

Table 2: OTUs and their frequency of detection and isolation, with criteria used for their identification, including sequence accession numbers.

<b>Class; Order; Family</b>	<b>OTU</b>	<b>N5<sup>1</sup></b>	<b>N8<sup>1</sup></b>	<b>CL<sup>3</sup></b>	<b>GenBank Accession</b>	<b>Criterion for identification</b>
<b><u>Dothideomycetes</u></b>						
Botryosphaerales; Family undet.	Botryosphaerales sp. 1	0	2	0	KM216369	Sequence similarity of 98% to AY843079, an unnamed fungal isolate from rock surfaces, and up to 86% to several species of Botryosphaerales, including KC869997, <i>Diplodia seriata</i> culture-collection CBS:134701 and FJ888478, <i>Diplodia alatafructa</i> CMW22721 Sequence similarity up to 90% to several species of Botryosphaerales, including EU603293, <i>Botryosphaeria viticola</i> and EF591921, <i>Dothiorella moneti</i>
	Botryosphaerales sp. 3	1	0	0	KM216350	
Capnodiales; Family undet.	Capnodiales sp. 1	0	1	0	KJ406762	Phylogenetic analysis, Figure 1
	Capnodiales sp. 2	1	1	0	KJ406757	Phylogenetic analysis, Figure 1
	Capnodiales sp. 3	1	0	0	KM216329	Phylogenetic analysis, Figure 1
	<i>Phaeotheca fissurella</i>	3	13	0	KM216349	Sequence similarity of 99% to AJ244255.1, <i>Phaeotheca fissurella</i> CBS 520.89, less than 90% similarity to any other sequence from identified fungi.
Davidiellaceae	<i>Davidiella</i> sp. 1	8	3	0	KM216336	Sequence similarity of 99.8% to a range of <i>Davidiella</i> and <i>Cladosporium</i> (anamorph of <i>Davidiella</i> ) species, including, <i>D. tassiana</i> ; <i>D. macrospora</i> ; <i>C. ramotenellum</i> ; <i>C. cucumerinum</i> .
	Davidiellaceae sp. 1	3	0	0	KM216333	Sequence similarity of 93-94% to four species of <i>Rachicladosporium</i>
	Davidiellaceae sp. 2	1	0	0	KM216347	Sequence similarity of 93-95% to four species of <i>Rachicladosporium</i> .
Mycosphaerellaceae	<i>Dothistroma septosporum</i>	2	16	0	KJ406805	Phylogenetic analysis, Figure 2

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	Mycosphaerellaceae sp. 1	3	2	0	KJ406789	Phylogenetic analysis, Figure 2
	Mycosphaerellaceae sp. 2	0	1	0	KJ406794	Phylogenetic analysis, Figure 2
	Mycosphaerellaceae sp. 3	0	1	0	KJ406799	Phylogenetic analysis, Figure 2
	<i>Phaeothecoidea</i> sp. 1	4	0	0	KJ406802	Phylogenetic analysis, Figure 2
	<i>Phaeothecoidea</i> sp. 2	1	0	0	KJ406792	Phylogenetic analysis, Figure 2
	<i>Phaeothecoidea</i> sp. 3	0	2	0	KJ406797	Phylogenetic analysis, Figure 2
	<i>Pseudocercospora</i> sp. 1	1	0	0	KJ406795	Phylogenetic analysis, Figure 2
	<i>Ramularia stellenboschensis</i>	1	0	0	KJ406791	Phylogenetic analysis, Figure 2
Order undet.;						
Family undet.	Dothideomycetes sp. 2	1	1	0	KJ406840	Sequence similarity of 98-99% to a range of Dothideomycete spp., including AJ279448, <i>Epicoccum nigrum</i> .
Teratosphaeriaceae	<i>Devriesia</i> sp.	0	1	0	KM216374	Sequence similarity of 93% to AY692088.1, <i>Devriesia thermoturans</i>
	<i>Teratosphaeria</i> aff. <i>associata</i>	2	0	0	KJ406767	Phylogenetic analysis, Figure 1
	<i>Teratosphaeria</i> aff. <i>capensis</i>	1	0	0	KJ406771	Phylogenetic analysis, Figure 1
	<i>Teratosphaeria</i> aff. <i>parva</i>	1	4	0	KJ406775	Phylogenetic analysis, Figure 1
	<i>Teratosphaeria</i> aff. <i>suttonii</i>	1	0	0	KJ406763	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 01	0	4	0	KJ406774	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 02	0	2	0	KJ406778	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 03	3	12	0	KM216368	Phylogenetic analysis, Figure 1

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	Teratosphaeriaceae sp. 04	1	7	0	KJ406777	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 05	2	0	0	KJ406766	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 06	2	0	0	KJ406768	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 07	1	0	0	KJ406760	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 08	2	2	0	KJ406759	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 09	1	0	0	KJ406770	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 10	3	0	0	KJ406764	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 11	0	1	0	KJ406783	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 12	0	1	0	KJ406782	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 13	0	6	0	KJ406779	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 14	4	0	0	KJ406758	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 15	0	4	0	KJ406776	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 16	1	5	0	KJ406786	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 17	1	0	0	KJ406785	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 18	2	4	0	KJ406787	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp. 19	1	0	0	KJ406788	Phylogenetic analysis, Figure 1
	Teratosphaeriaceae sp.	0	1	0	KJ406780	Phylogenetic analysis, Figure 1

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	20					
	Teratosphaeriaceae sp.	2	6	0	KJ406769	Phylogenetic analysis, Figure 1
	21					
	Teratosphaeriaceae sp.	0	3	0	KJ406781	Phylogenetic analysis, Figure 1
	22					
	Teratosphaeriaceae sp.	9	33	0	KJ406784	Phylogenetic analysis, Figure 1
	23					
	Teratosphaeriaceae sp.	0	5	0	KM216373	Phylogenetic analysis, Figure 1
	25					
	Teratosphaeriaceae sp.	15	2	0	KJ406761	Phylogenetic analysis, Figure 1
	26					
Dothideales;						
Dothioraceae	<i>Aureobasidium pullulans</i>	2	2	2	KJ407004	Phylogenetic analysis, Figure 3
	<i>Sydowia polyspora</i>	10	2	3	KJ407006	Phylogenetic analysis, Figure 3
Family undet.	Dothideales sp. 1	1	0	0	KJ406831	Phylogenetic analysis, Figure 3
Pleosporales						
Didymellaceae	<i>Leptosphaerulina</i> sp. 1	1	0	0	KJ406837	Sequence similarity of up to 99.8% to accessions from several <i>Leptosphaerulina</i> spp., including KJ796400, <i>L. chartarum</i> .
	Didymellaceae sp. 2	0	3	0	KM216364	Sequence similarity of 98% to a range of <i>Peyronellaea</i> and <i>Phoma</i> species, including GU237818, <i>Peyronellaea aurea</i> .
Lophiostomataceae	<i>Lophiostoma corticola</i>	0	2	1	KJ407013	Sequence similarity of 99.5% to multiple accessions of <i>Lophiostoma corticola</i> , including HE774481.
Montagnulaceae	<i>Paraphaeosphaeria michotii</i>	3	0	0	KJ406849	Sequence similarity of 99.8% to multiple accessions of <i>Paraphaeosphaeria michotii</i> , including JX496079, and 98% similarity to other <i>Paraphaeosphaeria</i> species.
Phaeosphaeriaceae	<i>Phaeosphaeria</i> sp. 3	1	0	0	KJ406845	Sequence similarity of 98-99% to a range of

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Pleosporaceae	<i>Allewia eureka</i>	0	1	0	KM216382	<i>Phaeosphaeria</i> species, including JX981464, <i>P. culmorum</i> . Sequence similarity of 99% to JN383490, <i>Embellisia eureka</i> (syn. <i>Allewia eureka</i> ), and up to 97% sequence similarity to several other species of <i>Alternaria</i> including, KC584222, <i>A. triglochynicola</i> CBS 119676
Sporormiaceae	<i>Preussia/Sporormiella</i> sp. 1	0	1	0	KJ406868	Phylogenetic analysis, Figure 4
	<i>Preussia/Sporormiella</i> sp. 2	0	0	3	KJ407017	Phylogenetic analysis, Figure 4
	<i>Preussia/Sporormiella</i> sp. 3	1	0	0	KJ406867	Phylogenetic analysis, Figure 4
	<i>Preussia/Sporormiella</i> sp. 4	0	1	0	KJ406866	Phylogenetic analysis, Figure 4
	<i>Preussia/Sporormiella</i> sp. 5	0	1	1	KJ407014	Phylogenetic analysis, Figure 4
	<i>Preussia/Sporormiella</i> sp. 6	0	1	0	KJ406865	Phylogenetic analysis, Figure 4
	<i>Preussia/Sporormiella</i> sp. 7	2	0	0	KJ406863	Phylogenetic analysis, Figure 4
Family undet.	Pleosporales sp. 1	0	5	0	KJ406858	Sequence similarity of up to 97% to several species of <i>Peyronellaea</i> and <i>Phoma</i> , including GU237847 <i>Peyronellaea obtusa</i>
	Pleosporales sp. 2	2	1	7	KJ407009	Sequence similarity of 99-100% to species of <i>Microsphaeropsis</i> , <i>Phoma</i> , and <i>Atracidymella</i> , including JX681101, <i>Microsphaeropsis olivacea</i> .
	Pleosporales sp. 3	0	1	0	KJ406852	Sequence similarity of 99-100% to a range of Pleosporales species, including JX496099, <i>Paraconiothyrium brasiliense</i> .
	Pleosporales sp. 4	0	2	0	KJ406853	Sequence identity with a range of Pleosporales species, including EU295638, <i>Paraconiothyrium brasiliense</i> .

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	Pleosporales sp. 6	0	1	0	KM216359	Sequence similarity of up to 93% to a range of Pleosporales species, including EU295638, <i>Paraconiothyrium brasiliense</i> .
<b><u>Eurotiomycetes</u></b>						
Chaetothyriales; Herpotrichiellaceae	<i>Exophiala eucalyptorum</i>	2	0	0	KJ406880	Sequence similarity of 99.6-100% to two accessions of <i>Exophiala eucalyptorum</i> , including EU035417, sequence similarity of up to 96% to other Chaetothyriales species. Sequence similarity of 98% to DQ914677, <i>Exophiala</i> sp., sequence similarity of up to 83% to other Chaetothyriales species. Sequence similarity of 95-96% to two accessions of <i>Exophiala eucalyptorum</i> , including EU035417, sequence similarity of up to 90% to other Chaetothyriales species.
	<i>Exophiala</i> sp. 1	0	1	0	KJ406883	
	<i>Exophiala</i> sp. 2	0	1	0	KJ406881	
Family undet.	Chaetothyriales sp. 1	3	0	0	KJ406877	Sequence similarity of 80-89% to a range of <i>Phaeococcomyces</i> species, including KJ152783, <i>P. mexicanus</i> .
	Chaetothyriales sp. 2	4	1	0	KJ406875	Sequence similarity of 80-87% to a range of <i>Phaeococcomyces</i> species, including KJ152783, <i>P. mexicanus</i> .
	Chaetothyriales sp. 3	1	0	0	KJ406884	Sequence similarity up to 93% to a range of Chaetothyriales spp., including EU035415, <i>Cyphellophora hylomeconis</i> .
Eurotiales; Trichocomaceae	<i>Aspergillus</i> sp. 1	0	1	0	KJ406885	Sequence similarity of 93-94% to several accessions of <i>A. conicus</i> , including EF652039, up to 91% similarity to other <i>Aspergillus</i> species. Sequence similarity of 99% to several species of <i>Aspergillus</i> , including AY373877, <i>A. ustus</i> . Sequence similarity of 99% to several species of
	<i>Aspergillus</i> sp. 2	0	6	0	KJ406901	
	<i>Aspergillus</i> sp. 3	0	0	1	KJ407020	

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	<i>Penicillium</i> sp.1	1	0	0	KJ406888	<i>Aspergillus</i> , including KJ775589, <i>A. versicolor</i> . Sequence similarity of 96% to several species of <i>Penicillium</i> , including KJ775589, <i>P. chrysogenum</i> .
	<i>Penicillium</i> sp. 2	4	0	0	KJ406887	Sequence similarity of 96% to several species of <i>Penicillium</i> , including AY373906, <i>P. corylophilum</i> .
	<i>Penicillium</i> sp. 3	1	0	0	KJ406890	Sequence similarity of 96% to several species of <i>Penicillium</i> , including AF033463, <i>P. namyslowskii</i> .
	<i>Penicillium</i> sp. 4	1	0	0	KJ406894	Sequence identity with several species of <i>Penicillium</i> , including KJ775635, <i>P. glabrum</i> .
	<i>Penicillium</i> sp. 5	0	0	3	KJ407018	Sequence similarity of 95% to several species of <i>Penicillium</i> , including AY373898, <i>P. brevicompactum</i> .
<b><u>Lecanoromycetes</u></b>						
Acarosporales; Family undet.	Acarosporales sp. 1	0	1	0	KM624595	Sequence similarity of up to 88% to several <i>Acarospora</i> species, including GU184115.1, <i>A. rosulata</i> .
<b><u>Leotiomyces</u></b>						
Helotiales; Dermateaceae	<i>Mollisia</i> sp. 1	0	0	2	KM216327	Over 99% similarity to several species of <i>Mollisia</i> , including <i>M. melaleuca</i> (AY259136), <i>M. cinerea</i> (AY259135), and <i>M. fusca</i> (AY259137)
Helotiaceae	<i>Varicosporium</i> aff. <i>elodeae</i>	1	0	0	KM216334	Sequence similarity of 98% to several accessions of <i>Varicosporium elodeae</i> , including JN655610.1.
Sclerotiniaceae	<i>Torrendiella eucalypti</i>	2	0	0	KM216355	Sequence similarity of 99% to AY755335, <i>Torrendiella eucalypti</i> , and 95% sequence

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Family undet.	<i>Cyclaneusma minus</i> 'simile'	8	17	2	KM216324	similarity to several other species of <i>Torreodiella</i> Sequence identity with reference isolates of <i>Cyclaneusma minus</i> 'simile' and 90-91% sequence similarity to <i>C. minus</i> 'verum' and <i>C. niveum</i> .
	<i>Cyclaneusma minus</i> 'verum'	9	2	3	KJ407021	Sequence identity with reference isolates of <i>Cyclaneusma minus</i> 'verum', 99% sequence similarity to <i>C. niveum</i> and 90% sequence similarity to <i>C. minus</i> 'simile'.
	Helotiales sp. 1	0	0	4	KM216322	Sequence similarity of up to 98% to several Helotiales species, including <i>Cadophora malorum</i> and <i>Mollisia dextrinospora</i>
	Helotiales sp. 2	0	0	2	KM216321	Sequence similarity of 99% to HQ608100.1, unidentified ascomycete, and up to 94% to several Helotiales species including EU940165.1, <i>Cyathicula microspora</i> .
	Helotiales sp. 3	0	1	0	KM216383	Sequence similarity of up to 92% to several Helotiales species, including KC464643 <i>Lachnellula tricolor</i> .
	Helotiales sp. 4	1	0	0	KM216351	Sequence similarity of up to 86% to several Helotiales species, including <i>Arachnopeziza</i> spp.
	<i>Meliniomyces</i> sp.	1	0	0	KM216335	Sequence similarity of 98% to several accessions of <i>Meliniomyces bicolor</i> , including HQ157926.1.
Phacidiales; Phacidiaceae	<i>Phacidium lacerum</i>	2	1	1	KF013549	Sequence identity with reference isolate NZFS504, 99% sequence similarity to <i>Strasseria geniculata</i> , KF013550.
Order undet., Family undet.	Leotiomycetes sp. 1	3	0	0	KJ406966	Sequence similarity of 90-91% to a range of <i>Collophora</i> spp., including JN808839, <i>C. hispanica</i> .
	Leotiomycetes sp. 2	0	1	0	KJ406972	Sequence similarity of up to 90% to a range of

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						Leotiomycete spp., including HQ533008, <i>Claussenomyces</i> sp.
Rhytismatales; Rhytismataceae	<i>Lophodermium aff. conigenum</i> <i>Lophodermium pinastri</i>	4 14	0 12	21 78	KJ407029 KJ407045	Phylogenetic analysis, Figure 5; Supplementary Figure 1 Phylogenetic analysis, Figure 6; Supplementary Figure 2
Family undet.	<i>Fulvoflamma</i> sp.	1	0	0	KM216341	Sequence similarity of 92% to DQ195779, <i>Fulvoflamma eucalypti</i> CPC 11243, and up to 99% to unknown Leotiomycetes species.
<b><u>Pezizomycetes</u></b>						
Pezizales; Family undet.	Pezizales sp. 1	0	0	2	KJ407055	Sequence similarity of 97% to EU552114, <i>Conoplea fusca</i> CBS 113475 and up to 95% to several species of <i>Plectaria</i>
	Pezizales sp. 3	0	0	1	KJ407058	Sequence similarity of up to 92% to several <i>Plectania</i> spp.
Pezizaceae	<i>Chromelosporium carneum</i>	0	0	2	KJ407060	Sequence identity with several accessions of <i>Chromelosporium carneum</i> , including JF440586 and up to 91% similarity to other Pezizaceae spp.
<b><u>Saccharomycetes</u></b>						
Saccharomycetales; Family undet.	<i>Candida sake</i>	0	1	0	KM216377	Sequence similarity of 99% to several accessions of <i>Candida sake</i> including AJ549822, and up to 90% similarity to several other <i>Candida</i> species.
<b><u>Sordariomycetes</u></b>						
Hypocreales;						

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Nectriaceae	<i>Fusarium</i> sp.	0	0	1	KM216320	Sequence similarity of 98% to several accessions of <i>Fusarium lateritium</i> , including FJ228190, and up to 96% to several other <i>Fusarium</i> and <i>Gibberella</i> species.
Coniochaetales; Coniochaetaceae	<i>Coniochaeta</i> sp. 1	0	0	73	KJ407067	Phylogenetic analysis, Figure 7.
	<i>Coniochaeta</i> sp. 2	0	0	4	KJ407066	Phylogenetic analysis, Figure 7.
Sordariales; Lasiosphaeriaceae	<i>Bagadiella</i> sp. 1	1	0	0	KM216344	Sequence similarity of 98-99% to several <i>Bagadiella</i> species, including JF951141, <i>B. victoriae</i> CPC 17688; GQ303269, <i>B. lunata</i> CBS 124762 and JF951142, <i>B. koalae</i> CPC 17682
	<i>Fimetariella rabenhorstii</i>	0	0	9	KJ407070	Sequence similarity of 99-100% to multiple accessions of <i>Fimetariella rabenhorstii</i> , including KM519659 and up to 93% to other Sordariomycete spp.
	<i>Lasiosphaeria</i> sp. 1	0	0	2	KJ407064	Sequence similarity of 97-99% to several accessions of <i>Lasiosphaeria lanuginosa</i> and <i>L. ovina</i> , including AY587916 and up to 93% to other <i>Lasiosphaeria</i> spp.
Family undet.	Sordariales sp. 1	1	0	0	KJ406980	Sequence similarity of up to 90% to a range of Sordariales spp., including GQ154539, <i>Coniochaeta africana</i> .
Xylariales; Amphisphaeriaceae	<i>Pestalotiopsis</i> sp. 1	0	0	1	KJ406990	Sequence similarity of up to 99.4% to a range of <i>Pestalotiopsis</i> spp., including EU342212, <i>P. neglecta</i> .
	<i>Pestalotiopsis</i> sp. 2	1	0	0	KJ406983	Sequence similarity of up to 98% to a range of <i>Pestalotiopsis</i> spp., including EU552147, <i>P. maculiformans</i> .
Xylariaceae	<i>Anthostomella pinea</i>	0	0	3	KJ406992	Sequence similarity of 99.4% to HQ599578,

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	<i>Biscogniauxia</i> sp. 1	0	0	3	KJ406987	<i>Anthostomella pinea</i> , less than 90% sequence similarity to sequences from any other identified fungi available on the INSDs. Sequence similarity of 99% to JN225897, <i>Biscogniauxia</i> sp., and up to 96% to several <i>Biscogniauxia</i> species, including JX507805, <i>B. uniapiculata</i> .
	<i>Nemania diffusa</i>	0	0	13	KJ406996	Sequence similarity of 98-99% to multiple accessions of <i>Nemania diffusa</i> , including DQ68238.
	<i>Rosellinia</i> sp. 1	0	0	1	KJ406999	Sequence similarity of up to 94% to several <i>Rosellinia</i> species, including KC477236, <i>R. corticium</i> .
	<i>Xylaria castorea</i>	0	0	3	KJ406994	Sequence identity with three accessions of <i>Xylaria castorea</i> , including JN225908, and up to 97% sequence similarity with a range of other <i>Xylaria</i> species.
	Xylariaceae sp. 1	0	0	19	KJ407000	Sequence similarity of 99% to JN225905.1, an unidentified Xylariaceae, and 86-91% to several species of <i>Hypoxylon</i> , including JQ009321, <i>H. vinosopulvinatum</i> .
	Xylariaceae sp. 2	0	0	7	KJ406985	Sequence similarity of up to 85% to several <i>Annulohypoxylon</i> and <i>Hypoxylon</i> species, including EF026139, <i>Annulohypoxylon squamulosus</i> .
	Xylariaceae sp. 3	0	0	1	KJ406986	Sequence similarity of 99% to JN225894, an unidentified Xylariaceae, and up to 93% to several <i>Hypoxylon</i> species, including JN979427, <i>H. hypomiltum</i> .
	Xylariaceae sp. 4	0	0	1	KJ406984	Sequence similarity of up to 83% to several <i>Hypoxylon</i> species, including KC968932, <i>H. rickii</i> .

Ascomycota;

<b><u>Class; Order; Family</u></b>	<b>OTU</b>	<b>N5<sup>1</sup></b>	<b>N8<sup>1</sup></b>	<b>CL<sup>3</sup></b>	<b>GenBank Accession</b>	<b>Criterion for identification</b>
Class, Order and Family undet.	Ascomycota sp. 1	3	7	0	KM216353	High sequence similarity in the 5.8S region only to a range of ascomycete species including AY843154.1, <i>Phaeococcomyces nigricans</i> .
	Ascomycota sp. 2	0	11	0	KM216358	Sequence similarity of 95% to AJ244255.1, <i>Phaeotheca fissurella</i> CBS 520.89, up to 88% similarity to a range of other genera including <i>Teratosphaeria</i> .
	Ascomycota sp. 3	1	0	0	KM216354	High sequence similarity in the 5.8S region only to a range of ascomycete species including AY843154.1, <i>Phaeococcomyces nigricans</i> , up to 87% similarity to several uncultured ascomycete clones, including FR682186.1.
	Ascomycota sp. 4	0	1	0	KM216378	High sequence similarity in the 5.8S region only to a range of ascomycete species including FJ172275.1, <i>Aquapoterium pinicola</i> .
	Ascomycota sp. 6	0	1	0	KM216360	High sequence similarity in the 5.8S region only to a range of ascomycete species including JN628167.1, <i>Scleroconidioma sphagnicola</i> .
	Ascomycota sp. 8	2	0	0	KJ406964	Up to 87% sequence similarity to a range of Ascomycota, mainly species of <i>Phacidium</i> and other Phacidiales.
	<i>Strasseria geniculata</i>	2	6	3	KJ407023	Sequence identity with reference isolates NZFS506 and MC7964/2, 99% similarity to <i>Phacidium lacerum</i> KF013549.
<b><u>Agaricomycetes</u></b>						
Agaricales;						
Physalacriaceae	<i>Armillaria</i> aff. <i>luteobubalina</i>	2	0	0	KM624597	Sequence similarity of 98% to several accessions of <i>Armillaria luteobubalina</i> , including AF394916.1,
Strophariaceae	<i>Pholiota multicingulata</i>	2	0	0	KM216337	Sequence identical to HQ533029, <i>Pholiota multicingulata</i> , and up to 93% similarity to several other <i>Pholiota</i> species.

<b>Class; Order; Family</b>	<b>OTU</b>	<b>N5<sup>1</sup></b>	<b>N8<sup>1</sup></b>	<b>CL<sup>3</sup></b>	<b>GenBank Accession</b>	<b>Criterion for identification</b>
Boletales;						
Serpulaceae	<i>Serpula himantioides</i>	1	0	0	KM216346	Sequence similarity of 99.5% to many accessions of <i>Serpula himantioides</i> , including GU187545.1 and 96% to <i>S. lacrymans</i> .
Cantharellales;						
Ceratobasidiaceae	<i>Ceratobasidium</i> sp. 1	0	0	2	KM216319	Sequence similarity of 95% to AJ427401 <i>Ceratobasidium papillatum</i> , and up to 92% similarity to several other <i>Ceratobasidium</i> and <i>Rhizoctonia</i> species.
<b><u>Tremellomycetes</u></b>						
Cystofilobasidiales;						
Cystofilobasidiaceae	<i>Udeniomyces pyricola</i>	0	1	0	KM216371	Sequence similarity of 99% to AF44402.1, <i>Udeniomyces pyricola</i> , 98% to AY841862, <i>U. pseudopyricola</i> , and up to 85% similarity to a range of other <i>Udeniomyces</i> species.
Tremellales;						
Tremellaceae	<i>Cryptococcus</i> aff. <i>amylolyticus</i>	1	0	0	KM216348	Sequence similarity of 97% to several accessions of <i>Cryptococcus</i> aff. <i>amylolyticus</i> , including EF363150.1
	<i>Cryptococcus</i> sp. 1	1	0	0	KM216340	Sequence similarity of up to 99.6% to several accessions of <i>Cryptococcus wieringaes</i> , including FN824493.1 and up to 96% to several other <i>Cryptococcus</i> species.
	<i>Cryptococcus</i> sp. 2	1	0	0	KM216339	Sequence similarity of up to 87% to several species of <i>Cryptococcus</i> , including JN942258.1, <i>C. aerius</i> ,
	<i>Cryptococcus victoriae</i>	2	1	0	KM216343	Sequence similarity of up to 99.8% to many accessions of <i>Cryptococcus victoriae</i> , including HQ615694.1
	<i>Tremella</i> sp.	2	2	0	KM216338	Sequence similarity of 99% to DQ242633.1, <i>Tremella</i> sp., and up to 83% similarity to a range

Class; Order; Family	OTU	N5 <sup>1</sup>	N8 <sup>1</sup>	CL <sup>3</sup>	GenBank Accession	Criterion for identification
	Tremellaceae sp. 1	1	0	0	KM624601	of identified <i>Tremella</i> species. Sequence similarity of up to 94% to a range of Tremellaceae, including <i>Cryptococcus fagi</i> and <i>Tremella neofoliacea</i>
	Tremellaceae sp. 2*	1	0	0	KM624602	Up to 90% sequence similarity to a range of Tremellaceae species, including AF444404, <i>Fellomyces horovitziae</i> .
Trichosporonaceae	<i>Trichosporon</i> aff. <i>dulcitum</i>	0	1	0	KM216365	Sequence similarity of 99% to Af444428.1, <i>Trichosporon dulcitum</i> , and 98% to several other <i>Trichosporon</i> species.
Basidiomycota; Order and family undet.	Basidiomycota sp. 1	1	0	0	KM624603	Up to 92% sequence similarity to several species of <i>Rhodotorula</i> and <i>Sporobolomyces</i> , including FN424107.1, <i>R. aff. diffluens</i> .
	Basidiomycota sp. 2	2	0	0	KM624606	High sequence similarity in the 5.8S region only to a range of basidiomycete species including JN620354, <i>Bensingtonia</i> sp.
	Basidiomycota sp. 5	0	0	1	KM624590	Up to 92% sequence similarity to several uncultured fungal clones, and 86% to a range of basidiomycete species, including JF908470.1, <i>Mycena senesii</i> .
	Basidiomycota sp. 7	2	0	1	KM624589	Sequence similarity of up to 86% to a range of basidiomycete species, including <i>Armillaria novae-zelandiae</i>

<sup>1</sup>N5 represents the frequency of occurrence in 34 bulk needle samples from 12 x 5y.o. plantations

<sup>2</sup>N8 represents the frequency of occurrence in 36 bulk needle samples from a single 8 y.o. plantation.

<sup>3</sup>CL represents the number of isolates (out of the 286 that were sequenced).