

#AV500K  
**Prep 500**

PARCEL

VARIETY

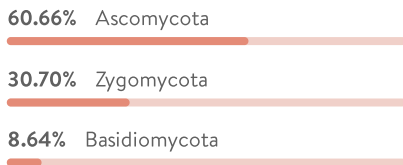
DATE

19-Jun-2019

**MICROBIAL POPULATION**

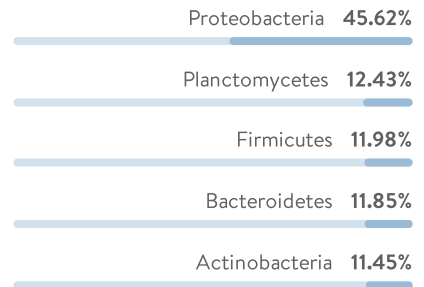
All the information shown in this microbial report is based on the detected presence of **482** different species.

FUNGAL  
PHYLUM DISTRIBUTION



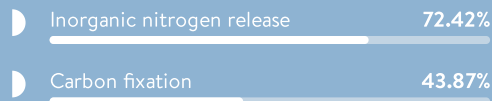
FUNGUS BACTERIA

BACTERIAL  
PHYLUM DISTRIBUTION

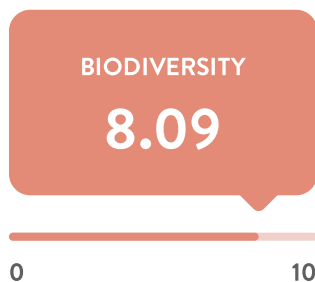


CONCLUSIONS

STRENGTHS



**BIOSUSTAINABILITY**



Richness, evenness and equilibrium of microbial species



Capability of soil microbial communities to perform multiple functions

## BACTERIAL QUANTIFICATION

### METHODOLOGY

The absolute quantification of bacterial communities using **Next-Gen sequencing** enables the cell number measurements and, thus, the knowledge of the total microbial loads among a sample

The present analysis relies on the application of a **spike-in of exogenous bacterial** with known microbial composition into crude soil amendment samples, under the ZymoBionics Spike-in Control I technology. After sequencing and data processing, the relative abundance of the exogenous bacterial strains and the known Spike-in cell input were used to transform relative abundances of all bacteria strains in the sample to absolute abundance.

Data in this report correspond to the average absolute abundance obtained from three technical replicates.

### LIST OF MAJOR BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

IN THIS ORDER OF MAGNITUDE

16 Microorganisms  
42.01% of the whole quantification

**e+8**

1	<i>Chthoniobacter sp.</i>	2.78E+08
2	<i>Devosia insulae</i>	2.40E+08
3	<i>Planctomyces sp.</i>	2.23E+08
4	<i>Rhodoplanes sp.</i>	2.13E+08
5	<i>Devosia sp.</i>	1.64E+08
6	<i>Ohtaekwangia sp.</i>	1.46E+08
7	<i>Phenylobacterium sp.</i>	1.42E+08
8	<i>Pirellula sp.</i>	1.40E+08
9	<i>Rhodopirellula sp.</i>	1.38E+08
10	<i>Pseudolabrys sp.</i>	1.28E+08
11	<i>Phycisphaera sp.</i>	1.19E+08
12	<i>Steroidobacter sp.</i>	1.18E+08

13	<i>Rhodococcus sp.</i>	1.14E+08
14	<i>Blastocatella sp.</i>	1.05E+08
15	<i>Gemmatimonas sp.</i>	1.05E+08
16	<i>Pricia sp.</i>	1.02E+08

IN THIS ORDER OF MAGNITUDE

63 Microorganisms  
43.66% of the whole quantification

**e+7**

17	<i>Mesorhizobium tianshanense</i>	9.71E+07
18	<i>Clostridium sp.</i>	9.60E+07
19	<i>Novosphingobium sp.</i>	9.21E+07
20	<i>Mycobacterium sp.</i>	8.97E+07
21	<i>Hyphomicrobium sp.</i>	8.64E+07
22	<i>Mesorhizobium sp.</i>	8.61E+07
23	<i>Pseudomonas flexibilis</i>	8.03E+07

## LIST OF MAJOR BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

24	<i>Pusillimonas</i> sp.	7.50E+07	43	<i>Cellulomonas xylanilytica</i>	3.88E+07
25	<i>Mesorhizobium ciceri</i>	7.24E+07	44	<i>Xiphinematobacter</i> sp.	3.85E+07
26	<i>Escherichia</i> sp.	7.23E+07	45	<i>Microthrix</i> sp.	3.66E+07
27	<i>Altererythrobacter</i> sp.	6.94E+07	46	<i>Singulisphaera</i> sp.	3.58E+07
28	<i>Filomicrobium</i> sp.	6.86E+07	47	<i>Weeksella</i> sp.	3.52E+07
29	<i>Aquicella</i> sp.	6.54E+07	48	<i>Nocardioides</i> sp.	3.39E+07
30	<i>Reyranella</i> sp.	5.73E+07	49	<i>Ilumatobacter</i> sp.	3.26E+07
31	<i>Opitutus</i> sp.	5.59E+07	50	<i>Truepera</i> sp.	3.25E+07
32	<i>Acidovorax</i> sp.	5.56E+07	51	<i>Sphingopyxis</i> sp.	3.17E+07
33	<i>Luteimonas mephitis</i>	5.53E+07	52	<i>Filimonas</i> sp.	3.02E+07
34	<i>Isosphaera</i> sp.	5.41E+07	53	<i>Luteibacter</i> sp.	2.94E+07
35	<i>Legionella</i> sp.	4.98E+07	54	<i>Chryseolinea</i> sp.	2.87E+07
36	<i>Bradyrhizobium</i> sp.	4.70E+07	55	<i>Agromyces bauzanensis</i>	2.85E+07
37	<i>Blastopirellula</i> sp.	4.38E+07	56	<i>Blastococcus aggregatus</i>	2.70E+07
38	<i>Marmoricola</i> sp.	4.36E+07	57	<i>Stenotrophomonas</i> sp.	2.67E+07
39	<i>Azospira</i> sp.	4.09E+07	58	<i>Butyrivibrio</i> sp.	2.27E+07
40	<i>Pelagibius</i> sp.	4.03E+07	59	<i>Gemmata</i> sp.	2.17E+07
41	<i>Pilimelia pattaloongensis</i>	3.98E+07	60	<i>Taibaiella</i> sp.	1.96E+07
42	<i>Methylobacillus flagellatus</i>	3.94E+07	61	<i>Balneimonas</i> sp.	1.94E+07

LIST OF MAJOR BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

62	<i>Pedomicrobium sp.</i>	1.80E+07
63	<i>Brevundimonas alba</i>	1.77E+07
64	<i>Georgenia satyanarayanai</i>	1.66E+07
65	<i>Agaricicola sp.</i>	1.65E+07
66	<i>Bradyrhizobium elkanii</i>	1.56E+07
67	<i>Phaeosporillum fulvum</i>	1.52E+07
68	<i>Bauldia sp.</i>	1.49E+07
69	<i>Caenimonas sp.</i>	1.48E+07
70	<i>Arenibacter sp.</i>	1.37E+07
71	<i>Pseudospirillum sp.</i>	1.35E+07
72	<i>Pedosphaera sp.</i>	1.35E+07
73	<i>Cellvibrio sp.</i>	1.34E+07
74	<i>Anaerostipes sp.</i>	1.29E+07
75	<i>Rhodobium sp.</i>	1.29E+07
76	<i>Turicibacter sp.</i>	1.27E+07
77	<i>Alysiosphaera sp.</i>	1.08E+07

78	<i>Massilia sp.</i>	9.25E+06
79	<i>Arthrobacter sp.</i>	8.62E+06
80	<i>Lautropia sp.</i>	8.55E+06
81	<i>Bacillus coahuilensis</i>	6.84E+06
82	<i>Coprococcus sp.</i>	6.62E+06
83	<i>Bacillus sp.</i>	4.67E+06
84	<i>Paenibacillus sp.</i>	3.83E+06
85	<i>Bacillus aryabhatai</i>	2.15E+06

NOTES

Genus predictions ('sp') that have species appearing in the CDFA list provided. (Species might or might not be present)

Species that appears explicitly highlighted in the CDFA list

IN THIS ORDER OF MAGNITUDE

8 Microorganisms  
0.86% of the whole quantification

**e+6**

# PLANT HEALTH IMPROVEMENT

Biocontrol agents, plant growth promoting organisms

## BIOCONTROL



Microbial species grouped according to the type of pest they encounter, capable of preventing pathogenic species from taking hold or proliferation

Fungicide agents

NOT DETECTED

Bactericide agents

NOT DETECTED

Insecticide agents

NOT DETECTED

Nematicide agents

NOT DETECTED

## HORMONE PRODUCTION



Microbial species grouped according to the type of phytohormone they generate

Auxin production (IAA)

CELL DIVISION

STEM ELONGATION

8.16%

Cytokinin production (CK)

CELL PROLIFERATION

CELL DIFFERENTIATION

4.56%

Gibberellin production (GA)

STEM ELONGATION

GERMINATION

FLOWERING

0.97%

## STRESS ADAPTATION



Microbial species grouped according to their relationship with the metabolisms linked to the capability to withstand stress conditions

Exopolysaccharide production

NUTRIENT TRAP

SALINITY PROTECT.

DROUGHT PROTECT.

4.65%

ACC deaminase (ACC-d)

PATHOGEN PROTECT.

SALINITY PROTECT.

DROUGHT PROTECT.

5.48%

Heavy metal solubilization

BIOREMEDIATION

DETOXIFICATION

ALLEVIATE HEAVY METAL STRESS

3.36%

Salicylic acid (SA)

DROUGHT PROTECT.

SALINITY PROTECT.

ALLEVIATE HEAVY METAL STRESS

0.03%

Salt tolerance

SALINITY PROTECT.

ROOT GROWTH PROMOTION

4.10%

Abscisic acid (ABA)

GROWTH REGULATION

PLANT RESISTANCE

INCREASE YIELDS

0.04%

Siderophore production

IRON AVAILABILITY

BIOFERTILIZER

40.73%

# NUTRITION

Nutritional status based on the presence and mobilization of certain compounds

## MAJOR COMPOUNDS



### Carbon

#### GAIN

Carbon fixation 43.87%

#### LOSS

Aerobic respiration 85.13%

Fermentation 70.95%

Methanogenesis 45.42%

#### INDIRECT BENEFITS

Organic matter release 33.34%



### Nitrogen

#### NUTRIENT SUPPLY

Inorganic nitrogen release 72.42%

#### NUTRIENT COMPETITION

Inorganic nitrogen consumption 54.52%

#### INDIRECT BENEFITS

Inorganic nitrogen cycle health 1.5 / 2



### Phosphorus

#### NUTRIENT SUPPLY

Inorganic P solubilization 42.58%

#### NUTRIENT COMPETITION

Inorganic P consumption 65.64%

#### INDIRECT BENEFITS

Organic P assimilation 72.76%



### Potassium

#### NUTRIENT SUPPLY

Potassium solubilization 42.58%

#### NUTRIENT COMPETITION

Potassium consumption 80.16%

## MINOR COMPOUNDS



### Iron

Iron assimilation 43.30%



### Calcium

Calcium transport 73.18%



### Zinc

Zinc transport equilibrium 69.19%



### Copper

Copper export 62.00%



### Manganese

Manganese transport equilibrium 40.96%



### Magnesium

Magnesium transport 73.12%



### Sulfur

Sulfur cycle equilibrium 1.32 / 2



### Chlorine

Chlorine transport 82.00%

# APPENDIX

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

1	<i>Parvibaculum sp.</i>	2.92E+07	20	<i>Kaistia sp.</i>	9.92E+06
2	<i>Saccharimonas sp.</i>	2.58E+07	21	<i>Caulobacter henricii</i>	9.87E+06
3	<i>Mariprofundus sp.</i>	2.51E+07	22	<i>Nitrosococcus sp.</i>	9.85E+06
4	<i>Conexibacter sp.</i>	2.26E+07	23	<i>Sporocytophaga sp.</i>	9.68E+06
5	<i>Sphingopyxis alaskensis</i>	1.67E+07	24	<i>Nitrososphaera sp.</i>	9.67E+06
6	<i>Solirubrobacter sp.</i>	1.66E+07	25	<i>Haliangium sp.</i>	9.59E+06
7	<i>Coxiella sp.</i>	1.54E+07	26	<i>Aquamicrobium sp.</i>	9.36E+06
8	<i>Bdellovibrio sp.</i>	1.45E+07	27	<i>Ilumatobacter fluminis</i>	9.20E+06
9	<i>Luteimonas composti</i>	1.36E+07	28	<i>Achromobacter xylosoxidans</i>	9.03E+06
10	<i>Muricauda sp.</i>	1.31E+07	29	<i>Ensifer sp.</i>	8.97E+06
11	<i>Mogibacterium sp.</i>	1.29E+07	30	<i>Nitrolancea sp.</i>	8.63E+06
12	<i>Sandaracinus sp.</i>	1.26E+07	31	<i>Constrictibacter sp.</i>	8.45E+06
13	<i>Patulibacter sp.</i>	1.21E+07	32	<i>Rhizomicrobium sp.</i>	8.27E+06
14	<i>Bythopirellula sp.</i>	1.20E+07	33	<i>Achromobacter sp.</i>	8.23E+06
15	<i>Aeromicrobium sp.</i>	1.19E+07	34	<i>Thermomonas sp.</i>	8.04E+06
16	<i>Woodsholea sp.</i>	1.17E+07	35	<i>Bryobacter sp.</i>	7.78E+06
17	<i>Brevundimonas bullata</i>	1.11E+07	36	<i>Demequina sp.</i>	7.66E+06
18	<i>Brevundimonas sp.</i>	1.00E+07	37	<i>Roseiflexus sp.</i>	6.76E+06
19	<i>Hyphomicrobium zavarzinii</i>	1.00E+07	38	<i>Mycobacterium celatum</i>	6.69E+06

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

39	<i>Spingomonas</i> sp.	6.56E+06
40	<i>Haloferula</i> sp.	6.16E+06
41	<i>Ochrobactrum rhizogenes</i>	6.15E+06
42	<i>Erythrobacter</i> sp.	6.08E+06
43	<i>Lysobacter</i> sp.	5.74E+06
44	<i>Nocardioides koreensis</i>	5.46E+06
45	<i>Pedobacter</i> sp.	5.29E+06
46	<i>Dokdonella</i> sp.	5.25E+06
47	<i>Defluviicoccus</i> sp.	5.07E+06
48	<i>Caldilinea</i> sp.	5.04E+06
49	<i>Stella</i> sp.	5.03E+06
50	<i>Flavisolibacter</i> sp.	5.00E+06
51	<i>Methanobrevibacter</i> sp.	4.88E+06
52	<i>Pseudomarcicurvus</i> sp.	4.79E+06
53	<i>Phaselicystis</i> sp.	4.71E+06
54	<i>Alterococcus</i> sp.	4.61E+06
55	<i>Sandarakinorhabdus</i> sp.	4.39E+06
56	<i>Acinetobacter lwoffii</i>	4.26E+06
57	<i>Bosea</i> sp.	4.24E+06
58	<i>Azoarcus</i> sp.	4.06E+06
59	<i>Amaricoccus</i> sp.	4.02E+06
60	<i>Pseudomonas</i> sp.	3.71E+06
61	<i>Sneathiella</i> sp.	3.62E+06
62	<i>Actinocorallia</i> sp.	3.61E+06
63	<i>Ornatilinea</i> sp.	3.59E+06
64	<i>Nitrosomonas</i> sp.	3.40E+06
65	<i>Bythopirellula goksoyri</i>	3.38E+06
66	<i>Subsaxibacter</i> sp.	3.34E+06
67	<i>Fodinicola</i> sp.	3.17E+06
68	<i>Ensifer meliloti</i>	3.17E+06
69	<i>Agrobacterium tumefaciens</i>	3.12E+06
70	<i>Anaeromyxobacter</i> sp.	3.09E+06
71	<i>Aequorivita</i> sp.	2.96E+06
72	<i>Pleomorphomonas</i> sp.	2.94E+06
73	<i>Beutenbergia cavernae</i>	2.75E+06
74	<i>Anaerotruncus</i> sp.	2.74E+06
75	<i>Thauera</i> sp.	2.65E+06
76	<i>Comamonas composti</i>	2.56E+06
77	<i>Sedimentibacter</i> sp.	2.55E+06
78	<i>Xanthomonas</i> sp.	2.52E+06



## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

79	<i>Sedimentibacter hongkongensis</i>	2.50E+06
80	<i>Pelagicoccus</i> sp.	2.45E+06
81	<i>Brevundimonas diminuta</i>	2.45E+06
82	<i>Nakamurella</i> sp.	2.45E+06
83	<i>Ruminococcus</i> sp.	2.40E+06
84	<i>Hydrogenoanaerobacterium</i> sp.	2.38E+06
85	<i>Pseudomonas peli</i>	2.25E+06
86	<i>Peredibacter</i> sp.	2.25E+06
87	<i>Bosea eneae</i>	2.23E+06
88	<i>Hirschia</i> sp.	2.22E+06
89	<i>Methylothermobacter mobilis</i>	2.19E+06
90	<i>Croceibacter</i> sp.	2.17E+06
91	<i>Blastomonas</i> sp.	2.15E+06
92	<i>Dongia</i> sp.	2.10E+06
93	<i>Sphingobium</i> sp.	2.06E+06
94	<i>Bacillus firmus</i>	2.05E+06
95	<i>Simiduia</i> sp.	2.04E+06
96	<i>Citricoccus xinjiangensis</i>	2.03E+06
97	<i>Pseudomonas litoralis</i>	2.01E+06
98	<i>Ardenscatena</i> sp.	1.97E+06
99	<i>Sorangium</i> sp.	1.96E+06
100	<i>Ignavibacterium</i> sp.	1.93E+06
101	<i>Actinotalea</i> sp.	1.88E+06
102	<i>Ruminococcus flavefaciens</i>	1.87E+06
103	<i>Pontibacter</i> sp.	1.85E+06
104	<i>Noviherbaspirillum</i> sp.	1.85E+06
105	<i>Adhaeribacter terreus</i>	1.85E+06
106	<i>Luteolibacter</i> sp.	1.84E+06
107	<i>Rubricoccus</i> sp.	1.83E+06
108	<i>Iamia majanohamensis</i>	1.81E+06
109	<i>Pelagibacterium halotolerans</i>	1.80E+06
110	<i>Marinicella</i> sp.	1.74E+06
111	<i>Leucobacter</i> sp.	1.72E+06
112	<i>Owenweeksia</i> sp.	1.72E+06
113	<i>Tistlia consotensis</i>	1.68E+06
114	<i>Gaiella</i> sp.	1.64E+06
115	<i>Dichotomicrobium</i> sp.	1.63E+06
116	<i>Rhodanobacter</i> sp.	1.62E+06
117	<i>Alkaliphilus</i> sp.	1.62E+06
118	<i>Affifella</i> sp.	1.62E+06

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

119	<i>Phyllobacterium sp.</i>	1.59E+06	139	<i>Sufflavibacter sp.</i>	1.05E+06
120	<i>Dietzia maris</i>	1.55E+06	140	<i>Haloplasma sp.</i>	1.01E+06
121	<i>Arthrobacter cereus</i>	1.48E+06	141	<i>Azospirillum sp.</i>	9.98E+05
122	<i>Williamsia faeni</i>	1.46E+06	142	<i>Parvularcula sp.</i>	9.92E+05
123	<i>Kaistobacter sp.</i>	1.44E+06	143	<i>Arthrospira sp.</i>	9.51E+05
124	<i>Atopobium sp.</i>	1.42E+06	144	<i>Oscillospira sp.</i>	9.45E+05
125	<i>Thalassobaculum sp.</i>	1.39E+06	145	<i>Haliaea sp.</i>	9.24E+05
126	<i>Rhodomicrobium sp.</i>	1.37E+06	146	<i>Limnobacter sp.</i>	8.47E+05
127	<i>Jatrophihabitans sp.</i>	1.33E+06	147	<i>Rhizobacter globosum</i>	8.43E+05
128	<i>Inquilinus sp.</i>	1.32E+06	148	<i>Fimbriimonas sp.</i>	8.35E+05
129	<i>Micromonospora hermanusense</i>	1.30E+06	149	<i>Captivus sp.</i>	8.16E+05
130	<i>Ornithinimicrobium pekingense</i>	1.28E+06	150	<i>Waddlia sp.</i>	8.05E+05
131	<i>Flavobacterium sp.</i>	1.28E+06	151	<i>Bacteriovorax sp.</i>	8.04E+05
132	<i>Collinsella sp.</i>	1.24E+06	152	<i>Nitrospira sp.</i>	7.91E+05
133	<i>Aeribacillus sp.</i>	1.23E+06	153	<i>Singulisphaera acidiphila</i>	7.57E+05
134	<i>Blautia sp.</i>	1.22E+06	154	<i>Chitinophaga sp.</i>	6.98E+05
135	<i>Nafulsella sp.</i>	1.15E+06	155	<i>Nannocystis exedens</i>	6.93E+05
136	<i>Streptomyces sp.</i>	1.14E+06	156	<i>Blastococcus sp.</i>	6.83E+05
137	<i>Lysinibacillus sp.</i>	1.11E+06	157	<i>Roseomonas sp.</i>	6.83E+05
138	<i>Sphaerobacter sp.</i>	1.08E+06	158	<i>Acetitomaculum sp.</i>	6.81E+05

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

159	<i>Pseudoxanthomonas sp.</i>	6.78E+05	179	<i>Ochrobactrum latifolia</i>	4.97E+05
160	<i>Micromonospora sp.</i>	6.47E+05	180	<i>Agromyces flavus</i>	4.90E+05
161	<i>Ferruginibacter sp.</i>	6.38E+05	181	<i>Arenimonas sp.</i>	4.88E+05
162	<i>Anaerosporobacter populeti</i>	6.32E+05	182	<i>Protochlamydia sp.</i>	4.74E+05
163	<i>Cryomorpha sp.</i>	6.28E+05	183	<i>Georgenia sp.</i>	4.73E+05
164	<i>Longispora sp.</i>	6.23E+05	184	<i>Nocardia rhamnosiphila</i>	4.73E+05
165	<i>Methanosphaera cuniculi</i>	6.18E+05	185	<i>Cohnella arctica</i>	4.66E+05
166	<i>Methylovirgula ligni</i>	6.01E+05	186	<i>Roseburia sp.</i>	4.48E+05
167	<i>Asticcacaulis biprosthecium</i>	6.00E+05	187	<i>Anaerobranca sp.</i>	4.43E+05
168	<i>Koribacter sp.</i>	6.00E+05	188	<i>Pilimelia sp.</i>	4.35E+05
169	<i>Bacillus decolorationis</i>	5.99E+05	189	<i>Planifilum sp.</i>	4.21E+05
170	<i>Arthrobacter alkaliphilus</i>	5.93E+05	190	<i>Methyloversatilis sp.</i>	4.00E+05
171	<i>Rheinheimera aquimaris</i>	5.85E+05	191	<i>Defluviimonas sp.</i>	3.99E+05
172	<i>Anaerosporobacter sp.</i>	5.78E+05	192	<i>Bdellovibrio bacteriovorus</i>	3.95E+05
173	<i>Rickettsia prowazekii</i>	5.69E+05	193	<i>Coprothermobacter sp.</i>	3.95E+05
174	<i>Fontimonas thermophila</i>	5.56E+05	194	<i>Rhodococcus equi</i>	3.95E+05
175	<i>Dietzia sp.</i>	5.52E+05	195	<i>Halocella sp.</i>	3.94E+05
176	<i>Propionicicella sp.</i>	5.26E+05	196	<i>Brachybacterium conglomeratum</i>	3.90E+05
177	<i>Arcticibacter sp.</i>	5.04E+05	197	<i>Solibacter sp.</i>	3.83E+05
178	<i>Fluviicola sp.</i>	5.03E+05	198	<i>Ferrovibrio sp.</i>	3.77E+05

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

199	<i>Nitrososphaera gargensis</i>	3.77E+05	219	<i>Rubellimicrobium</i> sp.	2.52E+05
200	<i>Cellulosilyticum</i> sp.	3.60E+05	220	<i>Halomonas</i> sp.	2.31E+05
201	<i>Ruminococcus albus</i>	3.45E+05	221	<i>Anaerovorax</i> sp.	2.29E+05
202	<i>Marinoscillum</i> sp.	3.36E+05	222	<i>Solimonas</i> sp.	2.28E+05
203	<i>Enhygromyxa</i> sp.	3.17E+05	223	<i>Euzebya</i> sp.	2.20E+05
204	<i>Adlercreutzia</i> sp.	3.14E+05	224	<i>Granulicella</i> sp.	2.20E+05
205	<i>Thalassospira</i> sp.	2.91E+05	225	<i>Nitrospira defluvii</i>	2.20E+05
206	<i>Lysinibacillus boronitolerans</i>	2.90E+05	226	<i>Rubrobacter</i> sp.	2.20E+05
207	<i>Parasegetibacter</i> sp.	2.89E+05	227	<i>Arthrobacter nitroguajacolicus</i>	2.20E+05
208	<i>Oenococcus oeni</i>	2.87E+05	228	<i>Niastella</i> sp.	2.10E+05
209	<i>Thioalkalispira</i> sp.	2.86E+05	229	<i>Porifericola</i> sp.	2.10E+05
210	<i>Planctomyces maris</i>	2.83E+05	230	<i>Armatimonas</i> sp.	2.05E+05
211	<i>Haloactinopolyspora</i> sp.	2.82E+05	231	<i>Sphingomonas dokdonensis</i>	2.05E+05
212	<i>Paracoccus chinensis</i>	2.72E+05	232	<i>Oceanobacillus</i> sp.	2.05E+05
213	<i>Cellulosilyticum lentocellum</i>	2.67E+05	233	<i>Litorilinea</i> sp.	2.04E+05
214	<i>Rhodobacter</i> sp.	2.65E+05	234	<i>Bacillus alkalitelluris</i>	2.02E+05
215	<i>Nordella</i> sp.	2.63E+05	235	<i>Geodermatophilus</i> sp.	2.01E+05
216	<i>Verrucomicrobium</i> sp.	2.54E+05	236	<i>Pedosphaera parvula</i>	2.00E+05
217	<i>Bacillus clausii</i>	2.54E+05	237	<i>Pseudomonas azotoformans</i>	2.00E+05
218	<i>Sphingobacterium</i> sp.	2.53E+05	238	<i>Paenibacillus koleovorans</i>	1.99E+05

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

239	<i>Comamonas sp.</i>	1.99E+05
240	<i>Amoebophilus sp.</i>	1.91E+05
241	<i>Mycobacterium hassiacum</i>	1.91E+05
242	<i>Nitrosoarchaeum sp.</i>	1.91E+05
243	<i>Rickettsia sp.</i>	1.91E+05
244	<i>Smithella sp.</i>	1.91E+05
245	<i>Smaragdicooccus niigatensis</i>	1.90E+05
246	<i>Pantoea sp.</i>	1.90E+05
247	<i>Litorilina aerophila</i>	1.90E+05
248	<i>Tsakamurella pulmonis</i>	1.90E+05
249	<i>Prosthecobacter sp.</i>	1.90E+05
250	<i>Acidiferrobacter sp.</i>	1.89E+05
251	<i>Saccharomonospora azurea</i>	1.89E+05
252	<i>Salana sp.</i>	1.89E+05
253	<i>Bacillus gibsonii</i>	1.80E+05
254	<i>Agrobacterium sp.</i>	1.58E+05
255	<i>Corynebacterium sp.</i>	1.57E+05
256	<i>Tepidimicrobium sp.</i>	1.53E+05
257	<i>Geminicoccus sp.</i>	1.51E+05
258	<i>Pedobacter roseus</i>	1.50E+05
259	<i>Thiothrix sp.</i>	1.46E+05
260	<i>Alistipes sp.</i>	1.42E+05
261	<i>Desulfosporosinus meridiei</i>	1.41E+05
262	<i>Hymenobacter sp.</i>	1.37E+05
263	<i>Umezawaea tangerina</i>	1.37E+05
264	<i>Pseudonocardia halophobica</i>	1.36E+05
265	<i>Rhizobium sp.</i>	1.36E+05
266	<i>Roseibacillus sp.</i>	1.36E+05
267	<i>Tumebacillus sp.</i>	1.32E+05
268	<i>Neptunomonas sp.</i>	1.32E+05
269	<i>Desulfocapsa sp.</i>	1.28E+05
270	<i>Dethiobacter sp.</i>	1.28E+05
271	<i>Chloroflexus sp.</i>	1.26E+05
272	<i>Alteromonas sp.</i>	1.14E+05
273	<i>Catenibacterium sp.</i>	1.13E+05
274	<i>Clostridium neonatale</i>	1.12E+05
275	<i>Agromyces ulmi</i>	1.10E+05
276	<i>Cerasicoccus sp.</i>	1.10E+05
277	<i>Criblamydia sp.</i>	1.10E+05
278	<i>Pseudoxanthomonas spadix</i>	1.10E+05

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

279	<i>Sphingomonas wittichii</i>	1.10E+05	299	<i>Ammoniphilus sp.</i>	9.03E+04
280	<i>Terrabacter sp.</i>	1.10E+05	300	<i>Alkanibacter sp.</i>	8.22E+04
281	<i>Turneriella parva</i>	1.10E+05	301	<i>Flavobacterium gelidilacus</i>	8.22E+04
282	<i>Microbispora sp.</i>	1.05E+05	302	<i>Thermobacillus sp.</i>	8.22E+04
283	<i>Oceanibaculum sp.</i>	1.03E+05	303	<i>Flavobacterium reichenbachii</i>	8.16E+04
284	<i>Sphingobacterium multivorum</i>	1.03E+05	304	<i>Tepidimicrobium ultunense</i>	8.12E+04
285	<i>Stenotrophomonas acidaminiphila</i>	1.03E+05	305	<i>Epulopiscium sp.</i>	7.60E+04
286	<i>Sporosarcina sp.</i>	9.99E+04	306	<i>Pseudomonas luteola</i>	7.60E+04
287	<i>Geobacillus sp.</i>	9.80E+04	307	<i>Atopostipes sp.</i>	7.55E+04
288	<i>Actinopolymorpha cephalotaxi</i>	9.57E+04	308	<i>Methylobacterium sp.</i>	7.55E+04
289	<i>Asticcacaulis solisilvae</i>	9.57E+04	309	<i>Amycolatopsis pigmentata</i>	7.32E+04
290	<i>Enterorhabdus sp.</i>	9.57E+04	310	<i>Aureimonas phyllosphaerae</i>	7.32E+04
291	<i>Methylotenera sp.</i>	9.57E+04	311	<i>Brachymonas sp.</i>	7.32E+04
292	<i>Thiobacillus sp.</i>	9.57E+04	312	<i>Chelativorans sp.</i>	7.32E+04
293	<i>Limnobacter thiooxidans</i>	9.50E+04	313	<i>Crossiella sp.</i>	7.32E+04
294	<i>Chlorochromatium sp.</i>	9.43E+04	314	<i>Kocuria rhizophila</i>	7.32E+04
295	<i>Glycomyces mongolensis</i>	9.43E+04	315	<i>Desulfotomaculum sp.</i>	7.14E+04
296	<i>Halorhodospira sp.</i>	9.43E+04	316	<i>Clostridium perfringens</i>	6.63E+04
297	<i>Panacagrimonas sp.</i>	9.43E+04	317	<i>Acetivibrio sp.</i>	6.38E+04
298	<i>Rhabdochlamydia sp.</i>	9.43E+04	318	<i>Acidothermus sp.</i>	6.38E+04

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

319	<i>Methylosula</i> sp.	6.38E+04
320	<i>Pleomorphomonas diazotrophica</i>	6.38E+04
321	<i>Reichenbachiella</i> sp.	6.38E+04
322	<i>Cryptosporangium</i> sp.	6.29E+04
323	<i>Cytophaga</i> sp.	6.29E+04
324	<i>Syntrophomonas</i> sp.	6.29E+04
325	<i>Thermincola</i> sp.	6.29E+04
326	<i>Acinetobacter johnsonii</i>	5.87E+04
327	<i>Caldicoprobacter</i> sp.	5.83E+04
328	<i>Bacillus thermolactis</i>	5.71E+04
329	<i>Catelliglobospora</i> sp.	5.49E+04
330	<i>Garciella</i> sp.	5.49E+04
331	<i>Rhodococcus corynebacterioides</i>	5.49E+04
332	<i>Roseococcus</i> sp.	5.49E+04
333	<i>Thermoflavimicrobium</i> sp.	5.14E+04
334	<i>Plantactinospira</i> sp.	4.78E+04
335	<i>Pseudonocardia</i> sp.	4.78E+04
336	<i>Rhodococcus tukisamuensis</i>	4.78E+04
337	<i>Catellatospora citrea</i>	4.72E+04
338	<i>Gluconobacter cerinus</i>	4.72E+04
339	<i>Roseomonas frigidaquae</i>	4.72E+04
340	<i>Paenibacillus aestivum</i>	4.61E+04
341	<i>Undibacterium</i> sp.	4.57E+04
342	<i>Chitinophaga soli</i>	4.39E+04
343	<i>Zeaxanthinibacter</i> sp.	4.39E+04
344	<i>Paenibacillus taiwanensis</i>	4.37E+04
345	<i>Gracilibacillus</i> sp.	4.08E+04
346	<i>Acinetobacter ursingii</i>	3.83E+04
347	<i>Flaviumibacter</i> sp.	3.83E+04
348	<i>Lactococcus lactis</i>	3.83E+04
349	<i>Alcanivorax indicus</i>	3.77E+04
350	<i>Arenicella</i> sp.	3.77E+04
351	<i>Desemzia</i> sp.	3.77E+04
352	<i>Aneurinibacillus</i> sp.	3.71E+04
353	<i>Alicyclobacillus</i> sp.	3.19E+04
354	<i>Faecalibacterium</i> sp.	3.19E+04
355	<i>Microtetraspora malaysiensis</i>	3.19E+04
356	<i>Streptosporangium roseum</i>	3.14E+04
357	<i>Thermopolyspora</i> sp.	3.14E+04
358	<i>Tepidimicrobium ferriphilum</i>	3.14E+04

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

359	<i>Gracilibacter sp.</i>	2.73E+04
360	<i>Coprobacillus sp.</i>	2.69E+04
361	<i>Lutibacterium sp.</i>	2.69E+04
362	<i>Proteiniborus sp.</i>	2.69E+04
363	<i>Tissierella sp.</i>	2.69E+04
364	<i>Brassicibacter mesophilus</i>	2.44E+04
365	<i>Kroppenstedtia eburnea</i>	2.36E+04
366	<i>Melghirimyces thermohalophilus</i>	2.36E+04
367	<i>Caldalkalibacillus sp.</i>	2.20E+04
368	<i>Clostridium bowmanii</i>	2.13E+04
369	<i>Paenibacillus alginolyticus</i>	1.69E+04
370	<i>Paenibacillus darangshiensis</i>	1.45E+04
371	<i>Acetanaerobacterium sp.</i>	0.00E+00
372	<i>Acholeplasma sp.</i>	0.00E+00
373	<i>Acidiphilium sp.</i>	0.00E+00
374	<i>Acidocella sp.</i>	0.00E+00
375	<i>Acinetobacter sp.</i>	0.00E+00
376	<i>Actinoplanes sp.</i>	0.00E+00
377	<i>Adhaeribacter sp.</i>	0.00E+00
378	<i>Algoriphagus sp.</i>	0.00E+00
379	<i>Alkalibacter sp.</i>	0.00E+00
380	<i>Anaerofustis sp.</i>	0.00E+00
381	<i>Anaerolinea sp.</i>	0.00E+00
382	<i>Anaerosinus sp.</i>	0.00E+00
383	<i>Anaerospora sp.</i>	0.00E+00
384	<i>Atopococcus sp.</i>	0.00E+00
385	<i>Bacteroides sp.</i>	0.00E+00
386	<i>Bavariicoccus seileri</i>	0.00E+00
387	<i>Beggiatoa sp.</i>	0.00E+00
388	<i>Brachymonas denitrificans</i>	0.00E+00
389	<i>Brevibacillus agri</i>	0.00E+00
390	<i>Byssovorax sp.</i>	0.00E+00
391	<i>Caldanaerocella sp.</i>	0.00E+00
392	<i>Caloramator sp.</i>	0.00E+00
393	<i>Chelatococcus sp.</i>	0.00E+00
394	<i>Christensenella sp.</i>	0.00E+00
395	<i>Chryseobacterium indologenes</i>	0.00E+00
396	<i>Chryseobacterium sp.</i>	0.00E+00
397	<i>Cohnella sp.</i>	0.00E+00
398	<i>Criblamydia sequanensis</i>	0.00E+00



## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

399	<i>Cryptanaerobacter sp.</i>	0.00E+00
400	<i>Dehalobacter sp.</i>	0.00E+00
401	<i>Dehalobacterium sp.</i>	0.00E+00
402	<i>Denitratisoma sp.</i>	0.00E+00
403	<i>Desulfitibacter sp.</i>	0.00E+00
404	<i>Desulfobulbus sp.</i>	0.00E+00
405	<i>Desulfosporosinus sp.</i>	0.00E+00
406	<i>Desulfovibrio africanus</i>	0.00E+00
407	<i>Desulfuromonas sp.</i>	0.00E+00
408	<i>Eilatimonas sp.</i>	0.00E+00
409	<i>Elioraea tepidiphila</i>	0.00E+00
410	<i>Entotheonella sp.</i>	0.00E+00
411	<i>Fastidiosipila sp.</i>	0.00E+00
412	<i>Flavisolibacter ginsengisoli</i>	0.00E+00
413	<i>Flavobacterium succinicans</i>	0.00E+00
414	<i>Flavonifractor sp.</i>	0.00E+00
415	<i>Geobacter humireducens</i>	0.00E+00
416	<i>Gluconobacter oxydans</i>	0.00E+00
417	<i>Glycomyces arizonensis</i>	0.00E+00
418	<i>Granulosicoccus sp.</i>	0.00E+00
419	<i>Halarsenatibacter sp.</i>	0.00E+00
420	<i>Hamadaea yuxiensis</i>	0.00E+00
421	<i>Herpetosiphon sp.</i>	0.00E+00
422	<i>Intestinimonas sp.</i>	0.00E+00
423	<i>Kiloniella sp.</i>	0.00E+00
424	<i>Kribbella sp.</i>	0.00E+00
425	<i>Legionella pneumophila</i>	0.00E+00
426	<i>Longilinea sp.</i>	0.00E+00
427	<i>Longispora albida</i>	0.00E+00
428	<i>Luedemannella helvata</i>	0.00E+00
429	<i>Lutispora sp.</i>	0.00E+00
430	<i>Metachlamydia lacustris</i>	0.00E+00
431	<i>Methanobacterium sp.</i>	0.00E+00
432	<i>Methanoculleus sp.</i>	0.00E+00
433	<i>Methanomassiliicoccus sp.</i>	0.00E+00
434	<i>Methylacidiphilum sp.</i>	0.00E+00
435	<i>Methylobacter marinus</i>	0.00E+00
436	<i>Methylomicrobium sp.</i>	0.00E+00
437	<i>Microlunatus sp.</i>	0.00E+00
438	<i>Micromonospora columellifera</i>	0.00E+00

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance


439	<i>Myxococcus sp.</i>	0.00E+00
440	<i>Neochlamydia sp.</i>	0.00E+00
441	<i>Niabella sp.</i>	0.00E+00
442	<i>Nitriliruptor sp.</i>	0.00E+00
443	<i>Nocardia coubleae</i>	0.00E+00
444	<i>Nocardioides simplex</i>	0.00E+00
445	<i>Novispirillum sp.</i>	0.00E+00
446	<i>Odyssella sp.</i>	0.00E+00
447	<i>Oscillibacter sp.</i>	0.00E+00
448	<i>Oxobacter sp.</i>	0.00E+00
449	<i>Paenibacillus edaphicus</i>	0.00E+00
450	<i>Paenibacillus sepulcri</i>	0.00E+00
451	<i>Paenibacillus taihuensis</i>	0.00E+00
452	<i>Paenibacillus turicensis</i>	0.00E+00
453	<i>Papillibacter sp.</i>	0.00E+00
454	<i>Parachlamydia acanthamoebae</i>	0.00E+00
455	<i>Pasteuria sp.</i>	0.00E+00
456	<i>Pelosinus fermentans</i>	0.00E+00
457	<i>Pelosinus sp.</i>	0.00E+00
458	<i>Pelotomaculum schinkii</i>	0.00E+00
459	<i>Pelotomaculum sp.</i>	0.00E+00
460	<i>Portibacter sp.</i>	0.00E+00
461	<i>Promicromonospora sukumoe</i>	0.00E+00
462	<i>Proteiniclasticum sp.</i>	0.00E+00
463	<i>Pseudobutyrvibrio sp.</i>	0.00E+00
464	<i>Pseudomonas graminis</i>	0.00E+00
465	<i>Pseudoxanthomonas mexicana</i>	0.00E+00
466	<i>Quadrisphaera sp.</i>	0.00E+00
467	<i>Rhizobium etli</i>	0.00E+00
468	<i>Rhodocytophaga aerolata</i>	0.00E+00
469	<i>Rickettsiella sp.</i>	0.00E+00
470	<i>Rickettsiella viridis</i>	0.00E+00
471	<i>Roseimicrobium sp.</i>	0.00E+00
472	<i>Rubritalea sp.</i>	0.00E+00
473	<i>Shimazuella sp.</i>	0.00E+00
474	<i>Simiduia areninigrae</i>	0.00E+00
475	<i>Skermanella sp.</i>	0.00E+00
476	<i>Sphaerisporangium rubeum</i>	0.00E+00
477	<i>Spirochaeta sp.</i>	0.00E+00
478	<i>Sporichthya sp.</i>	0.00E+00

## REMAINING BACTERIA DETECTED

Quantification based on number of cells per gram of soil amendment and grouped by abundance

479	 <i>Sporobacter sp.</i>	 0.00E+00
480	 <i>Sporomusa sp.</i>	 0.00E+00
481	 <i>Sporotomaculum sp.</i>	 0.00E+00
482	 <i>Streptococcus sp.</i>	 0.00E+00
483	 <i>Streptomyces serianimatus</i>	 0.00E+00
484	 <i>Symbiobacterium thermophilum</i>	 0.00E+00
485	 <i>Syntrophobacter sp.</i>	 0.00E+00
486	 <i>Tepidamorphus gemmatus</i>	 0.00E+00
487	 <i>Terrimonas sp.</i>	 0.00E+00
488	 <i>Thermaerobacter marianensis</i>	 0.00E+00
489	 <i>Trichococcus sp.</i>	 0.00E+00
490	 <i>Variovorax quadricarinatus</i>	 0.00E+00

## NOTES

 Genus predictions ('sp') that have species appearing in the CDFA list provided. (Species might or might not be present)

 Species that appears explicitly highlighted in the CDFA list

# APPENDIX

## RELATIVE FUNGAL ABUNDANCE

The relative abundance of the fungal communities is reported in %. Data in this report correspond to the average relative abundance obtained from three technical replicates. The absolute quantification of fungal communities using amplicon sequencing has not yet been validated at Biome Makers, Inc.

#	Genus & Species	Percentage	#	Genus & Species	Percentage
1	<i>Mortierella</i> sp.	30.3286%	19	<i>Aspergillus austroafricanus</i>	0.5068%
2	<i>Phialophora</i> sp.	20.7002%	20	<i>Wallemia muriae</i>	0.4684%
3	<i>Chrysosporium vallenarense</i>	10.5267%	21	<i>Cladorrhinum phialophoroides</i>	0.4377%
4	<i>Cirrenalia macrocephala</i>	8.3308%	22	<i>Chrysosporium lobatum</i>	0.3993%
5	<i>Wallemia sebi</i>	5.1981%	23	<i>Ajellomyces crescens</i>	0.3762%
6	<i>Gymnoascoideus</i> sp.	3.8775%	24	<i>Cryptococcus aerius</i>	0.3609%
7	<i>Oidiodendron truncatum</i>	3.1096%	25	<i>Cryptococcus podzolicus</i>	0.3455%
8	<i>Phialosimplex caninus</i>	1.9502%	26	<i>Lewia infectoria</i>	0.3302%
9	<i>Coprinellus bisporus</i>	1.8428%	27	<i>Aspergillus</i> sp.	0.3302%
10	<i>Pseudallescheria fimeti</i>	1.0365%	28	<i>Mortierella elongata</i>	0.2534%
11	<i>Monodictys castaneae</i>	1.0289%	29	<i>Westerdykella</i> sp.	0.2534%
12	<i>Chrysosporium</i> sp.	0.8446%	30	<i>Schizothecium carpinicola</i>	0.2303%
13	<i>Brachyphoris oviparasitica</i>	0.8292%	31	<i>Preussia flanaganiai</i>	0.2227%
14	<i>Sagenomella</i> sp.	0.7448%	32	<i>Conocybe karinae</i>	0.1766%
15	<i>Podospora communis</i>	0.7141%	33	<i>Lecythophora</i> sp.	0.1612%
16	<i>Scedosporium prolificans</i>	0.6373%	34	<i>Cryptococcus laurentii</i>	0.1536%
17	<i>Penicillium chrysogenum</i>	0.6143%	35	<i>Podospora</i> sp.	0.1536%
18	<i>Podospora decipiens</i>	0.5221%			

















## RELATIVE FUNGAL ABUNDANCE

The relative abundance of the fungal communities is reported in %. Data in this report correspond to the average relative abundance obtained from three technical replicates. The absolute quantification of fungal communities using amplicon sequencing has not yet been validated at Biome Makers, Inc.


#	Genus & Species	Percentage	#	Genus & Species	Percentage
36	<i>Cercophora</i> sp.	0.1459%	55	<i>Sarocladium glaucum</i>	0.0384%
37	<i>Aphanoascus mephitalis</i>	0.1459%	56	<i>Ascobolus</i> sp.	0.0307%
38	<i>Beauveria</i> sp.	0.1305%	57	<i>Mucor brunneogriseus</i>	0.0307%
39	<i>Arthroderma ciferrii</i>	0.1305%	58	<i>Cephalosporium serra</i>	0.0307%
40	<i>Penicillium</i> sp.	0.0921%	59	<i>Alternaria atra</i>	0.0307%
41	<i>Aspergillus niger</i>	0.0921%	60	<i>Mycocarachis inversa</i>	0.0307%
42	<i>Cercophora samala</i>	0.0845%	61	<i>Aspergillus deflectus</i>	0.0230%
43	<i>Millerozyma farinosa</i>	0.0845%	62	<i>Schizothecium curvisporum</i>	0.0154%
44	<i>Aspergillus sydowii</i>	0.0845%	63	<i>Polytolypa hysteric</i>	0.0154%
45	<i>Paecilomyces marquandii</i>	0.0691%	64	<i>Acremonium furcatum</i>	0.0154%
46	<i>Penicillium buchwaldii</i>	0.0691%	65	<i>Mortierella clonocystis</i>	0.0154%
47	<i>Mortierella oligospora</i>	0.0614%	66	<i>Cladorrhinum bulbiliosum</i>	0.0154%
48	<i>Psilocybe argentina</i>	0.0614%	67	<i>Ascobolus stercorarius</i>	0.0154%
49	<i>Aspergillus ruber</i>	0.0537%	68	<i>Penicillium sizovae</i>	0.0154%
50	<i>Fusarium pseudensiforme</i>	0.0537%	69	<i>Candida subhashii</i>	0.0154%
51	<i>Penicillium cyclopium</i>	0.0537%	70	<i>Penicillium brevicompactum</i>	0.0154%
52	<i>Amauroascus niger</i>	0.0537%	71	<i>Pichia fermentans</i>	0.0154%
53	<i>Paecilomyces</i> sp.	0.0461%	72	<i>Talaromyces purpureogenus</i>	0.0077%
54	<i>Fusarium lichenicola</i>	0.0384%	73	<i>Stilbella byssiseda</i>	0.0077%


RELATIVE FUNGAL ABUNDANCE

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#	Genus & Species	Percentage	#	Genus & Species	Percentage
74	 <i>Sistotrema</i> sp.	 0.0077%			
75	 <i>Pilobolus sphaerosporus</i>	 0.0077%			
76	 <i>Cercospora apii</i>	 0.0077%			
77	 <i>Cryptococcus terreus</i>	 0.0077%			
78	 <i>Pyrenochaetopsis leptospora</i>	 0.0077%			
79	 <i>Pterula echo</i>	 0.0077%			
80	 <i>Penicillium menorum</i>	 0.0077%			
81	 <i>Psathyrella</i> sp.	 0.0077%			

NOTES

 Genus predictions ('sp') that have species appearing in the CDFA list provided. (Species might or might not be present)

 Species that appears explicitly highlighted in the CDFA list

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