

Appendix S1: Spatial position of diploid (2x) and tetraploid (4x) plants of *Centaurea stoebe* s.l. and soil samples sampled from a sympatric population at Sandberg hill. For comparison, our sampling (darker colored set) is superimposed over the map of Mráz et al. (2012b; lighter colored set). Please note that our sampling did not involve the diploid plants from the central part of the study site, as this part of the Nature Reserve - being the closest to the hiking path - was seriously damaged by trampling in 2011.

Appendix S2: List of samples and their characteristics: ploidy, root colonization by arbuscular mycorrhizal fungi (AMF) and dark septate endophytes (DSE), and soil variables.

Sample	Ploidy	AMF colonization (%)	DSE colonization (%)		pH (H2O)		CEC (mmolckg ⁻¹)		C total (%)	C organic (%)	N (%)	P (mg kg ⁻¹)
1)	Ca (mg kg ⁻¹)	Mg (mg kg ⁻¹)	K (mg kg ⁻¹)									
CS01	2x	96.0	8.1	7.03	75.36	1.37	0.92	0.12	11.87	1311.22	79.74	115.23
CS02	2x	96.0	26.3	7.09	71.09	1.09	0.71	0.09	13.11	1279.53	60.58	70.29
CS03	2x	96.0	4.7	7.00	99.82	2.21	1.36	0.20	18.29	1745.59	100.19	162.34
CS04	2x	90.6	16.7	6.90	80.26	1.65	1.18	0.14	13.33	1407.96	84.48	105.83
CS05	2x	92.7	8.3	7.30	48.00	0.59	0.45	0.04	6.33	811.11	52.37	114.12
CS06	2x	91.5	11.5	7.24	39.35	0.29	0.21	0.02	4.48	713.59	32.38	30.57
CS07	2x	85.0	3.5	7.09	57.25	0.77	0.60	0.07	5.44	997.35	60.72	87.60
CS08	2x	99.5	26.4	7.24	56.77	0.78	0.74	0.12	7.15	982.90	54.46	110.19
CS09	2x	94.5	4.8	7.13	38.78	0.67	0.59	0.06	16.09	651.79	47.34	80.38
CS10	2x	94.5	7.5	7.01	48.56	0.92	0.64	0.08	9.39	813.73	60.68	100.71
CS11	2x	15.3	7.6	8.02	151.23	0.26	0.12	0.02	9.46	2924.96	43.68	39.91
CS12	2x	98.5	6.6	7.94	125.97	0.60	0.43	0.05	12.70	2377.01	60.31	68.74
CS13	2x	98.5	6.5	7.49	92.45	0.98	0.62	0.08	12.51	1669.93	77.34	89.00
CS14	2x	94.0	21.9	7.50	288.22	4.53	2.95	0.37	17.82	5017.15	368.94	260.81
CS15	2x	93.5	9.5	7.37	216.90	4.90	3.95	0.44	17.54	3835.38	262.40	127.51
CS16	4x	98.5	5.3	7.16	59.58	0.98	0.81	0.09	18.76	953.44	72.91	213.78
CS17	4x	96.5	5.9	7.22	78.92	1.04	0.92	0.09	9.10	1376.37	83.43	113.43
CS18	4x	95.1	8.7	7.03	51.42	1.32	1.01	0.11	8.07	847.71	57.02	157.22
CS19	4x	98.1	31.3	7.03	36.55	0.42	0.41	0.03	8.95	626.95	48.66	39.07
CS20	4x	91.1	3.5	7.57	43.18	0.32	0.29	0.03	8.14	782.72	33.25	32.22
CS21	4x	95.5	38.1	7.42	41.00	0.23	0.22	0.02	5.82	734.86	35.49	41.13
CS22	4x	99.0	5.4	7.33	54.68	0.68	0.50	0.06	7.82	971.64	46.77	76.62
CS23	4x	91.8	6.6	7.68	73.18	0.63	0.55	0.05	8.09	1296.49	54.09	138.91
CS24	4x	93.1	2.0	7.23	38.05	0.89	0.82	0.07	7.52	611.19	43.85	139.12
CS25	4x	17.8	0.0	8.22	120.82	0.22	0.10	0.01	11.02	2344.56	34.09	19.06
CS26	4x	92.5	4.8	8.24	107.97	0.25	0.14	0.03	9.77	2086.63	33.52	20.69
CS27	4x	96.6	7.1	7.84	59.09	0.43	0.39	0.03	8.84	1096.43	34.98	46.96
CS28	4x	78.0	6.7	7.96	59.49	0.29	0.25	0.02	7.60	1125.35	29.61	22.13
CS29	4x	67.0	10.3	8.04	58.42	0.32	0.24	0.02	9.65	1102.15	27.14	34.60

GenBank results			UNITE results					
SEQ TITLE	Accession	Description	Query length	E value	Similarity (%)	Coverage (%)	Accession	Species
hypothesis	Description	E value	Similarity (%)	Coverage (%)				
CL2_001	AJ567734	Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6	103	2.36E-36	97	98.1	FJ769308SH219474.07FU	
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.07E-46 100 100								
CL2_002	KF836972	Rhizophagus intraradices isolate E6_53 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	113	2.38E-43	96.5	100	HE775296 SH001003.07FU	
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.48E-47 98.2 98.2								
CL2_003	AJ567734	Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6	103	4.56E-39	98	96.1	AJ567734 SH001103.07FU	
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 8.26E-42 98 96.1								
CL2_004	FJ769312	Glomus intraradices clone M50_22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	105	5.01E-45	100	100	HF674808 SH175559.07FU	
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.05E-48 100 100								
CL2_005	KM376421	Rhizophagus sp. P5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	108	2.22E-43	99.1	100	KM376421 SH497058.07FU	
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 4.00E-46 99.1 100								
CL2_006	AJ567771	Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone PvI2.9	97	7.52E-36	100	100	KJ209706 SH001017.07FU	
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.24E-40 100 100								
CL2_007	KF836957	Rhizophagus intraradices isolate E4_42 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	112	3.72E-47	99.1	100	KF836957 SH001003.07FU	
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 6.65E-50 99.1 100								
CL2_008	KF836965	Glomus sp. 25 ZHNL-2013b isolate E6_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	114	3.13E-48	99.1	100	KF836965 SH001026.07FU	
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 5.58E-51 99.1 100								
CL2_009	KM376416	Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	108	4.02E-40	96.3	100	KF939972 SH001323.07FU	
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.28E-47 100 100								
CL2_010	KF836947	Glomus sp. 8 ZHNL-2013k isolate E3_35 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	111	2.31E-43	99.1	100	HE775312 SH001325.07FU	
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.75E-48 99.1 100								

CL2_011 KM056661 Dominikia sp. JB-2014 clone Da-22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 7.02E-43 100 100 KM056660 SH521585.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_aurea; 1.27E-45 100 100

CL2_012 AM743194 Glomus sp. G60-80 ITS1, 23S rRNA gene and ITS2, isolate G60-80 111 3.01E-29 91.6 96.4 KF206512 SH001328.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.05E-45 98.2 98.2

CL2_013 KF836936 Glomus sp. 8 ZHNL-2013i isolate E2_15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 104 8.94E-42 99 100 KF836936 SH001284.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.62E-44 99 100

CL2_014 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 101 1.88E-37 97 98 FJ769308SH219474.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.42E-40 99 100

CL2_015 KM376416 Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence 110 6.13E-38 94.5 100 KF939955 SH001284.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 9.63E-48 98.2 100

CL2_016 KM376416 Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence 98 7.16E-30 96.9 100 KF939989 SH001284.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.81E-35 98 100

CL2_017 KP756523 Glomus sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 1.45E-13 85.1 100 JX096596 SH019349.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.42E-40 99 100

CL2_018 KP756525 Glomus sp. 2 SL-2017 isolate TS5 clone 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 2.03E-18 85.6 98.1 JX096596 SH019349.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.05E-40 95.3 100

CL2_019 JF439170 Glomus sp. 8 SUN-2011 isolate 08_62_6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 1.12E-40 98.1 98.1 JF439098SH176083.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.02E-43 100 98.1

CL2_020 KY591440 Glomus sp. clone G-jav2-ITS1_OTU-0-413_2 internal transcribed spacer 1 and 5.8S ribosomal RNA gene, partial sequence 166 7.20E-60 94.4 97.6 HQ895792 SH017484.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.08E-69 96.4 100

CL2_021 AJ504633 Glomus sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 105 1.54E-32 94.3 100 EF393596 SH176129.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.26E-39 95.2 100

CL2_022 JF439189 Glomus sp. 7 SUN-2011 isolate 08_40_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 2.50E-36 96.1 96.3 FJ769298SH176092.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo

meraceae_sp; 3.70E-40 96.2 98.1

CL2_023 HG938304 Dominikia bernensis genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate FO310, clone 310.5 101 1.27E-39 99 100 HG938304 SH524902.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_bernensis; 2.30E-42 99 100

CL2_024 AJ504633 Glomus sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 107 3.71E-34 93.4 99.1 AJ504633 SH176129.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 6.69E-37 93.4 99.1

CL2_025 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 100 9.61E-35 95.8 96 FJ769308SH219474.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.43E-38 99 98

CL2_026 KM376416 Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence 109 1.73E-38 95.4 100 KF939972 SH001323.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.41E-50 100 100

CL2_027 AJ567737 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone v41.3 111 4.19E-40 99.1 98.2 AM384942 SH001071.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.79E-48 99.1 100

CL2_028 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 93 7.04E-36 98.9 100 KJ564159 SH176142.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.30E-38 98.9 100

CL2_029 KF836902 Glomus sp. 8 ZHNL-2013s isolate C19_51 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 96 6.49E-24 94.7 97.9 JQ218218 SH000331.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.64E-33 97.8 95.8

CL2_030 KR105642 Dominikia duoreactiva isolate 271-9 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 96 5.33E-25 92.5 96.9 EF393596 SH176129.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.43E-32 93.5 96.9

CL2_031 KY076494 Rhizophagus irregularis strain 8 RCAM00320 clone 8-48-5 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 106 1.46E-45 100 100 JX375234 SH490604.07FU

k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassified_Fungi;g__unclassified_Fungi;s__Fungi_sp; 2.63E-48 100 100

CL2_032 KP756533 Glomus sp. 1 SL-2017 isolate SR4 clone 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 5.51E-32 95.3 100 JX096603 SH017240.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.92E-37 95.2 97.2

CL2_033 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 101 1.88E-37 96 100 AJ567734 SH001103.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 3.42E-40 96 100

CL2_034 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 95 8.30E-29 93.6 98.9 FN397320 SH001356.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.92E-36 97.9 98.9
 CL2_035 AJ517460 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone Sp8 (15.9) 99 8.29E-42 100 100 AJ517456 SH197521.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.51E-44 100 100
 CL2_036 KP756523 Glomus sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 103 1.94E-18 85.4 100 JX096596 SH019349.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.22E-36 96.1 100
 CL2_037 AJ504633 Glomus sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 107 4.52E-33 93.5 100 EF393596 SH176129.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.57E-38 94.4 100
 CL2_038 KJ564158 Dominikia achra strain 146-1 clone 24 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 1.01E-33 97.8 100 AY236252 SH176101.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.53E-37 97.8 100
 CL2_039 KJ564169 Dominikia indica strain 211-1 clone 43 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 1.91E-37 97 97.1 KJ564166 SH174581.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.47E-40 97 97.1
 CL2_040 KF836929 Glomus sp. 8 ZHNL-2013g isolate E1_31 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 9.20E-42 98.1 100 JX276911 SH001284.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.90E-46 100 100
 CL2_041 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 98 1.13E-33 97.9 95.9 FJ769308 SH219474.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.87E-38 100 98
 CL2_042 KF836936 Glomus sp. 8 ZHNL-2013i isolate E2_15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 1.45E-32 96 98 JX276899 SH176070.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.60E-43 98 100
 CL2_043 GQ205050 Glomus irregulare strain DAOM 240159 clone 84F12 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 5.23E-45 99.1 100 GQ205050 SH175527.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_irregularis; 9.40E-48 99.1 100
 CL2_044 EF989116 Funneliformis mosseae clone V444 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence >gi|326486548|gb|HQ386976.1| Uncultured Glomus clone ABRII 1739-Yazd 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 2.71E-42 99.1 98.1 AM992833 SH184262.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.40E-45 99.1 99.1
 CL2_045 KM056659 Dominikia sp. JB-2014 clone Da-2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 2.98E-41 99 100 JQ218221 SH017159.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 1.27E-45 100 100
 CL2_046 KJ564169 Dominikia indica strain 211-1 clone 43 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 101 1.27E-39 98 99 KJ564166 SH174581.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 2.30E-42 98 99
 CL2_047 KF836902 Glomus sp. 8 ZHNL-2013s isolate C19_51 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 98 2.85E-22 90.6 98 JX096575 SH000326.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 2.07E-36 95.9 100
 CL2_048 KM376416 Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer
 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence 113 1.40E-33 92
 100 KF939968 SH001284.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomero
 mycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.80E-44 96.5 100
 CL2_049 AM743194 Glomus sp. G60-80 ITS1, 23S rRNA gene and ITS2, isolate G60-80 104 8.94E-23 92.8 93.3
 FJ553212SH000330.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 7.84E-36 96.2 100
 CL2_050 HG969387 Glomus invermaium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and
 28S rRNA gene, isolate Att1646, clone ECU102P20 106 1.12E-40 98.1 100 HF674807 SH175587.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 1.12E-46 99.1 100
 CL2_051 JF439179Glomus sp. 8 SUN-2011 isolate 08_48_29 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 168 6.79E-72 98.2 100 KJ484721 SH200414.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomero
 mycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 5.29E-79 99.4 100
 CL2_052 KF836928 Glomus sp. 3 ZHNL-2013b isolate E1_29 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 102 6.25E-31 94.8 95.1 FJ008644SH001278.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 2.19E-36 99 95.1
 CL2_053 JF439161Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 94 9.95E-28 94.5 96.8 FN397384 SH024970.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 2.90E-34 95.7 100
 CL2_054 KP756523 Glomus sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 102 2.84E-16 88 98 JX096620 SH019350.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomero
 mycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.51E-26 90.9 97.1
 CL2_055 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 94 3.47E-27 93.6 100 FN397320 SH001356.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 1.01E-33 96.8 100
 CL2_056 AJ504627 Glomus sp. R22.2 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA
 gene, clone R22.2 101 1.88E-37 97 100 EU359265 SH199963.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 8.04E-42 98 100
 CL2_057 KJ564158 Dominikia achra strain 146-1 clone 24 18S ribosomal RNA gene, partial sequence; internal

transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 8.28E-35 98.9 100 KJ564157 SH176144.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.53E-37 98.9 100

CL2_058 AJ567352 Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone U3.2 111 3.44E-41 99.1 95.5 GU322944 SH175570.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.45E-45 99.1 95.5

CL2_059 KF836902 Glomus sp. 8 ZHNL-2013s isolate C19_51 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 104 2.10E-24 88.2 98.1 JQ218218 SH000331.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.74E-35 95.2 100

CL2_060 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 94 1.68E-37 98.9 100 JF439161SH024970.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.10E-40 98.9 100

CL2_061 EF989114 Funneliformis mosseae clone V143 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence >gi|213053600|gb|FJ008599.1| Uncultured Glomus clone 077 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 3.97E-40 98.1 100 HG425919 SH184262.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.38E-45 100 98.1

CL2_062 KF836935 Glomus sp. 8 ZHNL-2013m isolate E2_13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 105 9.07E-42 99 100 JX096607 SH176120.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.34E-45 100 100

CL2_063 FJ769312 Glomus intraradices clone M50_22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 104 1.62E-38 97.1 100 HF674808 SH175559.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.92E-41 97.1 100

CL2_064 KY076493 Rhizophagus irregularis strain 8 RCAM00320 clone 8-48-4 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 104 2.56E-42 100 100 HG425873 SH175545.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.63E-45 100 100

CL2_065 KP756533 Glomus sp. 1 SL-2017 isolate SR4 clone 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 113 8.86E-30 90.3 100 HG425911 SH535765.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.14E-40 93.8 100

CL2_066 JF439181 Glomus sp. 8 SUN-2011 isolate 08_48_42 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 5.88E-38 98.1 96.3 FJ769298SH176092.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.14E-43 98.1 98.1

CL2_067 HG969387 Glomus invermaium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate Att1646, clone ECU102P20 110 4.71E-33 94.5 100 HE775307 SH175629.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.63E-48 99.1 100

CL2_068 KF836907 *Glomus* sp. 28 ZHNL-2013 isolate D2_19 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 103 1.07E-40 99 97.1 KF836907 SH004981.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__*Glomus*;s__*Glomus*_sp; 1.94E-43 99 97.1

CL2_069 KF836902 *Glomus* sp. 8 ZHNL-2013s isolate C19_51 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 99 1.95E-24 91.8 98 JX096575 SH000326.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.42E-43 99 100

CL2_070 KC182043 *Glomus macrocarpum* clone HSp135-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 8.27E-35 97.8 100 UDB025485 SH017240.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__*Glomus*;s__*Glomus*_macrocarpum; 1.53E-37 97.8 100

CL2_071 AJ567734 *Glomus intraradices* 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 99 5.23E-38 99 100 AJ567734 SH001103.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__*Rhizophagus*;s__*Rhizophagus*_sp; 9.54E-41 99 100

CL2_072 AJ567734 *Glomus intraradices* 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 103 2.88E-16 83.3 93.2 JX096612 SH001340.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.75E-27 88.1 98.1

CL2_073 KC182043 *Glomus macrocarpum* clone HSp135-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 3.30E-27 94.5 100 UDB025485 SH017240.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__*Glomus*;s__*Glomus*_macrocarpum; 6.10E-30 94.5 100

CL2_074 KJ564162 *Dominikia achra* strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 3.30E-27 95.6 100 KJ564159 SH176142.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.10E-30 95.6 100

CL2_075 KY965417 *Glomus* sp. clone OTU25 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 109 4.08E-21 87.9 98.2 JQ951563 SH202639.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.93E-45 98.1 96.3

CL2_076 AJ557008 *Glomus intraradices* 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 25S rRNA gene (partial), isolate D2 107 3.97E-40 98.1 96.3 HG425880 SH001003.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.86E-44 99 96.3

CL2_077 AJ504633 *Glomus* sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 100 9.61E-35 99 100 EF393596 SH176129.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.43E-38 99 100

CL2_078 FJ769310 *Glomus intraradices* clone M31/17 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 109 3.57E-47 100 100 KP954735 SH175735.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.41E-50 100 100

CL2_079 KJ564162 *Dominikia achra* strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 96 8.44E-29 92.7 100 FN397320 SH001356.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo

meraceae_sp; 3.19E-40 99 100
CL2_080 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 105 1.26E-33 96 95.2 FJ769308SH219474.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.99E-43 99 97.1
CL2_081 AJ567771 Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone PvI2.9 96 9.01E-35 100 100 AJ567771 SH001017.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.65E-37 100 100
CL2_082 AJ518854 Glomus sp. R1.1 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone R1.189 1.18E-32 97.8 100 AJ518854 SH001320.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.20E-35 97.8 100
CL2_083 AM743194 Glomus sp. G60-80 ITS1, 23S rRNA gene and ITS2, isolate G60-80 109 2.41E-30 94.2 95.4 FJ553212SH000330.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.09E-40 96.2 95.4
CL2_084 JF439120Glomus sp. 8 SUN-2011 isolate B21-11 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 105 4.70E-39 98.1 100 JF439120SH001335.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 8.48E-42 98.1 100
CL2_085 JF439189Glomus sp. 7 SUN-2011 isolate 08_40_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 109 5.66E-32 93.1 93.6 FJ769298SH176092.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.32E-39 94.5 100
CL2_086 HG938301 Dominikia bernensis genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate FO310, clone 310.1 108 2.54E-17 82.8 91.7 JX096612 SH001340.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.07E-24 85.7 97.2
CL2_087 AF197919 Glomus intraradices strain MD211 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence 105 9.07E-42 99 100 AF197919 SH001093.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.64E-44 99 100
CL2_088 AJ557009 Glomus intraradices 18S rRNA gene (partial),ITS1, 5.8S rRNA gene, ITS2 and 25S rRNA gene (partial), isolate B3 100 1.25E-39 100 100 AJ557009 SH001025.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_irregularis; 2.27E-42 100 100
CL2_089 AJ504627 Glomus sp. R22.2 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone R22.2 100 5.31E-38 97 100 GQ388461 SH001278.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.87E-43 99 100
CL2_090 JF439117Glomus sp. 13 SUN-2011 isolate B21-15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 100 6.06E-31 95.9 98 HG425981 SH529448.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.77E-41 99 98
CL2_091 KY965421 Glomus sp. clone OTU29 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 226 2.46E-41 95.8 52.7 KJ564151 SH192875.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.57E-15 90.4 32.3

CL2_092 FM992377 Rhizophagus irregularis 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), isolate Att690-23 (DAOM197198), clone pHS111-8 108 1.60E-32 92.5 98.1 JX096621 SH001070.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.36E-36 95.3 98.1

CL2_093 KF836935 Glomus sp. 8 ZHNL-2013m isolate E2_13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 109 3.35E-41 96.3 100 JX096607 SH176120.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.93E-45 97.2 100

CL2_094 JF439106 Glomus mosseae isolate B22-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 109 1.85E-44 98.2 100 HF970208 SH204223.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.32E-47 99.1 100

CL2_095 KP756533 Glomus sp. 1 SL-2017 isolate SR4 clone 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 109 4.65E-33 93.6 100 HG425911 SH535765.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.01E-44 97.2 100

CL2_096 KR105642 Dominikia duoreactiva isolate 271-9 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 110 5.75E-13 79.4 92.7 JX096612 SH001340.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.08E-25 86 97.3

CL2_097 KF836972 Rhizophagus intraradices isolate E6_53 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 112 3.48E-41 95.5 100 KF836972 SH175543.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 6.23E-44 95.5 100

CL2_098 KF836965 Glomus sp. 25 ZHNL-2013b isolate E6_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 118 2.53E-43 95.8 100 KF836965 SH001026.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.49E-46 95.8 100

CL2_099 JF439192 Glomus sp. 8 SUN-2011 isolate 08_6_11 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 165 2.48E-58 92.1 100 JX276918 SH200419.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.26E-61 92.1 100

CL2_100 JF439150 Glomus sp. 8 SUN-2011 isolate S08-13-18 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 166 3.04E-57 93.9 98.8 KF939966 SH204357.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.36E-78 98.8 100

CL2_101 KF836923 Glomus sp. 11 ZHNL-2013f isolate D6_34 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 172 1.11E-18 83.8 61 JX096602 SH192876.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.83E-28 94.4 62.2

CL2_102 KY965421 Glomus sp. clone OTU29 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 212 1.04E-26 75.9 100 KJ564157 SH176144.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.04E-19 98.2 26.9

CL2_103 KF836957 Rhizophagus intraradices isolate E4_42 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 9.45E-42 100 100 AM495184 SH001003.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.28E-47 100 100

CL2_104 KY965417 Glomus sp. clone OTU25 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 108 1.40E-20 88.7 98.1 JQ951563 SH202639.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.15E-46 99.1 100

CL2_105 GQ205050 Glomus irregulare strain DAOM 240159 clone 84F12 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 2.71E-42 97.2 100 GQ205050 SH175527.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_irregularis; 4.87E-45 97.2 100

CL2_106 KF836955 Rhizophagus intraradices isolate E4_29 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 3.30E-41 98.1 100 KF836955 SH525002.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 5.93E-44 98.1 100

CL2_107 KY965417 Glomus sp. clone OTU25 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 108 5.23E-26 89.6 98.1 JQ951563 SH202639.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.07E-43 97.1 97.2

CL2_108 KF836954 Rhizophagus intraradices isolate E4_22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 4.83E-39 95.3 100 KF836954 SH175542.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 8.70E-42 95.3 100

CL2_109 HE817875 Rhizophagus intraradices genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, strain MUCL52327, clone pSC-Ri003 107 2.19E-43 98.1 100 KJ484708 SH175542.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.95E-46 98.1 100

CL2_110 AJ504633 Glomus sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 107 3.05E-35 95.3 99.1 AJ504633 SH176129.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 5.49E-38 95.3 99.1

CL2_111 AM743194 Glomus sp. G60-80 ITS1, 23S rRNA gene and ITS2, isolate G60-80 107 3.48E-28 92.5 100 JQ218218 SH000331.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.70E-40 96.2 98.1

CL2_112 KF836929 Glomus sp. 8 ZHNL-2013g isolate E1_31 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 109 7.37E-18 90.5 77.1 JX096612 SH001340.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.91E-35 91.7 100

CL2_113 KF836972 Rhizophagus intraradices isolate E6_53 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 110 6.55E-44 98.1 98.2 KF836972 SH175543.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 1.17E-46 98.1 98.2

CL2_114 KF836965 Glomus sp. 25 ZHNL-2013b isolate E6_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 9.33E-42 98.1 97.2 KF836965 SH001026.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.68E-44 98.1 97.2
 CL2_115 AJ567352 Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone U3.2 110 1.04E-47 100 100 AJ567352 SH174867.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.86E-50 100 100
 CL2_116 AJ567737 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone v41.3 110 3.39E-41 100 96.4 KC222869 SH001003.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.17E-46 99.1 100
 CL2_117 AJ534718 Glomus claroideum 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone 1a30.2 112 8.73E-49 100 100 HG425958 SH525475.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Claroideoglomeraceae;g__unclassified_Claroideoglomeraceae;s__Claroideoglomeraceae_sp; 1.56E-51 100 100
 CL2_118 KF836966 Glomus sp. 7 ZHNL-2013c isolate E6_6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 3.97E-40 98 94.4 FJ769298SH176092.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.68E-44 98.1 99.1
 CL2_119 KF836965 Glomus sp. 25 ZHNL-2013b isolate E6_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 113 1.23E-40 95.6 100 AJ872037 SH001026.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.30E-44 95.6 100
 CL2_120 KF836965 Glomus sp. 25 ZHNL-2013b isolate E6_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 115 1.35E-46 98.3 100 KF836965 SH001026.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.40E-49 98.3 100
 CL2_121 AM743194 Glomus sp. G60-80 ITS1, 23S rRNA gene and ITS2, isolate G60-80 107 3.48E-28 92.5 100 FJ553212SH000330.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.70E-40 96.1 96.3
 CL2_122 KF836965 Glomus sp. 25 ZHNL-2013b isolate E6_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 118 2.53E-43 95.8 100 KF836965 SH001026.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.49E-46 95.8 100
 CL2_123 KY590135 Glomeraceae sp. clone G-jav2-ITS1_OTU-0-146_14 internal transcribed spacer 1 and 5.8S ribosomal RNA gene, partial sequence 138 8.42E-38 89.1 100 GQ388487 SH017793.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.12E-63 98.6 100
 CL2_124 KR105642 Dominikia duoreactiva isolate 271-9 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 139 7.96E-32 100 66.9 EF393596 SH176129.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.27E-36 100 66.9
 CL2_125 KF646116 Glomus sp. 81 AM-2013 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 151 4.26E-61 98 100 KF646116 SH470097.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 7.45E-64 98 100
 CL2_126 JF439157 Glomus sp. 8 SUN-2011 isolate 08_34_8 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 164 1.55E-73 100 100 JF439157SH200418.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.66E-76
 100 100
 CL2_127 AJ504641 Glomus sp. 1v17.2 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA
 gene, clone 1v17.2 107 1.14E-40 96.3 100 EU747860 SH191191.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomero
 mycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.24E-47 99.1 100
 CL2_128 AM980861 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene and ITS2, clone FL2z_5 107
 9.33E-42 97.2 100 AM980861 SH175546.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intr
 aradices; 1.68E-44 97.2 100
 CL2_129 KY591440 Glomus sp. clone G-jav2-ITS1_OTU-0-413_2 internal transcribed spacer 1 and 5.8S ribosomal
 RNA gene, partial sequence 169 1.16E-62 95.3 100 HQ895792 SH017484.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 7.41E-71 96.4 100
 CL2_130 JF439179 Glomus sp. 8 SUN-2011 isolate 08_48_29 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 172 2.61E-58 94 97.7 KF939973 SH200417.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 4.47E-61 94 97.7
 CL2_131 KF836929 Glomus sp. 8 ZHNL-2013g isolate E1_31 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 107 4.53E-14 87.2 72.9 JX096612 SH001340.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomero
 mycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.24E-28 88.5 97.2
 CL2_132 JF439150 Glomus sp. 8 SUN-2011 isolate S08-13-18 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 173 3.90E-75 98.8 100 JF439150 SH017478.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 6.68E-78
 98.8 100
 CL2_133 KY965418 Glomus sp. clone OTU26 small subunit ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit
 ribosomal RNA gene, partial sequence 179 9.60E-20 77.4 98.9 JX096602 SH192876.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 6.11E-28 92.5 59.8
 CL2_134 KY591440 Glomus sp. clone G-jav2-ITS1_OTU-0-413_2 internal transcribed spacer 1 and 5.8S ribosomal
 RNA gene, partial sequence 191 2.62E-08 80.2 47.6 AY236237 SH216618.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 9.77E-83 97.9 100
 CL2_135 GQ205066 Glomus irregulare strain DAOM 229457 clone 11910R 18S ribosomal RNA gene, partial
 sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence;
 and 28S ribosomal RNA gene, partial sequence 106 6.20E-44 99.1 100 AJ872040 SH001003.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 2.63E-48 100 100
 CL2_136 KF836966 Glomus sp. 7 ZHNL-2013c isolate E6_6 18S ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal
 RNA gene, partial sequence 106 5.80E-38 99 92.5 KF836966 SH176130.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.05E-40
 99 92.5
 CL2_137 KY965417 Glomus sp. clone OTU25 small subunit ribosomal RNA gene, partial sequence; internal
 transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit
 ribosomal RNA gene, partial sequence 106 1.12E-21 89.4 98.1 JQ951563 SH202639.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glo
 meraceae_sp; 3.90E-46 100 100
 CL2_138 KM376416 Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer
 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence 106 7.07E-37 96.2

100 JX096623 SH001284.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.05E-40 96.2 100

CL2_139 KM376422 Rhizophagus sp. S9 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 9.20E-42 100 100 GU322941 SH001015.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.75E-45 99.1 100

CL2_140 JF439189 Glomus sp. 7 SUN-2011 isolate 08_40_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 1.66E-38 97 95.3 FJ769298 SH176092.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.12E-46 99.1 100

CL2_141 KM376421 Rhizophagus sp. P5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 2.67E-42 99 96.3 KM376421 SH497058.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 4.81E-45 99 96.3

CL2_142 AJ567739 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone v41.7 106 2.16E-43 100 100 AM384946 SH175605.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.90E-46 100 100

CL2_143 AJ504633 Glomus sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 107 9.97E-29 93 93.5 EF393596 SH176129.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.92E-35 94 93.5

CL2_144 KJ564143 Kamienskia perpusilla strain 169-3 clone 22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 3.21E-41 99 98.1 KJ564139 SH181726.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 5.79E-44 99 98.1

CL2_145 KF836960 Glomus sp. 8 ZHNL-2013b isolate E5_12 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 2.50E-36 97.2 100 JX276911 SH001284.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.70E-42 97.2 100

CL2_146 HG969392 Glomus invermaium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate Att1646, clone ECU102P25 106 2.03E-37 96.2 100 AJ872051 SH001036.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.66E-44 100 100

CL2_147 HE817878 Rhizophagus intraradices genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, strain MUCL52327, clone pSC-Ri006 106 2.31E-30 93.9 93.4 JX276885 SH204107.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.59E-42 98 93.4

CL2_148 KP756533 Glomus sp. 1 SL-2017 isolate SR4 clone 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 2.47E-17 86.8 100 JN195709 SH200110.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.06E-24 87.7 100

CL2_149 KR105642 Dominikia duoreactiva isolate 271-9 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 1.56E-13 82.7 92.5 AY969845 SH001338.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.75E-26 88.1 95.3

CL2_150 AM743194 Glomus sp. G60-80 ITS1, 23S rRNA gene and ITS2, isolate G60-80 106 4.46E-33 94.3 100

GQ388291 SH176072.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.55E-38 97.2 100

CL2_151 AJ567352 Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone U3.2 107 3.97E-40 99.1 100 GU322944 SH175570.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.05E-43 99.1 100

CL2_152 KY965417 Glomus sp. clone OTU25 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 108 2.71E-23 87 100 JQ951563 SH202639.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.87E-45 98.1 97.2

CL2_153 KM376421 Rhizophagus sp. P5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 9.45E-42 98.1 100 KM376421 SH497058.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.70E-44 98.1 100

CL2_154 HG969387 Glomus invermaium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate Att1646, clone ECU102P20 106 1.20E-27 93.1 96.2 HE775307 SH175629.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.05E-40 98.1 100

CL2_155 KJ564143 Kamienskia perpusilla strain 169-3 clone 22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 1.40E-39 97.2 100 KJ564139 SH181726.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.52E-42 97.2 100

CL2_156 HE817878 Rhizophagus intraradices genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, strain MUCL52327, clone pSC-Ri006 105 1.03E-34 95.2 100 JX276885 SH204107.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.85E-46 99 100

CL2_157 KY965422 Glomus sp. clone OTU30 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 108 2.38E-30 92.5 98.1 KF836907 SH004981.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.27E-33 92.3 96.3

CL2_158 KP756523 Glomus sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 105 2.43E-17 88.3 98.1 JX096620 SH019350.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.75E-31 91.2 97.1

CL2_159 HE817879 Rhizophagus intraradices genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, strain MUCL52327, clone pSC-Ri007 105 8.49E-36 96.2 100 FR873158 SH175567.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.26E-39 97.1 100

CL2_160 KY965417 Glomus sp. clone OTU25 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 108 6.38E-25 90.6 98.1 JX388537 SH522230.07FU

k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassified_Fungi;g__unclassified_Fungi;s__Fungi_sp; 1.40E-45 98.1 100

CL2_161 KP756533 Glomus sp. 1 SL-2017 isolate SR4 clone 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 105 7.95E-30 96.2 100 HG425911 SH535765.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.52E-37 98.1 100

CL2_162 AJ504633 Glomus sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA

gene, clone I16.6 105 3.38E-28 92.4 100 EF393596 SH176129.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.38E-34 93.3 100

CL2_163 KF836935 Glomus sp. 8 ZHNL-2013m isolate E2_13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 1.95E-31 93.5 100 KF939972 SH001323.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.74E-40 97.2 100

CL2_164 JF439173 Glomus intraradices isolate 08_45_20 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 6.37E-44 98.1 100 FR693660 SH001008.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.40E-48 99.1 100

CL2_165 AJ567352 Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone U3.2 109 4.96E-39 98.1 96.3 GU322944 SH175570.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.01E-44 98.1 96.3

CL2_166 AJ518862 Glomus sp. 4.2.3 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.2.3 105 2.96E-35 97 95.2
GQ388586 SH199959.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.96E-43 98.1 100

CL2_167 KF836929 Glomus sp. 8 ZHNL-2013g isolate E1_31 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 105 4.70E-39 97.1 97.1 KF836929 SH176112.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 8.48E-42 97.1 97.1

CL2_168 KP756523 Glomus sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 105 5.36E-13 84.2 90.5 JX096596 SH019349.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.38E-34 92.9 94.3

CL2_169 JF439173 Glomus intraradices isolate 08_45_20 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 109 6.05E-38 96.1 93.6 FR693660 SH001008.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.91E-42 97.1 93.6

CL2_170 KP756533 Glomus sp. 1 SL-2017 isolate SR4 clone 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 109 1.25E-27 89.9 100 JN195709 SH200110.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.82E-30 89 100

CL2_171 AJ504633 Glomus sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 105 1.75E-25 90.5 100 EF393596 SH176129.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.75E-31 91.4 100

CL2_172 JF439118 Glomus intraradices isolate B21-18 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 104 1.73E-44 100 100 JF439118 SH175575.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 3.12E-47 100 100

CL2_173 AJ518862 Glomus sp. 4.2.3 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.2.3 104 1.97E-37 96.1 99 AJ518862 SH199957.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.56E-40

96.1 99

- CL2_174 KF836951 Glomus sp. 11 ZHNL-2013r isolate E4_13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 104 6.87E-37 96.2 100 KF836920 SH527348.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.24E-39 96.2 100
- CL2_175 KM376416 Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence 104 5.64E-38 98.1 100 JX096623 SH001284.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.12E-47 100 100
- CL2_176 KY590148 Glomus sp. clone G-ela1-ITS1_OTU-0-056_44 internal transcribed spacer 1 and 5.8S ribosomal RNA gene, partial sequence 111 1.90E-25 100 65.8 JN581945 SH027190.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.29E-49 99.1 100
- CL2_177 KF836965 Glomus sp. 25 ZHNL-2013b isolate E6_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 111 2.17E-37 95.3 96.4 KF836965 SH001026.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.88E-40 95.3 96.4
- CL2_178 KY965417 Glomus sp. clone OTU25 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 111 9.85E-23 88.1 98.2 JQ951563 SH202639.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.15E-44 97.2 96.4
- CL2_179 HG969387 Glomus invermaium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate Att1646, clone ECU102P20 111 4.78E-33 92.8 100 HE775307 SH175629.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.15E-43 96.4 100
- CL2_180 AJ518862 Glomus sp. 4.2.3 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.2.3104 2.92E-35 97 96.2 AM076596 SH176069.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.33E-45 99 100
- CL2_181 KJ484716 Uncultured Glomeromycota clone Y_10 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 104 2.60E-24 89.9 95.2 JX363251 SH522230.07FU
k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassified_Fungi;g__unclassified_Fungi;s__Fungi_sp; 3.56E-40 97 95.2
- CL2_182 EF989111 Rhizophagus intraradices clone V164 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 113 4.02E-34 93.4 93.8 FJ008650 SH174866.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.69E-38 92.9 100
- CL2_183 KF836940 Glomus sp. 6 ZHNL-2013d isolate E2_44 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 104 1.73E-44 100 100 KF836940 SH004948.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.12E-47 100 100
- CL2_184 AJ567737 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone v41.3 114 4.35E-40 98.2 95.6 HE775296 SH001003.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.29E-46 98.2 97.4
- CL2_185 AJ567738 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone v48c4 114 1.25E-40 95.6 100 AM495148 SH001003.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.23E-45 96.5 100
 CL2_186 KF836965 Glomus sp. 25 ZHNL-2013b isolate E6_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 114 1.97E-44 96.5 100 KF836965 SH001026.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.52E-47 96.5 100
 CL2_187 AJ567352 Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone U3.2 104 2.92E-35 99 96.2 GU322944 SH175570.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.51E-38 99 96.2
 CL2_188 KP756523 Glomus sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 104 5.29E-13 84.2 91.3 JX096596 SH019349.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.95E-32 92.9 94.2
 CL2_189 HG938301 Dominikia bernensis genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate FO310, clone 310.1 104 5.64E-19 85.4 92.3 JX096612 SH001340.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.73E-31 93.3 100
 CL2_190 KY590133 Glomeraceae sp. clone G-cla3-ITS1_OTU-0-139_4 internal transcribed spacer 1 and 5.8S ribosomal RNA gene, partial sequence 127 5.41E-27 89.3 96.1 GQ388487 SH017793.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.73E-30 90.6 100
 CL2_191 KY590133 Glomeraceae sp. clone G-cla3-ITS1_OTU-0-139_4 internal transcribed spacer 1 and 5.8S ribosomal RNA gene, partial sequence 137 6.00E-46 93.3 97.8 GQ388487 SH017793.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.46E-50 94.9 100
 CL2_192 AJ504633 Glomus sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 103 1.59E-38 98 99 AJ504633 SH176129.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.88E-41 98 99
 CL2_193 KF836929 Glomus sp. 8 ZHNL-2013g isolate E1_31 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 103 1.31E-39 99 98.1 KF836929 SH176112.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.37E-42 99 98.1
 CL2_194 KF646116 Glomus sp. 81 AM-2013 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 145 2.39E-32 90.4 93.1 KF646116 SH470097.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.19E-35 90.4 93.1
 CL2_195 AJ504627 Glomus sp. R22.2 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone R22.2 103 6.34E-31 92.2 100 GQ388564 SH176087.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.82E-37 95.1 100
 CL2_196 KM056661 Dominikia sp. JB-2014 clone Da-22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 161 1.25E-17 100 36.6 KC965597 SH017159.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.14E-21 100 37.3
 CL2_197 KY591440 Glomus sp. clone G-jav2-ITS1_OTU-0-413_2 internal transcribed spacer 1 and 5.8S ribosomal RNA gene, partial sequence 164 4.44E-55 93.8 97.6 HQ895792 SH017484.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.34E-64 95.7 100

CL2_198 JF439184 *Glomus intraradices* isolate 08_62_38 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 103 2.21E-30 94.9 95.1 JX096621 SH001070.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.35E-37 98 95.1

CL2_199 KF836914 *Rhizophagus intraradices* isolate D3_28 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 103 1.49E-32 93.2 100 AM114024 SH175544.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.57E-44 99 100

CL2_200 KP756523 *Glomus* sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 103 5.21E-13 81.6 100 JX096596 SH019349.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.31E-26 88.1 98.1

CL2_201 KP867533 Uncultured fungus clone 136890 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence 166 2.67E-45 91.6 100 JX096602 SH192876.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.08E-49 91 100

CL2_202 KJ564169 *Dominikia indica* strain 211-1 clone 43 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 103 6.77E-37 97 97.1 KJ564166 SH174581.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.23E-39 97 97.1

CL2_203 KJ564156 *Dominikia iranica* strain 187-2-2 clone 23 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 169 1.41E-23 82.8 100 JX096602 SH192876.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.95E-46 90.3 97.6

CL2_204 KF836969 *Glomus* sp. 11 ZHNL-2013j isolate E6_35 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 170 2.58E-20 100 35.3 JX096580 SH017482.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.04E-24 92.8 48.8

CL2_205 JF439183 *Glomus* sp. 5 SUN-2011 isolate 08_62_26 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 4.50E-39 98 97.1 EF619695 SH175543.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.34E-42 98 98

CL2_206 AJ518862 *Glomus* sp. 4.2.3 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.2.3102 3.03E-41 100 100 FR693662 SH017154.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.70E-46 100 100

CL2_207 AJ504627 *Glomus* sp. R22.2 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone R22.2 102 4.21E-33 93.1 100 FJ769332 SH176133.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.70E-46 100 100

CL2_208 KF836923 *Glomus* sp. 11 ZHNL-2013f isolate D6_34 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 175 8.18E-27 80.2 98.3 JX096618 SH012309.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 7.73E-52 93.4 95.4

CL2_209 AJ517452 *Glomus intraradices* 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene

(partial), clone Sp3 (11.2) 102 2.04E-43 100 100 AJ517451 SH197525.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_Rhizophagus;s_Rhizophagus_sp;
3.70E-46 100 100

CL2_210 KF646116 Glomus sp. 81 AM-2013 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 183 1.78E-16 94 36.6 AY236237 SH216618.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_unclassified_Glomeraceae;s_Glomeraceae_sp; 1.48E-29 86.4 96.2

CL2_211 KJ564156 Dominikia iranica strain 187-2-2 clone 23 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 184 3.47E-19 78 96.2 JX096602 SH192876.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_unclassified_Glomeraceae;s_Glomeraceae_sp; 6.32E-28 88.9 63.6

CL2_212 KF836924 Glomus sp. 11 ZHNL-2013p isolate E1_3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 1.91E-37 97 97.1 KF836922 SH527348.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_Glomus;s_Glomus_sp; 3.47E-40 97 97.1

CL2_213 KY591439 Glomus sp. clone G-cla3-ITS1_OTU-0-053_27 internal transcribed spacer 1 and 5.8S ribosomal RNA gene, partial sequence 195 1.48E-11 82.1 48.7 AY236237 SH216618.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_unclassified_Glomeraceae;s_Glomeraceae_sp; 1.30E-87 97.4 100

CL2_214 NO HIT AY236237 SH216618.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_unclassified_Glomeraceae;s_Glomeraceae_sp; 1.59E-23 97.1 34

CL2_215 KY965421 Glomus sp. clone OTU29 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 211 4.99E-37 79.1 100 FJ362330SH017476.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_unclassified_Glomeraceae;s_Glomeraceae_sp; 5.33E-17 91.4 33.2

CL2_216 KF836924 Glomus sp. 11 ZHNL-2013p isolate E1_3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 1.57E-38 97 99 KF836922 SH527348.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_Glomus;s_Glomus_sp; 2.85E-41 97 99

CL2_217 KY965421 Glomus sp. clone OTU29 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 214 2.81E-21 74.3 100 AJ567795 SH017795.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_unclassified_Glomeraceae;s_Glomeraceae_sp; 2.31E-15 88.8 37.4

CL2_218 KF836924 Glomus sp. 11 ZHNL-2013p isolate E1_3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 1.57E-38 97 99 KF836922 SH527348.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_Glomus;s_Glomus_sp; 2.85E-41 97 99

CL2_219 GQ205056 Glomus irregulare strain DAOM 240159 clone 84F13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 1.79E-31 93.9 97.1 AM076618 SH175544.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_unclassified_Glomeraceae;s_Glomeraceae_sp; 1.21E-39 98 97.1

CL2_220 KF836952 Glomus sp. 7 ZHNL-2013d isolate E4_15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 2.33E-36 95.1 100 KF836952 SH487564.07FU
k_Fungi;p_Glomeromycota;c_Glomeromycetes;o_Glomerales;f_Glomeraceae;g_Glomus;s_Glomus_sp; 4.22E-39 95.1 100

CL2_221 KJ564169 *Dominikia indica* strain 211-1 clone 43 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 5.48E-38 97.1 100 KJ564166 SH174581.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.93E-41 97.1 100

CL2_222 KF836935 *Glomus* sp. 8 ZHNL-2013m isolate E2_13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 2.33E-36 99 98 JX096607 SH176120.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.93E-41 100 98

CL2_223 HG938304 *Dominikia bernensis* genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate FO310, clone 310.5 101 5.39E-38 98 100 HG938304 SH524902.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_bernensis; 9.80E-41 98 100

CL2_224 KF836970 *Glomus* sp. 11 ZHNL-2013o isolate E6_49 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 102 2.04E-43 100 100 KF836970 SH017159.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.70E-46 100 100

CL2_225 KF836941 *Glomus* sp. 11 ZHNL-2013m isolate E2_57 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 8.55E-42 100 98 KF836941 SH524990.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.55E-44 100 98

CL2_226 KF836968 *Glomus* sp. 11 ZHNL-2013l isolate E6_9 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 3.63E-40 98 100 KM056663 SH521585.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_aurea; 6.60E-43 98 100

CL2_227 AJ504627 *Glomus* sp. R22.2 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone R22.2 101 2.15E-30 94.1 100 FJ769319SH219472.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.77E-37 97 100

CL2_228 AJ518862 *Glomus* sp. 4.2.3 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.2.3101 1.45E-32 97 99 FR693652 SH199964.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.16E-36 96 99

CL2_229 KX485375 *Glomus macrocarpum* strain SAC-2 clone 3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 103 1.31E-39 97.1 100 JX096609 SH017249.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.57E-45 99 100

CL2_230 KJ564169 *Dominikia indica* strain 211-1 clone 43 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 1.88E-37 99 96 KJ564166 SH174581.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.42E-40 99 96

CL2_231 HG938301 *Dominikia bernensis* genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate FO310, clone 310.1 101 7.02E-43 100 100 HG938301 SH000327.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_bernensis; 1.27E-45 100 100

CL2_232 KP756523 *Glomus* sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 2.80E-16 86.1 100 JX096596 SH019349.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 7.06E-30 93.5 92.1
 CL2_233 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 103 2.36E-36 96.1 100 FJ769308SH219474.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.23E-39 98 98.1
 CL2_234 AJ504633 Glomus sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 103 1.22E-33 96.1 100 EF393596 SH176129.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.01E-40 97.1 100
 CL2_235 KF836902 Glomus sp. 8 ZHNL-2013s isolate C19_51 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 9.13E-29 91.9 98 JQ218218 SH000331.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.53E-36 97 98
 CL2_236 KF836902 Glomus sp. 8 ZHNL-2013s isolate C19_51 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 1.04E-21 88.9 98 JX096575 SH000326.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.12E-33 94.1 100
 CL2_237 JF439191 Glomus sp. 11 SUN-2011 isolate 08_6_3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 3.63E-40 99 100 JF439191SH200029.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 6.60E-43 99 100
 CL2_238 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 101 1.76E-31 95.6 89.1 FJ769308SH219474.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.20E-34 98.9 89.1
 CL2_239 KF836951 Glomus sp. 11 ZHNL-2013r isolate E4_13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 4.15E-33 93.9 97 KC965597 SH017159.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.18E-37 94.9 97
 CL2_240 KF836906 Glomus sp. 27 ZHNL-2013a isolate D1_45 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 8.01E-36 98 100 KF836903 SH197524.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.45E-38 98 100
 CL2_241 KY076494 Rhizophagus irregularis strain 8 RCAM00320 clone 8-48-5 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 104 1.09E-40 99 96.2 JX375234 SH490604.07FU
 k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassified_Fungi;g__unclassified_Fungi;s__Fungi_sp; 1.97E-43 99 96.2
 CL2_242 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 101 6.15E-31 95.9 96 FJ769308SH219474.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.81E-41 99 98
 CL2_243 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 101 1.19E-33 93.9 98 FJ769308SH219474.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.77E-37 97 100
 CL2_244 GQ205050 Glomus irregulare strain DAOM 240159 clone 84F12 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S

ribosomal RNA gene, partial sequence 101 6.57E-37 96.9 97 GQ205050 SH175527.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_irregularis; 1.19E-39 96.9 97

CL2_245 KF836966 Glomus sp. 7 ZHNL-2013c isolate E6_6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 7.50E-30 93 99 EF989100 SH176098.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.90E-33 92.9 97

CL2_246 KM056659 Dominikia sp. JB-2014 clone Da-2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 101 6.57E-37 96.9 97 KM056659 SH521585.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_aurea; 1.19E-39 96.9 97

CL2_247 KF836966 Glomus sp. 7 ZHNL-2013c isolate E6_6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 100 9.61E-35 98 100 KF836966 SH176130.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.75E-37 98 100

CL2_248 KJ564169 Dominikia indica strain 211-1 clone 43 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 100 4.36E-39 99 100 KJ564166 SH174581.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.94E-42 99 100

CL2_249 JF439117 Glomus sp. 13 SUN-2011 isolate B21-15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 100 4.98E-32 95.9 98 FR693658 SH001280.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.39E-45 100 100

CL2_250 AJ567352 Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone U3.2 105 2.96E-35 98 97.1 GU322944 SH175570.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.53E-38 98 97.1

CL2_251 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 100 2.75E-35 97.9 97 AJ567734 SH001103.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 5.01E-38 97.9 97

CL2_252 AJ517452 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone Sp3 (11.2) 100 1.52E-38 100 100 AJ517451 SH197525.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 2.77E-41 100 100

CL2_253 KJ564150 Dominikia disticha strain 237-1 clone 18 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 100 2.75E-16 84.8 99 KM208142 SH524085.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.03E-27 91 100

CL2_254 KP756523 Glomus sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 105 2.43E-17 85.7 100 JX096596 SH019349.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.11E-33 91.4 100

CL2_255 JF439183 Glomus sp. 5 SUN-2011 isolate 08_62_26 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 105 3.85E-40 100 100 HG425884 SH175545.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.96E-43 100 100

CL2_256 AJ567734 *Glomus intraradices* 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 100 1.74E-31 96.6 88 AJ567734 SH001103.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 3.16E-34 96.6 88

CL2_257 KJ564169 *Dominikia indica* strain 211-1 clone 43 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 100 2.75E-35 98 99 KJ564166 SH174581.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.01E-38 98 99

CL2_258 JF439196 *Glomus intraradices* isolate N22_2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 100 9.00E-29 93 100 JF439196SH175775.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 1.64E-31 93 100

CL2_259 AJ504627 *Glomus* sp. R22.2 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone R22.2 100 2.75E-35 95 100 GQ388310 SH176141.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.27E-42 98 100

CL2_260 KP756523 *Glomus* sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 100 7.89E-17 84.7 98 JX096596 SH019349.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.43E-29 91.8 97

CL2_261 AJ567352 *Glomus intraradices* 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone U3.2 106 8.61E-36 99 95.3 GU322944 SH175570.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.45E-39 99 95.3

CL2_262 AJ504633 *Glomus* sp. I16.6 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone I16.6 100 1.34E-26 94.9 98 AJ504633 SH176129.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.43E-29 94.9 98

CL2_263 KF836929 *Glomus* sp. 8 ZHNL-2013g isolate E1_31 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 2.03E-37 95.3 100 JX276911 SH001284.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.05E-40 96.2 100

CL2_264 JF439189 *Glomus* sp. 7 SUN-2011 isolate 08_40_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 1.56E-32 94.3 100 JF439162SH176130.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.81E-35 94.3 100

CL2_265 KY076493 *Rhizophagus irregularis* strain 8 RCAM00320 clone 8-48-4 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 106 9.20E-42 98.1 100 HG425873 SH175545.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.66E-44 98.1 100

CL2_266 AJ567734 *Glomus intraradices* 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 99 3.30E-34 95.8 96 FJ769308SH219474.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.94E-38 99 98

CL2_267 KF836900 *Glomus* sp. 8 ZHNL-2013h isolate C13_30 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 99 8.86E-29 97.9 98 KF939989 SH001284.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.05E-40 96.2 100

mycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.09E-33 97.9 97
 CL2_268 KF836914 Rhizophagus intraradices isolate D3_28 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 99 2.54E-29 94.9 100 AM076615 SH175544.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.54E-41 99 100
 CL2_269 KJ564169 Dominikia indica strain 211-1 clone 43 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 99 1.15E-33 97 100 KJ564166 SH174581.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.10E-36 97 100
 CL2_270 KF836961 Glomus sp. 6 ZHNL-2013c isolate E5_13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 99 1.50E-38 99 100 KF836961 SH489933.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.73E-41 99 100
 CL2_271 FJ769312 Glomus intraradices clone M50_22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 106 8.61E-36 96.2 100 HF674808 SH175559.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.55E-38 96.2 100
 CL2_272 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 99 2.71E-35 97.9 98 AJ567734 SH001103.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 4.94E-38 97.9 98
 CL2_273 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 99 1.71E-31 93.7 96 FJ769308 SH219474.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.56E-35 96.9 98
 CL2_274 KF836902 Glomus sp. 8 ZHNL-2013s isolate C19_51 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 99 1.95E-24 91.8 98 JX096575 SH000326.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.42E-38 98 100
 CL2_275 KF836906 Glomus sp. 27 ZHNL-2013a isolate D1_45 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 99 3.09E-28 94.9 100 KF939971 SH015411.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.72E-37 99 100
 CL2_276 KF836900 Glomus sp. 8 ZHNL-2013h isolate C13_30 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 99 1.08E-27 95.9 98 KF939972 SH001323.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.33E-32 97.9 97
 CL2_277 AJ504627 Glomus sp. R22.2 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone R22.2 99 1.31E-26 92.8 98 FJ769308 SH219474.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.33E-32 93.8 98
 CL2_278 AJ517452 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone Sp3 (11.2) 99 9.45E-35 98 100 AJ517451 SH197525.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.72E-37 98 100
 CL2_279 KM376416 Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence 99 1.31E-26 94.9 100 KF939972 SH001323.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.63E-32 99 100
 CL2_280 KF836928 Glomus sp. 3 ZHNL-2013b isolate E1_29 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 99 2.71E-35 97.9 98 KF836928 SH017159.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.94E-38 97.9 98
 CL2_281 JF439189 Glomus sp. 7 SUN-2011 isolate 08_40_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 107 2.50E-36 96.9 90.7 FJ769298SH176092.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.14E-43 99 92.5
 CL2_282 KY965414 Glomeromycotina sp. clone OTU22 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 98 3.25E-15 86.7 100 JX096596 SH019349.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 7.23E-36 95.8 96.9
 CL2_283 KF836907 Glomus sp. 28 ZHNL-2013 isolate D2_19 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 98 7.16E-30 96.9 98 KF836907 SH004981.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.31E-32 96.9 98
 CL2_284 KM376416 Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence 107 1.06E-34 95.2 97.2 KF939972 SH001323.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.70E-42 99 97.2
 CL2_285 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 98 2.67E-35 98.9 95.9 AJ567734 SH001103.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 4.87E-38 98.9 95.9
 CL2_286 HG969387 Glomus invermaium genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate Att1646, clone ECU102P20 107 1.06E-34 95.1 96.3 HF674807 SH175587.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.50E-39 96.3 100
 CL2_287 AJ567772 Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone PvI2.10 98 1.38E-32 98 100 KJ209706 SH001017.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.93E-37 98 100
 CL2_288 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 98 1.38E-32 96.8 95.9 FN397384 SH024970.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.69E-41 99 100
 CL2_289 AJ518864 Glomus sp. 4.4 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.4 98 1.58E-25 93.5 93.9 FJ769308 SH219474.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.94E-30 92.7 98
 CL2_290 MF966034 Fungal sp. clone ITS1_OTU_2206 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence 98 9.95E-22 89.4 95.9 KM208142 SH524085.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.07E-34 95.8 96.9
 CL2_291 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene

(partial), clone a43c6 98 1.68E-31 95.7 95.9 FJ769308SH219474.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.23E-36 99 98

CL2_292 KJ564169 Dominikia indica strain 211-1 clone 43 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 98 1.38E-32 97.9 95.9 KJ564166 SH174581.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.52E-35 97.9 95.9

CL2_293 AJ518843 Glomus sp. 4.1 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.1 98 4.82E-32 93.9 100 FJ769296 SH199961.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.28E-40 98 100

CL2_294 AJ504627 Glomus sp. R22.2 partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and partial 28S rRNA gene, clone R22.2 98 4.82E-32 95.9 100 GQ388573 SH176087.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.21E-42 99 100

CL2_295 KF836936 Glomus sp. 8 ZHNL-2013i isolate E2_15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 98 3.25E-34 97.9 98 HG425981 SH529448.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.87E-38 97.9 98

CL2_296 AJ517453 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone Sp3 (11.3) 98 1.48E-38 98 100 AJ517450 SH197521.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.15E-39 98.9 94.9

CL2_297 KF836902 Glomus sp. 8 ZHNL-2013s isolate C19_51 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 98 3.47E-21 90.4 95.9 JX096575 SH000326.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.52E-35 95.8 98

CL2_298 AJ567772 Glomus intraradices 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone Pv12.10 98 1.38E-32 98 100 KJ209706 SH001017.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.93E-37 98 100

CL2_299 KX485374 Glomus macrocarpum strain SAC-2 clone 1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 98 1.21E-20 90.8 100 HE775305 SH000346.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.07E-34 99 98

CL2_300 HG938301 Dominikia bernensis genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate FO310, clone 310.1 98 1.21E-20 88.2 94.9 JX321802 SH489719.07FU
k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassified_Fungi;g__unclassified_Fungi;s__Fungi_sp; 1.70E-37 97.9 96.9

CL2_301 KP756533 Glomus sp. 1 SL-2017 isolate SR4 clone 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 108 2.54E-36 94.4 100 JX096615 SH017245.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.87E-45 97.2 100

CL2_302 AJ518843 Glomus sp. 4.1 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.1 97 1.12E-33 95.8 99 FJ769296 SH199961.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.66E-41 99 99

CL2_303 AJ518843 Glomus sp. 4.1 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal

transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.1 97 6.17E-37 97.9 100 FJ769296 SH199961.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.61E-42 99 100

CL2_304 AJ517453 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone Sp3 (11.3) 97 3.00E-09 82.5 100 AJ517456 SH197521.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.91E-11 82.5 100

CL2_305 AJ567734 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone a43c6 97 1.12E-33 98.9 97.9 AJ567734 SH001103.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 2.04E-36 98.9 97.9

CL2_306 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 97 1.27E-26 90.6 99 FN397320 SH001356.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.04E-36 96.9 99

CL2_307 KF836933 Glomus sp. 27 ZHNL-2013c isolate E2_10 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 97 5.78E-31 95.9 100 KF939958 SH197522.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.04E-36 100 100

CL2_308 KM056665 Dominikia sp. JB-2014 clone Da-33 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 97 5.42E-25 90.6 99 GQ388414 SH199955.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.13E-29 92.6 97.9

CL2_309 KF836907 Glomus sp. 28 ZHNL-2013 isolate D2_19 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 97 7.04E-30 95.8 97.9 KF836907 SH004981.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.29E-32 95.8 97.9

CL2_310 AJ518843 Glomus sp. 4.1 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.1 97 1.36E-32 94.8 100 FJ769296 SH199961.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.80E-38 95.9 100

CL2_311 AJ518843 Glomus sp. 4.1 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.1 96 1.10E-33 96.8 97.9 FJ769296 SH199961.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.50E-42 100 97.9

CL2_312 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 96 9.01E-35 97.8 96.9 FN397384 SH024970.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.50E-42 100 97.9

CL2_313 KP756523 Glomus sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 96 3.84E-14 87.5 100 JX096596 SH019349.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.04E-33 95.7 97.9

CL2_314 AJ517460 Glomus intraradices 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone Sp8 (15.9) 96 8.44E-29 94.8 100 AJ517456 SH197521.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp;

1.55E-31 94.8 100

CL2_315 KX758125 *Kamienskia divaricata* strain 240-8 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 109 1.33E-14 84 97.2 KJ484704 SH497462.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.36E-17 82.7 95.4

CL2_316 KF836914 *Rhizophagus intraradices* isolate D3_28 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 96 2.58E-35 98.9 97.9 KF836914 SH001017.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 4.73E-38 98.9 97.9

CL2_317 FR750200 *Rhizophagus irregularis* 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), isolate from Poland (trap culture), clone pMK108-9 109 2.25E-43 98.1 98.2 FR750194 SH175543.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_irregularis; 4.05E-46 98.1 98.2

CL2_318 AJ518843 *Glomus* sp. 4.1 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.1 96 1.99E-30 94.6 96.9 FJ769296 SH199961.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.36E-38 97.8 96.9

CL2_319 MF966034 Fungal sp. clone ITS1_OTU_2206 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, complete sequence; and 5.8S ribosomal RNA gene, partial sequence 96 1.43E-19 89.1 95.8 KM208142 SH524085.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.30E-29 93.5 96.9

CL2_320 AM743194 *Glomus* sp. G60-80 ITS1, 23S rRNA gene and ITS2, isolate G60-80 109 1.98E-31 93.6 100 KF206512 SH001328.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.63E-38 97.1 96.3

CL2_321 KR105642 *Dominikia duoreactiva* isolate 271-9 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 96 4.37E-26 92.5 96.9 EF393596 SH176129.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.43E-32 93.5 96.9

CL2_322 AJ517460 *Glomus intraradices* 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), clone Sp8 (15.9) 96 2.95E-09 83.9 96.9 AJ517456 SH197521.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 5.41E-12 83.9 96.9

CL2_323 JF439183 *Glomus* sp. 5 SUN-2011 isolate 08_62_26 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 110 6.55E-44 98.2 100 HG425884 SH175545.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.17E-46 98.2 100

CL2_324 AJ518843 *Glomus* sp. 4.1 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone 4.1 95 1.60E-31 96.8 97.9 FJ769296 SH199961.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.98E-36 97.8 97.9

CL2_325 JF439111 *Glomus* sp. 9 SUN-2011 isolate B22-17 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 95 1.71E-18 91.1 94.7 KJ484647 SH521403.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.15E-21 85.3 100

CL2_326 KR105639 *Dominikia duoreactiva* isolate 271-12 18S ribosomal RNA gene, partial sequence; internal

transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 95 4.59E-32 97.7 92.6 KR105639 SH001312.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_duoreactiva; 8.43E-35 97.7 92.6

CL2_327 KR105642 Dominikia duoreactiva isolate 271-9 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 95 1.50E-25 92.4 96.8 EF393596 SH176129.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.25E-32 93.5 96.8

CL2_328 KR105639 Dominikia duoreactiva isolate 271-12 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 94 2.50E-35 97.9 100 KR105639 SH001312.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_duoreactiva; 4.60E-38 97.9 100

CL2_329 KM376416 Glomeraceae sp. BBM S3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence 111 1.12E-34 92.8 100 KF939972 SH001323.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.76E-44 97.3 100

CL2_330 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 94 8.17E-29 93.6 100 FN397320 SH001356.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.32E-38 98.9 100

CL2_331 KY965422 Glomus sp. clone OTU30 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence 111 2.03E-31 91.5 95.5 KF836907 SH004981.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 6.57E-31 90.6 95.5

CL2_332 KP756523 Glomus sp. 2 SL-2017 isolate SR6 clone 5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 111 1.67E-13 82.9 100 JX096620 SH019350.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.00E-49 100 100

CL2_333 AJ517204 Glomus sp. 'Bad Sachsa'; 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 and ITS2, clone Sp6(7.4) 112 2.20E-37 97.1 92.9 AY236296 SH212911.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.24E-42 96.4 98.2

CL2_334 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 94 3.47E-27 93.4 96.8 FN397320 SH001356.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.10E-40 100 96.8

CL2_335 KR105642 Dominikia duoreactiva isolate 271-9 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 94 2.67E-22 92.2 95.7 EF393596 SH176129.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.23E-29 93.3 95.7

CL2_336 NR_121445 Glomus macrocarpum E W5581 ITS region; from TYPE material 93 4.44E-32 95.7 100 FR750526 SH200108.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_macrocarpum; 8.19E-35 95.7 100

CL2_337 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 93 9.78E-28 94.5 97.8 KJ484659 SH521403.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.30E-38 98.9 100
 CL2_338 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 93 4.44E-32 97.8 100 KF939960 SH024973.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.30E-38 98.9 97.8
 CL2_339 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 93 2.30E-29 93.5 100 FN397320 SH001356.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.72E-36 98.9 100
 CL2_340 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 93 8.57E-35 97.8 100 KJ564159 SH176142.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.58E-37 97.8 100
 CL2_341 JF439111 Glomus sp. 9 SUN-2011 isolate B22-17 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 93 2.46E-16 90.9 94.6 KJ484647 SH521403.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.07E-20 86 100
 CL2_342 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 92 6.48E-30 95.7 100 JF439161 SH024970.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.20E-32 95.7 100
 CL2_343 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 92 1.25E-32 97.8 100 KJ484647 SH521403.07FU
 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.62E-36 97.8 100
 CL2_344 KJ564158 Dominikia achra strain 146-1 clone 24 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 92 1.52E-31 98.8 92.4 KJ564157 SH176144.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.81E-34 98.8 92.4
 CL2_345 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 92 2.75E-28 94.4 96.7 FN397320 SH001356.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.82E-34 98.9 96.7
 CL2_346 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 92 4.36E-32 97.8 100 KJ564159 SH176142.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.06E-35 97.8 100
 CL2_347 KY590133 Glomeraceae sp. clone G-cla3-ITS1_OTU-0-139_4 internal transcribed spacer 1 and 5.8S ribosomal RNA gene, partial sequence 138 8.99E-44 92.6 97.8 GQ388487 SH017793.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.50E-47 93.5 100
 CL2_348 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 7.26E-23 92.3 100 KJ564159 SH176142.07FU
 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp;

meraceae_sp; 1.34E-25 92.3 100

CL2_349 KP756534 Glomus sp. 1 SL-2017 isolate SR4 clone 3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 143 5.95E-40 93.7 100 EU350772 SH200111.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.98E-26 81.8 100

CL2_350 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 5.22E-31 97.8 97.8 KJ484659 SH521403.07FU

k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.77E-34 96.7 100

CL2_351 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 5.22E-31 98.9 97.8 FN397384 SH024970.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.94E-35 100 97.8

CL2_352 KF836978 Glomus sp. 8 ZHNL-2013a isolate E14_27 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 155 6.13E-72 100 100 KF836930 SH200435.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.07E-74 100 100

CL2_353 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 7.75E-29 94.5 100 KJ564159 SH176142.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.44E-31 94.5 100

CL2_354 KF836923 Glomus sp. 11 ZHNL-2013f isolate D6_34 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 162 4.99E-67 97.5 100 FJ362330 SH017476.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.46E-70 98.1 98.8

CL2_355 AJ699063 Glomus mycorrhizal symbiont of Marchantia foliacea 18S rRNA gene (partial) and ITS1 (partial), Otira valley, clone 2 163 2.98E-19 80.6 88.3 AJ699063 SH466345.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.12E-22 80.6 88.3

CL2_356 JF439111 Glomus sp. 9 SUN-2011 isolate B22-17 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 1.60E-18 92 95.6 JF439111 SH024974.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.96E-21 92 95.6

CL2_357 AF480159 Glomus sp. 5018 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA, complete sequence; and internal transcribed spacer 2, partial sequence 91 2.89E-15 84.7 93.4 HF674801 SH000348.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.39E-38 100 100

CL2_358 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 4.89E-25 92.1 97.8 AY236252 SH176101.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.13E-29 93.3 97.8

CL2_359 KF836969 Glomus sp. 11 ZHNL-2013j isolate E6_35 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 91 6.79E-36 98.9 100 KF836969 SH521585.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.26E-38 98.9 100

CL2_360 HG938301 Dominikia bernensis genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and

28S rRNA gene, isolate FO310, clone 310.1 90 2.84E-15 88 83.3 JQ218218 SH000331.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.32E-29 98.7 87.8

CL2_361 KJ564158 Dominikia achra strain 146-1 clone 24 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 90 2.84E-34 98.9 97.8 KJ564157 SH176144.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.27E-37 98.9 97.8

CL2_362 JF439161 Glomus sp. 9 SUN-2011 isolate 08_48_1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 90 2.04E-23 94.3 97.8 KJ484647 SH521403.07FU
k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.84E-36 100 97.8

CL2_363 KJ564162 Dominikia achra strain 146-1 clone 83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 90 4.21E-32 97.7 97.8 KJ564159 SH176142.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.81E-35 97.7 97.8

CL2_364 KJ564156 Dominikia iranica strain 187-2-2 clone 23 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 171 1.53E-29 86 100 JX096602 SH192876.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.12E-68 96.5 100

CL2_365 KJ564158 Dominikia achra strain 146-1 clone 24 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 89 3.39E-33 98.9 100 KJ564157 SH176144.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.31E-36 98.9 100

CL2_366 KR105639 Dominikia duoreactiva isolate 271-12 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 89 1.27E-19 91 100 KR105639 SH001312.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_duoreactiva; 2.35E-22 91 100

CL2_367 FR750544 Glomus macrocarpum 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene (partial), specimen voucher W5293, clone pHS094-6 89 1.76E-30 97.8 100 FR750544 SH200108.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_macrocarpum; 3.27E-33 97.8 100

CL2_368 KC182043 Glomus macrocarpum clone HSp135-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 88 6.02E-30 98.9 100 KC182043 SH200108.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_macrocarpum; 1.12E-32 98.9 100

CL2_369 KJ564158 Dominikia achra strain 146-1 clone 24 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 88 1.73E-30 98.9 100 KJ564157 SH176144.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.22E-33 98.9 100

CL2_370 KC182043 Glomus macrocarpum clone HSp135-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 88 3.80E-26 95.5 100 UDB025485 SH017240.07FU
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_macrocarpum; 7.09E-29 95.5 100

CL2_371 AJ518854 Glomus sp. R1.1 18S rRNA gene (partial), 5.8S rRNA gene, 28S rRNA gene (partial), internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), clone R1.187 1.69E-30 97.7 100 AJ504630 SH001320.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.16E-33 97.7 100

CL2_372 AH005838 Racocetra castanea clone pRIBSc 18S ribosomal RNA genes, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 25S ribosomal RNA gene, partial sequence 81 3.60E-32 100 100 EF393617 SH203809.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;g__Racocetra;s__Racocetra_sp; 1.50E-30 97.5 98.8

CL2_373 HG938301 Dominikia bernensis genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate FO310, clone 310.1 81 1.87E-10 87.3 77.8 JQ218218 SH000331.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.90E-21 98.5 82.7

CL2_374 MG459216 Cetraspora armeniaca isolate Ce-7 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 79 6.23E-29 100 100 FN547603 SH203803.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;g__Cetraspora;s__Cetraspora_gi
lmorei; 2.15E-28 94.9 100

CL2_375 NR_111105 Racocetra castanea BEG 1 ITS region; from TYPE material >gi|21388570|emb|AJ313171.1|
Scutellospora castanea 5.8S rRNA gene, internal transcribed spacer 1 (ITS1) and internal transcribed spacer 2 (ITS2), isolate BEG1 78 2.59E-27 98.7 98.7 FR750140 SH019941.07FU

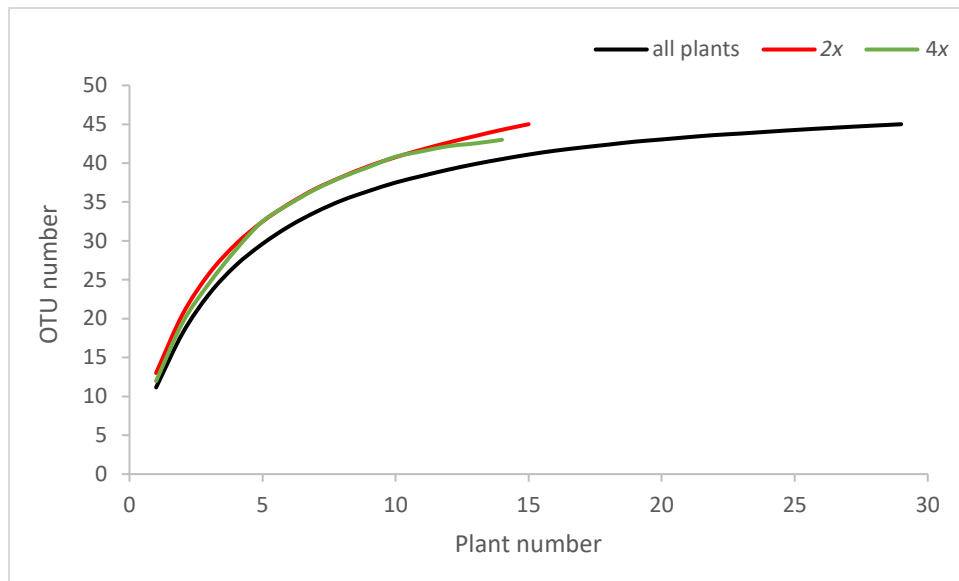
k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;g__Dentiscutata;s__Dentiscutata
_erythropus; 7.37E-28 94.9 100

CL2_376 MG459217 Cetraspora armeniaca isolate Ce-8 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence 78 5.71E-23 96.2 100 FN547603 SH203803.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;g__Cetraspora;s__Cetraspora_gi
lmorei; 1.09E-25 96.2 100

CL2_377 FN423707 Scutellospora castanea 18S rRNA gene (partial), ITS1 and 5.8S rRNA gene (partial), clone 12_3_1 77 4.89E-30 100 100 FR750140 SH019941.07FU

k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;g__Dentiscutata;s__Dentiscutata
_erythropus; 3.74E-25 94.8 100



Appendix S4: Species accumulation curves calculated for all plants of *Centaurea stoebe* s.l. sampled at the Sandberg site as well as for each cytotyp e separately.

SEQ TITLE	STATUS	Sel Result	Accession	Description	E value	Max score	Total score	Query from					
Query to	Hit from	Hit to	Identity	Positive	Similarity[%]	Coverage[%]	Query length						
CL2_001	blastn	01-May	SH219474.07FU FJ769308 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp;	1.07E-46	187.033	206	1	103	55	157	103	103	100,0
CL2_002	blastn	01-May	SH001003.07FU HE775296 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp;	3.48E-47	188.837	208	3	113	224	333	109	109	98,2
CL2_003	blastn	01-May	SH001103.07FU AJ567734 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp;	8.26E-42	170.803	188	1	99	55	153	97	97	98,0
CL2_004	blastn	01-May	SH175559.07FU HF674808 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp;	9.05E-48	190.64	210	1	105	454	350	105	105	100,0
CL2_005	blastn	01-May	SH497058.07FU KM376421 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp;	4.00E-46	185.23	204	1	108	189	297	107	107	99,1
CL2_006	blastn	01-May	SH001017.07FU KJ209706 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp;	3.24E-40	165.393	182	1	97	244	343	97	97	100,0
CL2_007	blastn	01-May	SH001003.07FU KF836957 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices;	6.65E-50	197.854	218	1	112	244	355	111	111	99,1
CL2_008	blastn	01-May	SH001026.07FU KF836965 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp;	5.58E-51	201.46	222	1	114	244	357	113	113	99,1
CL2_009	blastn	01-May	SH001323.07FU KF939972 k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp;	3.28E-47	188.837	208	1	108	244	352	108	108	100,0
CL2_010	blastn	01-May	SH001325.07FU HE775312 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp;	9.75E-48	190.64	210	1	111	222	333	110	110	99,1
CL2_011	blastn	01-May	SH521585.07FU KM056660 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_aurea;	1.27E-45	183.427	202	1	101	243	343	101	101	100,0
CL2_012	blastn	01-May	SH001328.07FU KF206512 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp;	5.05E-45	181.623	200	3	111	190	299	107	107	98,2
CL2_013	blastn	01-May	SH001284.07FU KF836936 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp;	1.62E-44	179.82	198	1	104	244	346	103	103	99,0
CL2_014	blastn	01-May	SH219474.07FU FJ769308 k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp;	1.07E-46	187.033	206	1	103	55	157	103	103	100,0

lassified_Glomeraceae;s__Glomeraceae_sp; 3.42E-40 165.393 182 1 101 55 157 100 100 99,0
100,0 101

CL2_015 blastn 01-May
SH001284.07FU|KF939955|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomero
mycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 9.63E-48
190.64 210 1 110 244 353 108 108 98,2 100,0 110

CL2_016 blastn 01-May
SH001284.07FU|KF939989|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomero
mycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.81E-35
147.359 162 1 98 244 347 96 96 98,0 100,0 98

CL2_017 blastn 01-May
SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomerom
ycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.42E-40
165.393 182 1 101 242 344 100 100 99,0 100,0 101

CL2_018 blastn 01-May
SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomerom
ycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.05E-40
167.196 184 1 106 242 344 101 101 95,3 100,0 106

CL2_019 blastn 01-May
SH176083.07FU|JF439098|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_sp; 2.02E-43 176.213 194 1 104 242 347 104 104 100,0 98,1 106

CL2_020 blastn 01-May
SH017484.07FU|HQ895792|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__u
nclassified_Glomeraceae;s__Glomeraceae_sp; 3.08E-69 262.775 290 1 166 240 405 160 160
96,4 100,0 166

CL2_021 blastn 01-May
SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
classified_Glomeraceae;s__Glomeraceae_sp; 1.26E-39 163.589 180 1 105 456 559 100 100
95,2 100,0 105

CL2_022 blastn 01-May
SH176092.07FU|FJ769298|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unc
lassified_Glomeraceae;s__Glomeraceae_sp; 3.70E-40 165.393 182 1 105 55 157 101 101 96,2
98,1 107

CL2_023 blastn 01-May
SH524902.07FU|HG938304|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__D
ominikia;s__Dominikia_bernensis; 2.30E-42 172.606 190 1 101 240 341 100 100 99,0 100,0
101

CL2_024 blastn 01-May
SH176129.07FU|AJ504633|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_sp; 6.69E-37 154.573 170 2 107 32 134 99 99 93,4 99,1 107

CL2_025 blastn 01-May
SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unc
lassified_Glomeraceae;s__Glomeraceae_sp; 1.43E-38 159.983 176 1 98 55 154 97 97 99,0
98,0 100

CL2_026 blastn 01-May
SH001323.07FU|KF939972|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomero
mycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.41E-50
197.854 218 1 109 244 352 109 109 100,0 100,0 109

CL2_027 blastn 01-May
SH001071.07FU|AM384942|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__u
nclassified_Glomeraceae;s__Glomeraceae_sp; 2.79E-48 192.443 212 1 111 378 487 110 110
99,1 100,0 111

CL2_028 blastn 01-May
SH176142.07FU|KJ564159|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un

classified_Glomeraceae;s__Glomeraceae_sp; 1.30E-38 159.983 176 1 93 244 335 92 92 98,9
100,0 93

CL2_029 blastn 01-May
SH000331.07FU|JQ218218|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.64E-33 141.949 156 1 92 259 354 90 90 97,8
95,8 96

CL2_030 blastn 01-May
SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.43E-32 138.342 152 1 93 456 547 87 87 93,5
96,9 96

CL2_031 blastn 01-May
SH490604.07FU|JX375234|k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassified_Fungi;g__unclassified_Fungi;s__Fungi_sp; 2.63E-48 192.443 212 1 106 78 183 106 106
100,0 100,0 106

CL2_032 blastn 01-May
SH017240.07FU|JX096603|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.92E-37 156.376 172 1 104 242 344 99 99 95,2 97,2 107

CL2_033 blastn 01-May
SH001103.07FU|AJ567734|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 3.42E-40 165.393 182 1 101 55 155 97 97 96,0 100,0
101

CL2_034 blastn 01-May
SH001356.07FU|FN397320|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.92E-36 150.966 166 2 95 70 163 92 92 97,9
98,9 95

CL2_035 blastn 01-May
SH197521.07FU|AJ517456|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.51E-44 179.82 198 1 99 55 153 99 99 100,0 100,0 99

CL2_036 blastn 01-May
SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.22E-36
152.769 168 1 103 242 344 99 99 96,1 100,0 103

CL2_037 blastn 01-May
SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.57E-38 159.983 176 1 107 456 559 101 101
94,4 100,0 107

CL2_038 blastn 01-May
SH176101.07FU|AY236252|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.53E-37 156.376 172 1 91 191 281 89 89 97,8
100,0 91

CL2_039 blastn 01-May
SH174581.07FU|KJ564166|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.47E-40 165.393 182 1 99 132 230 96 96 97,0
97,1 102

CL2_040 blastn 01-May
SH001284.07FU|JX276911|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.90E-46 185.23
204 1 106 222 328 106 106 100,0 100,0 106

CL2_041 blastn 01-May
SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.87E-38 158.179 174 1 96 55 154 96 96 100,0
98,0 98

CL2_042 blastn 01-May
SH176070.07FU|JX276899|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.30E-38 159.983 176 1 93 244 335 92 92 98,9
100,0 93

classified_Glomeraceae;s__Glomeraceae_sp; 6.60E-43 174.41 192 1 101 222 322 99 99 98,0
100,0 101

CL2_043 blastn 01-May
SH175527.07FU|GQ205050|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_irregularis; 9.40E-48 190.64 210 1 108 5 112 107 107 99,1
100,0 108

CL2_044 blastn 01-May
SH184262.07FU|AM992833|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.40E-45 183.427 202 1 107 460 567 106 106
99,1 99,1 108

CL2_045 blastn 01-May
SH017159.07FU|JQ218221|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.27E-45 183.427 202 1 101 237 337 101 101
100,0 100,0 101

CL2_046 blastn 01-May
SH174581.07FU|KJ564166|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.30E-42 172.606 190 2 101 133 232 98 98 98,0
99,0 101

CL2_047 blastn 01-May
SH000326.07FU|JX096575|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.07E-36 152.769 168 1 98 242 340 94 94 95,9
100,0 98

CL2_048 blastn 01-May
SH001284.07FU|KF939968|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.80E-44
179.82 198 1 113 244 354 109 109 96,5 100,0 113

CL2_049 blastn 01-May
SH000330.07FU|FJ553212|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.84E-36 150.966 166 1 104 362 468 100 100 96,2
100,0 104

CL2_050 blastn 01-May
SH175587.07FU|HF674807|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.12E-46 187.033 206 1 106 437 542 105 105
99,1 100,0 106

CL2_051 blastn 01-May
SH200414.07FU|KJ484721|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 5.29E-79
295.235 326 1 168 222 388 167 167 99,4 100,0 168

CL2_052 blastn 01-May
SH001278.07FU|FJ008644|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.19E-36 152.769 168 6 102 59 157 96 96 99,0
95,1 102

CL2_053 blastn 01-May
SH024970.07FU|FN397384|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.90E-34 145.556 160 1 94 522 428 90 90 95,7
100,0 94

CL2_054 blastn 01-May
SH019350.07FU|JX096620|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.51E-26
118.505 130 2 100 248 350 90 90 90,9 97,1 102

CL2_055 blastn 01-May
SH001356.07FU|FN397320|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.01E-33 143.752 158 1 94 69 163 91 91 96,8
100,0 94

CL2_056 blastn 01-May

SH199963.07FU|EU359265|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.04E-42 170.803 188 1 101 33 132 99 99 98,0 100,0 101

CL2_057 blastn 01-May

SH176144.07FU|KJ564157|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.53E-37 156.376 172 1 91 244 333 90 90 98,9 100,0 91

CL2_058 blastn 01-May

SH175570.07FU|GU322944|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.45E-45 183.427 202 6 111 59 163 105 105 99,1 95,5 111

CL2_059 blastn 01-May

SH000331.07FU|JQ218218|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.74E-35 149.163 164 1 104 259 363 99 99 95,2 100,0 104

CL2_060 blastn 01-May

SH024970.07FU|JF439161|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.10E-40 165.393 182 1 94 244 337 93 93 98,9 100,0 94

CL2_061 blastn 01-May

SH184262.07FU|HG425919|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.38E-45 183.427 202 1 105 222 327 105 105 100,0 98,1 107

CL2_062 blastn 01-May

SH176120.07FU|JX096607|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.34E-45 183.427 202 1 105 242 347 105 105 100,0 100,0 105

CL2_063 blastn 01-May

SH175559.07FU|HF674808|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.92E-41 169 186 1 104 454 350 101 101 97,1 100,0 104

CL2_064 blastn 01-May

SH175545.07FU|HG425873|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.63E-45 181.623 200 1 104 296 400 104 104 100,0 100,0 104

CL2_065 blastn 01-May

SH535765.07FU|HG425911|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.14E-40 167.196 184 1 113 242 351 106 106 93,8 100,0 113

CL2_066 blastn 01-May

SH176092.07FU|FJ769298|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.14E-43 174.41 192 1 105 55 157 103 103 98,1 98,1 107

CL2_067 blastn 01-May

SH175629.07FU|HE775307|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.63E-48 190.64 210 1 110 222 330 109 109 99,1 100,0 110

CL2_068 blastn 01-May

SH004981.07FU|KF836907|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.94E-43 176.213 194 1 100 244 343 99 99 99,0 97,1 103

CL2_069 blastn 01-May

SH000326.07FU|JX096575|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.42E-43 174.41 192 1 99 242 340 98 98 99,0 100,0 99

CL2_070 blastn 01-May
SH017240.07FU|UDB025485|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_macrocarpum; 1.53E-37 156.376 172 1 91 14 104 89 89 97,8 100,0 91

CL2_071 blastn 01-May
SH001103.07FU|AJ567734|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 9.54E-41 167.196 184 1 99 55 155 98 98 99,0 100,0 99

CL2_072 blastn 01-May
SH001340.07FU|JX096612|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.75E-27 122.112 134 1 101 244 342 89 89 88,1 98,1 103

CL2_073 blastn 01-May
SH017240.07FU|UDB025485|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_macrocarpum; 6.10E-30 131.129 144 1 91 14 104 86 86 94,5 100,0 91

CL2_074 blastn 01-May
SH176142.07FU|KJ564159|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.10E-30 131.129 144 1 91 244 335 87 87 95,6 100,0 91

CL2_075 blastn 01-May
SH202639.07FU|JQ951563|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.93E-45 181.623 200 1 105 5 109 103 103 98,1 96,3 109

CL2_076 blastn 01-May
SH001003.07FU|HG425880|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.86E-44 178.016 196 5 107 248 349 102 102 99,0 96,3 107

CL2_077 blastn 01-May
SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.43E-38 159.983 176 1 100 456 559 99 99 99,0 100,0 100

CL2_078 blastn 01-May
SH175735.07FU|KP954735|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.41E-50 197.854 218 1 109 55 163 109 109 100,0 100,0 109

CL2_079 blastn 01-May
SH001356.07FU|FN397320|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.19E-40 165.393 182 1 96 69 163 95 95 99,0 100,0 96

CL2_080 blastn 01-May
SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.99E-43 176.213 194 1 102 55 155 101 101 99,0 97,1 105

CL2_081 blastn 01-May
SH001017.07FU|AJ567771|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.65E-37 156.376 172 1 96 55 155 96 96 100,0 100,0 96

CL2_082 blastn 01-May
SH001320.07FU|AJ518854|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.20E-35 149.163 164 1 89 31 118 87 87 97,8 100,0 89

CL2_083 blastn 01-May
SH000330.07FU|FJ553212|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.09E-40 167.196 184 3 106 364 466 100 100 96,2 95,4 109

CL2_084 blastn 01-May
SH001335.07FU|JF439120|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 8.48E-42 170.803 188 1 105 242 346 103 103 98,1 100,0 105

CL2_085 blastn 01-May
SH176092.07FU|FJ769298|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.32E-39 163.589 180 1 109 55 160 103 103 94,5 100,0 109

CL2_086 blastn 01-May
SH001340.07FU|JX096612|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.07E-24 113.095
124 1 105 244 342 90 90 85,7 97,2 108

CL2_087 blastn 01-May
SH001093.07FU|AF197919|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.64E-44 179.82 198 1 105 5 110 104 104 99,0 100,0 105

CL2_088 blastn 01-May
SH001025.07FU|AJ557009|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_irregularis; 2.27E-42 172.606 190 1 100 32 133 100 100 100,0 100,0 100

CL2_089 blastn 01-May
SH001278.07FU|GQ388461|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.87E-43 176.213 194 1 100 55 154 99 99 99,0 100,0 100

CL2_090 blastn 01-May
SH529448.07FU|HG425981|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.77E-41 169 186 1 98 222 318 97 97 99,0 98,0 100

CL2_091 blastn 01-May
SH192875.07FU|KJ564151|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.57E-15 82.4379 90 154 226 340 413 66 66 90,4 32,3 226

CL2_092 blastn 01-May
SH001070.07FU|JX096621|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.36E-36 152.769 168 3 108 246 352 101 101 95,3 98,1 108

CL2_093 blastn 01-May
SH176120.07FU|JX096607|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.93E-45 181.623 200 1 109 242 347 106 106 97,2 100,0 109

CL2_094 blastn 01-May
SH204223.07FU|HF970208|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.32E-47 188.837 208 1 109 222 329 108 108 99,1 100,0 109

CL2_095 blastn 01-May
SH535765.07FU|HG425911|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.01E-44 178.016 196 1 109 242 351 106 106 97,2 100,0 109

CL2_096 blastn 01-May
SH001340.07FU|JX096612|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.08E-25 114.899
126 1 107 244 342 92 92 86,0 97,3 110

CL2_097 blastn 01-May
SH175543.07FU|KF836972|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 6.23E-44 178.016 196 1 112 244 353 107 107 95,5 100,0 112

CL2_098 blastn 01-May
SH001026.07FU|KF836965|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.49E-46 185.23 204 1 118 244 357 113 113 95,8 100,0 118

CL2_099 blastn 01-May
SH200419.07FU|JX276918|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.26E-61 235.724 260 1 165 222 385 152 152 92,1 100,0 165

CL2_100 blastn 01-May
SH204357.07FU|KF939966|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.36E-78 291.629 322 1 166 244 409 164 164 98,8 100,0 166

CL2_101 blastn 01-May

SH192876.07FU|JX096602|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.83E-28 125.719 138 66 172 300 414 101 101 94,4 62,2 172
CL2_102 blastn 01-May

SH176144.07FU|KJ564157|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.04E-19 98.6682 108 156 212 277 333 56 56 98,2 26,9 212
CL2_103 blastn 01-May

SH001003.07FU|AM495184|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.28E-47 188.837 208 1 108 425 533 108 108 100,0 100,0 108
CL2_104 blastn 01-May

SH202639.07FU|JQ951563|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.15E-46 187.033 206 1 108 5 111 107 107 99,1 100,0 108
CL2_105 blastn 01-May

SH175527.07FU|GQ205050|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_irregularis; 4.87E-45 181.623 200 1 108 5 112 105 105 97,2 100,0 108
CL2_106 blastn 01-May

SH525002.07FU|KF836955|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 5.93E-44 178.016 196 1 108 244 353 106 106 98,1 100,0 108
CL2_107 blastn 01-May

SH202639.07FU|JQ951563|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.07E-43 176.213 194 1 105 5 109 102 102 97,1 97,2 108
CL2_108 blastn 01-May

SH175542.07FU|KF836954|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 8.70E-42 170.803 188 1 107 244 350 102 102 95,3 100,0 107
CL2_109 blastn 01-May

SH175542.07FU|KJ484708|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.95E-46 185.23 204 1 107 222 328 105 105 98,1 100,0 107
CL2_110 blastn 01-May

SH176129.07FU|AJ504633|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 5.49E-38 158.179 174 2 107 32 134 101 101 95,3 99,1 107
CL2_111 blastn 01-May

SH000331.07FU|JQ218218|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.70E-40 165.393 182 1 105 259 360 101 101 96,2 98,1 107
CL2_112 blastn 01-May

SH001340.07FU|JX096612|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.91E-35 149.163 164 1 109 244 350 100 100 91,7 100,0 109
CL2_113 blastn 01-May

SH175543.07FU|KF836972|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 1.17E-46 187.033 206 3 110 246 353 106 106 98,1 98,2 110
CL2_114 blastn 01-May

SH001026.07FU|KF836965|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.68E-44 179.82 198 1 104 244 347 102 102 98,1 97,2 107
CL2_115 blastn 01-May

SH174867.07FU|AJ567352|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.86E-50 199.657 220 1 110 55 164 110 110 100,0 100,0 110
CL2_116 blastn 01-May

SH001003.07FU|KC222869|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.17E-46 187.033 206 1 110 244 355 109 109 99,1 100,0 110
CL2_117 blastn 01-May

SH525475.07FU|HG425958|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Claroideoglomerac

eae;g__unclassified_Claroideoglomeraceae;s__Claroideoglomeraceae_sp; 1.56E-51 203.264 224 1 112 222 333
 112 112 100,0 100,0 112
 CL2_118 blastn 01-May
 SH176092.07FU|FJ769298|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.68E-44 179.82 198 2 107 56 160 104 104 98,1 99,1 107
 CL2_119 blastn 01-May
 SH001026.07FU|AJ872037|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.30E-44 178.016 196 1 113 5 116 108 108 95,6 100,0 113
 CL2_120 blastn 01-May
 SH001026.07FU|KF836965|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.40E-49 196.05 216 1 115 244 357 113 113 98,3 100,0 115
 CL2_121 blastn 01-May
 SH000330.07FU|FJ553212|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.70E-40 165.393 182 3 105 364 464 99 99 96,1 96,3 107
 CL2_122 blastn 01-May
 SH001026.07FU|KF836965|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.49E-46 185.23 204 1 118 244 357 113 113 95,8 100,0 118
 CL2_123 blastn 01-May
 SH017793.07FU|GQ388487|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.12E-63 241.134 266 1 138 55 192 136 136 98,6 100,0 138
 CL2_124 blastn 01-May
 SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.27E-36 152.769 168 1 93 456 552 93 93 100,0 66,9 139
 CL2_125 blastn 01-May
 SH470097.07FU|KF646116|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 7.45E-64 244.741 270 1 151 33 183 148 148 98,0 100,0 151
 CL2_126 blastn 01-May
 SH200418.07FU|JF439157|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.66E-76 286.219 316 1 164 244 410 164 164 100,0 100,0 164
 CL2_127 blastn 01-May
 SH191191.07FU|EU747860|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.24E-47 188.837 208 1 107 138 244 106 106 99,1 100,0 107
 CL2_128 blastn 01-May
 SH175546.07FU|AM980861|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 1.68E-44 179.82 198 1 107 14 120 104 104 97,2 100,0 107
 CL2_129 blastn 01-May
 SH017484.07FU|HQ895792|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.41E-71 268.185 296 1 169 240 405 163 163 96,4 100,0 169
 CL2_130 blastn 01-May
 SH200417.07FU|KF939973|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.47E-61 235.724 260 1 168 244 409 158 158 94,0 97,7 172
 CL2_131 blastn 01-May
 SH001340.07FU|JX096612|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.24E-28 125.719 138 1 104 244 342 92 92 88,5 97,2 107
 CL2_132 blastn 01-May
 SH017478.07FU|JF439150|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 6.68E-78 291.629 322 1 173 242 416 171 171 98,8 100,0 173
 CL2_133 blastn 01-May

SH192876.07FU|JX096602|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.11E-28 125.719 138 68 174 301 412 99 99 92,5 59,8 179
CL2_134 blastn 01-May

SH216618.07FU|AY236237|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.77E-83 307.859 340 1 191 191 386 187 187 97,9 100,0
191
CL2_135 blastn 01-May

SH001003.07FU|AJ872040|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.63E-48 192.443 212 1 106 68 173 106 106 100,0 100,0
106
CL2_136 blastn 01-May

SH176130.07FU|KF836966|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.05E-40 167.196 184 2 99 245 343 97 97 99,0 92,5 106
CL2_137 blastn 01-May

SH202639.07FU|JQ951563|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.90E-46 185.23 204 1 106 5 111 106 106 100,0 100,0
106
CL2_138 blastn 01-May

SH001284.07FU|JX096623|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.05E-40 167.196
184 1 106 242 345 102 102 96,2 100,0 106
CL2_139 blastn 01-May

SH001015.07FU|GU322941|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.75E-45 181.623 200 1 106 55 161 105 105 99,1 100,0
106
CL2_140 blastn 01-May

SH176092.07FU|FJ769298|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.12E-46 187.033 206 1 106 55 160 105 105 99,1 100,0 106
CL2_141 blastn 01-May

SH497058.07FU|KM376421|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 4.81E-45 181.623 200 5 107 195 297 102 102 99,0 96,3 107
CL2_142 blastn 01-May

SH175605.07FU|AM384946|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.90E-46 185.23 204 1 106 195 301 106 106 100,0 100,0
106
CL2_143 blastn 01-May

SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.92E-35 147.359 162 8 107 462 559 94 94 94,0 93,5 107
CL2_144 blastn 01-May

SH181726.07FU|KJ564139|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 5.79E-44 178.016
196 1 104 244 348 103 103 99,0 98,1 106
CL2_145 blastn 01-May

SH001284.07FU|JX276911|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.70E-42 170.803
188 1 107 222 328 104 104 97,2 100,0 107
CL2_146 blastn 01-May

SH001036.07FU|AJ872051|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.66E-44 179.82 198 1 106 34 141 106 106 100,0 100,0 106
CL2_147 blastn 01-May

SH204107.07FU|JX276885|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.59E-42 170.803 188 8 106 228 326 97 97 98,0 93,4 106
CL2_148 blastn 01-May

SH200110.07FU|JN195709|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.59E-42 170.803 188 8 106 228 326 97 97 98,0 93,4 106

classified_Glomeraceae;s__Glomeraceae_sp; 7.06E-24 111.292 122 1 106 457 563 93 93 87,7 100,0
106
CL2_149 blastn 01-May
SH001338.07FU|AY969845|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.75E-26 118.505
130 6 106 11 107 89 89 88,1 95,3 106
CL2_150 blastn 01-May
SH176072.07FU|GQ388291|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.55E-38 159.983 176 1 106 55 162 103 103 97,2 100,0
106
CL2_151 blastn 01-May
SH175570.07FU|GU322944|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.05E-43 176.213 194 1 107 55 163 106 106 99,1 100,0
107
CL2_152 blastn 01-May
SH202639.07FU|JQ951563|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.87E-45 181.623 200 1 105 5 109 103 103 98,1 97,2 108
CL2_153 blastn 01-May
SH497058.07FU|KM376421|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.70E-44 179.82 198 1 108 189 297 106 106 98,1 100,0 108
CL2_154 blastn 01-May
SH175629.07FU|HE775307|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.05E-40 167.196 184 1 106 222 330 104 104 98,1 100,0
106
CL2_155 blastn 01-May
SH181726.07FU|KJ564139|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.52E-42 172.606
190 1 108 244 351 105 105 97,2 100,0 108
CL2_156 blastn 01-May
SH204107.07FU|JX276885|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.85E-46 185.23 204 1 105 222 326 104 104 99,0 100,0
105
CL2_157 blastn 01-May
SH004981.07FU|KF836907|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.27E-33 141.949 156 1 104 244 343 96 96 92,3 96,3 108
CL2_158 blastn 01-May
SH019350.07FU|JX096620|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.75E-31 136.539
150 2 103 248 351 93 93 91,2 97,1 105
CL2_159 blastn 01-May
SH175567.07FU|FR873158|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.26E-39 163.589 180 1 105 211 314 102 102 97,1 100,0
105
CL2_160 blastn 01-May
SH522230.07FU|JX388537|k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassified_Fungi;g__unclassified_Fungi;s__Fungi_sp; 1.40E-45 183.427 202 1 108 77 183 106 106 98,1 100,0
108
CL2_161 blastn 01-May
SH535765.07FU|HG425911|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.52E-37 154.573 170 1 105 242 351 103 103 98,1 100,0
105
CL2_162 blastn 01-May
SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.38E-34 145.556 160 1 105 456 559 98 98 93,3 100,0

105

CL2_163 blastn 01-May

SH001323.07FU|KF939972|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.74E-40 165.393 182 1 108 244 352 105 105 97,2 100,0 108

CL2_164 blastn 01-May

SH001008.07FU|FR693660|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.40E-48 190.64 210 1 108 270 377 107 107 99,1 100,0 108

CL2_165 blastn 01-May

SH175570.07FU|GU322944|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.01E-44 178.016 196 5 109 60 163 103 103 98,1 96,3 109

CL2_166 blastn 01-May

SH199959.07FU|GQ388586|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.96E-43 174.41 192 1 105 55 157 103 103 98,1 100,0 105

CL2_167 blastn 01-May

SH176112.07FU|KF836929|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 8.48E-42 170.803 188 4 105 247 348 99 99 97,1 97,1 105

CL2_168 blastn 01-May

SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.38E-34 145.556 160 7 105 249 344 92 92 92,9 94,3 105

CL2_169 blastn 01-May

SH001008.07FU|FR693660|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.91E-42 170.803 188 8 109 276 377 99 99 97,1 93,6 109

CL2_170 blastn 01-May

SH200110.07FU|JN195709|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.82E-30 131.129 144 1 109 457 563 97 97 89,0 100,0 109

CL2_171 blastn 01-May

SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.75E-31 136.539 150 1 105 456 559 96 96 91,4 100,0 105

CL2_172 blastn 01-May

SH175575.07FU|JF439118|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 3.12E-47 188.837 208 1 104 244 347 104 104 100,0 100,0 104

CL2_173 blastn 01-May

SH199957.07FU|AJ518862|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.56E-40 165.393 182 2 104 32 133 99 99 96,1 99,0 104

CL2_174 blastn 01-May

SH527348.07FU|KF836920|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.24E-39 163.589 180 1 104 244 344 100 100 96,2 100,0 104

CL2_175 blastn 01-May

SH001284.07FU|JX096623|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.12E-47 188.837 208 1 104 242 345 104 104 100,0 100,0 104

CL2_176 blastn 01-May

SH027190.07FU|JN581945|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.29E-49 196.05 216 1 111 6 116 110 110 99,1 100,0 111

CL2_177 blastn 01-May

SH001026.07FU|KF836965|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl

omus;s__Glomus_sp; 3.88E-40 165.393 182 5 111 250 357 102 102 95,3 96,4 111
 CL2_178 blastn 01-May
 SH202639.07FU|JQ951563|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.15E-44 178.016 196 1 107 5 109 104 104 97,2 96,4 111
 CL2_179 blastn 01-May
 SH175629.07FU|HE775307|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.15E-43 176.213 194 1 111 222 330 107 107 96,4 100,0 111
 CL2_180 blastn 01-May
 SH176069.07FU|AM076596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.33E-45 183.427 202 1 104 55 158 103 103 99,0 100,0 104
 CL2_181 blastn 01-May
 SH522230.07FU|JX363251|k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassified_Fungi;g__unclassified_Fungi;s__Fungi_sp; 3.56E-40 165.393 182 6 104 83 181 96 96 97,0 95,2 104
 CL2_182 blastn 01-May
 SH174866.07FU|FJ008650|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.69E-38 159.983 176 1 113 55 162 105 105 92,9 100,0 113
 CL2_183 blastn 01-May
 SH004948.07FU|KF836940|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.12E-47 188.837 208 1 104 244 347 104 104 100,0 100,0 104
 CL2_184 blastn 01-May
 SH001003.07FU|HE775296|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.29E-46 185.23 204 4 114 225 333 109 109 98,2 97,4 114
 CL2_185 blastn 01-May
 SH001003.07FU|AM495148|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.23E-45 181.623 200 1 114 382 493 110 110 96,5 100,0 114
 CL2_186 blastn 01-May
 SH001026.07FU|KF836965|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 3.52E-47 188.837 208 1 114 244 357 110 110 96,5 100,0 114
 CL2_187 blastn 01-May
 SH175570.07FU|GU322944|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.51E-38 159.983 176 5 104 60 163 99 99 99,0 96,2 104
 CL2_188 blastn 01-May
 SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.95E-32 138.342 152 7 104 249 344 91 91 92,9 94,2 104
 CL2_189 blastn 01-May
 SH001340.07FU|JX096612|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.73E-31 136.539 150 1 104 244 350 97 97 93,3 100,0 104
 CL2_190 blastn 01-May
 SH017793.07FU|GQ388487|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.73E-30 132.932 146 1 127 55 192 115 115 90,6 100,0 127
 CL2_191 blastn 01-May
 SH017793.07FU|GQ388487|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.46E-50 199.657 220 1 137 55 192 130 130 94,9 100,0 137
 CL2_192 blastn 01-May
 SH176129.07FU|AJ504633|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.88E-41 169 186 2 103 32 134 100 100 98,0 99,0 103
 CL2_193 blastn 01-May

SH176112.07FU|KF836929|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.37E-42 172.606 190 1 101 244 345 100 100 99,0 98,1 103
CL2_194 blastn 01-May

SH470097.07FU|KF646116|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.19E-35 149.163 164 1 135 33 174 122 122 90,4 93,1 145
CL2_195 blastn 01-May

SH176087.07FU|GQ388564|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.82E-37 156.376 172 1 103 55 154 98 98 95,1 100,0 103
CL2_196 blastn 01-May

SH017159.07FU|KC965597|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.14E-21 102.275 112 102 161 47 107 60 60 100,0 37,3 161
CL2_197 blastn 01-May

SH017484.07FU|HQ895792|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.34E-64 246.544 272 1 164 240 405 157 157 95,7 100,0 164
CL2_198 blastn 01-May

SH001070.07FU|JX096621|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.35E-37 154.573 170 3 100 246 346 96 96 98,0 95,1 103
CL2_199 blastn 01-May

SH175544.07FU|AM114024|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.57E-44 178.016 196 1 103 5 106 102 102 99,0 100,0 103
CL2_200 blastn 01-May

SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.31E-26 120.309 132 1 101 242 340 89 89 88,1 98,1 103
CL2_201 blastn 01-May

SH192876.07FU|JX096602|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.08E-49 197.854 218 1 166 244 414 151 151 91,0 100,0 166
CL2_202 blastn 01-May

SH174581.07FU|KJ564166|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.23E-39 163.589 180 1 100 132 230 97 97 97,0 97,1 103
CL2_203 blastn 01-May

SH192876.07FU|JX096602|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.95E-46 185.23 204 1 165 244 407 149 149 90,3 97,6 169
CL2_204 blastn 01-May

SH017482.07FU|JX096580|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.04E-24 114.899 126 88 170 323 407 77 77 92,8 48,8 170
CL2_205 blastn 01-May

SH175543.07FU|EF619695|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.34E-42 172.606 190 1 100 6 105 98 98 98,0 98,0 102
CL2_206 blastn 01-May

SH017154.07FU|FR693662|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.70E-46 185.23 204 1 102 265 366 102 102 100,0 100,0 102
CL2_207 blastn 01-May

SH176133.07FU|FJ769332|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.70E-46 185.23 204 1 102 55 156 102 102 100,0 100,0 102
CL2_208 blastn 01-May

SH012309.07FU|JX096618|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__unclassified_Glomeromycota_sp; 1.04E-24 114.899 126 88 170 323 407 77 77 92,8 48,8 170

ycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 7.73E-52 205.067
226 1 167 241 416 156 156 93,4 95,4 175
CL2_209 blastn 01-May
SH197525.07FU|AJ517451|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rh
izophagus;s__Rhizophagus_sp; 3.70E-46 185.23 204 1 102 55 156 102 102 100,0 100,0 102
CL2_210 blastn 01-May
SH216618.07FU|AY236237|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__u
nclassified_Glomeraceae;s__Glomeraceae_sp; 1.48E-29 131.129 144 1 176 191 383 152 152 86,4 96,2 183
CL2_211 blastn 01-May
SH192876.07FU|JX096602|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
classified_Glomeraceae;s__Glomeraceae_sp; 6.32E-28 125.719 138 68 184 300 414 104 104 88,9 63,6 184
CL2_212 blastn 01-May
SH527348.07FU|KF836922|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_sp; 3.47E-40 165.393 182 4 102 247 345 96 96 97,0 97,1 102
CL2_213 blastn 01-May
SH216618.07FU|AY236237|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__u
nclassified_Glomeraceae;s__Glomeraceae_sp; 1.30E-87 324.089 358 1 195 191 386 190 190 97,4 100,0
195
CL2_214 blastn 01-Mar
SH216618.07FU|AY236237|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__u
nclassified_Glomeraceae;s__Glomeraceae_sp; 1.59E-23 111.292 122 137 206 316 386 68 68 97,1 34,0 206
CL2_215 blastn 01-May
SH017476.07FU|FJ362330|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unc
lassified_Glomeraceae;s__Glomeraceae_sp; 5.33E-17 89.6514 98 140 209 119 188 64 64 91,4 33,2 211
CL2_216 blastn 01-May
SH527348.07FU|KF836922|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_sp; 2.85E-41 169 186 2 102 245 345 98 98 97,0 99,0 102
CL2_217 blastn 01-Apr
SH017795.07FU|AJ567795|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
classified_Glomeraceae;s__Glomeraceae_sp; 2.31E-15 84.2413 92 135 214 109 187 71 71 88,8 37,4 214
CL2_218 blastn 01-May
SH527348.07FU|KF836922|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_sp; 2.85E-41 169 186 2 102 245 345 98 98 97,0 99,0 102
CL2_219 blastn 01-May
SH175544.07FU|AM076618|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__u
nclassified_Glomeraceae;s__Glomeraceae_sp; 1.21E-39 163.589 180 1 99 55 154 97 97 98,0 97,1 102
CL2_220 blastn 01-May
SH487564.07FU|KF836952|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_sp; 4.22E-39 161.786 178 1 102 244 345 97 97 95,1 100,0 102
CL2_221 blastn 01-May
SH174581.07FU|KJ564166|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
classified_Glomeraceae;s__Glomeraceae_sp; 9.93E-41 167.196 184 1 102 132 232 99 99 97,1 100,0
102
CL2_222 blastn 01-May
SH176120.07FU|JX096607|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
classified_Glomeraceae;s__Glomeraceae_sp; 9.93E-41 167.196 184 1 100 242 344 100 100 100,0 98,0
102
CL2_223 blastn 01-May
SH524902.07FU|HG938304|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__D
ominikia;s__Dominikia_bernensis; 9.80E-41 167.196 184 1 101 240 341 99 99 98,0 100,0 101
CL2_224 blastn 01-May
SH017159.07FU|KF836970|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_sp; 3.70E-46 185.23 204 1 102 244 345 102 102 100,0 100,0 102
CL2_225 blastn 01-May

SH524990.07FU|KF836941|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.55E-44 179.82 198 1 99 244 342 99 99 100,0 98,0 101
CL2_226 blastn 01-May

SH521585.07FU|KM056663|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_aurea; 6.60E-43 174.41 192 1 101 241 341 99 99 98,0 100,0 101
CL2_227 blastn 01-May

SH219472.07FU|FJ769319|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.77E-37 156.376 172 1 101 55 154 98 98 97,0 100,0 101
CL2_228 blastn 01-May

SH199964.07FU|FR693652|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.16E-36 152.769 168 2 101 271 370 96 96 96,0 99,0 101
CL2_229 blastn 01-May

SH017249.07FU|JX096609|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.57E-45 181.623 200 1 103 242 344 102 102 99,0 100,0 103
CL2_230 blastn 01-May

SH174581.07FU|KJ564166|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.42E-40 165.393 182 2 98 133 230 96 96 99,0 96,0 101
CL2_231 blastn 01-May

SH000327.07FU|HG938301|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_bernensis; 1.27E-45 183.427 202 1 101 240 340 101 101 100,0 100,0 101
CL2_232 blastn 01-May

SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 7.06E-30 131.129 144 1 93 242 333 87 87 93,5 92,1 101
CL2_233 blastn 01-May

SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.23E-39 163.589 180 3 103 57 157 99 99 98,0 98,1 103
CL2_234 blastn 01-May

SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.01E-40 167.196 184 1 103 456 559 100 100 97,1 100,0 103
CL2_235 blastn 01-May

SH000331.07FU|JQ218218|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.53E-36 150.966 166 1 99 259 360 96 96 97,0 98,0 101
CL2_236 blastn 01-May

SH000326.07FU|JX096575|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.12E-33 143.752 158 1 101 242 340 95 95 94,1 100,0 101
CL2_237 blastn 01-May

SH200029.07FU|JF439191|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 6.60E-43 174.41 192 1 101 242 341 100 100 99,0 100,0 101
CL2_238 blastn 01-May

SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.20E-34 145.556 160 10 99 63 154 89 89 98,9 89,1 101
CL2_239 blastn 01-May

SH017159.07FU|KC965597|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.18E-37 154.573 170 4 101 10 107 93 93 94,9 97,0 101
CL2_240 blastn 01-May

SH197524.07FU|KF836903|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.45E-38 159.983 176 1 101 244 347 99 99 98,0 100,0 101
CL2_241 blastn 01-May

SH490604.07FU|JX375234|k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassi

fied_Fungi;g__unclassified_Fungi;s__Fungi_sp; 1.97E-43 176.213 194 5 104 84 183 99 99 99,0 96,2 104
 CL2_242 blastn 01-May
 SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unc
 lassified_Glomeraceae;s__Glomeraceae_sp; 2.81E-41 169 186 1 99 55 154 98 98 99,0 98,0 101
 CL2_243 blastn 01-May
 SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unc
 lassified_Glomeraceae;s__Glomeraceae_sp; 1.77E-37 156.376 172 1 101 55 157 98 98 97,0 100,0 101
 CL2_244 blastn 01-May
 SH175527.07FU|GQ205050|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__R
 hizophagus;s__Rhizophagus_irregularis; 1.19E-39 163.589 180 1 98 5 102 95 95 96,9 97,0 101
 CL2_245 blastn 01-May
 SH176098.07FU|EF989100|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
 classified_Glomeraceae;s__Glomeraceae_sp; 3.90E-33 141.949 156 2 99 56 152 91 91 92,9 97,0 101
 CL2_246 blastn 01-May
 SH521585.07FU|KM056659|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__D
 ominikia;s__Dominikia_aurea; 1.19E-39 163.589 180 4 101 243 340 95 95 96,9 97,0 101
 CL2_247 blastn 01-May
 SH176130.07FU|KF836966|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
 omus;s__Glomus_sp; 1.75E-37 156.376 172 1 100 244 347 98 98 98,0 100,0 100
 CL2_248 blastn 01-May
 SH174581.07FU|KJ564166|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
 classified_Glomeraceae;s__Glomeraceae_sp; 7.94E-42 170.803 188 1 100 132 232 99 99 99,0 100,0 100
 CL2_249 blastn 01-May
 SH001280.07FU|FR693658|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
 classified_Glomeraceae;s__Glomeraceae_sp; 4.39E-45 181.623 200 1 100 268 367 100 100 100,0 100,0 100
 CL2_250 blastn 01-May
 SH175570.07FU|GU322944|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__u
 nclassified_Glomeraceae;s__Glomeraceae_sp; 1.53E-38 159.983 176 4 105 58 163 100 100 98,0 97,1 105
 CL2_251 blastn 01-May
 SH001103.07FU|AJ567734|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rh
 izophagus;s__Rhizophagus_sp; 5.01E-38 158.179 174 1 97 55 153 95 95 97,9 97,0 100
 CL2_252 blastn 01-May
 SH197525.07FU|AJ517451|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rh
 izophagus;s__Rhizophagus_sp; 2.77E-41 169 186 1 100 55 156 100 100 100,0 100,0 100
 CL2_253 blastn 01-May
 SH524085.07FU|KM208142|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomero
 mycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.03E-27 123.915
 136 1 100 222 322 91 91 91,0 100,0 100
 CL2_254 blastn 01-May
 SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomerom
 ycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.11E-33 141.949
 156 1 105 242 344 96 96 91,4 100,0 105
 CL2_255 blastn 01-May
 SH175545.07FU|HG425884|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__u
 nclassified_Glomeraceae;s__Glomeraceae_sp; 6.96E-43 174.41 192 1 105 233 341 105 105 100,0 100,0 105
 CL2_256 blastn 01-May
 SH001103.07FU|AJ567734|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rh
 izophagus;s__Rhizophagus_sp; 3.16E-34 145.556 160 11 98 65 152 85 85 96,6 88,0 100
 CL2_257 blastn 01-May
 SH174581.07FU|KJ564166|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
 classified_Glomeraceae;s__Glomeraceae_sp; 5.01E-38 158.179 174 2 100 133 232 97 97 98,0 99,0 100

CL2_258 blastn 01-May
SH175775.07FU|JF439196|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 1.64E-31 136.539 150 1 100 242 343 93 93 93,0 100,0 100

CL2_259 blastn 01-May
SH176141.07FU|GQ388310|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.27E-42 172.606 190 1 100 55 154 98 98 98,0 100,0 100

CL2_260 blastn 01-May
SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.43E-29 129.325 142 1 97 242 334 89 89 91,8 97,0 100

CL2_261 blastn 01-May
SH175570.07FU|GU322944|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.45E-39 161.786 178 6 106 59 163 100 100 99,0 95,3 106

CL2_262 blastn 01-May
SH176129.07FU|AJ504633|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.43E-29 129.325 142 3 100 33 134 93 93 94,9 98,0 100

CL2_263 blastn 01-May
SH001284.07FU|JX276911|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.05E-40 167.196 184 1 106 222 328 102 102 96,2 100,0 106

CL2_264 blastn 01-May
SH176130.07FU|JF439162|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.81E-35 149.163 164 1 106 244 346 100 100 94,3 100,0 106

CL2_265 blastn 01-May
SH175545.07FU|HG425873|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.66E-44 179.82 198 1 106 296 400 104 104 98,1 100,0 106

CL2_266 blastn 01-May
SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.94E-38 158.179 174 1 97 55 153 96 96 99,0 98,0 99

CL2_267 blastn 01-May
SH001284.07FU|KF939989|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.09E-33 143.752 158 1 96 244 345 94 94 97,9 97,0 99

CL2_268 blastn 01-May
SH175544.07FU|AM076615|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.54E-41 167.196 184 1 99 55 155 98 98 99,0 100,0 99

CL2_269 blastn 01-May
SH174581.07FU|KJ564166|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.10E-36 152.769 168 1 99 132 232 96 96 97,0 100,0 99

CL2_270 blastn 01-May
SH489933.07FU|KF836961|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.73E-41 169 186 1 99 244 343 98 98 99,0 100,0 99

CL2_271 blastn 01-May
SH175559.07FU|HF674808|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.55E-38 159.983 176 1 106 454 350 102 102 96,2 100,0 106

CL2_272 blastn 01-May
SH001103.07FU|AJ567734|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 4.94E-38 158.179 174 3 99 57 155 95 95 97,9 98,0 99

CL2_273 blastn 01-May

SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.56E-35 149.163 164 1 97 55 153 94 94 96,9 98,0 99
CL2_274 blastn 01-May
SH000326.07FU|JX096575|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.42E-38 159.983 176 1 99 242 340 97 97 98,0 100,0 99
CL2_275 blastn 01-May
SH015411.07FU|KF939971|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.72E-37 156.376 172 1 99 244 345 98 98 99,0 100,0 99
CL2_276 blastn 01-May
SH001323.07FU|KF939972|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.33E-32 140.146 154 1 96 244 350 94 94 97,9 97,0 99
CL2_277 blastn 01-May
SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.33E-32 140.146 154 1 97 55 153 91 91 93,8 98,0 99
CL2_278 blastn 01-May
SH197525.07FU|AJ517451|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.72E-37 156.376 172 1 99 55 156 97 97 98,0 100,0 99
CL2_279 blastn 01-May
SH001323.07FU|KF939972|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 4.63E-32 138.342 152 1 99 244 352 98 98 99,0 100,0 99
CL2_280 blastn 01-May
SH017159.07FU|KF836928|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 4.94E-38 158.179 174 3 99 246 344 95 95 97,9 98,0 99
CL2_281 blastn 01-May
SH176092.07FU|FJ769298|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.14E-43 174.41 192 7 105 59 157 98 98 99,0 92,5 107
CL2_282 blastn 01-May
SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 7.23E-36 150.966 166 1 95 242 334 91 91 95,8 96,9 98
CL2_283 blastn 01-May
SH004981.07FU|KF836907|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.31E-32 140.146 154 1 96 244 342 93 93 96,9 98,0 98
CL2_284 blastn 01-May
SH001323.07FU|KF939972|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.70E-42 170.803 188 4 107 247 352 103 103 99,0 97,2 107
CL2_285 blastn 01-May
SH001103.07FU|AJ567734|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 4.87E-38 158.179 174 3 96 57 152 93 93 98,9 95,9 98
CL2_286 blastn 01-May
SH175587.07FU|HF674807|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.50E-39 161.786 178 1 107 437 542 103 103 96,3 100,0 107
CL2_287 blastn 01-May
SH001017.07FU|KJ209706|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.93E-37 154.573 170 1 98 244 343 96 96 98,0 100,0 98

CL2_288 blastn 01-May

SH024970.07FU|FN397384|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.69E-41 169 186 1 98 522 426 97 97 99,0 100,0 98

CL2_289 blastn 01-May

SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.94E-30 132.932 146 1 96 55 153 89 89 92,7 98,0 98

CL2_290 blastn 01-May

SH524085.07FU|KM208142|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.07E-34 145.556 160 2 96 223 319 91 91 95,8 96,9 98

CL2_291 blastn 01-May

SH219474.07FU|FJ769308|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.23E-36 150.966 166 1 96 55 153 95 95 99,0 98,0 98

CL2_292 blastn 01-May

SH174581.07FU|KJ564166|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.52E-35 149.163 164 5 98 137 232 92 92 97,9 95,9 98

CL2_293 blastn 01-May

SH199961.07FU|FJ769296|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.28E-40 165.393 182 1 98 55 151 96 96 98,0 100,0 98

CL2_294 blastn 01-May

SH176087.07FU|GQ388573|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.21E-42 172.606 190 1 98 55 152 97 97 99,0 100,0 98

CL2_295 blastn 01-May

SH529448.07FU|HG425981|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.87E-38 158.179 174 1 96 222 318 94 94 97,9 98,0 98

CL2_296 blastn 01-May

SH197521.07FU|AJ517450|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.15E-39 163.589 180 1 93 55 147 92 92 98,9 94,9 98

CL2_297 blastn 01-May

SH000326.07FU|JX096575|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.52E-35 149.163 164 3 98 244 340 92 92 95,8 98,0 98

CL2_298 blastn 01-May

SH001017.07FU|KJ209706|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.93E-37 154.573 170 1 98 244 343 96 96 98,0 100,0 98

CL2_299 blastn 01-May

SH000346.07FU|HE775305|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.07E-34 145.556 160 1 96 222 323 95 95 99,0 98,0 98

CL2_300 blastn 01-May

SH489719.07FU|JX321802|k__Fungi;p__unclassified_Fungi;c__unclassified_Fungi;o__unclassified_Fungi;f__unclassified_Fungi;g__unclassified_Fungi;s__Fungi_sp; 1.70E-37 156.376 172 2 96 78 173 93 93 97,9 96,9 98

CL2_301 blastn 01-May

SH017245.07FU|JX096615|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.87E-45 181.623 200 1 108 242 349 105 105 97,2 100,0 108

CL2_302 blastn 01-May

SH199961.07FU|FJ769296|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.66E-41 169 186 2 97 56 151 95 95 99,0 99,0 97

CL2_303 blastn 01-May

SH199961.07FU|FJ769296|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.61E-42 170.803 188 1 97 55 151 96 96 99,0 100,0 97

CL2_304 blastn 01-May
SH197521.07FU|AJ517456|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.91E-11 69.8143 76 1 97 55 153 80 80 82,5 100,0 97

CL2_305 blastn 01-May
SH001103.07FU|AJ567734|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 2.04E-36 152.769 168 1 95 55 152 94 94 98,9 97,9 97

CL2_306 blastn 01-May
SH001356.07FU|FN397320|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.04E-36 152.769 168 2 97 70 163 93 93 96,9 99,0 97

CL2_307 blastn 01-May
SH197522.07FU|KF939958|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.04E-36 152.769 168 1 97 244 348 97 97 100,0 100,0 97

CL2_308 blastn 01-May
SH199955.07FU|GQ388414|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.13E-29 127.522 140 1 95 55 150 88 88 92,6 97,9 97

CL2_309 blastn 01-May
SH004981.07FU|KF836907|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.29E-32 140.146 154 1 95 244 341 91 91 95,8 97,9 97

CL2_310 blastn 01-May
SH199961.07FU|FJ769296|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.80E-38 158.179 174 1 97 55 151 93 93 95,9 100,0 97

CL2_311 blastn 01-May
SH199961.07FU|FJ769296|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.50E-42 170.803 188 1 94 55 148 94 94 100,0 97,9 96

CL2_312 blastn 01-May
SH024970.07FU|FN397384|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.50E-42 170.803 188 1 94 522 429 94 94 100,0 97,9 96

CL2_313 blastn 01-May
SH019349.07FU|JX096596|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.04E-33 143.752 158 1 94 242 334 90 90 95,7 97,9 96

CL2_314 blastn 01-May
SH197521.07FU|AJ517456|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 1.55E-31 136.539 150 1 96 55 153 91 91 94,8 100,0 96

CL2_315 blastn 01-May
SH497462.07FU|KJ484704|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.36E-17 87.848 96 4 107 224 323 86 86 82,7 95,4 109

CL2_316 blastn 01-May
SH001017.07FU|KF836914|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_intraradices; 4.73E-38 158.179 174 1 94 244 339 93 93 98,9 97,9 96

CL2_317 blastn 01-May
SH175543.07FU|FR750194|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_irregularis; 4.05E-46 185.23 204 1 107 292 398 105 105 98,1 98,2 109

CL2_318 blastn 01-May
SH199961.07FU|FJ769296|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.36E-38 159.983 176 2 94 56 148 91 91 97,8 96,9 96

CL2_319 blastn 01-May
SH524085.07FU|KM208142|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.30E-29 129.325 142 2 94 223 319 87 87 93,5 96,9 96

CL2_320 blastn 01-May

SH001328.07FU|KF206512|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.63E-38 158.179 174 3 107 190 296 102 102 97,1 96,3 109
CL2_321 blastn 01-May

SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.43E-32 138.342 152 1 93 456 547 87 87 93,5 96,9 96
CL2_322 blastn 01-May

SH197521.07FU|AJ517456|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Rhizophagus;s__Rhizophagus_sp; 5.41E-12 71.6177 78 4 96 59 153 78 78 83,9 96,9 96
CL2_323 blastn 01-May

SH175545.07FU|HG425884|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.17E-46 187.033 206 1 110 233 341 108 108 98,2 100,0 110
CL2_324 blastn 01-May

SH199961.07FU|FJ769296|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.98E-36 152.769 168 1 93 55 148 91 91 97,8 97,9 95
CL2_325 blastn 01-May

SH521403.07FU|KJ484647|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 3.15E-21 102.275 112 1 95 222 314 81 81 85,3 100,0 95
CL2_326 blastn 01-May

SH001312.07FU|KR105639|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_duoreactiva; 8.43E-35 147.359 162 8 95 247 332 86 86 97,7 92,6 95
CL2_327 blastn 01-May

SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.25E-32 140.146 154 1 92 456 547 86 86 93,5 96,8 95
CL2_328 blastn 01-May

SH001312.07FU|KR105639|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Dominikia;s__Dominikia_duoreactiva; 4.60E-38 158.179 174 1 94 241 332 92 92 97,9 100,0 94
CL2_329 blastn 01-May

SH001323.07FU|KF939972|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.76E-44 179.82 198 1 111 244 352 108 108 97,3 100,0 111
CL2_330 blastn 01-May

SH001356.07FU|FN397320|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.32E-38 159.983 176 1 94 69 163 93 93 98,9 100,0 94
CL2_331 blastn 01-May

SH004981.07FU|KF836907|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 6.57E-31 134.736 148 1 106 244 343 96 96 90,6 95,5 111
CL2_332 blastn 01-May

SH019350.07FU|JX096620|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 8.00E-49 194.247 214 1 111 242 353 111 111 100,0 100,0 111
CL2_333 blastn 01-May

SH212911.07FU|AY236296|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.24E-42 170.803 188 1 110 191 300 106 106 96,4 98,2 112
CL2_334 blastn 01-May

SH001356.07FU|FN397320|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 3.10E-40 165.393 182 2 92 70 160 91 91 100,0 96,8 94
CL2_335 blastn 01-May

SH176129.07FU|EF393596|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.23E-29 129.325 142 2 91 457 547 84 84 93,3 95,7 94
CL2_336 blastn 01-May

SH200108.07FU|FR750526|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_macrocarpum; 8.19E-35 147.359 162 1 93 242 333 89 89 95,7 100,0 93
CL2_337 blastn 01-May
SH521403.07FU|KJ484659|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.30E-38 159.983 176 1 93 222 313 92 92 98,9 100,0 93
CL2_338 blastn 01-May
SH024973.07FU|KF939960|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.30E-38 159.983 176 1 91 244 334 90 90 98,9 97,8 93
CL2_339 blastn 01-May
SH001356.07FU|FN397320|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.72E-36 150.966 166 1 93 69 163 92 92 98,9 100,0 93
CL2_340 blastn 01-May
SH176142.07FU|KJ564159|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.58E-37 156.376 172 1 93 244 335 91 91 97,8 100,0 93
CL2_341 blastn 01-May
SH521403.07FU|KJ484647|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.07E-20 100.472 110 1 93 222 314 80 80 86,0 100,0 93
CL2_342 blastn 01-May
SH024970.07FU|JF439161|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.20E-32 140.146 154 1 92 244 337 88 88 95,7 100,0 92
CL2_343 blastn 01-May
SH521403.07FU|KJ484647|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 6.62E-36 150.966 166 1 92 222 314 90 90 97,8 100,0 92
CL2_344 blastn 01-May
SH176144.07FU|KJ564157|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.81E-34 145.556 160 8 92 250 333 84 84 98,8 92,4 92
CL2_345 blastn 01-May
SH001356.07FU|FN397320|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 9.82E-34 143.752 158 2 90 70 160 88 88 98,9 96,7 92
CL2_346 blastn 01-May
SH176142.07FU|KJ564159|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 8.06E-35 147.359 162 1 92 244 335 90 90 97,8 100,0 92
CL2_347 blastn 01-May
SH017793.07FU|GQ388487|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.50E-47 188.837 208 1 138 55 192 129 129 93,5 100,0 138
CL2_348 blastn 01-May
SH176142.07FU|KJ564159|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.34E-25 116.702 128 1 91 244 335 84 84 92,3 100,0 91
CL2_349 blastn 01-May
SH200111.07FU|EU350772|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.98E-26 118.505 130 1 143 33 168 117 117 81,8 100,0 143
CL2_350 blastn 01-May
SH521403.07FU|KJ484659|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 2.77E-34 145.556

160 1 91 222 313 88 88 96,7 100,0 91
CL2_351 blastn 01-May
SH024970.07FU|FN397384|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.94E-35 147.359 162 1 89 522 431 89 89 100,0 97,8 91
CL2_352 blastn 01-May
SH200435.07FU|KF836930|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.07E-74 280.808 310 1 155 244 398 155 155 100,0 100,0 155
CL2_353 blastn 01-May
SH176142.07FU|KJ564159|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.44E-31 136.539 150 1 91 244 335 86 86 94,5 100,0 91
CL2_354 blastn 01-May
SH017476.07FU|FJ362330|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.46E-70 266.382 294 1 160 28 187 157 157 98,1 98,8 162
CL2_355 blastn 01-May
SH466345.07FU|AJ699063|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.12E-22 105.882 116 20 163 1839 1983 116 116 80,6 88,3 163
CL2_356 blastn 01-May
SH024974.07FU|JF439111|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 2.96E-21 102.275 112 1 87 242 333 80 80 92,0 95,6 91
CL2_357 blastn 01-May
SH000348.07FU|HF674801|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 4.39E-38 158.179 174 1 91 456 547 91 91 100,0 100,0 91
CL2_358 blastn 01-May
SH176101.07FU|AY236252|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 2.13E-29 129.325 142 1 89 191 275 83 83 93,3 97,8 91
CL2_359 blastn 01-May
SH521585.07FU|KF836969|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Glomus;s__Glomus_sp; 1.26E-38 159.983 176 1 91 244 334 90 90 98,9 100,0 91
CL2_360 blastn 01-May
SH000331.07FU|JQ218218|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.32E-29 127.522 140 12 90 284 363 78 78 98,7 87,8 90
CL2_361 blastn 01-May
SH176144.07FU|KJ564157|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 5.27E-37 154.573 170 3 90 246 333 87 87 98,9 97,8 90
CL2_362 blastn 01-May
SH521403.07FU|KJ484647|k__Fungi;p__Glomeromycota;c__unclassified_Glomeromycota;o__unclassified_Glomeromycota;f__unclassified_Glomeromycota;g__unclassified_Glomeromycota;s__Glomeromycota_sp; 1.84E-36 152.769 168 1 88 222 310 88 88 100,0 97,8 90
CL2_363 blastn 01-May
SH176142.07FU|KJ564159|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 7.81E-35 147.359 162 1 88 244 329 86 86 97,7 97,8 90
CL2_364 blastn 01-May
SH192876.07FU|JX096602|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 1.12E-68 260.971 288 1 171 244 414 165 165 96,5 100,0 171
CL2_365 blastn 01-May
SH176144.07FU|KJ564157|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__unclassified_Glomeraceae;s__Glomeraceae_sp; 6.31E-36 150.966 166 1 89 244 333 88 88 98,9 100,0 89
CL2_366 blastn 01-May

SH001312.07FU|KR105639|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__D
ominikia;s__Dominikia_duoreactiva; 2.35E-22 105.882 116 1 89 241 332 81 81 91,0 100,0 89
CL2_367 blastn 01-May

SH200108.07FU|FR750544|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_macrocarpum; 3.27E-33 141.949 156 1 89 242 330 87 87 97,8 100,0 89
CL2_368 blastn 01-May

SH200108.07FU|KC182043|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_macrocarpum; 1.12E-32 140.146 154 1 88 244 334 87 87 98,9 100,0 88
CL2_369 blastn 01-May

SH176144.07FU|KJ564157|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
classified_Glomeraceae;s__Glomeraceae_sp; 3.22E-33 141.949 156 1 88 244 333 87 87 98,9 100,0
88
CL2_370 blastn 01-May

SH017240.07FU|UDB025485|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_macrocarpum; 7.09E-29 127.522 140 1 88 14 104 84 84 95,5 100,0 88
CL2_371 blastn 01-May

SH001320.07FU|AJ504630|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__Gl
omus;s__Glomus_sp; 3.16E-33 141.949 156 1 87 31 118 85 85 97,7 100,0 87
CL2_372 blastn 01-May

SH203809.07FU|EF393617|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;g__
Racocetra;s__Racocetra_sp; 1.50E-30 132.932 146 2 81 466 544 78 78 97,5 98,8 81
CL2_373 blastn 01-May

SH000331.07FU|JQ218218|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Glomerales;f__Glomeraceae;g__un
classified_Glomeraceae;s__Glomeraceae_sp; 8.90E-21 100.472 110 12 78 284 354 66 66 98,5 82,7 81
CL2_374 blastn 01-May

SH203803.07FU|FN547603|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;
g__Cetraspora;s__Cetraspora_gilmorei;2.15E-28 125.719 138 1 79 293 371 75 75 94,9 100,0 79
CL2_375 blastn 01-May

SH019941.07FU|FR750140|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;
g__Dentiscutata;s__Dentiscutata_erythropus; 7.37E-28 123.915 136 1 78 191 268 74 74 94,9 100,0
78
CL2_376 blastn 01-May

SH203803.07FU|FN547603|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;
g__Cetraspora;s__Cetraspora_gilmorei;1.09E-25 116.702 128 1 78 293 371 75 75 96,2 100,0 78
CL2_377 blastn 01-May

SH019941.07FU|FR750140|k__Fungi;p__Glomeromycota;c__Glomeromycetes;o__Diversisporales;f__Gigasporaceae;
g__Dentiscutata;s__Dentiscutata_erythropus; 3.74E-25 114.899 126 1 77 191 268 73 73 94,8 100,0
77

Appendix S5: Results of analysis of variance (ANOVA) with statistic values, degrees of freedom and *P* values.**A) Results of one-way ANOVA showing differences between rhizosphere soil of field-sampled diploid (2x) vs. tetraploid (4x) plants.**

Variable	df	<i>F</i>	<i>P</i>
pH _{H2O}	1	3.760	0.063
CEC (mmol _c kg ⁻¹)	1	3.871	0.059
C _{org} (%)	1	4.716	0.039
N (%)	1	6.001	0.021
P (mg kg ⁻¹)	1	2.353	0.136
K (mg kg ⁻¹)	1	3.776	0.062
Ca (mg kg ⁻¹)	1	3.383	0.076
Mg (mg kg ⁻¹)	1	8.663	0.006

B) Results of two-way ANOVA showing effects of ploidy level, substrate and their interaction on colonization of *Centaurea stoebe* roots by arbuscular mycorrhizal fungi (AMF) and dark septate endophytes (DSE) in the greenhouse experiment.

Factor	df	AMF colonization						DSE colonization	
		Total		Arbuscular		Vesicular			
		<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>
Ploidy	1	3.343	0.078	0.001	0.982	0.461	0.503	0.096	0.759
Substrate	1	3.010	0.094	3.459	0.073	0.103	0.751	1.378	0.250
Ploidy × substrate	1	1.778	0.193	1.645	0.210	0.251	0.620	0.007	0.932

C) Results of three-way ANOVA showing effects of ploidy level, substrate, inoculation with arbuscular mycorrhizal fungi and their interactions on *Centaurea stoebe* growth and phosphorus uptake in the greenhouse experiment.

Factor	df	Leaf number		Longest leaf length		Shoot dry mass		Root dry mass		Root / shoot ratio		Shoot phosphorus concentration	
		<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>	<i>F</i>	<i>P</i>
Ploidy	1	0.083	0.775	18.079	<0.0001	6.574	0.013	4.377	0.041	12.353	0.001	3.487	0.067
Substrate	1	61.582	<0.0001	70.698	<0.0001	126.310	<0.0001	90.152	<0.0001	2.719	0.105	0.162	0.689
Inoculation	1	4.521	0.038	0.021	0.887	16.608	0.002	56.499	<0.0001	22.466	<0.0001	130.76	<0.0001
Ploidy × substrate	1	0.000	0.985	0.824	0.368	5.319	0.025	1.062	0.307	0.149	0.701	0.334	0.566
Ploidy × inoculation	1	0.554	0.460	0.009	0.924	0.040	0.841	7.188	0.010	1.403	0.241	0.523	0.473
Substrate × inoculation	1	1.143	0.290	1.427	0.237	2.445	0.124	5.872	0.019	0.423	0.518	0.122	0.728
Ploidy × substrate × inoculation	1	0.406	0.527	0.037	0.849	0.102	0.751	2.951	0.091	2.346	0.131	2.640	0.110

[illegible]

Appendix S8: Community matrix of operational taxonomical units (OTUs) of arbuscular mycorrhizal fungi in roots of *Centaurea stoebe* s.l. in the data set downsampled to 225 reads per sample. Data represent read numbers in each sample.

Sample	OTU_1	OTU_2	OTU_3	OTU_4	OTU_5	OTU_6	OTU_7	OTU_8	OTU_9	OTU_10	OTU_11	OTU_12	OTU_13	OTU_14	OTU_15	OTU_16	OTU_17	OTU_18	OTU_19	OTU_20	OTU_21	OTU_22	OTU_23	OTU_24	OTU_25	OTU_26	OTU_27	OTU_28	OTU_29	OTU_31	OTU_32	OTU_34	OTU_35	OTU_36													
OTU_37	OTU_38	OTU_39	OTU_41	OTU_42	OTU_43	OTU_44	OTU_45	OTU_46	OTU_48	OTU_49	OTU_50-OTU_225 / sample																																				
CS01	0	0	0	0	0	99	1	1	0	0	11	0	0	0	0	105	0	0	0	0	0	1	0	0	0	0	0	3	1	0	0	3	0	0	0	0	0	9	225								
CS02	0	0	0	0	115	0	4	7	2	0	0	0	0	0	0	0	1	5	0	8	0	0	2	0	15	9	0	1	0	1	0	0	4	2	0	1	0	0	0	48	0	0	16	225			
CS03	4	0	0	0	0	123	0	42	0	0	0	0	0	0	0	0	11	0	0	0	0	0	33	0	0	0	0	5	6	0	0	0	0	0	0	0	0	1	0	0	8	225					
CS04	0	0	0	0	0	95	0	0	0	0	0	0	0	0	0	0	51	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0	3	0	0	0	0	0	27	0	0	10	225				
CS05	0	0	1	0	0	0	0	0	0	0	0	0	10	0	0	7	0	0	0	0	0	6	0	33	10	0	14	0	0	2	0	0	0	0	0	0	0	0	3	11	21	107	0	0	12	225	
CS06	0	0	0	14	3	0	0	1	0	10	0	38	0	0	5	0	0	0	0	16	0	3	0	1	0	0	0	0	2	0	4	0	0	0	1	0	0	8	8	21	88	0	0	2	17	225	
CS07	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	186	1	0	3	0	0	13	0	0	0	0	0	5	0	0	0	0	12	0	1	0	8	225		
CS08	0	0	0	0	0	0	0	0	0	0	78	2	0	0	0	0	0	0	0	5	0	6	3	2	6	0	0	0	0	2	0	0	0	0	0	0	0	0	0	118	0	2	1	11	225		
CS09	2	1	0	0	0	0	9	5	0	24	0	0	0	0	2	0	0	0	0	1	33	0	3	0	0	0	0	0	1	0	0	0	0	0	0	0	3	0	0	2	4	134	0	0	15	225	
CS10	10	0	0	0	0	0	1	1	0	7	72	0	0	0	0	0	0	0	0	45	0	3	0	0	0	0	2	0	0	0	0	0	0	0	5	0	0	0	0	75	0	2	0	12	225		
CS11	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	33	0	12	0	0	167	0	0	1	7	225	
CS12	0	0	0	0	8	4	0	0	0	0	0	0	94	0	0	0	0	0	0	0	62	0	22	0	0	0	1	3	6	2	0	14	0	0	0	0	0	0	0	0	0	0	0	13	225		
CS13	0	0	0	0	0	0	0	1	0	0	45	56	0	2	0	0	0	0	0	0	14	0	1	0	10	6	0	0	0	0	13	0	0	0	0	2	0	0	0	5	0	0	70	0	0	12	225
CS14	1	0	0	0	0	36	0	6	0	2	2	0	0	0	0	0	0	0	1	0	0	10	0	4	2	0	0	0	0	0	1	1	0	0	0	0	24	0	0	135	0	0	13	225			
CS15	0	0	0	0	0	2	0	0	0	0	4	0	0	0	0	0	0	4	8	0	22	0	12	12	0	0	1	0	0	0	0	0	0	0	1	0	0	2	0	0	100	56	1	0	13	225	
CS16	1	0	0	0	0	0	17	1	0	0	94	0	0	0	0	0	14	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	95	0	0	8	225		
CS17	0	1	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	201	0	0	0	4	225			
CS18	2	0	1	0	0	0	0	80	2	0	4	1	0	0	0	13	0	12	37	0	30	0	6	4	2	3	1	0	2	0	0	0	0	0	1	0	0	0	0	24	0	0	18	225			
CS19	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	5	0	0	0	0	0	0	36	0	0	1	0	0	0	1	0	0	0	0	0	0	2	1	29	136	0	0	10	225			
CS20	0	0	0	0	0	4	0	51	0	12	0	0	0	0	0	0	0	0	0	14	0	28	0	0	0	0	0	1	4	0	2	0	4	0	4	0	0	0	1	1	6	93	0	0	14	225	
CS21	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0	84	0	117	1	0	0	0	5	5	0	0	0	0	0	0	0	0	3	0	0	0	0	7	0	0	9	225	
CS22	2	0	0	0	0	28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	152	0	0	0	0	4	0	0	0	0	0	0	0	0	0	38	0	0	1	0	38	0	0	6	225
CS23	1	0	0	61	4	0	0	0	0	0	0	4	0	0	0	0	0	0	0	3	0	26	0	0	0	0	0	5	0	0	0	0	0	0	3	0	1	0	0	11	0	0	106	0	0	11	225
CS24	87	0	0	1	0	0	0	28	0	12	3	0	0	0	0	0	0	0	0	1	11	0	5	1	3	1	0	3	0	0	3	0	0	0	1	0	0	0	0	65	0	0	15	225			
CS25	0	0	0	0	15	0	0	0	50	0	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	2	0	0	0	2	2	0	1	0	139	0	0	9	225			
CS26	0	0	0	0	0	34	0	0	0	65	0	0	1	0	0	0	0	0	0	63	2	0	0	0	0	0	13	0	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	10	225		
CS27	0	0	0	67	9	12	0	0	0	32	0	0	11	0	0	0	0	0	0	65	0	0	0	0	0	0	0	3	0	1	0	0	3	0	0	21	0	1	0	0	0	0	0	11	225		
CS28	0	0	0	0	97	0	0	0	0	0	0	0	0	0	0	0	1	0	85	9	0	6	0	0	0	1	3	2	1	0	1	0	0	0	2	16	0	0	0	1	0	0	13	225			
CS29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	164	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	31	17	0	0	0	2	0	0	7	225			
Presence in no. of samples	9	2	3	5	4	16	3	12	5	8	17	9	3	1	4	7	3	1	11	14	2	23	6	7	12	3	12	12	7	12	1	7	4	4	8	11	2	1	10	7	5	25	1	4	3		
Read no.	110	2	3	151	20	543	19	311	40	179	342	289	22	2	19	205	7	2	418	335	3	743	19	52	60	6	38	45	18	49	1	31	9	13	45	107	35	2	69	25	81	1989	56	6	4		

Appendix S9: Summary of operational taxonomical units (OTUs) of arbuscular mycorrhizal fungi (AMF) in roots of *Centaurea stoebe* s.l.

OTU no.	Read no.	Proportion (%)	Subphyllum	Class	Order	Family	Genus	Species
OTU 1	187	0.90	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 2	2	0.01	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 3	14	0.07	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 4	741	3.56	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 5	74	0.36	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 6	2557	12.30	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Dominikia
OTU 7	85	0.41	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 8	545	2.62	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Dominikia
OTU 9	57	0.27	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 10	600	2.89	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Dominikia
OTU 11	797	3.83	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 12	568	2.73	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 13	102	0.49	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 14	3	0.01	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 15	23	0.11	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 16	300	1.44	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 17	18	0.09	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 18	7	0.03	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Kamienkia
OTU 19	2480	11.93	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 20	783	3.77	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Dominikia
OTU 21	11	0.05	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 22	1739	8.36	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 23	46	0.22	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 24	262	1.26	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 25	259	1.25	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 26	18	0.09	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 27	119	0.57	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 28	90	0.43	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 29	64	0.31	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 30	2	0.01	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 31	92	0.44	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 32	53	0.25	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 33	5	0.02	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 34	86	0.41	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 35	23	0.11	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 36	27	0.13	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 37	120	0.58	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 38	616	2.96	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		
OTU 39	35	0.17	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Funneliformis
OTU 40	2	0.01	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Septoglomus
OTU 41	2	0.01	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Glomus
OTU 42	557	2.68	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Glomus
OTU 43	30	0.14	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Rhizophagus
OTU 44	98	0.47	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Rhizophagus
OTU 45	5810	27.95	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Rhizophagus irregularis
OTU 46	666	3.20	Glomeromycotina	Glomeromycetes	Glomerales	Glomeraceae		Rhizophagus

OTU 47	2	0.01	Glomeromycotina	Glomeromycetes	Glomerales	Claroideoglomeraceae	Claroideoglomus
OTU 48	9	0.04	Glomeromycotina	Glomeromycetes	Diversisporales	Gigasporaceae	Racocetra
OTU 49	4	0.02	Glomeromycotina	Glomeromycetes	Diversisporales	Gigasporaceae	Cetraspora