnological interest)	9,22		34	8	5176	42		
Vanderwaltozyma polyspora	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	DSM 70294	Gp0000053	AAZN01	19237	uncertain; yeast; close relative of S. cerevisiae	14,674	7,80	411	281	5767	33	Sanger	
Zygosaccharomyces bailii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	ISA1307	Gp0045431	CBTC01	236361	spoilage yeast; acetic acid tolerant	12,141		281		4723	42,5		
Zygosaccharomyces rouxii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycetaceae	CBS 732	Gp0002712	GCA_000026365.1	12502	food spoilage yeast (Halotolerant and osmotolerant)	9,764	11,10	9		5332	39	Sanger	

Hanseniaspora uvarum	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycodaceae	34-9	Gp0097581	JPPO02	254213	saprotroph	8,1	234,00	103	41	4061	31,6	Illumina HiSeq
Hanseniaspora valbyensis	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycodaceae	NRRL Y-1626	Gp0007245	JGI	64991	traditional use	11,46	53,00	1163	647	4800		454; Illumina
Hanseniaspora vineae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycodaceae	T02/19AF	Gp0090029	JFAV02	238564	industrial importance	11,383	121,00	305			37,4	Illumina GAIIx
Arthroascus fermentans	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycopsidaceae	17710 v1.0		1040501		fermenting yeast	14,37	89,20	115	46	5449		Illumina
Saccharomycopsis malanga	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Saccharomycopsidaceae	JCM 7620	Gp0144036	BCGJ01	313788	uncertain	16,72	190,00	229	44		37,8	HiSeq 2500
Sugiyamaella (Candida) lignohabita	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Trichomonascaceae	CBS 10342			308900	industrial importance (biorefinery)	15,98			5	5135	44,9	
Sugiyamaella americana	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Trichomonascaceae	NRRL YB-2067 v1.0		1040555		insect-associated (beetles)	16,48	100,00	223	52	6288		Illumina
Sympodiomyces attinorum	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Trichomonascaceae	NRRL Y-27639 v1.0		1040561		insect-associated (ants)	14,02	89,30	66	14	6184		Illumina
Trichomonascus petasosporus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Trichomonascaceae	NRRL YB-2093	Gp0150175	1042933	332934	saprotrophic yeast	14,46	91,90	175	79			Illumina
Wickerhamiella domercqiae	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Trichomonascaceae	JCM 9478	Gp0144044	BCGM01	313791	pharmaceutical importance (anticancer sophorolipid producing)	8,47	344,00	50	4		48,4	HiSeq 2500
Wickerhamomyces anomalus	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Wickerhamomycetaceae	NRRL Y-366	Gp0008963	AEGI02	52059	industrial importance (wine yeast); spoilage; biocontrol (mycotoxic compo	14,15	97,57	207	46	6423	35,1	454; Illumina
Wickerhamomyces ciferrii	Ascomycota	Saccharomycotina	Saccharomycetes	Saccharomycetidae	Saccharomycetales	Wickerhamomycetaceae	NRRL Y-1031	Gp0038328	CAIF01	169887	pharmaceutical importance (sphingolipid biosynthesis pathway)	15,901		364		6702	30,4	
Pneumocystis jirovecii (carinii)	Ascomycota	Taphrinomycotina	Pneumocystidomycetes	Pneumocystidomycetidae	Pneumocystidales	Pneumocystidaceae	SE8	Gp0038459	CAKM01	68827	parasite (obligate); colonizes lungs (pneumonia)	8,15	675,50	355	355	3520	28,4	454; Illumina
Pneumocystis murina	Ascomycota	Taphrinomycotina	Pneumocystidomycetes	Pneumocystidomycetidae	Pneumocystidales	Pneumocystidaceae	B123	Gp0037048	AFWA01	70803	parasite (obligate); colonizes lungs (pneumonia)	7,451	214,90	17		3609	26,9	454; Illumina
Schizosaccharomyces cryophilus	Ascomycota	Taphrinomycotina	Schizosaccharomycetes	Schizosaccharomycetidae	Schizosaccharomycetales	Schizosaccharomycetaceae	OY26	Gp0008116	ACQJ02	38373	uncertain; yeast (fission)	11,56	51,00	202	34	5180	37,7	454
Schizosaccharomyces japonicus	Ascomycota	Taphrinomycotina	Schizosaccharomycetes	Schizosaccharomycetidae	Schizosaccharomycetales	Schizosaccharomycetaceae	yFS275	Gp0002702	AATM02	13640	model organism; yeast (fission)	11,73	9,00	87	32	4878	44	Sanger
Schizosaccharomyces octosporus	Ascomycota	Taphrinomycotina	Schizosaccharomycetes	Schizosaccharomycetidae	Schizosaccharomycetales	Schizosaccharomycetaceae	yFS286	Gp0002701	ABHY03	13639	uncertain; yeast (fission)	11,63	39,00	18	5	4986	37,5	Sanger
Schizosaccharomyces pombe	Ascomycota	Taphrinomycotina	Schizosaccharomycetes	Schizosaccharomycetidae	Schizosaccharomycetales	Schizosaccharomycetaceae	972h-	Gp0000701	GCA_000002945.2	13836	model organism	12,591		8	4	6953	36	
Saitoella complicata	Ascomycota	Taphrinomycotina	Taphrinomycetes	Taphrinomycetidae	Taphrinales	Protomycetaceae	NRRL Y-17804	Gp0038417	BACD02	63243	saprotroph	14,14	52,49	74	35	7034	52,5	454; Illumina
Taphrina deformans	Ascomycota	Taphrinomycotina	Taphrinomycetes	Taphrinomycetidae	Taphrinales	Taphrinaceae	PYCC 5710	Gp0038420	CAHR02	74523	plant pathogen (peach)	13,394		517	403	4668	49,5	
Taphrina flavorubra	Ascomycota	Taphrinomycotina	Taphrinomycetes	Taphrinomycetidae	Taphrinales	Taphrinaceae	JCM 22207	Gp0103452	BAVW01	257906	plant pathogen (Prunus fruit)	15,73	200,00	1266	865		49,6	Illumina HiSeq
Taphrina populina	Ascomycota	Taphrinomycotina	Taphrinomycetes	Taphrinomycetidae	Taphrinales	Taphrinaceae	JCM 22190	Gp0124247	BAVX01	271741	plant pathogen (cottonwood)	12	200,00	408	335		47,4	Illumina HiSeq
Taphrina wiesneri	Ascomycota	Taphrinomycotina	Taphrinomycetes	Taphrinomycetidae	Taphrinales	Taphrinaceae	JCM 22204	Gp0103453	BAVU01	257904	plant pathogen (cherry trees)	13,1	200,00	359	225		48,1	Illumina HiSeq

Sequenced Basidiomycota species

	Classification											Genome statistics						
SPECIES	**PHYLUM**	**SUBPHYLUM**	**CLASS**	**SUBCLASS**	**ORDER**	**FAMILY**	**Strain**	**GOLD Accession**	**GENOME Accession**	**NCBI Project ID**	**Significance**	**Size (Mb)**	**coverage**	**# of contigs**	**# of scaffolds**	**# genes**	**GC**	**Technology**
Agaricus bisporus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Agaricaceae	JB137-s8	Gp0003193	JGI	61007	edible; saprotroph	30,2	46	254	29	10438		454; Illumina
Leucoagaricus gongylophorus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Agaricaceae	Ac12	Gp0042023	ANIS01	179280	insect symbiont	101,58	15	92785	92785		35,1	454
Leucoagaricus sp. SymC.cos	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Agaricaceae	SymC.cos	Gp0143237	LSHD01	295288	insect-associated (ants)	119,03	27	33952	20457	12136	44,4	Illumina HiSeq
Macrolepiota fuliginosa	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Agaricaceae	MF-IS2	Gp0024456	JGI	218801	saprotroph	46,4	165,4	4852	3478	15801		Illumina HiSeq
Amanita brunnescens	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Amanitaceae	BX004	Gp0096753	JNHV01	236753	mycorrhizal	57,56	25	24247	17039			Illumina HiSeq
Amanita inopinata	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Amanitaceae	Kibby_2008	Gp0096754	JNHW01	236757	saprotroph	22,12	900	6054	5912		47,9	Illumina HiSeq
Amanita jacksonii	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Amanitaceae	TRTC16861	Gp0067868	AYNK01	226613	ectomycorrhizal	30,9	100	5557	4516			
Amanita muscaria var. guesso	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Amanitaceae	BX008	Gp0096755	JNHX01	236758	ectomycorrhizal	67,64	250	23945	17515	18091	47,5	Illumina HiSeq
Amanita polypyramis	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Amanitaceae	BW_CC	Gp0096756	JNHY01	236755	ectomycorrhizal	23,56	150	6521	5295		47,3	
Amanita thiersii	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Amanitaceae	SKay4041	Gp0005144	JGI	82749	saprotroph	33,69	135,9	2164	1446	10354		
Bolbitius vitellinus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Bolbitiaceae	SZMC-NL-1	Go0125832	1097215	334996	saprotroph	51,24	65	428	428	14483		PacBio
Clavaria fumosa	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Clavariaceae	KM175152	Gp0145123	CVRD01	287237	saprotroph	70,47		114209	111201		55,7	Illumina HiSeq
Cortinarius glaucopus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Cortinariaceae	AT 2004 27	Gp0019356	JGI	213332	ectomycorrhizal	63,45	107,00	2103	769	20377		Illumina HiSeq
Hebeloma cylindrosporum	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Cortinariaceae	h7	Gp0005977	JGI	207849	mycorrhizal	38,23	113	526	176	15382		Illumina; PacBio; 454; Sanger
Crepidotus sp. BD-2015	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Crepidotaceae	MCA163	Gp0145126	CVRE01	287237	uncertain	70,26		793879	182032		54,3	IonTorrent
Crepidotus variabilis	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Crepidotaceae	CBS 506.95	v1.0	1056714		saprotroph	38,58	111,20	1097	435	14573		Illumina
Fistulina hepatica	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Fistulinaceae	ATCC 6442	Gp0017025	JYFI01	196028	saprotroph; wood-decay	33,85	137,9	914	588	11391	50,2	Illumina; PacBio
Laccaria amethystina	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Hydnangiaceae	LaAM-08-1	Gp0010080	JGI	196025	ectomycorrhizal	52,2	156,5	4756	1299	21066		454; Illumina HiSeq
Laccaria bicolor	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Hydnangiaceae	S238N-H82	Gp0002644	JGI	19043	ectomycorrhizal	60,71	9,90	584	55	23132	47	Sanger
Hypsizygus marmoreus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Lyophyllaceae	51987-8	Gp0143018	LUEZ01	312409	saprotroph; edible	41,63	287,30	999	340	15561	48,7	Illumina HiSeq; MiSeq
Termitomyces sp. J132	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Lyophyllaceae	J132	Gp0076039	JDCH01	193471	insect-cultivated fungus	67,3	81	4863	2335	11398	46,3	Illumina HiSeq
Marasmius fiardii	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Marasmiaceae	PR-910	Gp0035332	1016747	200608	uncertain	59,45	96,1	2986	1124	17098		Illumina HiSeq
Moniliophthora perniciosa	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Marasmiaceae	FA553	Gp0002607	ABRE01	28951	plant pathogen (cacao)	26,663		25056		16443	48	Sanger
Moniliophthora roreri	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Marasmiaceae	MCA 2997	Gp0049167	AWSO01	213737	plant pathogen (pod rot of cacao)	52,204	15,00	3280		17910	46,9	454; Illumina
Mycena chlorophos	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Mycenaceae		Gp0149686	BAYG01	317219	bioluminescent saprotroph	43,6	420	25660		17445	55,6	Illumina
Mycena galopus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Mycenaceae	ATCC-6205	Go0035333	1016743	196020	saprtotroph	211,36	80,09557307	1364	1364	49694		PacBio
Panellus stipticus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Mycenaceae	LUM	Gp0046822	1018599	245622	saprotroph	53,17	112,20	3730	1562	15860		Illumina
Crucibulum laeve	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Nidulariaceae	CBS 166.37	v1.0	1059303		saprotroph	44,73	106,60	1536	574	14218		Illumina
Cyathus striatus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Nidulariaceae	AH 40144	Go0111615	1056738	333390	saprtotroph; bird's nest fungus	91,18		1562	1562	23513		Illumina; PacBio
Lentinula edodes	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Omphalotaceae	L-54	Gp0006482		17581	edible	40,2	11,00		767	13382		454; SOLiD
Omphalotus olearius	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Omphalotaceae	VT 653.13	Gp0039058	AHIW01	79063	bioluminescent mushroom	28,15	85,3	1535	868	8171	47,4	Illumina
Rhodocollybia butyracea	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Omphalotaceae	AH 40177	v1.0	1056720		saprotroph	96,28		1482	1482	22870		PacBio
Armillaria gallica	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Physalacriaceae	Ar21-2	Gp0072259	JGI	242129	saprotroph; pathogen (root rot; opportunistic tree p	85,34	41,8	1529	319	25704		Illumina HiSeq
Armillaria ostoyae	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Physalacriaceae	28-4	v1.0	1032462		plant pathogen; conifer root rot (parasitic or saprop	58,01	67,6	693	229	20811		PacBio
Cylindrobasidium torrendii	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Physalacriaceae	FP15055 ss-	Gp0034230	JNEL01	196018	saproptroph	31,57	134,3	1222	1149	13940		Illumina HiSeq
Flammulina velutipes	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Physalacriaceae	W23	Gp0041101	AQHU01	191864	model organism	35,64	37,20	513	11		49,8	454
Guyanagaster necrorhiza	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Physalacriaceae	MCA 3950	Gp0036668		234669	saprotroph	53,69	81,5	656	168			Illumina HiSeq
Oudemansiella mucida	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Physalacriaceae	CBS 558.79	Go0111942	1056768		saprtotroph; white-rot	61,73	131,00	1386	1386	18562		PacBio
Pleurotus eryngii	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Pleurotaceae	ATCC 90797	v1.0	1056780		bioremediation; edible	44,61	96,7	1684	609	15960		
Pleurotus ostreatus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Pleurotaceae	PC15	Gp0017839	AYUK01	81933	saprotrophic (white rot)	34,342	8,7	13	12	12460	50,9	Sanger
Pluteus cervinus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Pluteaceae	NL-1719	v1.0	1063679		saprotroph	52,19	138,20	3329	1887	19818		Illumina
Volvariella volvacea	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Pluteaceae	PYd21	Gp0038369	ANCH01	171553	edible mushroom	36,626	90,00	2304			48,8	Illumina GAII
Coprinellus micaceus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Psathyrellaceae	FP101781 v	Gp0072267	1031312	247835	saprotroph	77,39	74,8	704	704	23559		PacBio
Coprinellus pellucidus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Psathyrellaceae	TEP2b		1074556		coprophilous	41,56	167,7	2262	1355	16047		Illumina
Coprinopsis cinerea	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Psathyrellaceae	okayama7#	Gp0002605	AACS02	1447	model organism	36,19	10	68	68	13657	52	Sanger
Coprinopsis marcescibilis	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Psathyrellaceae	CBS121175	Gp0092282	1040687	247837	coprophilous	38,91	94,40	1269	817	14632		Illumina
Pterula gracilis	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Pterulaceae	CBS309.79	v1.0	1019505		developmentally interesting	34,77	88,4	852	221	12873		Illumina
Schizophyllum commune	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Schizophyllaceae	H4-8	Gp0003179	ADMJ01	32757	saprotroph; opportunistic human pathogen	38,67	8,29	72	25	16319	57,5	Sanger
Galerina marginata	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Strophariaceae	CBS 339.88	Gp0017026	AYUM01	207683	saprotroph (white rot); toxic	59,42	34,30	1272	414	21461	48	454; Illumina
Gymnopilus chrysopellus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Strophariaceae	PR-1187	Gp0033092	JGI	196058	saprotroph	47,22	142,5	2046	1949	18193		Illumina HiSeq
Gymnopilus junonius	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Strophariaceae	AH 44721	Go0111649	1056762		saptrotroph; white-rot; hallucinogenic	59,46	101,97	1174	1174	16444		Illumina; PacBio
Hypholoma sublateritium	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Strophariaceae	FD-334 SS-4	Gp0010136		70685	industrial importance	48,03	152	1329	704	17911	51	454; Illumina
Baeospora myosura	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Tricholomataceae	KM189292	Gp0145125	CEMG01	287237	saprotroph	61,02		190914	1824890		50,5	
Gymnopus androsaceus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Tricholomataceae	JB14	Gp0046757	JGI	234428	saprotrophic (white rot); important in carbon cycle	89,15		2519	2516	29375		Illumina
Gymnopus luxurians	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Tricholomataceae	FD-317 M1	Gp0010138	JGI	68535	saprotroph	66,28	29,73	1848	383	22057	45	454; Illumina
Lepista nuda	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Tricholomataceae	CBS 247.69	v1.0	1056744		saprotroph; edible	43,49	93,4	2234	822	14880		Illumina
Macrocystidia cucumis	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Tricholomataceae	KM177596	Gp0145124	CEMH01	287237	saprotroph	46,75		210056	204508		48,8	
Tricholoma matsutake	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Agaricales	Tricholomataceae	945	Gp0017903		200596	ectomycorrhizal (edible)	175,76	100,4	16714	2546	22885		Illumina HiSeq; PacBio
Anomoporia bombycina	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Amylocorticales	Amylocorticiaceae	ATCC 6450	Go0109871	1051233	333831	uncertain	44,48	126,1	4856	1600	14617		Illumina
Plicaturopsis crispa	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Amylocorticales	Amylocorticiaceae	FD-325 SS-3	Gp0010137	JGI	207847	saprotrophic (white rot)	34,5	33,81	956	316	13626		454; Illumina
Athelia rolfsii	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Atheliales	Atheliaceae	1010	Gp0106003	JZWR01	259929	plant pathogen (blight of vegetables)	59,72	24	20290			46,4	IonTorrent; PGM
Fibulorhizoctonia psychrophila	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Atheliales	Atheliaceae	CBS 109695	Gp0025527	1006934	196049	psychrophile; spoilage	95,13	30,5	3901	1918	32946		Illumina HiSeq
Piloderma croceum	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Atheliales	Atheliaceae	F 1598	Gp0000933		61203	ectomycorrhizal	59,33	102,8	4469	715	21583		Illumina
Auricularia subglabra	Basidiomycota	Agaricomycotina	Agaricomycetes	Auriculariomycetidae	Auriculariales	Auriculariaceae	SS-5	Gp0006909	JGI	60553	saprotrophic (white rot)	74,92	46,57	4323	1531	23577	58,6	Sanger; 454; Illumina
Exidia glandulosa	Basidiomycota	Agaricomycotina	Agaricomycetes	Auriculariomycetidae	Auriculariales	Auriculariaceae	HHB12029	Gp0024457	JGI	196053	saproptroph	78,17	83,7	4024	1727	26765		Illumina HiSeq
Aporpium (Elmerina) caryae	Basidiomycota	Agaricomycotina	Agaricomycetes	Auriculariomycetidae	Auriculariales	Incertae sedis	L-13461	Gp0033151	1009626	218032	lignocellulotic cosmopolitan fungus	39,53	26,00	731	533	16571		Illuminal; PacBio
Boletus edulis	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Boletaceae	BED1	Gp0016927	JGI	200598	mycorrhizal	46,64	135	4723	1099	16933		Illumina
Xerocomus badius	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Boletaceae	84.06	v1.0	1019549		ectomycorrhizal	38,39	166,4	2580	1390	14938		Illumina
Phlebopus portentosus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Boletinellaceae	PP33	Gp0109113	JROP02	260232	ectomycorrhizal; edible	30,35	70	295	108		49	Illumina HiSeq
Coniophora puteana	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Coniophoraceae	RWD-64-59	Gp0001002	AEIT01	53977	saprotroph (brown rot)	42,97	49,54	1034	210	13761	52,4	454; Illumina
Leucogyrophana mollusca	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Hygrophoropsidaceae	KUC201207	Gp0036250	JGI	239087	saprotroph	35,19	110,2	1347	1262	14619		Illumina HiSeq
Gyrodon lividus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Paxillaceae	BX	Gp0019392	JGI	234843	ectomycorrhizal	43,05	113,5	1390	369	11779		Illumina HiSeq
Hydnomerulius pinastri	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Paxillaceae	MD-312	Gp0012784	JGI	207871	saprotroph (brown rot)	38,28	41,30	2315	603	13270		454; Illumina HiSeq
Paxillus ammoniavirescens	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Paxillaceae	Pou09.2	v1.0	1047709		ectomycorrhizal	35,76	176,50	2244	1194	13473		Illumina
Paxillus involutus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Paxillaceae	ATCC 2001	Gp0003197		60449	ectomycorrhizal	58,3	36,2	6222	2681	17968		454; Illumina
Paxillus rubicundulus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Paxillaceae	Ve08.2h10	Gp0010108		243391	ectomycorrhizal	53,01	133,9	7170	6945	22065		Illumina
Rhizopogon salebrosus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Rhizopogonaceae	TDB-379	Gp0003891		207841	mycorrhizal; model organism	82,29	120,8	5710	1976	18900		Illumina HiSeq
Rhizopogon vinicolor	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Rhizopogonaceae	AM-OR11-0	Gp0032994		196085	ectomycorrhizal	36,1	153,70	3018	2310	14469		Illumina
Pisolithus microcarpus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Sclerodermataceae	441	Gp0002173	JGI	60815	mycorrhizal	53,03	87,1	5476	1064	21064		Illumina HiSeq; 454; Sanger
Pisolithus tinctorius	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Sclerodermataceae	Marx 270	Gp0004800	JGI	207840	Mycorrhizal	71,01	74	5915	610	22701		Illumina
Scleroderma citrinum	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Sclerodermataceae	Foug A	Gp0017844		207859	ectomycorrhizal	56,14	80,70	3919	938	21012		Illumina
Serpula lacrymans	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Serpulaceae	S7.9	Gp0003188	AEQB01	32885	saprotroph (brown rot)	42,73	8	375	36	12789	45	Sanger
Suillus americanus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Suillaceae	EM31	v1.0	1052751		mycorrhizal	50,81	92	3604	1307	17163		Illumina
Suillus brevipes	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Suillaceae	Sb2	Gp0024399	JGI	218802	ectomycorrhizal	51,71	101,70	4139	1550	22453		Illumina HiSeq
Suillus decipiens	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Suillaceae	EM49	v1.0	1052769		mycorrhizal; edible	62,78	91,3	3648	1391	16894		Illumina
Suillus granulatus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Suillaceae	EM37	v1.0	1052757		mycorrhizal	42,34	80,3	1869	628	15802		Illumina
Suillus hirtellus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Suillaceae	EM16	v1.0	1052775		ectomycorrhizal	49,94	109,5	1626	644	17067		Illumina
Suillus luteus	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Boletales	Suillaceae	UH-Slu-Lm8	Gp0025675	JGI	242126	ectomycorrhizal	37,01	93,60	2113	1944	18316		454; Illumina HiSeq
Botryobasidium botryosum	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Cantharellales	Botryobasidiaceae	FD-172 SS1	Gp0010010	JGI	69807	saprotroph	46,67	31,02	1446	334	16526	52	454; Illumina
Cantharellus anzutake	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Cantharellales	Cantharellaceae	C23	Gp0022296	1006245	245611	ectomycorrhizal	120,17		614	614	16968		Illumina HiSeq
Rhizoctonia solani	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Cantharellales	Ceratobasidiaceae	AG-1 IB	Gp0041102	CAOJ01	170144	plant pathogen (broad host range)	47,66	25	3979	1600	15157	48	454
Clavulina sp. PMI_390	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Cantharellales	Clavulinaceae	PMI_390	Gp0039948	JGI	243946	ectomycorrhizal	41,64	131,2	1435	683	15452		Illumina HiSeq
Hydnum rufescens	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Cantharellales	Hydnaceae	UP504	v2.0	1019557		ectomycorrhizal; edible	67,14	102,00	2013	1072	18665		Illumina
Tulasnella calospora	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Cantharellales	Tulasnellaceae	AL13/4D	Gp0012815	JGI	207843	mycorrhizal	62,39	136	6848	1335	19659		Illumina HiSeq

Dendrothele bispora	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Corticiales	Corticiaceae	CBS 962.96	Gp0034229	JGI	196017	saproptroph	130,65	103	6351	3942	33645		Illumina HiSeq	
Limonomyces culmigenus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Corticiales	Corticiaceae	CBS 661.85				plant pathogen (turfgrass)	36,1	211		8889		57,8		
Punctularia strigosozonata	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Corticiales	Corticiaceae	HHB-11173	Gp0007184	AEGM01	52407	saprotrophic (white rot)	34,17	45,55	1327	195	11538	55,2	Sanger; 454; Illumina	
Sphaerobolus stellatus	Basidiomycota	Agaricomycotina	Agaricomycetes	Phallomycetidae	Geastrales	Geastraceae	SS14	Gp0017850		207858	saprotroph	176,37	57,5	13156	1460	35274		Illumina	
Sclerogaster hysterangioides	Basidiomycota	Agaricomycotina	Agaricomycetes	Phallomycetidae	Geastrales	Sclerogastraceae	SCL2.BST		1019437	256708	uncertain	124,26		901	901	16656		Illumina; PacBio	
Gloeophyllum trabeum	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Gloeophyllales	Gloeophyllaceae	ATCC 1153	Gp0005491	AFVP01	64553	saprotroph (brown rot)	37,18	54,00	1454	442	11885	53,2	Sanger; 454; Illumina	
Heliocybe sulcata	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Gloeophyllales	Gloeophyllaceae	OMC1185	v1.0	1047715		saprotroph (brown rot)	31,95	82,2	491		12570			
Neolentinus lepideus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Gloeophyllales	Gloeophyllaceae	HHB14362	Gp0025087	JGI	196054	saprotroph (brown rot)	35,64	92,4	1215	331	13164		Illumina HiSeq	
Gautieria morchelliformis	Basidiomycota	Agaricomycotina	Agaricomycetes	Phallomycetidae	Gomphales	Gomphaceae	GMNE.BST	v1.0	1019425		uncertain, hypogeal	122,81		1220	1220	20331		PacBio	
Ramaria acris	Basidiomycota	Agaricomycotina	Agaricomycetes	Phallomycetidae	Gomphales	Gomphaceae	UT-36052-T	Gp0035336	JGI	196021	ectomycorrhizal	105,46	78,90	5927	1553	19287		Illumina	
Fomitiporia mediterranea	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Hymenochaetales	Hymenochaetaceae	MF3/22	Gp0006428	AEJJ01	56107	saprotrophic (white rot)	63,35	39,35	5766	1412	11333	40,8	Sanger; 454; Illumina	
Onnia scaura	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Hymenochaetales	Hymenochaetaceae	P-53A	Gp0035335	1016751	245618	saprotroph; wood-decomposinbg	37,1	88,8	2066	834	12895		Illumina HiSeq	
Phellinus noxius	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Hymenochaetales	Hymenochaetaceae	OVT-YTM/9	Gp0070880	AYOR01	226629	plant pathogen (broad host range, typically trees)	31,259	35,00	1434			41,6	Ion Torrent	
Porodaedalea chrysoloma	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Hymenochaetales	Hymenochaetaceae	FP-135951	Go0033091	1009630	200594	plant pathogen (conifer parasite; white pocket rot)	44,69	50,00	1684	496	13562		Illumina; PacBio	
Porodaedalea niemelaei	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Hymenochaetales	Hymenochaetaceae	PN71-100-li	Go0072274	1032455	333975	plant pathogen (conifer white rot)	53,34		951	951	14467		PacBio	
Sanghuangporus baumii	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Hymenochaetales	Hymenochaetaceae	821	Gp0150193	LNZH02	304358	pharmaceutical importance (medicinal mushroom)	31,64	186,00	339	217	8455	47,6	Illumina	
Rickenella fibula	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Hymenochaetales	Rickenellaceae	HBK330-10	v1.0	1064682		saprotroph, probable	59,35	91,45	529	529	18897		PacBio	
Schizopora paradoxa	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Hymenochaetales	Schizoporaceae	KUC8140	Gp0036252	JGI	239088	wood-inhabiting	44,41	108	1342	1291	17098		Illumina HiSeq	
Jaapia argillacea	Basidiomycota	Agaricomycotina	Agaricomycetes	Agaricomycetidae	Jaapiales	Jaapiaceae	MUCL 3360	Gp0012165	AYUL01	207685	saprotroph	45,05	20,58	1182	295	16419	49,8	454; Illumina	
Mutinus elegans	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Phallales	Phallaceae	ME.BST	v1.0	1019445		saprotroph	52,78	85,3	3570	1095	14626		Illumina	
Taiwanofungus camphoratus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Coriolaceae	S27	Gp0109109	JNBV01	244959	pharmaceutical importance (traditional medicine)	32,16	878,00	348	360		50,6	Illumina GAIIx; 454	
Trametes cinnabarina	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Coriolaceae	DSM 3022	Gp0107556	JSYY01	261270	saprotrophic (white rot)	31,62	180,00	9648		10233	55,6	Illumina HiSeq	
Trametes hirsuta	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Coriolaceae	072	Gp0124682	LIYB01	271118	saprotrophic (white rot)	33,62	101,00	1022	140		56,8	Illumina HiSeq; MiSeq	
Trametes sp. AH28-2	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Coriolaceae	AH28-2	Gp0124683	LJJJ01	294859	saprotrophic (white rot); industrial importance (lacc	38,9	100,00	502	306		58,8	Illumina HiSeq	
Antrodia sinuosa	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Fomitopsidaceae	LB1	Gp0019259	JGI	196036	saprotroph	30,17	128,10	1482	1387	11327		Illumina HiSeq	
Daedalea quercina	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Fomitopsidaceae	L-15889	Gp0025092	JGI	196055	saprotroph	32,74	144,4	1025	357	12199		Illumina HiSeq	
Fomitopsis pinicola	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Fomitopsidaceae	FP-58527 S	Gp0008479	AEHC02	52941	saprotroph (brown rot)	41,61	85,9	988	504	13885	55,8	Illumina; PacBio	
Laetiporus sulphureus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Fomitopsidaceae	93-53	Gp0025315	JGI	196057	saprotroph	39,92	85,20	1207	403	13774		Illumina HiSeq	
Postia placenta	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Fomitopsidaceae	MAD 698	Gp0017841	ABWF01	19789	saprotroph (brown rot)	90,9	7,20	10568	1243	17173	54	Sanger	
Ganoderma lucidum	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Ganodermataceae	BCRC 3718	Gp0038562	AGAX00000000.1	61379	traditional use	43,29		194			56,1	454; Illumina; Sanger	
Ganoderma sp. 10597 SS1	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Ganodermataceae	10597 SS1	Gp0010017	JGI	68313	saprotroph	39,52	33,74	503	156	12910		Sanger; 454; Illumina	
Trametopsis cervina	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Hapalopilaceae	CIRM-BRFM 1824	v1.0	1051569		biocontrol (mycoparasite)	29,82	89	310	110	11836		Illumina	
Hydnopolyporus fimbriatus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Meripilaceae	CBS384.51	Go0111656	1051179	334190	saprotroph	34,57	92,20	894	256	12424		Illumina	
Bjerkandera adusta	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Meruliaceae	HHB-1282	Gp0008855	JGI	74757	saprotrophic (white rot)	42,73	47,59	1263	508	15473		454; Illumina	
Ceriporiopsis (Gelatoporia) sul	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Meruliaceae	B	Gp0003878	JGI	60419	saprotrophic (white rot)	39	56,6		740	12125		454; Sanger	
Obba rivulosa	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Meruliaceae	3A-2	Gp0046819		247915	saprotrophic (white rot)	34,04	127	808	712	13206		Illumina	
Phlebia brevispora	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Meruliaceae	HHB-7030	Gp0010049	JGI	64423	saprotrophic (white rot)	49,96	42,56	3178	1645	16170		454; Illumina	not publically available
Phanerochaete carnosa	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Phanerochaetaceae	HHB-10118	Gp0003186	AEHB01	38425	saprotrophic (white rot)	46,29	58,10	2272	1137	13937	53,1	Sanger; 454; Illumina	
Phanerochaete chrysosporium	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Phanerochaetaceae	RP-78	Gp0000577	AADS01	135	saprotrophic (white rot)	35,15	10,60	1253	232	13602	57	Sanger	
Phlebiopsis gigantea	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Phanerochaetaceae	11061_1 CR	Gp0017782	JGI	207860	saprotrophic (white rot)	30,14	144,9	1195	573	11891		Illumina	
Cerrena unicolor	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	303	Gp0016934	JGI	207864	saprotrophic (white rot)	36	189,6	1462	547	12966		Illumina	
Dichomitus squalens	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	LYAD-421 S	Gp0008772	AEID01	53511	saproptroph	42,75	50,63	2852	542	12290	55,6	454; Illumina	
Fibroporia radiculosa	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	TFFH 294	Gp0018298	CAGC01	72357	saprotroph (brown rot)	28,378		1823	861	9262	51,2	Illumina GAII	
Leiotrametes sp. BRFM 1775	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	BRFM 1775	Gp0092279	1037392	252879	lignocellulolytic	34,52	142,4	598	549	13763		Illumina	
Lentinus polychrous	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	BCC7694	Gp0107385	JSYW01	261275	saprotroph; edible	38,05	180,00	10349			51		
Lentinus tigrinus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	ALCF2SS1-7	Gp0036550	1006930	200609	saprotroph	39,76	103,6	572	263	15653		Illumina HiSeq	
Lignosus rhinocerotis	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	TM02	Gp0106247	AXZM01	212725	pharmaceutical importance (traditional medicine)	34,31	100	2317	1338		53,7	Illumina HiSeq	
Polyporus arcularius	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	HHB13444	Gp0025526	JGI	196048	saprotrophic (white rot)	43,45	118,00	2601	2540	17525		Illumina HiSeq	
Polyporus brumalis	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	BRFM 1820	v1.0	1051563		saprotroph	45,72	94,9	1040	621	18244		Illumina	
Pycnoporus cinnabarinus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	BRFM 137		CCBP01	251621	saprotrophic (white rot)	33,67		2036	784	10442	55,6		
Pycnoporus coccineus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	CIRM1662	Gp0025336	JGI	254894	saprotrophic (white rot)	32,1	128,70	643	599	12798		Illumina HiSeq	
Pycnoporus sanguineus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	BRFM 1264		JGI		saprotrophic (white rot)	36,04		2046	657	14165			454
Trametes cingulata	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	BRFM 1805	v1.0	1051575		saprotrophic (white rot)	35	108,30	625	367	14110		Illumina	
Trametes elegans	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	CIRM1663	Gp0035623	JGI	239086	saprotrophic (white rot)	33,08	86,1	638	243	12851		Illumina	
Trametes ljubarskyi	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	CIRM1659	Gp0035668	JGI	239085	saprotrophic (white rot)	34	86,3	761	311	13180		Illumina HiSeq	
Trametes versicolor	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	FP-101664	Gp0007183	AEJI01	56097	saprotrophic (white rot)	44,794	40	977	283	14572	57,7		454
Trichaptum abietinum	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	L-15831 ss-	Gp0025314	JGI	210203	saprotrophic (white rot)	40,61	125,6	1345	587	14978		Illumina HiSeq	
Wolfiporia cocos	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Polyporaceae	MD-104 SS	Gp0001013	AEHD01	52943	saprotroph (brown rot); traditional use	50,48	40,48	2228	348	12746	52	Sanger; 454; Illumina	
Xenasmatella vaga	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Polyporales	Xenasmataceae	CBS212.54	Go0112339	1051167	333496	saprotroph	64,17	91,3	3416	1275	20933		Illumina	
Artomyces pyxidatus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Auriscalpiaceae	HHB10654	Gp0072265	JGI	239090	saprotroph	37,99	90,3	1188	477	15130		Illumina HiSeq	
Auriscalpium vulgare	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Auriscalpiaceae	FP105234-S	Gp0072261	1031308	247917	saprotroph	39,65	122,7	2195	1349	16945		Illumina HiSeq	
Lentinellus vulpinus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Auriscalpiaceae	AHS73672-sp	v1.0	1058270		saprotroph (white rot)	34,71	94,9	1554	578	13477			
Heterobasidion annosum	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Bondarzewiaceae	03012	Gp0093680	AOSL01	182499	plant pathogen (conifers)	31,009	66,5	2415			51,5	Illumina	
Heterobasidion irregulare	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Bondarzewiaceae	TC 32-1	Gp0002642	AEOJ01	46703	plant pathogen (conifers and hardwoods)	33,649	8,5	18	15	13272	52,2	Sanger	
Dentipellis sp.	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Hericiaceae	KUC8613	v1.0	1036192		bioremediation; white rot	36,71	88,6	1184	425	14320		Illumina	
Scytinostroma sp.	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Lachnocladiaceae	KUC9335	Go0112034	1036200	333305	uncertain	60,64	N/A		597	597	14908		PacBio	
Vararia minispora	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Lachnocladiaceae	EC-137	Gp0033094	1006141	196070	saprotroph	36,81	149,80	1675	1435	10962		Illumina HiSeq	
Peniophora aff. cinerea.	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Peniophoraceae	CBS 579.87	Gp0034226	JGI	196016	saprotroph	46,03	141,30	1236	1092	18952		Illumina HiSeq	
Peniophora sp.	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Peniophoraceae	CONTA	v1.0	1027012		uncertain	48,44	85,80	487	217	18999		Illumina	
Lactarius quietus	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Russulaceae	SC23		1006257		ectomycorrhizal	115,9	97,00	2812	2812	18943		PacBio	
Stereum hirsutum	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Russulales	Stereaceae	FP-91666 S	Gp0017898	AEGX01	52843	saprotrophic (white rot)	46,51	44,77	995	159	14072	51,3	Sanger; 454; Illumina	
Piriformospora indica	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Sebacinales	Sebacinaceae	DSM 11827	Gp0038661	CAFZ01	76339	endophyte	24,98	22,00	2398	1884	11767	50,7		454
Sebacina vermifera	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Sebacinales	Sebacinaceae	MAFF 3058	Gp0010103	JGI	207844	mycorrhizal (orchid)	38,09	117,20	2457	546	15312		454; Illumina	
Thelephora ganbajun	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Thelephorales	Thelephoraceae	P2	v1.0	1050999		ectomycorrhizal ; edible	36,34	176,8	2373	1241	12643		Illumina	
Sistotremastrum niveocremeu	Basidiomycota	Agaricomycotina	Agaricomycetes	Incertae sedis	Trechisporales	Hydnodontaceae	HHB9708 ss	Gp0025439	JGI	196047	saprotroph (brown rot)	33,86	143,50	1072	1028	13657		Illumina	
Cantharellus anzutake	Basidiomycota	Agaricomycotina	Dacrymycetes	Incertae sedis	Dacrymycetales	Cerinomycetaceae	C23		1006245		mycorrhizal;edible	120,17		614	614	16968		PacBio	
Cerinomyces ceraceus	Basidiomycota	Agaricomycotina	Dacrymycetes	Incertae sedis	Dacrymycetales	Cerinomycetaceae	ATCC 56525	v1.0	1051227		saprotroph (brown rot)	33,2	91,5	836	376	13489		Illumina	
Calocera cornea	Basidiomycota	Agaricomycotina	Dacrymycetes	Incertae sedis	Dacrymycetales	Dacrymycetaceae	HHB12733	Gp0025090	JGI	210204	saprotroph (brown rot)	33,24	85,00	1032	545	13177		Illumina HiSeq	
Calocera viscosa	Basidiomycota	Agaricomycotina	Dacrymycetes	Incertae sedis	Dacrymycetales	Dacrymycetaceae	TUFC12733	Gp0018721	JGI	200620	saprotrophic (white rot)	29,1	81,7	487	214	12378		Illumina HiSeq	
Dacryopinax sp. DJM-731 SS1	Basidiomycotates	Agaricomycotina	Dacrymycetes	Incertae sedis	Dacrymycetales	Dacrymycetaceae	DJM-731 SS	Gp0007449	AEUS01	62091	saprotroph (brown rot)	29,5	43,19	878	99	10242	52,2	Sanger; 454; Illumina	
Mrakia blollopis	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Cystofilobasidiales	Mrakiaceae	SK-4	Gp0150507	BBPU01	270040	cryophilic	30,48	140	167			53,7	PacBio	
Mrakia frigida	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Cystofilobasidiales	Mrakiaceae	JCM 7857	Gp0144037	BCJW01	313867	biocontrol (toxibn production); psychrotolerant	28,62	232	268	149		54	HiSeq 2500	
Phaffia (Xanthophyllomyces) c	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Cystofilobasidiales	Mrakiaceae	JCM 9681	Gp0144047	BCJZ01	313870	industrial importance (carotenoid)	19,11	326	120	43	6380	47,3	HiSeq 2500	
Phaffia rhodozyma	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Cystofilobasidiales	Mrakiaceae	CBS 7918	Gp0145386	LSVH01	306035	industrial importance (carotenoid biosynthesis)	18,76	10,5	376	345		47,2	Illumina GAIIx	
Filobasidium wieringae	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Filobasidiales	Filobasidiaceae	JCM 11695	Gp0143999	BCIV01	313844	saprotroph, probable	19,78	277,00	83	36		49,9	HiSeq 2500	
Naganishia (Cryptococcus) visl	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Filobasidiales	Filobasidiaceae	ANT03-052	Gp0022517	JGI	196045	psychrophile	19,69	146,7	137	50	7232		Illumina HiSeq	
Naganishia albida (Cryptococc	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Filobasidiales	Filobasidiaceae	NRRL Y-14(	Gp0143351	LKPZ01	291988	opportunistic human pathogen	24,81	43,00	834			53,8		
Solicoccozyma (Cryptococcus)	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Filobasidiales	Piskurozymaceae	JCM 11743	Gp0144000	BCIS01	313842	saprotroph	22,26	278,00	316	71		54,9	HiSeq 2500	
Solicoccozyma (Cryptococcus)	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Filobasidiales	Piskurozymaceae	JCM 24518	Gp0143989	BCLD01	313887	industrial importance (oleaginous)	24,12	152	782	79		49,4	HiSeq 2500	
Holtermannia corniformis	Basidiomycota	Agaricomycotina	Tremellomycetes	Incertae sedis	Holtermanniales	Incertae sedis	JCM 1743	Gp0144015	BCIJ01	313834	uncertain	20,72	288	417	129		55,2	HiSeq 2500	
Holtermanniella nyarrowii	Basidiomycota	Agaricomycotina	Tremellomycetes	Incertae sedis	Holtermanniales	Incertae sedis	JCM 11471	Gp0143981	BCIT01	313843	psychrophile	17,74	309,00	92	33		52,7	HiSeq 2500	
Bulleromyces albus	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Bulleraceae	JCM 2954	Gp0144027	BCIX01	313846	uncertain	19,42	271,00	20	8		54,3	HiSeq 2500	
Sirobasidium intermedium	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Bulleraceae	CBS7805	v1.0	1051197		saprotroph	21,96	92,6	230	102	9453		Illumina	
Dioszegia aurantiaca	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Bulleribasidiaceae	JCM 2956	Gp0150860	BCKN01	313875	uncertain; plant-associated	19,34	188,00	139	52		53,6	Illumina	
Dioszegia crocea	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Bulleribasidiaceae	JCM 2961	Gp0150857	BCKK01	313872	uncertain; plant-associated	20,6	258	86	26		53,2	Illumina	
Dioszegia cryoxerica	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Bulleribasidiaceae	ANT03-071	Gp0022518	JGI	196046	psychrophile	39,52	98,50	1318	865	15948		Illumina HiSeq	
Cryptococcus amylolentus	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cryptococcaceae	CBS 6039	Gp0042018	AWGJ01	200571	saprotroph	20,25	117,00	18	15	8503	53,4	Illumina	

Cryptococcus depauperatus	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cryptococcaceae	CBS 7841	Gp0041267	AWGK01	200572	parasite (mycoparasite on Lecanicillium lecanii)	15,8	130	157	68	6521	44,7	Illumina
Cryptococcus gattii	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cryptococcaceae	R265	Gp0002609	AAFP01	13691	human pathogen	17,5	6	701	28	6580	47,87	Sanger
Cryptococcus neoformans	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cryptococcaceae	JEC 21	Gp0000508	GCA_000091045.1	13856	human pathogen	19,05	12,5	37		6617	49	Sanger
Kwoniella (Cryptococcus) best	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cryptococcaceae	CBS 10118	Gp0037867	ASCK01	191321	saprotroph	24,36	63	42	12		47,3	Illumina
Kwoniella (Cryptococcus) deje	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cryptococcaceae	CBS 10117	Gp0038102	ASCJ01	191322	saprotroph	23,86	88	69	13		48,4	Illumina
Kwoniella heveanensis	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cryptococcaceae	BCC8398	Gp0038042	ASQB01	191335	saprotroph	25,469	30	114	67		51,9	Illumina
Kwoniella mangrovensis	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cryptococcaceae	CBS 8507	Gp0038044	ASQE01	191223	saprotroph (marine)	22,654	44	105	62		44,9	Illumina
Kwoniella pini (Cryptococcus p	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cryptococcaceae	CBS 10737	Gp0038280	ASCL01	191226	saprotroph	20,83	62	42	18		40,2	Illumina
Fellomyces penicillatus	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cuniculitremaceae	Phaff54-35	v1.0	1051257		uncertain	21,05	97,6	37	22	8340		Illumina
Kockovaella imperatae	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Cuniculitremaceae	NRRL Y-179	Go0115733	1075691	334695	uncertain; yeast	17,47	428,26	38	38	7393		PacBio
Phaeotremella (Cryptococcus)	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Phaeotremellaceae	JCM 9039	Gp0144038	BCHT01	313820	saprotroph	20,79	289	164	58		50,2	HiSeq 2500
Papiliotrema (Cryptococcus) fl	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Rhynchogastremataceae	NRRL Y-503	Gp0038499	CAUG01	185775	biocontrol (of fusarium head blight)	22,79		1269	712		58,5	
Papiliotrema (Cryptococcus) la	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Rhynchogastremataceae	RY1	Gp0044996	JDSR01	210827	occasional human pathogen	19,14	50	1154	1152		56,1	Illumina MiSeq
Fibulobasidium inconspicuum	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Sirobasidiaceae	Phaff89-39	v1.0	1052658		saprotroph, probable	20,29	91,6	169	31	8148		Illumina
Tremella fuciformis	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Tremellaceae	Tr26	Gp0120585	LBGW01	281519	biocontrol (mycoparasite)	23,64	40	3502			57	Illumina HiSeq
Tremella mesenterica	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Tremellales	Tremellaceae	DSM 1558	Gp0002624	AFVY01	32829	industrial importance; white rot	28,6	7,4	484	45	8313	46,7	Sanger
Phaeotremella (Cryptococcus)	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Phaeotremellaceae	JCM 13614	Gp0144002	BCHU01	313821	saprotroph	22,65	264	52	30		42,4	Illumina
Apiotrichum (Trichosporon) bi	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 1599	Gp0143984	BCJI01	313856	saprotrophic (cabbage)	23,65	209	135	16		56,5	HiSeq 2500
Apiotrichum (Trichosporon) di	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 9580	Gp0149825	BCFW01	313776	human allergen	24,51	271	92	28			Illumina
Apiotrichum (Trichosporon) gi	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 9941	Gp0144051	BCJN01	313859	saprotrophic (cabbage)	24,61	253	173	29			HiSeq 2500
Apiotrichum (Trichosporon) gr	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 10018	Gp0143992	BCJO01	313860	saprotrophic (soil)	24,11	231	62	17			HiSeq 2500
Apiotrichum (Trichosporon) la	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 2947	Gp0150864	BCKV01	313881	soil or animal-associated	30,62	178	182	26		59,6	Illumina
Apiotrichum (Trichosporon) m	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 9937	Gp0143035	BCFV01	313775	opportunistic human pathogen	24,87	258	149	61			HiSeq 2500
Apiotrichum (Trichosporon) ve	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 10691	Gp0150863	BCKJ01	313871	alkane-assimilating	31,62	196	174	35		59,6	Illumina
Cryptococcus sp. JCM 24511	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 24511	Gp0143988	BCLC01	313899	industrial importance (oleaginous)	28,18	103	232	55		58,5	HiSeq 2500
Cutaneotrichosporon (Cryptoc	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 1532	Gp0144007	BCJH01	313855	industrial importance (oleaginous)	18,64	305	182	75		57,9	HiSeq 2500
Trichosporon asahii	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	CBS 8904	Gp0037591	AMBO01	172216	human pathogen	25,299	12,4	420	194	8528	59,5	454; Illumina
Trichosporon chiarellii	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	MYA-4694	v1.0	1042939		insect-associated (ants)	24,81	86,7	82	7	7766		Illumina
Trichosporon cutaneum	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	B3	Gp0149983	LRUG01	310294	industrial importance (lipid production)	38,7	25	592			57,6	Illumina
Trichosporon guehoae	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 10690	Gp0143997	BCJX01	313868	saprotrophic (soil)	33,7	187	851	35		59,2	HiSeq 2500
Trichosporon oleaginosus	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	IBC0246	Gp0044565	JGI	239490	industrial importance (lipid producer); biotechnolog	19,84	115,8	196	180	8322		Illumina HiSeq
Trichosporon porosum	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 1458	Gp0144004	BCJG01	313854	saprotrophic (soil)	25,99	196	154	37		59	HiSeq 2500
Vanrija humicola	Basidiomycota	Agaricomycotina	Tremellomycetes	Tremellomycetidae	Trichosporonales	Trichosporonaceae	JCM 1457	Gp0144003	BCJF01	313853	saprotroph	22,65	313	72	10		62,7	HiSeq 2500
Basidioascus undulatus	Basidiomycota	Agaricomycotina	Wallemiomycetes	Incertae sedis	Geminibasidiales	Geminibasidiaceae	DAOM 241	Gp0094789	JTLS01	247992	xerotolerant	32,18	28	2993	2992		58	
Wallemia ichthyophaga	Basidiomycota	Agaricomycotina	Wallemiomycetes	Incertae sedis	Wallemiales	Wallemiaceae	EXF-994	Gp0041105	APLC01	193177	halophile	9,66	280	95	82	4863	45,3	Illumina HiSeq
Wallemia sebi	Basidiomycota	Agaricomycotina	Wallemiomycetes	Incertae sedis	Wallemiales	Wallemiaceae	CBS 633.66	Gp0005604	AFQX01	64975	xerophile	9,82	71	114	56	5284	40	454; Illumina
Agaricostilbum hyphaenes	Basidiomycota	Pucciniomycotina	Agaricostilbomycetes	Agaricostilbomycetidae	Agaricostilbales	Agaricostilbaceae	ATCC MYA-	Gp0036613	JGI	245617	uncertain (associated with palms)	17,89	197,7	121	108	7746		Illumina HiSeq
Chionosphaera apobasidialis	Basidiomycota	Pucciniomycotina	Agaricostilbomycetes	Agaricostilbomycetidae	Agaricostilbales	Chionosphaeraceae	52639	v1.0	1045315		parasite (lichens)	21,83	94,30	1183	398	9875		Illumina
Chionosphaera cuniculicola	Basidiomycota	Pucciniomycotina	Agaricostilbomycetes	Agaricostilbomycetidae	Agaricostilbales	Chionosphaeraceae	CBS10063	v1.0	1051203		insect-associated (conifer-inhabiting bark beetles)	14,16	89,4	43	19	7187		Illumina
Cystobasidiopsis (Sporobolom	Basidiomycota	Pucciniomycotina	Agaricostilbomycetes	Agaricostilbomycetidae	Agaricostilbales	Chionosphaeraceae	JCM 7595	Gp0149823	BCIO01	313839	uncertain	22,18	241,00	53	19		56,2	Illumina
Atractiellales sp. 95	Basidiomycota	Pucciniomycotina	Atractiellomycetes	Incertae sedis	Atractiellales	unknown	PMI 95	Gp0019383	JGI	234661	endophyte (root)	51,47	66,7	3076	1998	17606		Illumina HiSeq
Classicula fluitans	Basidiomycota	Pucciniomycotina	Classiculomycetes	Incertae sedis	Classiculales	Classiculaceae	ATCC 6471	Gp0036615	JGI	218039	aquatic	52,67	82,7	4363	1417	13270		Illumina HiSeq
Cystobasidium pallidum	Basidiomycota	Pucciniomycotina	Cystobasidiomycetes	Incertae sedis	Cystobasidiales	Cystobasidiaceae	JCM 3780	Gp0144029	BCIL01	313836	uncertain	21,72	259	257	69		49,7	HiSeq 2500
Erythrobasidium hasegawianu	Basidiomycota	Pucciniomycotina	Cystobasidiomycetes	Incertae sedis	Erythrobasidiales	Erythrobasidiaceae	ATCC 9536	Gp0036641	1019585	218035	uncertain	40,69	155,3	265	158	9521		Illumina HiSeq
Erythrobasidium yunnanense	Basidiomycota	Pucciniomycotina	Cystobasidiomycetes	Incertae sedis	Erythrobasidiales	Erythrobasidiaceae	JCM 10687	Gp0143996	BCJC01	313851	uncertain	20,93	252	35	11		51	HiSeq 2500
Naohidea sebacea	Basidiomycota	Pucciniomycotina	Cystobasidiomycetes	Incertae sedis	Naohideales	Naohideaceae	CBS 8477 (F	Gp0036591	1019588	218030	biocontrol (mycoparasite)	20,43	87,4	294	124	10410		Illumina HiSeq
Heterogastridium pycnidioide	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Heterogastridiales	Heterogastridiaceae	ATCC MYA-	Gp0036643		218038	parasite	17,58	109,00	296	117	7658		Illumina; PacBio; 454; Sanger
Hyalopycnis blepharistoma	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Heterogastridiales	Heterogastridiaceae	ATCC 48560	v1.0	1045309		saprotroph, probable	17,93	102,2	448	210	7872		Illumina
Meredithblackwellia eburnea	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Kriegeriales	Kriegeriaceae	MCA 4105	Gp0036543	1019597	223132	uncertain; yeast (budding)	30,68	112,00	201	52	11135		
Leucosporidiella creatinivora	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Leucosporidiales	Leucosporidiaceae	JCM 10699	Gp0150858	BCKL01	313873	aquatic saprotroph	27,97	190,00	296	122		58,7	Illumina
Microbotryum lychnidis-dioicz	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Microbotryales	Microbotryaceae	p1A1 Lamo	Gp0142947	CDLV01	285970	plant pathogen (anther smut of campion flowers)	3,47	3,00	1			55,5	
Microbotryum violaceum	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Microbotryales	Microbotryaceae	p1A1 Lamo	Gp0005981	AEIJ01	41281	plant pathogen (anther smut of Caryophyllaceae); s	26,138	15	2104	1231	7500	55,4	454
Rhodosporidium toruloides	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	MTCC 457	Gp0038702	AJMJ01	112573	industrial importance (lipid producer)	20,06	121,35	689	462	8171	62	Illumina GAIIx
Rhodotorula glutinis	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	ATCC 2040	Gp0009345	AEVR02	59971	industrial importance (lipid producer)	20,478	40	186		3361	61,9	Sanger; 454; Illumina
Rhodotorula graminis	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	WP1	Gp0003185	JGI	32711	endophyte	21,01	8,55	620	26	7283		454; Sanger
Rhodotorula minuta	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	MCA 4210	Gp0036376	JGI	218034	occasional human pathogen	20,82	94,7	57	38	7814		Illumina HiSeq
Rhodotorula mucilaginosa	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	C2.5t1	Gp0118226	JWTJ01	270792	human pathogen (fungemia)	19,98	70	1382	1034		60,5	
Rhodotorula sp. JG-1b	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	JG-1b	Gp0033786	LQXB01	195770	Opportunistic Pathogen	19,4	133,90	171	156	6790	60,6	Illumina HiSeq
Rhodotorula toruloides	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	JCM 10020	Gp0143993	BCIY01	313847	industrial importance (oleaginous)	20,49	143	127	88	8140	62	HiSeq 2500
Sporidiobolus salmonicolor	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	SPOSA6832	Gp0143875	CENE01	279947	opportunistic human pathogen	50,52		744	395	4672	61,3	Illumina HiSeq
Sporobolomyces linderae	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	CBS 7893 (F	Gp0036589	JGI	218037	uncertain; only known strain in existence	18,24	93,9	56	35	9062		Illumina HiSeq
Sporobolomyces roseus	Basidiomycota	Pucciniomycotina	Microbotryomycetes	Incertae sedis	Sporidiobolales	Sporidiobolaceae	IAM 13481	Gp0017897	JGI	207682	free-living; non-pathogenic	21,2	8,1		76	5536		Illumina
Mixia osmundae	Basidiomycota	Pucciniomycotina	Mixiomycetes	Incertae sedis	Mixiales	Mixiaceae	IAM 14324	Gp0010143	JGI	205560	plant pathogen (fern parasite)	13,63	150,9	204	156	6903	55,5	454; Illumina
Cronartium comandrae	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Cronartiaceae	C4	Gp0038527	AUZW01	190832	plant pathogen; rust fungus (pine)	68,6	549	54532	35717		40,7	Illumina HiSeq
Cronartium quercuum	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Cronartiaceae	G11	Gp0004798	JGI	67371	plant pathogen; rust fungus (fusiform rust of pine)	76,57	70,4	10431	1198	13903		Illumina
Cronartium ribicola	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Cronartiaceae	11-2	Gp0038568	AWVX01	190829	plant pathogen; rust fungus (pine)	94,3	629	59233	41096		41,3	Illumina HiSeq
Endocronartium harknessii	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Cronartiaceae	PhW48OC	Gp0038528	AXDO01	190831	plant pathogen; rust fungus (pine-pine gall rust)	56,94	671	41594	25178		40,9	Illumina HiSeq
Melampsora allii-populina	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Melampsoraceae	12AY07 v1.	Gp0047015	1026279	247510	plant pathogen; rust fungus (poplar)	335,73	104	3637	3637	23089		PacBio
Melampsora larici-populina	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Melampsoraceae	98AG31_30	Gp0002503	AECX01	46711	plant pathogen (poplar); rust fungus	101,1	6,79		462	16694	41	Sanger
Melampsora pinitorqua	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Melampsoraceae	Mpini7	Gp0038564	AUYS01	190833	plant pathogen (pine twisting rust); rust fungus	34,032	959,00	15326	1232500,00%		44,9	Illumina HiSeq
Puccinia arachidis	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Pucciniaceae	MRF11	Gp0118201	LBLN01	280565	plant pathogen (peanut)	87,62	24	130300			52,4	IonTorrent
Puccinia graminis	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Pucciniaceae	CRL 75-36-7	Gp0002677	AAWC01	18535	plant pathogen; rust fungus (cereals)	88,724	7,88	4563	393	16309	43,3	Sanger
Puccinia psidii	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Pucciniaceae	Aus_3	Gp0144693	LKHF01	295407	plant pathogen; rust fungus (guava)	129,78	30	151718	57309		30,6	Illumina HiSeq
Puccinia sorghi	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Pucciniaceae	Rojas	Gp0118202	LAVV01	277993	plant pathogen (maize); rust	99,53	85	28117	15715	21078	44,8	Illumina HiSeq
Puccinia striiformis	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Pucciniaceae	PST-08/21	Gp0039222	AORS01	181960	plant pathogen (wheat); rust fungus	56,267	23	50890			45,2	Illumina HiSeq
Puccinia triticina	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Pucciniaceae	1-1 BBBD	Gp0005826	ADAS01	36323	plant pathogen (wheat, barley, rye); rust fungus	162,948	16,00	38776	24423		47	454; Sanger
Uromyces viciae-fabae	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Pucciniales	Pucciniaceae	I2	Gp0117703	JNCO01	248166	plant pathogen (beans); rust	215,71	75	95849	59737		35,7	Illumina HiSeq
Septobasidium sp.	Basidiomycota	Pucciniomycotina	Pucciniomycetes	Incertae sedis	Septobasidiales	Septobasidiaceae	PNB30-8B	v1.0	1047727		endophyte	27,51	80,5	751	236	10893		Illumina
Tritirachium sp. CBS 265.96	Basidiomycota	Pucciniomycotina	Tritirachiomycetes	Incertae sedis	Tritirachiales	Tritirachiaceae	CBS 265.96	Gp0036339	JGI	218036	uncertain; mold	18,89	86,5	202	110	7254		Illumina
Ceraceosorus bombacis	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Ceraceosorales	Ceraceosoraceae	Cbombacis	Gp0143854	CCYA01	299044	plant pathogen (lumber tree); smut	26,1		8645	485	8022	51,9	
Ceraceosorus sp.	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Ceraceosorales	Ceraceosoraceae	MCA 4658	Gp0095870	1036212	254921	plant pathogen (lumber tree); smut	24,15	145	316	251	7822		Illumina
Meira miltonrushii	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Exobasidiales	Brachybasidiaceae	MCA 3882	Gp0091359	1036216	247836	mite-associate	17,38	99,60	117	32	7452		Illumina HiSeq
Meira nashicola	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Exobasidiales	Brachybasidiaceae	JCM 18503	Gp0144018	BCJU01	313865	probable plant pathogen (pear)	18,02	359	99	58		40	HiSeq 2500
Acaromyces ingoldii	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Exobasidiales	Cryptobasidiaceae	MCA 4198	v1.0	1036220		biocontrol (toxigenic on mite spp.)	19,33	91,4	50	28	8025		Illumina
Exobasidium vaccinii	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Exobasidiales	Exobasidiaceae	MPITM	Gp0034224	JGI	196015	plant pathogen (endoparasitic)	16,99	96,3	246	119	7453		Illumina HiSeq
Tilletiaria anomala	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Georgefischeriales	Tilletiariaceae	UBC 951	Gp0034232	JMSN01	196019	uncertain	18,7	25,2	289	289	6810	56	
Golubevia (Tilletiopsis) pallesc	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Golubeviales	Golubeviaceae	JCM 5230	Gp0144030	BCHO01	313816	biocontrol (of podwery mildew)	27,76	195	173	63		43,2	HiSeq 2500
Tilletiopsis washingtonensis	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Incertae sedis	Incertae sedis	MCA 4816	Gp0091365	1040192	247833	uncertain; yeast	18,76	84,7	218	38	7011		Illumina HiSeq
Tilletia caries	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Tilletiales	Tilletiaceae	DAOM 238	Gp0150383	LWDD01	317434	plant pathogen (bunt of wheat)	29,54	109	3552	2888	10204	56,1	Illumina
Tilletia controversa	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Tilletiales	Tilletiaceae	DAOM 236	Gp0150384	LWDE01	317433	plant pathogen (dwarf bunt of wheat)	28,84	94	3878	3586	9860	56,6	Illumina
Tilletia horrida	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Tilletiales	Tilletiaceae	QB-1	Gp0118397	LAXH01	280382	plant pathogen (rice); smut	20,11	154	1713	767		55,8	Illumina HiSeq
Tilletia indica	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Tilletiales	Tilletiaceae	DAOM 236	Gp0150415	LWDF01	314779	plant pathogen (Karnal bunt on wheat an triticale)	30,38	176	2207	1666		54,6	Illumina
Tilletia walkeri	Basidiomycota	Ustilaginomycotina	Exobasidiomycetes	Exobasidiomycetidae	Tilletiales	Tilletiaceae	DAOM 236	Gp0150493	LWDG01	314785	plant pathogen (Ryegrass bunt)	24,34	58,00	1208	972	7970	54,8	Illumina
Malassezia caprae	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	CBS 10434	Gp0132988	LFFV01	286710	opportunistic animal pathogen	7,58	479	237	229		59,8	Illumina HiSeq
Malassezia cuniculi	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	CBS 11721	Gp0133010	LFFW01	286710	skin-associated; lipophilic	7,46	298	90	76		59	Illumina HiSeq
Malassezia dermatis	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	JCM 11348	Gp0143980	BCKX01	313883	animal pathogen (dermatitis)	7,55	486,00	55	48		59	HiSeq 2500
Malassezia equina	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	CBS 9969	Gp0133467	LFFY01	286710	opportunistic animal pathogen	7,66	244,00	130	117		58	Illumina HiSeq

Malassezia furfur	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	CBS 1878	Gp0133469	LFGL01	286710	skin-associated; lipophilic	7,88	500	1777	1694		64,1	Illumina HiSeq	
Malassezia globosa	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	CBS 7966	Gp0003180	AAYY01	18719	human pathogen	8,958	7	67		1286	52	Sanger	
Malassezia japonica	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	JCM 11963	Gp0143982	BCKY01	313884	skin-associated; lipophilic	8,36	466,00	27	16		62,3	HiSeq 2500	
Malassezia nana	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	JCM 12085	Gp0143983	BCLA01	313886	opportunistic animal pathogen	7,58	489	29	13		58	HiSeq 2500	
Malassezia obtusa	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	CBS 7876	Gp0133473	LFGC01	286710	skin-associated; lipophilic	7,84	455	1905	1709		62,2	Illumina HiSeq	
Malassezia pachydermatis	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	CBS 1879	Gp0143141	LGAV01	288787	animal pathogen (dermatitis)	8,15	250	118	91	4202	55,1	Illumina HiSeq	
Malassezia restricta	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	CBS 7877	Gp0003181	AAXK01	18721	human pathogen	4,628	1	3812			55,3	Sanger	
Malassezia slooffiae	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	CBS 7956	Gp0132990	LFGK01	286710	opportunistic animal pathogen	8,43	262	1897	1641	4202	65,9	Illumina HiSeq	
Malassezia sympodialis	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	ATCC 4213	Gp0039243	CANK01	192188	opportunistic human and animal pathogen (cutaneo	7,67	130,00	87	65	3517	59,1	454; Illumina HiSeq	
Malassezia yamatoensis	Basidiomycota	Ustilaginomycotina	Malasseziomycetes	Incertae sedis	Malasseziales	Malasseziaceae	MY9725	Gp0133476	LFCX01	286710	human pathogen (dermatitis)	8,11	235,00	88	49		49,7	Illumina HiSeq	
Ustilaginomycotina sp. SA 807	Basidiomycota	Ustilaginomycotina	unknown	unknown	unknown	unknown	SA 807	Gp0042889	1019621	254893	uncertain; plant-associated	27,32	140,8	1563	1406	8060		Illumina HiSeq	
Melanotaenium endogenum	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Urocystidales	Melanotaeniaceae	CBS481.91	v1.0	1051185		plant pathogen (bedstraw); smut	19,17	97,9	316	87	6624		Illumina	
Kalmanozyma (Pseudozyma) b	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	GHG001	Gp0070930	AWXO01	217085	industrial importance	17,3254	585	132	45	5889	58,1	Illumina HiSeq	
Moesziomyces (Pseudozyma)	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	T-34	Gp0038467	BAFG01	186736	industrial importance	18,07	20	744	27	6640	61,1		454
Moesziomyces (Pseudozyma)	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	DSM70725	Gp0070929	AWNI01	215967	industrial importance	17,921	90	1968		6011	60,9	Illumina HiSeq	
Moesziomyces antarcticus	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	JCM 10317	Gp0103432	BBIZ01	257785	industrial importance (psychrophili lipid and lipase	18,11	200	276	197	6766	60,9	Illumina MiSeq	
Pseudozyma flocculosa	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	DAOM 196	Gp0044988	AOUS01	185206	biocontrol (powdery mildew)	23,305	28	1583	37	6877	65,3		454
Pseudozyma hubeiensis	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	SY62	Gp0040215	BAOW01	203274	industrial importance (biosurfactant producing)	18,44	200	159	74	7472	56,5	Illumina HiSeq	
Sporisorium reilianum	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	SRZ2	Gp0038426	GCA_000230245	64587	plant pathogen (maize); smut	18,39		818	23	6648	59,68		454
Sporisorium scitamineum	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	2014001	Gp0118304	JFOL01	240344	plant pathogen (sugarcane); smut	19,78	100	329	69		64,64	HiSeq 2500	
Ustilago esculenta	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	MMT	Gp0109108	JTLW01	263330	plant pathogen (wild rice); smut	20,2	139	298			54,4	Illumina HiSeq	
Ustilago hordei	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	Uh4857-4	Gp0038438	CAGI01	79049	plant pathogen (barley); smut	21,15		713		7230	51,9		
Ustilago maydis	Basidiomycota	Ustilaginomycotina	Ustilaginomycetes	Ustilaginomycetidae	Ustilaginales	Ustilaginaceae	521	Gp0000206	AACP01	1446	plant pathogen (maize and teosinte); smut	19,799	10	277		6631	54	Sanger	

Sequenced early-diverging fungal species

	Classification										Genome statistics							
SPECIES	**PHYLUM**	**SUBPHYLUM**	**CLASS**	**SUBCLASS**	**ORDER**	**FAMILY**	**Strain**	**GOLD Accession**	**GENOME Accession**	**NCBI Project ID**	**Significance**	**Size (Mb)**	**coverage**	**# of contigs**	**# of scaffolds**	**# genes**	**GC**	**Technology**
Allomyces macrogynus	Blastocladiomycota	none	Blastocladiomycetes	none	Blastocladiales	Blastocladiaceae	ATCC 38327	Gp0002500	ACDU00000000.1	20563	model organism (sexual cycle); cosmopolitan	57	11,39	8973	101			
Catenaria anguillulae	Blastocladiomycota	none	Blastocladiomycetes	none	Blastocladiales	Catenariaceae	PL171	Gp0016932	JGI	69551	biocontrol (nematode parasite)	41,34	93,4	2577	509		12804	Illumina; PacBio
Globomyces pollinis-pini	Chytridiomycota	none	Chytridiomycetes	Chytridiomycetidae	Rhizophydiales	Globomycetaceae	Arg68	Go0136949	1098991	331560	aquatic saprtotroph	21,65	163,00	1402	1155	11537		Illumina
Batrachochytrium dendrobatidis	Chytridiomycota	none	Chytridiomycetes	Chytridiomycetidae	Rhizophydiales	unknown	JEL423	Gp0002494	AATT01	13653	animal pathogen	23,89	7,40		70	8700	39,3	Sanger
Homoloaphlyctis polyrhiza	Chytridiomycota	none	Chytridiomycetes	Chytridiomycetidae	Rhizophydiales	unknown	JEL 142	Gp0039389	AFSM01	68115	saprotroph	26,11	11,00	14231	11986		49,7	454
Spizellomyces punctatus	Chytridiomycota	none	Chytridiomycetes	Chytridiomycetidae	Spizellomycetales	Spizellomycetaceae	DAOM BR117	Gp0002502	ACOE01	37881	model organism	23,906	9,38	329			48	Sanger
Gonapodya prolifera	Chytridiomycota	none	Monoblepharidomycetes		Monoblepharidales	Gonapodyaceae	JEL478	Gp0017029	JGI	207863	aqautic	48,79		1154	352	13902		Illumina
Rozella allomycis	Cryptomycota	none	none	none	none	unknown	CSF55	Gp0009558	JGI	223002	parasite (water moulds)	11,86	264,00	1128	1059	6350		454; Illumina HiSeq
Antonospora locustae	Microsporidia	-	-	-	-	Nosematidae	HM-2013	Gp0038411		185776	biocontrol; parasite (grasshoppers)	6,07	7,90	3116	3116	2606		Illumina
Edhazardia aedis	Microsporidia	-	-	-	-	Amblyosporidae	USNM 41457	Gp0038023	AFBI02	65125	parasite	46,6	20,00	2379		4281	22,5	454
Spraguea lophii	Microsporidia	-	-	-	-	Spraguidae	42_110	Gp0039328	ATCN01	73605	parasite (teleost fish)	4,98	70,00	1392		2596	23,4	Illumina GAii
Enterocytozoon bieneusi	Microsporidia	-	-	-	-	Enterocytozoonidae	H348	Gp0002463	ABGB01	21011	parasite	3,86		1743	1733	3806	34	
Nosema antheraeae	Microsporidia	-	-	-	-	Nosematidae	YY	Gp0038948	Silkworm pathogen data	183977	parasite (silkworm)	6,6			6215	3413	28	Sanger; Illumina
Nosema apis	Microsporidia	-	-	-	-	Nosematidae	BRL01	Gp0037550	ANPH01	66735	parasite (honeybee)	8,569	27	1133	554	2764	18,8	454
Nosema bombycis	Microsporidia	-	-	-	-	Nosematidae	CQ1	Gp0005763	ACJZ01	30919	parasite (silkworm)	15,7		3558	1605	4458	31	Sanger; Illumina
Nosema ceranae	Microsporidia	-	-	-	-	Nosematidae	BRL01	Gp0004758	ACOL01	32971	parasite (honeybee)	7,86	24,20	5465	5465	2614	25,3	454
Vittaforma corneae	Microsporidia	-	-	-	-	Nosematidae	ATCC 50505	Gp0038026	AEYK01	63501	opportunistic pathogen	3,213	68	314	220	2293	36,5	454
Encephalitozoon bieneusi	Microsporidia	-	-	-	-	Encephalitozoonidae	H348		ABGB01	28163	parasite	3,86	64	1743	1733	3632	33,7	454; Illumina
Encephalitozoon cuniculi	Microsporidia	-	-	-	-	Encephalitozoonidae	GB-M1	Gp0000710	GCA_000091225.1	13833	parasite	2,5		12	11	1997	48	454
Encephalitozoon hellem	Microsporidia	-	-	-	-	Encephalitozoonidae	ATCC 50504	Gp0039296	GCA_000277815.3	73047	parasite	2,25	53,00	12	12	1847		
Encephalitozoon intestinalis	Microsporidia	-	-	-	-	Encephalitozoonidae	ATCC 50506	Gp0006942	GCA_000146465.1	42703	parasite	2,22	40	12	11	1833	42	Sanger
Encephalitozoon romaleae	Microsporidia	-	-	-	-	Encephalitozoonidae	SJ-2008	Gp0039118	GCA_000280035.2	160949	parasite	2,19	300,00	13	13	1677	40,4	
Anncaliia algerae	Microsporidia	-	-	-	-	Tubulinosematidae	PRA109	Gp0038024	AOMV02	188094	parasite (aquatic)	17,5	341	8403	7113			Illumina
Nematocida parisii	Microsporidia	-	-	-	-	Incertae sedis	ERTm1	Gp0008837	JGI	51843	parasite (C.elegans)	4,07	97,00	115	65	2661	34,4	454
Pseudoloma neurophilia	Microsporidia	-	-	-	-	Glugeidae		Gp0048063	LGUB01	206217	parasite (zebrafish)	5,25	138,00	1603		3645		Illumina
Trachipleistophora hominis	Microsporidia	-	-	-	-	Pleistophoridae		Gp0038589	ANCC01	84343	parasite	8,498	32,50	1632	310	3253	34,1	454; SOLiD
Vavraia culicis	Microsporidia	-	-	-	-	Pleistophoridae	floridensis	Gp0009650	AEUG01	62117	parasite (mosquito)	6,118	27	501	379	2825	39,7	454
Hamiltosporidium tvaerminnensis	Microsporidia	-	-	-	-	Dubosqiidae	OER-3-3	Gp0008119	ACSZ01	39213	parasite	13,27		41786			26,5	
Nematocida displodere	Microsporidia	-	-	-	-	None	JUm2807	Gp0149837	LTDL01	312555	parasite (Caenorhabditis elegans)	3,1	2500,00	99	42	2278	49,1	Illumina
Nematocida ironsii	Microsporidia	-	-	-	-	None	ERTm5	Gp0149836	LTDK01	312551	parasite (Caenorhabditis elegans)	4,4	101,00	223	186	2709	33,5	Illumina
Nematocida sp. 1	Microsporidia	-	-	-	-	None	ERTm2	Gp0038029	AERB01	61785	parasite (Caenorhabditis elegans)	4,7	65,00	289	202	2493	38,4	454
Ordospora colligata	Microsporidia	-	-	-	-	Ordosporidae	OC4	Gp0101994	JOKQ01	210314	parasite (Daphnia)	2,29	627,00	15		1820	38,5	Illumina HiSeq
Mitosporidium daphniae	Microsporidia	-	-	-	-	unknown	UGP3	Gp0107713	JMKJ01	243305	parasite	5,64	300	612		3330	43	Illumina HiSeq
Rhizophagus irregularis	Mucoromycota	Glomeromycotina	Glomeromycetes	none	Glomerales	Glomeraceae	DAOM 197198	Gp0002623	AUPC01	208392	mycorrhizal (arbuscular)	91,08	100	28405	28371	30282	27,5	Sanger; 454; Illumina
Lobosporangium transversale	Mucoromycota	Mortierellomycotina	none	none	Mortierellales	Mortierellaceae	NRRL 3116 v1.0		1076126		industrial importance (lipid biosynthesis)	42,77	195,5	138	138	11822		PacBio
Mortierella alpina	Mucoromycota	Mortierellomycotina	none	none	Mortierellales	Mortierellaceae	ATCC 32222	Gp0005982	ADAG01	41211	industrial importance	38,042	31,70	1099			52	454; Illumina; Sanger
Mortierella elongata	Mucoromycota	Mortierellomycotina	none	none	Mortierellales	Mortierellaceae	AG-77	Gp0019300	JGI	196039	endophyte; saprotroph	49,96	112,80	3314	473	14964		Illumina HiSeq
Mortierella multidivaricata	Mucoromycota	Mortierellomycotina	none	none	Mortierellales	Mortierellaceae	RSA 2152 T	Go0145900	1098953	331667	saprotroph; soil; garlic-odour	37,67	184,76	217	217	12248		PacBio
Mortierella verticillata	Mucoromycota	Mortierellomycotina	none	none	Mortierellales	Mortierellaceae	NRRL 6337	Gp0002501	AEVJ01	20603	animal pathogen	41,912	225	701	56	12774	48,9	Illumina; Sanger
Backusella circina	Mucoromycota	Mucoromycotina	none	none	Mucorales	Backusellaceae	FSU 941	Gp0032377	JGI	196083	thermophile	48,65	100,50	2354	1095	17039		Illumina HiSeq
Blakeslea trispora	Mucoromycota	Mucoromycotina	none	none	Mucorales	Choanephoraceae	NRRL 2456 v1.0		1085219		industrial importance (beta-carotene); plant pathogen	37,51	80	328	328	11687		PacBio
Absidia (Chlamydoabsidia) padenii	Mucoromycota	Mucoromycotina	none	none	Mucorales	Cunninghamellaceae	NRRL 2977	Go0141635	1099015	331669	uncertain	34,33	139,05	117	117	13495		PacBio
Cunninghamella bertholletiae	Mucoromycota	Mucoromycotina	none	none	Mucorales	Cunninghamellaceae	B7461	Gp0044997	JNEL01	211905	human pathogen (mucoromycosis)	31,1	82,92	880			24,8	Illumina HiSeq
Cunninghamella elegans	Mucoromycota	Mucoromycotina	none	none	Mucorales	Cunninghamellaceae	B9769	Gp0038540	JNDR01	184885	degrades xenobiotics, some herbicides and fungicides	31,74	115,42	1380			24,5	Illumina HiSeq
Gongronella butleri	Mucoromycota	Mucoromycotina	none	none	Mucorales	Cunninghamellaceae	CBS 227.36	Go0141634	1098955	331668	industrial importance (chitosan production)	33,01	150,81	112	112	11004		PacBio
Hesseltinella vesiculosa	Mucoromycota	Mucoromycotina	none	none	Mucorales	Cunninghamellaceae	NRRL 3301	Gp0046759	1026982	243954	uncertain	25,86	157,80	1202	252	10675		Illumina
Lichtheimia corymbifera	Mucoromycota	Mucoromycotina	none	none	Mucorales	Lichtheimiaceae	CBS 429.75	Gp0039842	CBTN01	248798	human pathogen (mucoromycosis)	33,53		589	209	13404	43,9	HiSeq 2500; 454
Lichtheimia hyalospora	Mucoromycota	Mucoromycotina	none	none	Mucorales	Lichtheimiaceae	FSU 10163	Gp0033114	JGI	196074	industrial importance (thermotolerant)	33,28	140,1	2294	2222	12062		Illumina not publically available
Lichtheimia ramosa	Mucoromycota	Mucoromycotina	none	none	Mucorales	Lichtheimiaceae	:FSU:6197	Gp0119779		257263	opportunistic human pathogen (mucoromycosis)	30,71		85	74	11542	41,1	HiSeq 2500; 454
Phascolomyces articulosus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Lichtheimiaceae	RSA 2281	Go0126192	1098949	331828	coprophilous	47,61	121,30	150	150	14495		PacBio
Rhizomucor miehei	Mucoromycota	Mucoromycotina	none	none	Mucorales	Lichtheimiaceae	CAU432	Gp0037929	AGBC01	66605	industrial importance (thermophile)	27,442	16	3599	870		44,3	454; Illumina HiSeq
Rhizomucor variabilis	Mucoromycota	Mucoromycotina	none	none	Mucorales	Lichtheimiaceae	B7584	Gp0044976	JNES01	211914	human pathogen	33,037	59,39	967			37,8	Illumina HiSeq
Thermomucor indicae-seudaticae	Mucoromycota	Mucoromycotina	none	none	Mucorales	Lichtheimiaceae	HACC 243	Gp0107552	JSYX01	261109	industrial importance (dairy industry)	29,57	180,00	1958			45,8	Illumina HiSeq
Zychaea mexicana	Mucoromycota	Mucoromycotina	none	none	Mucorales	Lichtheimiaceae	RSA 1403	Go0126193	1098951	331829	coprophilous	50,64	260	357	357	14004		PacBio
Actinomucor elegans	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	JCM 22485	Gp0144022	BCHK01	313812	human pathogen; mucormycosis	34,17	317,00	494	192		35,9	HiSeq 2500
Apophysomyces elegans	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	B7760	Gp0038478	JNDQ01	184884	human pathogen (mucoromycosis); thermotolerant	38,5	53,91	1528				Illumina HiSeq
Apophysomyces trapeziformis	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	B9324	Gp0038504	JNDP01	184883	human pathogen (mucoromycosis)	35,8	102,48	1400				Illumina HiSeq
Cokeromyces recurvatus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	B5483	Gp0044990	JNEH01	211901	human pathogen (mucoromycosis)	29,34	63,16	2637			30,4	
Mucor (Kirkomyces) cordense	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	RSA 1222	Go0141636	1099019	331670	uncertain	40,95	157,38	150	150	16794		PacBio
Mucor ambiguus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	NBRC 6742	Gp0122235	BBKB01	275080	industrial importance (novel carbonyl reductase)	40,74	200,00	8422	1283	11343	40,7	Illumina MiSeq
Mucor circinelloides	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	1006PhL	Gp0023048	AOCY01	172437	opportunistic pathogen; model organism	36,348	45,00	1459	470	12410	39,5	Illumina
Mucor heterogamus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	NRRL 1489	Go0118600	1085225	332253	soil-associated; homothallic	54,49	285,03	1219	1219	14998		PacBio
Mucor indicus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	B7402	Gp0044788	JNEK01	211904	human pathogen (mucoromycosis)	39,797	55,80	3117			35,8	Illumina HiSeq
Mucor irregularis	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	B50	Gp0076107	AZYI01	232510	human pathogen (mucoromycosis)	33,966	293,00	1059	882		37,9	Illumina
Mucor racemosus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	B9645	Gp0044789	JNEI01	211902	human pathogen (mucoromycosis)	65,553	49,38	6360			32,5	Illumina HiSeq
Mucor ramosissimus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	97-1192	Gp0038503	JNEF01	186024	human pathogen (mucoromycosis)	42,9	73,11	4566			35,3	Illumina HiSeq
Mucor velutinosus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	B5328	Gp0038506	JNDK01	184878	human pathogen (mucoromycosis)	35,852	107,80	2411			40,5	Illumina HiSeq
Parasitella parasitica	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mucoraceae	CBS 412.66	Gp0144375	CCXP01	260023	biocontrol (mycoparasite)	44,91		22707	15637	13408	39	Illumina HiSeq
Mycotypha africana	Mucoromycota	Mucoromycotina	none	none	Mucorales	Mycotyphaceae	NRRL 2978	Go0118597	1085227	332250	soil-associated; dimorphic	29,2	610,54	40	40	10917		PacBio
Phycomyces blakesleeanus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Phycomycetaceae	NRRL1555	Gp0002659	JGI	61391	model organism	53,9	7,50	350	80	16528	50	Sanger
Rhizopus delemar	Mucoromycota	Mucoromycotina	none	none	Mucorales	Rhizopodaceae	RA 99-880	Gp0002678	AACW02	13066	opportunistic human pathogen	46,184	14	391	83	17703	35,6	Sanger
Rhizopus microsporus	Mucoromycota	Mucoromycotina	none	none	Mucorales	Rhizopodaceae	CCTCC M201021	Gp0038908	ANKS01	179339	traditional use	45,74	97,00	3374	3281	17676	36,9	Illumina
Rhizopus oryzae	Mucoromycota	Mucoromycotina	none	none	Mucorales	Rhizopodaceae	NRRL 13440	Gp0038511	JNDU01	186013	opportunistic human pathogen (mucormycosis); traditior	43,351	86,09	5022			35,4	Illumina HiSeq
Rhizopus stolonifer	Mucoromycota	Mucoromycotina	none	none	Mucorales	Rhizopodaceae	B9770	Gp0038545	JNDS01	184886	opportunistic human pathogen (mucoromycosis); black b	38,025	42,23	5567			35,5	Illumina HiSeq
Saksenaea oblongispora	Mucoromycota	Mucoromycotina	none	none	Mucorales	Saksenaeaceae	B3353	Gp0045177	JNEV01	211918	human pathogen (mucoromycosis)	40,75	72,7	1702			41,9	Illumina HiSeq
Saksenaea vasiformis	Mucoromycota	Mucoromycotina	none	none	Mucorales	Saksenaeaceae	B4078	Gp0038505	JNDT01	184887	human pathogen (mucoromycosis)	42,502	88,08	2417			42,7	Illumina HiSeq
Syncephalastrum monosporum	Mucoromycota	Mucoromycotina	none	none	Mucorales	Syncephalastraceae	B8922	Gp0045351	JNEN01	211907	human pathogen (mucoromycosis)	29,565	75,83	1284			48,3	Illumina HiSeq
Syncephalastrum racemosum	Mucoromycota	Mucoromycotina	none	none	Mucorales	Syncephalastraceae	B6101	Gp0038502	JNDN01	184881	human pathogen (mucoromycosis)	29,568	76,54	1035			47,2	Illumina HiSeq
Umbelopsis isabellina	Mucoromycota	Mucoromycotina	none	none	Mucorales	Umbelopsidaceae	NBRC 7884	Gp0087738	BAVE01	236720	oleaginous	22,588	200	84			42	SOLiD
Umbelopsis ramanniana	Mucoromycota	Mucoromycotina	none	none	Mucorales	Umbelopsidaceae	AG	Gp0019399	JGI	196032	saprotroph (soil)	23,08	112	239	198	9931		Illumina HiSeq
Anaeromyces robustus	Neocallimastigomycota	Incertae sedis	Neocallimastigomycetes	none	Neocallimastigales	Neocallimastigaceae	S4		1029442	330692	gut-associated; sheep	71,69	20	1035	1035	12832		PacBio
Neocallimastix californiae	Neocallimastigomycota	Incertae sedis	Neocallimastigomycetes	none	Neocallimastigales	Neocallimastigaceae	G1		1029446	262392	gut-associated; goat	193,03	20	1819	1819	20219		PacBio
Orpinomyces sp. C1A	Neocallimastigomycota	Incertae sedis	Neocallimastigomycetes	none	Neocallimastigales	Neocallimastigaceae	C1A	Gp0042060	ASRE01	200719	anaerobic gut fungus	100,954	94,4	32574			17	Illumina; PacBio
Piromyces finnis	Neocallimastigomycota	Incertae sedis	Neocallimastigomycetes	none	Neocallimastigales	Neocallimastigaceae	v3.0		1043531	330696	gut-associated; horse	56,46	??	232	232	10992		PacBio
Piromyces sp. E2	Neocallimastigomycota	Incertae sedis	Neocallimastigomycetes	none	Neocallimastigales	Neocallimastigaceae	ATCC 76762		16860	82799	anaerobic gut fungus	71,02	20	17217	1656	14648		
fungal sp. EF0021	unknown	unknown	unknown	unknown	unknown	unknown	EF0021	Gp0038366	AIET01	77807	endophyte (Taxus)	44,37	18	2051			47,1	454
fungal sp. No.11243	unknown	unknown	unknown	unknown	unknown	unknown	No.11243	Gp0150288	BBSH01	273823	industrial importance (lipopeptidolactone and ,3-beta-gl	21,72	135	25	20	9730	54	454; Sanger
Basidiobolus meristosporus	Zoopagomycota	Entomophthoromycotina	Basidiobolomycetes	none	Basidiobolales	Basidiobolaceae	B9252	Gp0044749	JNEO01	211908	human pathogen (mucoromycosis)	103,87	22,1	20930			41,9	Illumina HiSeq
Conidiobolus coronatus	Zoopagomycota	Entomophthoromycotina	Entomophthoromycetes	none	Entomophthorales	Ancylistaceae	NRRL 28638	Gp0010140	JGI	67455	human and animal pathogen (conidiobolomycosis)	39,9	16,31	7809	1050	10635		454
Conidiobolus incongruus	Zoopagomycota	Entomophthoromycotina	Entomophthoromycetes	none	Entomophthorales	Ancylistaceae	B7586	Gp0044993	JNEM01	211906	human and animal pathogen (conidiobolomycosis)	93,89	75,57	15486			22,4	Illumina HiSeq
Conidiobolus thromboides	Zoopagomycota	Entomophthoromycotina	Entomophthoromycetes	none	Entomophthorales	Ancylistaceae	FSU 785	Gp0032992	1015483	196084	biocontrol (entomopathogen)	24,64	127,3	873	799	8867		Illumina HiSeq
Coemansia reversa	Zoopagomycota	Kickxellomycotina	none	none	Kickxellales	Kickxellaceae	NRRL 1564	Gp0005603	JGI	68631	arthropod-associated	21,84	38,24	1063	346	7347	45	

Linderina pennispora	Zoopagomycota	Kickxellomycotina	none	none	Kickxellales	Kickxellaceae	ATCC 12442 v1.0	Gp0036322	1019509	243942	saprotroph (soil)	26,2	1	227	227	9351	PacBio
Martensiomyces pterosporus	Zoopagomycota	Kickxellomycotina	none	none	Kickxellales	Kickxellaceae	CBS 209.56	Gp0093918	1040168	251778	saprotroph	19,82	115,7	1156	529	8435	Illumina HiSeq
Ramicandelaber brevisporus	Zoopagomycota	Kickxellomycotina	none	none	Kickxellales	Kickxellaceae	CBS 109374	Gp0093945	JGI	251765	saprotroph (soil)	25,53	168,2	2789	1262	9281	Illumina HiSeq

Supplementary File 2: Cash crops, Food crops, and Gymnosperms

CASH CROP PATHOGENS

		Classification	Genome
SPECIES	**Significance**	**PHYLUM**	**Accession**
Ashbya gossypii	plant pathogen (insect-associated; cotton)	Ascomycota	Gp0000589
Ceratocystis adiposa	plant pathogen (black root in sugar cane)	Ascomycota	Gp0149937
Colletotrichum falcatum	plant pathogen (sugar-cane red rot)	Ascomycota	Gp0124244
Colletotrichum phormii	plant pathogen (anthracnose on flax)	Ascomycota	Go0111565
Colletotrichum simmondsii	plant pathogen (safflower oil crop)	Ascomycota	Gp0122385
Phoma herbarum	plant pathogen (hop & hemp)	Ascomycota	Gp0144010
Sporisorium scitamineum	plant pathogen (sugarcane); smut	Basidiomycota	Gp0118304
Verticillium longisporum	plant pathogen (canola)	Ascomycota	Gp0143280

GYMNOSPERM PATHOGENS

		Classification	Genome
SPECIES	**Significance**	**PHYLUM**	**Accession**
Aplosporella prunicola	probable tree pathogen	Ascomycota	Gp0019419
Armillaria ostoyae	plant pathogen; conifer root rot (parasitic or saprophytic)	Basidiomycota	
Botryosphaeria dothidea	plant pathogen (broad host range of trees and shrubs)	Ascomycota	Gp0038455
Caloscypha fulgens	plant pathogen (seed rot of conifers)	Ascomycota	
Ceraceosorus bombacis	plant pathogen (lumber tree); smut	Basidiomycota	Gp0143854
Ceraceosorus sp.	plant pathogen (lumber tree); smut	Basidiomycota	Gp0095870
Ceratocystis albifundus	plant pathogen (woody & herbaceaous)	Ascomycota	Gp0109102
Ceratocystis eucalypticola	probable plant pathogen (eucalyptus)	Ascomycota	Gp0121626
Ceratocystis platani	plant pathogen (trees)	Ascomycota	Gp0117548
Chrysoporthe austroafricana	plant pathogen (eucalyptus, Tibouchina, Syzygium)	Ascomycota	Gp0146002
Chrysoporthe cubensis	plant pathogen (eucalyptus, Tibouchina, Syzygium)	Ascomycota	Gp0117564
Chrysoporthe deuterocubensis	plant pathogen (eucalyptus, Tibouchina, Syzygium)	Ascomycota	Gp0117565
Colletotrichum salicis	plant pathogen (black canker of willow)	Ascomycota	Gp0090026
Cronartium comandrae	plant pathogen; rust fungus (pine)	Basidiomycota	Gp0038527
Cronartium quercuum	plant pathogen; rust fungus (fusiform rust of pine)	Basidiomycota	Gp0004798
Cronartium ribicola	plant pathogen; rust fungus (pine)	Basidiomycota	Gp0038568
Cryphonectria parasitica	plant pathogen (chestnut blight)	Ascomycota	Gp0002604
Diplodia pinea	plant pathogen (pines)	Ascomycota	Gp0093398
Diplodia scrobiculata	plant pathogen (conifer spp.)	Ascomycota	Gp0143864
Endocronartium harknessii	plant pathogen; rust fungus (pine-pine gall rust)	Basidiomycota	Gp0038528
Fusarium circinatum	plant pathogen (pitch canker of pines)	Ascomycota	Gp0005151
Grosmannia clavigera	plant pathogen; blue stain	Ascomycota	Gp0002583
Heterobasidion annosum	plant pathogen (conifers)	Basidiomycota	Gp0093680
Heterobasidion irregulare	plant pathogen (conifers and hardwoods)	Basidiomycota	Gp0002642
Hymenoscyphus fraxineus	plant pathogen (ash dieback)	Ascomycota	Gp0124450
Lecanosticta acicola	plant pathogen (pine)	Ascomycota	Gp0047147
Leptographium procerum	plant pathogen (pine)	Ascomycota	Gp0107386
Marssonina brunnea	plant pathogen (poplar leaf spot)	Ascomycota	Gp0038386
Melampsora allii-populina	plant pathogen; rust fungus (poplar)	Basidiomycota	Gp0047015
Melampsora larici-populina	plant pathogen (poplar); rust fungus	Basidiomycota	Gp0002503
Melampsora pinitorqua	plant pathogen (pine twisting rust); rust fungus	Basidiomycota	Gp0038564
Mycosphaerella laricina	plant pathogen (larch)	Ascomycota	Gp0047149
Mycosphaerella pini	plant pathogen (pine)	Ascomycota	Gp0017021
Ophiostoma novo-ulmi	plant pathogen (Dutch Elm Disease)	Ascomycota	Gp0038489
Phellinus noxius	plant pathogen (broad host range, typically trees)	Basidiomycota	Gp0070880
Porodaedalea chrysoloma	plant pathogen (conifer parasite; white pocket rot)	Basidiomycota	Go0033091
Porodaedalea niemelaei	plant pathogen (conifer white rot)	Basidiomycota	Go0072274
Setomelanomma holmii	plant pathogen (spruce needle drop)	Ascomycota	Gp0036261
Sphaerulina musiva	plant pathogen (poplar)	Ascomycota	Gp0008704
Sphaerulina populicola	plant pathogen (poplar)	Ascomycota	Gp0048413
Taphrina populina	plant pathogen (cottonwood)	Ascomycota	Gp0124247
Teratosphaeria nubilosa	plant pathogen (leaf spot of *Eucalyptus)*	Ascomycota	Gp0036290
Thielaviopsis paradoxa	plant pathogen (palm)	Ascomycota	Gp0144032

FOOD CROP PATHOGENS

			Classification	Genome
SPECIES	**Significance**	**Staple crop?**	**PHYLUM**	**Accession**
Grains				
Bipolaris maydis	plant pathogen (wheat)	x	Ascomycota	Gp0003183
Bipolaris oryzae	plant pathogen (rice)	x	Ascomycota	Gp0010035
Bipolaris sorokiniana	plant pathogen (cereals)	x	Ascomycota	Gp0004797
Bipolaris victoriae	plant pathogen (blight of oats)	x	Ascomycota	Gp0010034
Bipolaris zeicola	plant pathogen (sorghum, maize and apple)	x	Ascomycota	Gp0010036
Blumeria graminis	plant pathogen (mildew on grasses and cereals)	x	Ascomycota	Gp0038457
Cercospora zeae-maydis	plant pathogen (maize); toxin-producing	x	Ascomycota	Gp0002172
Claviceps fusiformis	plant pathogen (pearl millet)	x	Ascomycota	Gp0038970
Claviceps purpurea	plant pathogen (cereals)	x	Ascomycota	Gp0038662
Cochliobolus lunatus	plant pathogen (sorghum); pharmaceutical importance	x	Ascomycota	Gp0039341
Colletotrichum graminicola	plant pathogen (anthracnose in cereals)	x	Ascomycota	Gp0004788
Colletotrichum sublineola	plant pathogen (anthracnose in wild rice and sorghum)	x	Ascomycota	Gp0094476
Fusarium acuminatum	plant pathogen (cereals)	x	Ascomycota	Gp0043378
Fusarium avenaceum	plant pathogen (generalist, including grain crops)	x	Ascomycota	Gp0143156
Fusarium equiseti	plant pathogen (members of the Leguminoseae and some cereals)	x	Ascomycota	Gp0044229
Fusarium fujikuroi	plant pathogen (rice)	x	Ascomycota	Gp0039409
Fusarium graminearum	plant pathogen (wheat and barley)	x	Ascomycota	Gp0086804
Fusarium nygamai	plant pathogen (rice)	x	Ascomycota	Gp0124341
Fusarium pseudograminearum	plant pathogen (wheat)	x	Ascomycota	Gp0043380
Fusarium temperatum	plant pathogen (maize); opportunistic human pathogen	x	Ascomycota	Gp0093049
Fusarium verticillioides	plant pathogen (maize)	x	Ascomycota	Gp0002615
Gaeumannomyces graminis	plant pathogen (root rot of cereals)	x	Ascomycota	Gp0005124
Magnaporthe oryzae	plant pathogen (rice)	x	Ascomycota	Gp0039276
Melanconium sp. 1 NRRL 54901	plant pathogen (probable maize pathogen)	x	Ascomycota	Gp0019267
Parastagonospora nodorum	plant pathogen (wheat)	x	Ascomycota	Gp0002465
Puccinia graminis	plant pathogen; rust fungus (cereals)	x	Basidiomycota	Gp0002677
Puccinia sorghi	plant pathogen (maize); rust	x	Basidiomycota	Gp0118202
Puccinia striiformis	plant pathogen (wheat); rust fungus	x	Basidiomycota	Gp0039222
Puccinia triticina	plant pathogen (wheat, barley, rye); rust fungus	x	Basidiomycota	Gp0005826
Pyrenophora seminiperda	plant pathogen (necrotrophic; seeds of grasses/cereals)	x	Ascomycota	Gp0037221
Pyrenophora teres	plant pathogen (barley and some other crops)	x	Ascomycota	Gp0008318
Pyrenophora tritici-repentis	plant pathogen (cereals and grasses; necrotrophic)	x	Ascomycota	Gp0003140
Ramularia collo-cygni	plant pathogen (barley)	x	Ascomycota	Gs0120586
Sarocladium oryzae	plant pathogen (rice sheath rot)	x	Ascomycota	
Sclerotinia borealis	plant pathogen (cereals; sychrophilic)	x	Ascomycota	Gp0070994
Setosphaeria turcica	plant pathogen (maize)	x	Ascomycota	Gp0008856
Sporisorium reilianum	plant pathogen (maize); smut	x	Basidiomycota	Gp0038426
Tilletia caries	plant pathogen (bunt of wheat)	x	Basidiomycota	Gp0150383
Tilletia controversa	plant pathogen (dwarf bunt of wheat)	x	Basidiomycota	Gp0150384
Tilletia horrida	plant pathogen (rice); smut	x	Basidiomycota	Gp0118397
Tilletia indica	plant pathogen (Karnal bunt on wheat an triticale)	x	Basidiomycota	Gp0150415
Ustilaginoidea virens	plant pathogen (rice)	x	Ascomycota	Gp0115332
Ustilago esculenta	plant pathogen (wild rice); smut	x	Basidiomycota	Gp0109108
Ustilago hordei	plant pathogen (barley); smut	x	Basidiomycota	Gp0038438
Ustilago maydis	plant pathogen (maize and teosinte); smut	x	Basidiomycota	Gp0000206
Villosiclava virens	plant pathogen; (false smut of rice)	x	Ascomycota	Gp0094980
Zymoseptoria passerinii	plant pathogen (barley leaf blotch)	x	Ascomycota	Gp0010309
Zymoseptoria tritici	plant pathogen (wheat leaf blotch)	x	Ascomycota	Gp0010420
Fruit				
Alternaria arborescens	plant pathogen (tomato)		Ascomycota	Gp0038059
Botryotinia fuckeliana	plant pathogen (grapevines)		Ascomycota	Gp0002499
Ceratocystis manginecans	plant pathogen (mango)		Ascomycota	Gp0097242
Cladosporium fulvum	plant pathogen (leaf mold)		Ascomycota	
Colletotrichum fioriniae	plant pathogen (anthracnose in crops and wild plants)		Ascomycota	Gp0019317
Dactylonectria macrodidyma	plant pathogen (grapevine, avocado, and olive)		Ascomycota	Gp0117674
Diplodia seriata	plant pathogen (grapevine bot canker)		Ascomycota	Gp0117696
Eremothecium cymbalariae	plant pathogen (stigmatomycosis; fruit rot; crops)		Ascomycota	Gp0008918
Erysiphe necator	plant pathogen (powdery mildew of grape)		Ascomycota	Gp0117742
Eutypa lata	plant pathogen; grapevine dieback		Ascomycota	Gp0039198
Geotrichum candidum	plant pathogen (citrus)		Ascomycota	Gp0106203
Guignardia citricarpa	plant pathogen (citrus)		Ascomycota	Gp0041977
Huntiella omanensis	plant pathogen (weak mango pathogen)		Ascomycota	Gp0121623
Meira nashicola	probable plant pathogen (pear)		Basidiomycota	Gp0144018
Moniliophthora perniciosa	plant pathogen (cacao)		Basidiomycota	Gp0002607
Mycosphaerella eumusae	plant pathogen (banana)		Ascomycota	Gp0143045
Mycosphaerella fijiensis	plant pathogen (leaf spot of banana)		Ascomycota	Gp0002650
Neofusicoccum parvum	plant pathogen (grapevines)		Ascomycota	Gp0039200
Neonectria ditissima	plant pathogen (apple canker)		Ascomycota	Gp0144542
Passalora (Cladosporium) fulva	plant pathogen (tomato)		Ascomycota	Gp0039398
Peltaster fructicola	plant pathogen (apples)		Ascomycota	Gp0143846
Phaeoacremonium aleophilum	plant pathogen (grapevine trunk disease)		Ascomycota	Gp0039199
Phaeomoniella chlamydospora	plant pathogen (grapevine trunk disease)		Ascomycota	Gp0118145
Phyllosticta citriasiana	plant pathogen (citrus tan spot)		Ascomycota	Gp0032376
Phyllosticta citricarpa	plant pathogen (citrus black spot)		Ascomycota	Gp0144687

Plenodomus tracheiphilus	plant pathogen (citrus)		Ascomycota	Gp0039845
Pseudocercospora musae	plant pathogen (banana)		Ascomycota	Gp0143044
Puccinia psidii	plant pathogen; rust fungus (guava)		Basidiomycota	Gp0144693
Pyrenochaeta lycopersici	plant pathogen (tomato)		Ascomycota	Gp0090025
Rosellinia necatrix	plant pathogen (fruits)		Ascomycota	Gp0146048
Stemphylium lycopersici	plant pathogen (fruits)		Ascomycota	Gp0118324
Taphrina deformans	plant pathogen (peach)		Ascomycota	Gp0038420
Taphrina flavorubra	plant pathogen (Prunus fruit)		Ascomycota	Gp0103452
Taphrina wiesneri	plant pathogen (cherry trees)		Ascomycota	Gp0103453
Thielaviopsis punctulata	plant pathogen (date palm)		Ascomycota	Gp0118396
Valsa mali	plant pathogen (apple & pear)		Ascomycota	Gp0118828
Venturia pyrina	plant pathogen (hemibiotrophic; pear)		Ascomycota	Gp0095335
Vegetables				
Alternaria brassicicola	plant pathogen (Brassica dark leaf spot)		Ascomycota	Gp0002466
Athelia rolfsii	plant pathogen (blight of vegetables)		Basidiomycota	Gp0106003
Ceratocystis fimbriata	plant pathogen (sweet potato)	x	Ascomycota	Gp0006908
Colletotrichum higginsianum	plant pathogen (anthracnose in Brassicaceae)		Ascomycota	Gp0008317
Fusarium sambucinum	plant pathogen (potato dry rot); mycotoxin-producing	x	Ascomycota	Gp0144734
Helminthosporium solani	plant pathogen (potato)	x	Ascomycota	Gp0047673
Leptosphaeria maculans	plant pathogen (Brassica crops)		Ascomycota	Gp0010336
Ophiognomonia clavigignenti-juglar	plant pathogen (butternut)		Ascomycota	Gp0008964
Plectosphaerella cucumerina	plant pathogen (blight of cucurbits); nematophagous		Ascomycota	
Sclerotinia sclerotiorum	plant pathogen (broadest host range known)		Ascomycota	Gp0002703
Legumes				
Ascochyta rabiei	plant pathogen (blight on chickpea)		Ascomycota	Gp0150874
Colletotrichum incanum	plant pathogen (broad host range; including soybean)		Ascomycota	Gp0150230
Diaporthe aspalathi	plant pathogen (soybean stem canker)	x	Ascomycota	Gp0144055
Diaporthe longicolla	plant pathogen (soybean)	x	Ascomycota	Gp0038530
Eremothecium coryli	plant pathogen (soybean)	x	Ascomycota	Gp0097267
Erysiphe pisi	plant pathogen (powdery mildew of pea)		Ascomycota	Gp0008359
Fusarium virguliforme	plant pathogen (soybean)	x	Ascomycota	Gp0038801
Moniliophthora roreri	plant pathogen (pod rot of cacao)		Basidiomycota	Gp0049167
Mycosphaerella arachidis (Cercospo	plant pathogen (leaf spot on peanuts)		Ascomycota	Gp0150604
Puccinia arachidis	plant pathogen (peanut)		Basidiomycota	Gp0118201
Uromyces viciae-fabae	plant pathogen (beans); rust		Basidiomycota	Gp0117703
Multiple food crop types				
Alternaria alternata	plant pathogen (leaf spot)		Ascomycota	Gp0047507
Cercospora canescens	plant pathogen (leaf spot of various bean crops and tomato)		Ascomycota	Gp0037543
Colletotrichum gloeosporioides	plant pathogen (disease and anthracnose on a range of fuit and vegetables)		Ascomycota	Gp0038653
Colletotrichum orbiculare	plant pathogen (melons and cucumber)		Ascomycota	Gp0038654
Corynespora cassicola	plant pathogen (broad host range)	x	Ascomycota	Gp0086748
Fusarium oxysporum	plant pathogen (broad host range)		Ascomycota	Gp0037083
Macrophomina phaseolina	plant pathogen (broad host range)	x	Ascomycota	Gp0044758
Nectria haematococca	plant pathogen (broad host range)	x	Ascomycota	Gp0017718
Rhizoctonia solani	plant pathogen (broad host range)	x	Basidiomycota	Gp0041102
Verticillium alfalfae	plant pathogen (broad host range); wilt disease		Ascomycota	Gp0005850
Verticillium dahliae	plant pathogen (broad host range); wilt disease		Ascomycota	Gp0003474

Supplementary File 3

Phylogenetic placement of fungal orders described after Hibbett *et al.* (2007).

ASCOMYCOTA

(Lumbsch & Huhndorf, 2010)

- Abrothallales: (Pérez-Ortega *et al.*, 2014)
- Acrospermales, Dyfrolomycetales, Monoblastiales, Lichenotheliales, Strigulales: (Wijayawardene et al., 2014)
- Amphisphaeriales: (Senanayake *et al.*, 2015)
- Archaeorhizomycetes: (Rosling *et al.*, 2011)
- Ascosphaerales & Arachnomycetales: (Kirk *et al.*, 2008)
- Asterinales: (Hongsanan *et al.*, 2014)
- Asterotexiales: (Guatimosim *et al.*, 2014)
- Celotheliales: (Gueidan *et al.*, 2014)
- Dothideomycete families: (Schoch *et al.*, 2009a; Wijayawardene *et al.*, 2014)
- Eremithallales: (Lucking *et al.*, 2008)
- Geoglossomycetes & Geoglossales: (Schoch *et al.*, 2009b)
- Lecanoromycete families: (Miadlikowska *et al.*, 2014)
- Lecanoromycete orders (Arctomiales, Caliciales, Hymeneliales, Sarrameanales, Trapeliales): (Miadlikowska *et al.*, 2014)
- Lecideales: (Schmull *et al.*, 2011)
- Leotiomycete families: (Wang *et al.*, 2006)
- Mytilinidiales: (Boehm *et al.*, 2009)
- Natipusillales: (Hongsanan *et al.*, 2014)
- Phaeomoniellales: (Chen *et al.*, 2015)
- Saccharomycotina families: (Kurtzman, 2011)
- Sordariomycete families and orders (Amplistromatales, Annulatascales, Cordanales, Falcocladiales, Glomerellales, Jobellisiales, Koralionastetales, Magnaporthales, Pisorisporiales, Savoryellales, Togniniales): (Maharachchikumbura *et al.*, 2015)
- Taxonomic confusion exists at almost all taxonomic levels within the Leotiomycetes: (Johnston *et al.*, 2014)
- Trapeliales & Sarrameanales: (Hodkinson & Lendemer, 2011)
- Trypetheliales: (Hyde *et al.*, 2013)
- Tubeufiales: (Boonmee *et al.*, 2014)
- Umbilicariales: (Miadlikowska *et al.*, 2014)
- Valsariales: (Jaklitsch *et al.*, 2015)
- Venturiales: (Wijayawardene *et al.*, 2014; Zhang *et al.*, 2011)
- Xylonomycetes: (Gazis *et al.*, 2012)

BASIDIOMYCOTA

- Amylocorticiales & Jaapiales: (Binder *et al.*, 2010) Jaapials is sister to Agaricomycetidae
- Ceraceosorales: (Wang *et al.*, 2015)
- Geminibasidiales: (Nguyen *et al.*, 2013)
- Geminibasidiomycetes: (Nguyen *et al.*, 2015)
- Golubeviales: (Wang *et al.*, 2015)
- Holtermanniales: (Liu *et al.*, 2015)
- Kriegeriales: (Toome *et al.*, 2013)
- Lepidostromatales: (Hodkinson *et al.*, 2014)
- Moniliellales: (Wang *et al.*, 2014)
- Robbauerales: (Wang *et al.*, 2015)
- Trichosporonales: (Liu *et al.*, 2015)
- Tritirachiomycetes: (Schell *et al.*, 2011)
- Wallemiomycetes at base of Agaricomycotina: (Nguyen *et al.*, 2013)

EARLY-DIVERGING FUNGI

- Basidiobolales (Gryganskyi *et al.*, 2012)
- Cladochytriales (Mozley-Standridge *et al.*, 2009)
- Lobulomycetales (Simmons *et al.*, 2009)
- Mortierellomycotina (Hoffmann *et al.*, 2011)
- Olpidiomycota: Index Fungorum no. 42, Effectively published 27/12/2013 22:02:48 (ISSN 2049-2375), Nomenclatural novelties: Alexander B. Doweld; Publication Name: Index Fungorum 42: 1. 28 Dec 2013.
- Rhizophlyctidales (Letcher *et al.*, 2008)

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