

Understanding Soil Properties and the Relationship to Maize Yield Variability

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Aim

This project aimed to understand the relationship between maize yield and soil chemical, physical or biology properties.

Method

Two different properties, shown in Figure 1 were used for this study, one being Hamono's and the other Kennedy's. Soil was collected in December 2016 from the 0-10cm range and then from the 10-30cm range at both farms. Each sample consisted of 25 sample points which were composited and subsampled.

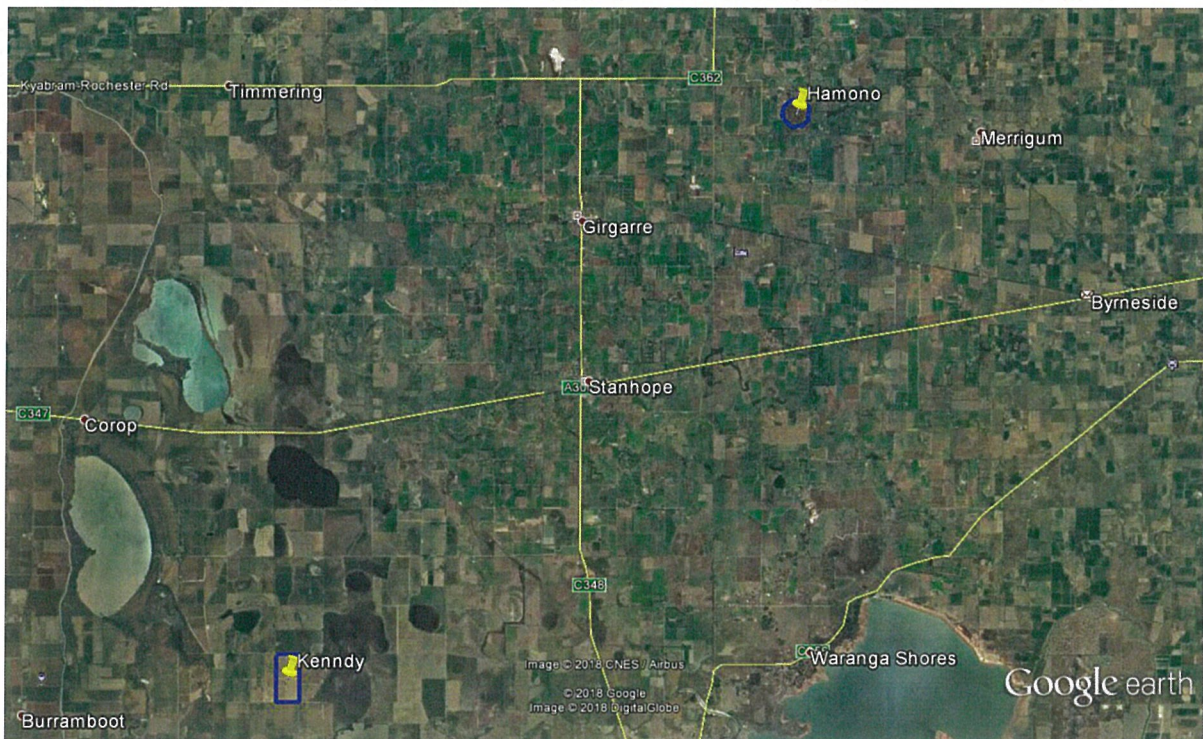
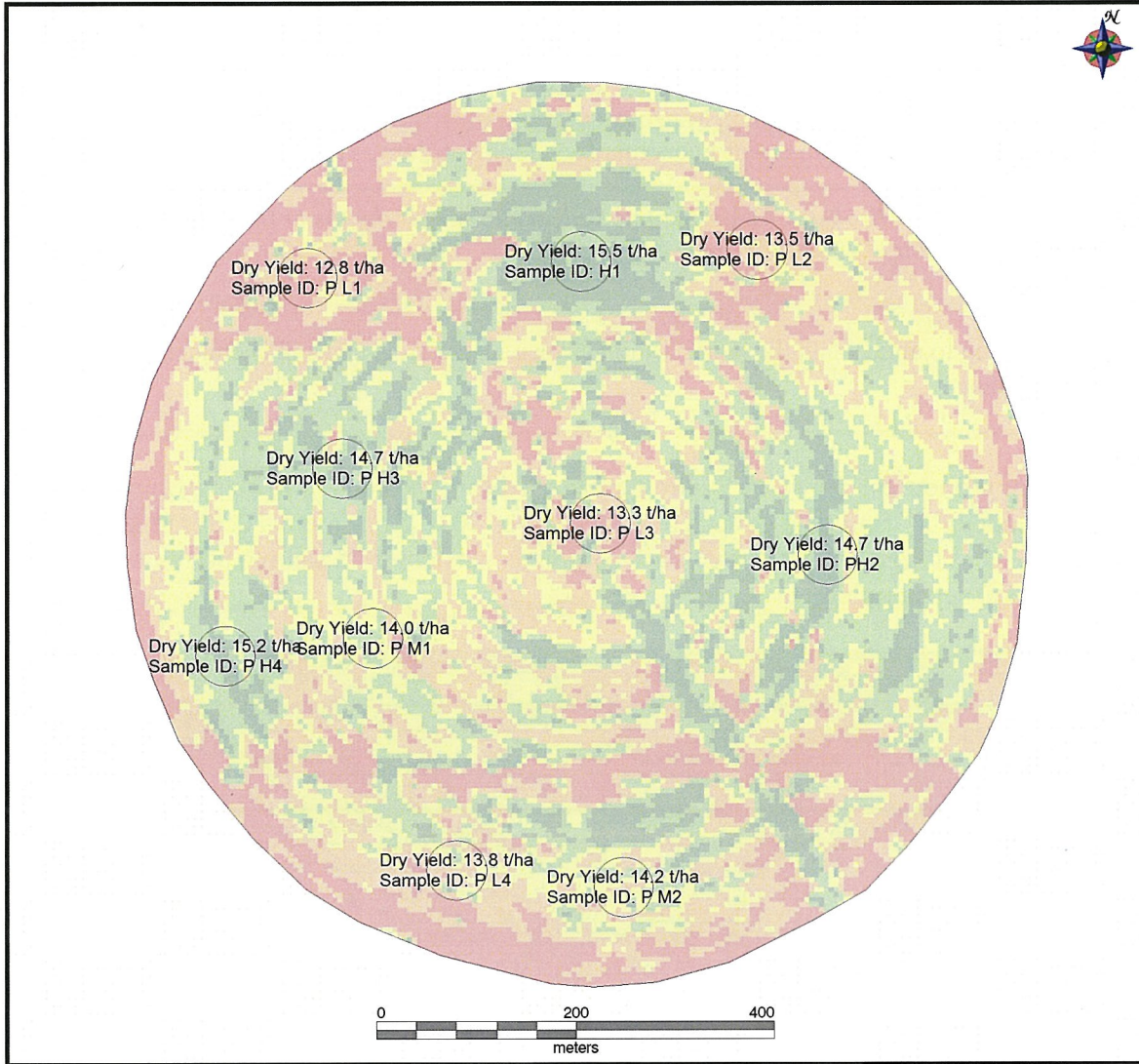


Figure 1: Location of the two properties

At the Hamono site 10 soil sample points were determined, with the selection based on the yield map data from the previous maize crop (summer 2015/16). These points were selected to represent 4 sections of the pivot which were low yielding, 4 sections that were high yielding, and 2 areas in the mid-yield range. The distribution of these points is shown in Figure 2. Average maize yield was calculated for a radius of 30, 50 and 70 meters around each sample point.

Dry Yield



precision
agriculture

Client: Nick O'Halloran
Farm: Irrigated Block
Paddock: Pivot
Crop: 2015 Wheat
Name: Average Yield 30m

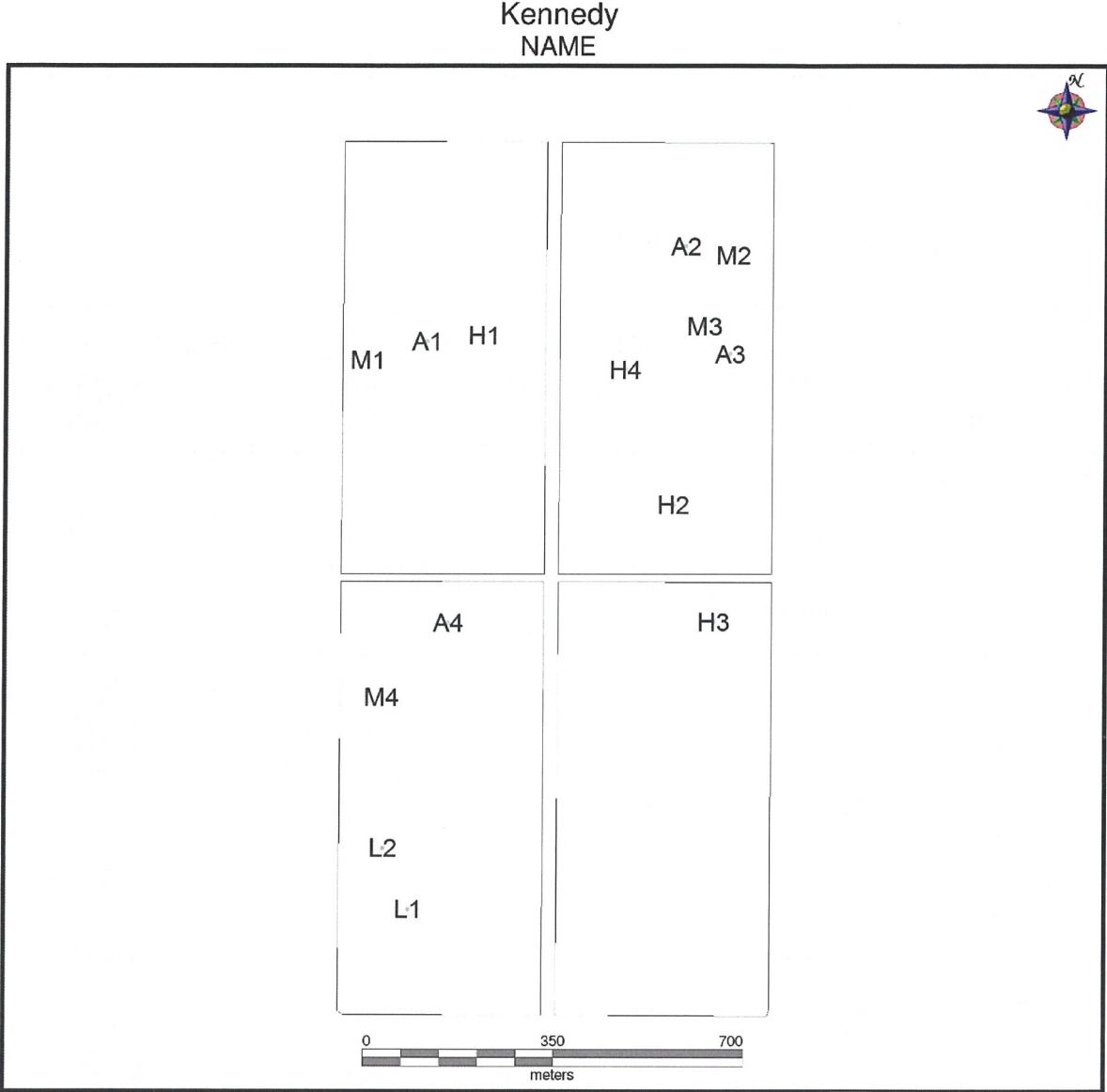
15.5 t/ha	0.28 ha	
15.2 t/ha	0.28 ha	
14.7 t/ha	0.56 ha	
14.2 t/ha	0.28 ha	
14.0 t/ha	0.28 ha	
13.8 t/ha	0.28 ha	
13.5 t/ha	0.28 ha	
13.3 t/ha	0.28 ha	
12.8 t/ha	0.28 ha	



Figure 2: Maize yield map

As yield data was not available for the Kennedy site the points were selected based on the NDVI data available from CSIRO, NDVI data was from (20/2/16) for the maize crop grown in summer 2015/16. Average NDVI value was taken from the 4 closest 30 m NDVI pixels to each

sample point. Points were then selected based on 4 points with the highest (H) NDVI, 4 points with a medium-high (A) NDVI, 4 with a medium (M) NDVI value and 2 with a low (L) NDVI value. The distribution of these points is shown in figure 3.



precision
agriculture

Client: Nick O'Halloran
Farm: Irrigated Block
Paddock: Kennedy
Name: Kennedy Strategic Soil Samp

- A1
- A2
- A3
- A4
- H1
- H2
- H3
- H4
- L1
- L2
- M1
- M2
- M3
- M4



Figure 3: Location of sampling points based on NDVI

Soil was sent to the APAL lab for full chemical analysis. Soil from the 0-10cm depth at the Hamono site was also sent to Melbourne University for DNA extraction. Bacterial and fungal sequences were then targeted with primers designed for the 27F and 519R regions of the 16S rRNA subunit.

Penetrometer resistance was also measure at each site to a depth of 45 cm using a cone penetrometer. Nine cone penetrometers readings were taken at each previously determined sampling point.

Results

Soil Chemistry test results are detailed in Appendix 1.

Data for 0-10cm range for Hamono was plotted against the average yield within 70m of each sample point. A regression line was added to each graph to determine potential relationship between each of the soil properties and yield. As the R^2 values become closer to 1.0, the better fit of the regression line. That is, the closer the line passes through all of the points. At Hamano's the strongest relationship was found between Soil Organic Carbon and average 70m yield (Figure 4).

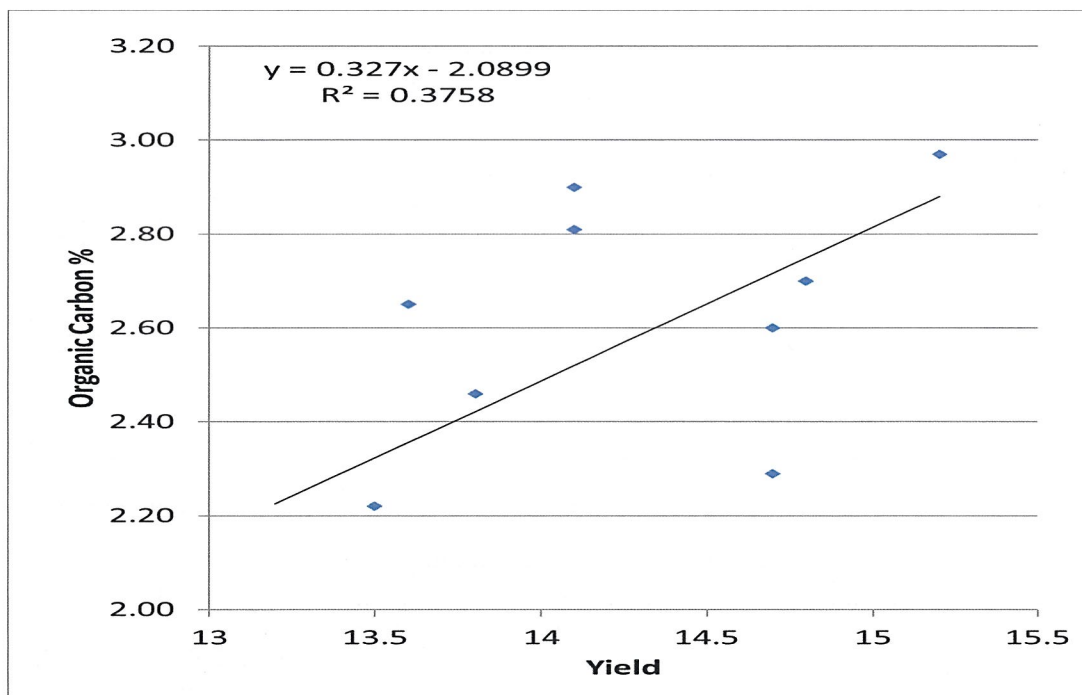


Figure 4: Organic Carbon and Yield at Hamono

Data for 0-10cm range for Kennedy was plotted against NDVI at each sample point. A regression line was added to each graph to determine potential relationships of soil properties to yield. As the R^2 values become closer to 1.0, the better fit of the regression line. That is, the closer the line passes through all of the points. At Kennedy's the strongest relationship was found between Colwell P and NDVI value (Figure 5).

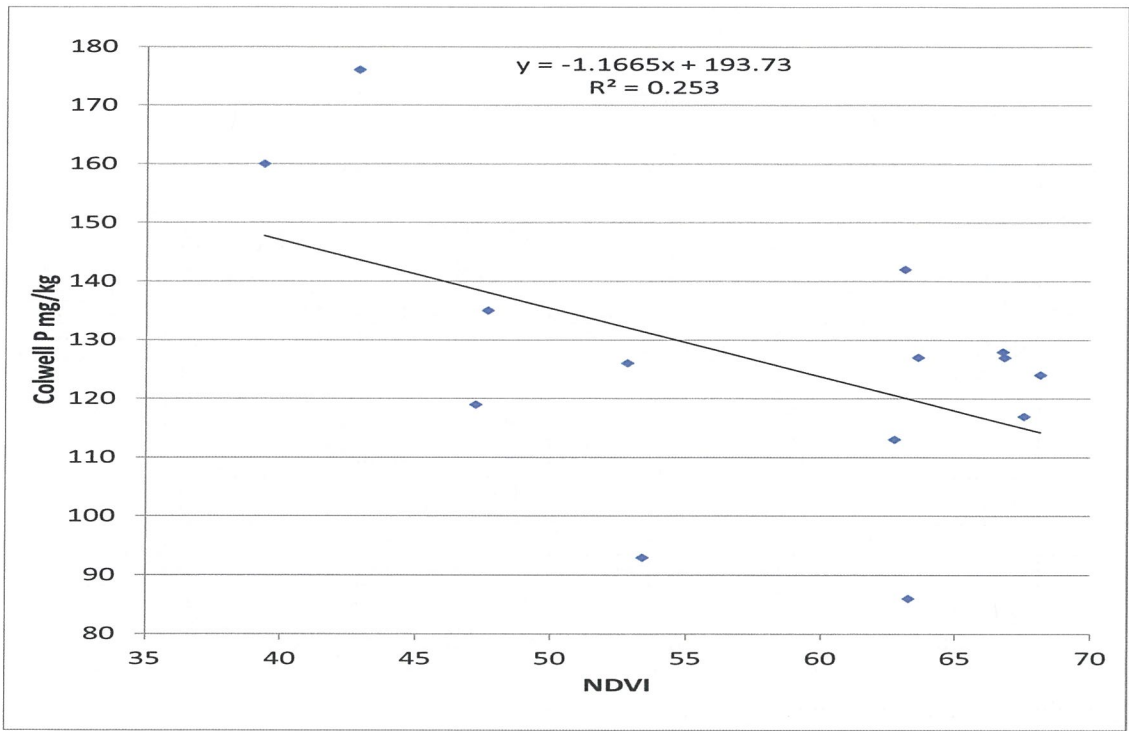


Figure 5: Colwell P and NDVI at Kennedy

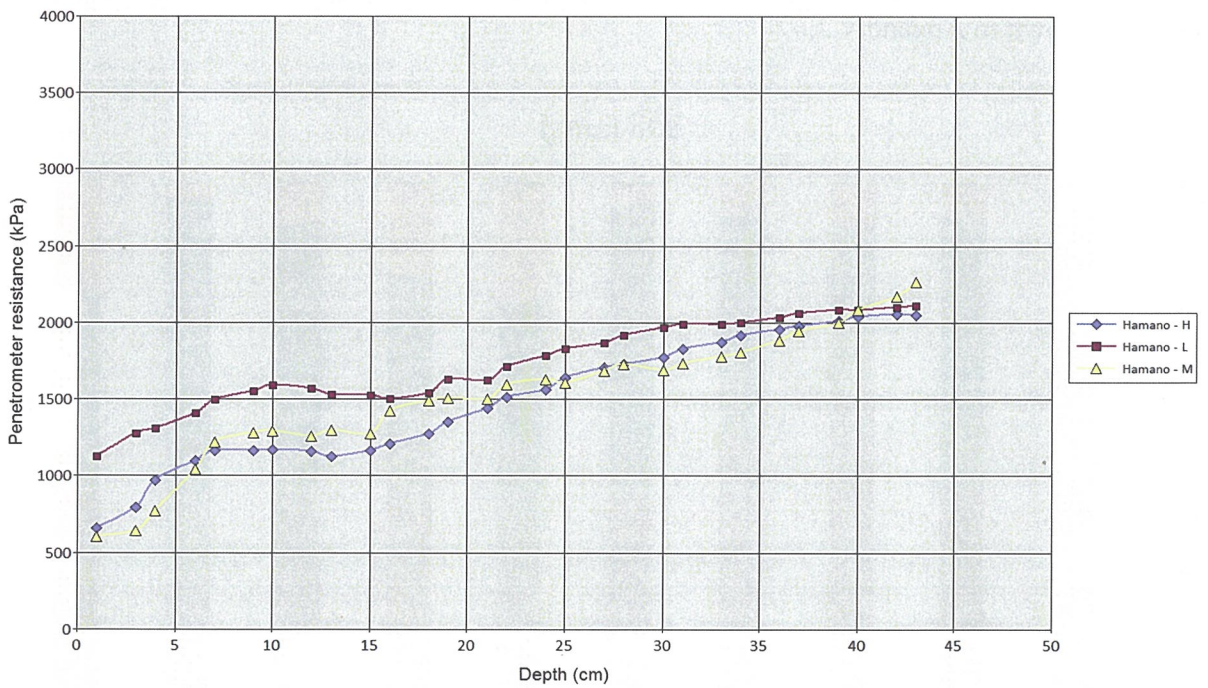


Figure 6: Soil Penetrometer Results from Hamono

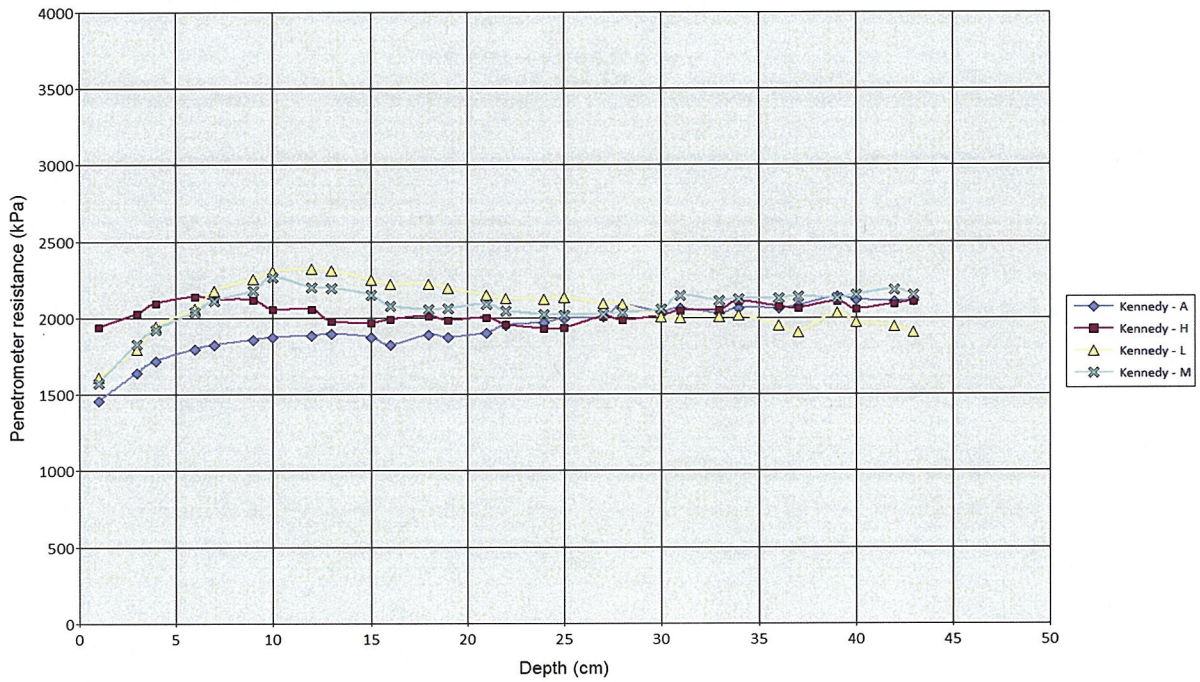


Figure 7: Soil Penetrometer Results from Kennedy

Soil fungi was classified into 7 fungal phyla and presented as the percentages. The table of results is shown in Appendix 2.

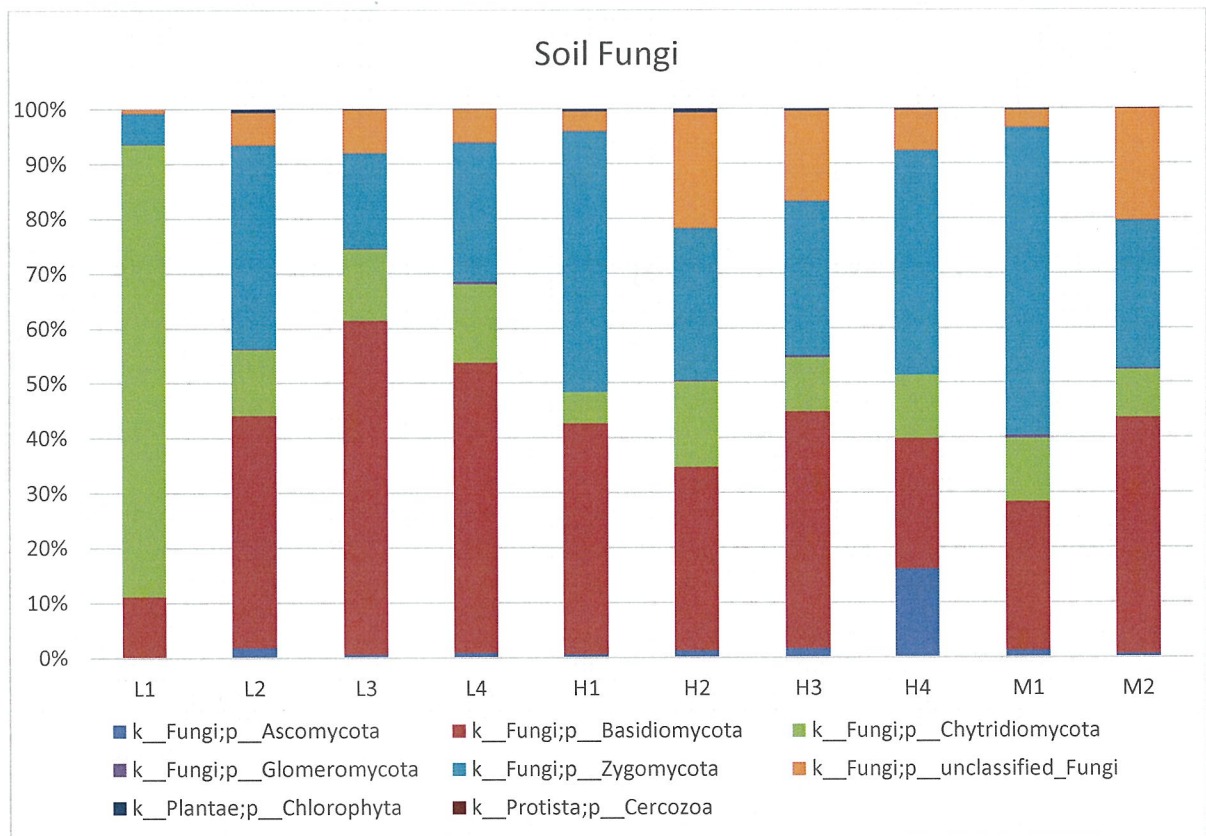


Figure 8: Fungi Composition of the Soil from Hamono

Soil fungi data for 0-10cm range for Hamono was plotted against the 70 m average yield at each sample point. A regression line was added to each graph to determine potential relationships of soil properties to yield. As the R^2 values become closer to 1.0, the better fit of the regression line. That is, the closer the line passes through all of the points. The strongest relationship was evident for *Chlorophyta* (Figure 9).

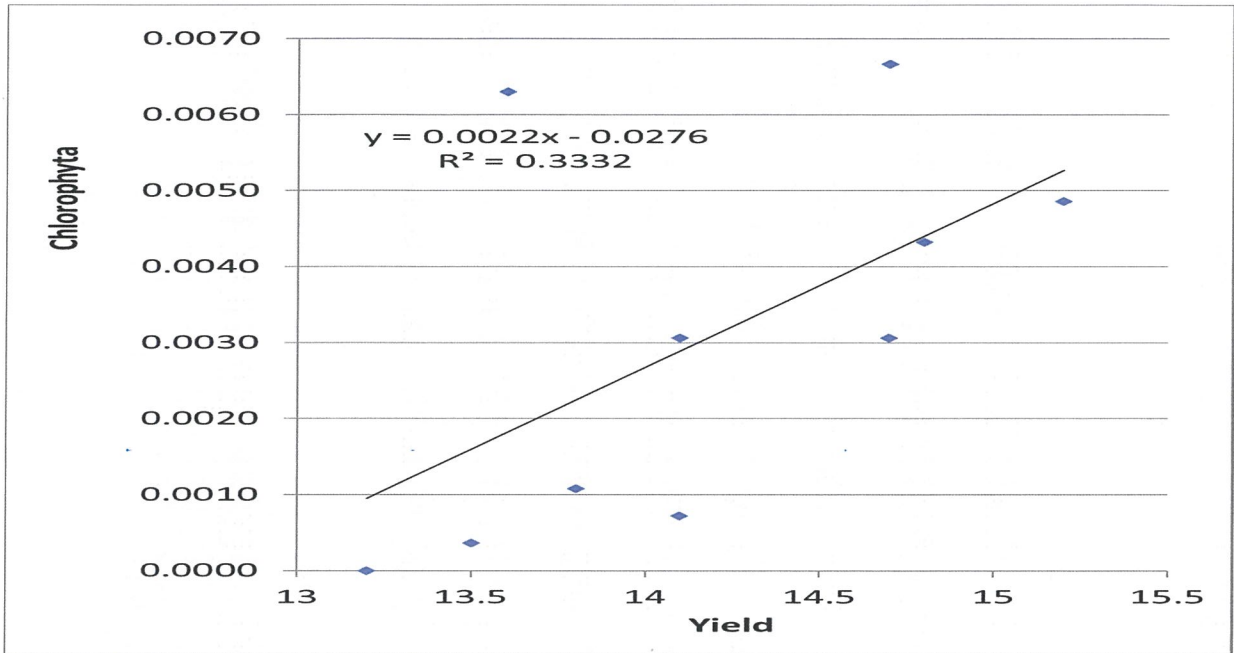


Figure 9: Soil Fungi: Chlorophyta and Yield from Hamono

Soil Bacteria was classified to 23 phyla, and 345 genera.

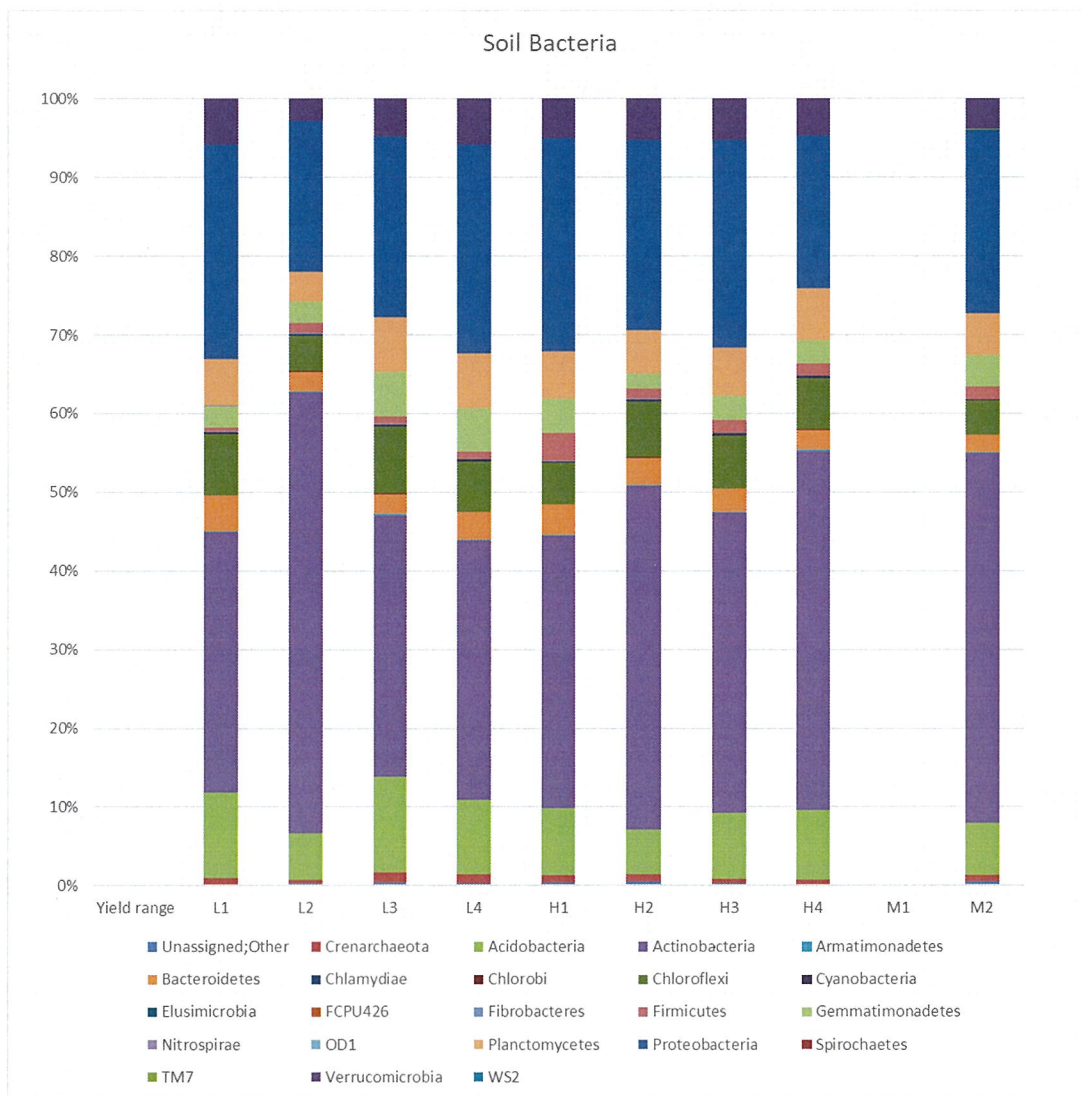


Figure 10: Bacteria Composition of Soil from Hamono

Soil bacterial data for 0-10cm range for Hamono was plotted against the yield for the 70m plots at each sample point. A regression line was added to each graph to determine potential relationships of soil properties to yield. As the R^2 values become closer to 1.0, the better fit of the regression line. That is, the closer the line passes through all of the points. The strongest relationship was evident for the phyla *Firmicutes* (Figure 11).

This phyla; *Firmicutes* was then further broken down to 16 different classifications, with some to the genera level, and others to family only. The regression analysis was also conducted with the strongest relationship was evident for the following:

- Phyla: *Firmicutes*; class: *Bacilli*; order: *Bacillales*; family: *Bacillaceae*; genera: *Bacillus* (Figure 12)
- Phyla: *Firmicutes*; class: *Clostridia*; order: *Clostridiales*; family: *Peptostreptococcaceae* phyla *Firmicutes* (Figure 13)

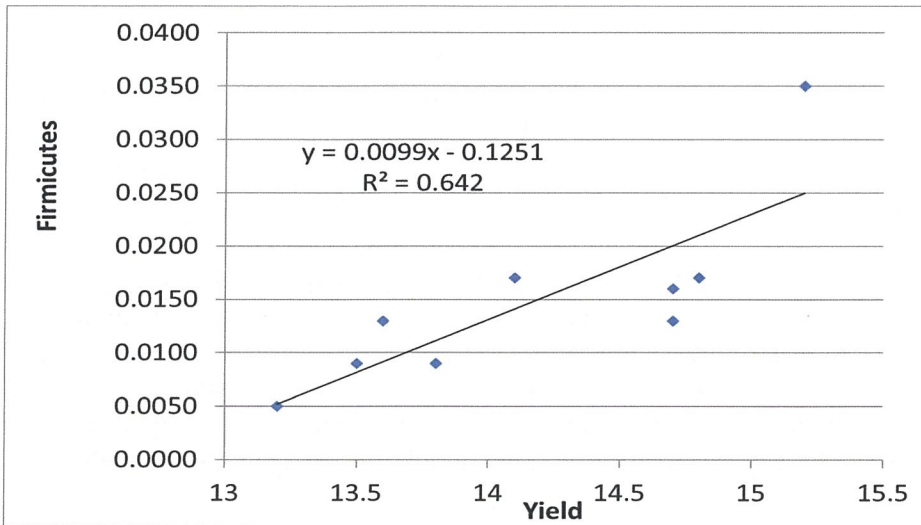


Figure 11: Soil Bacteria: Firmicutes and Yield from Hamono

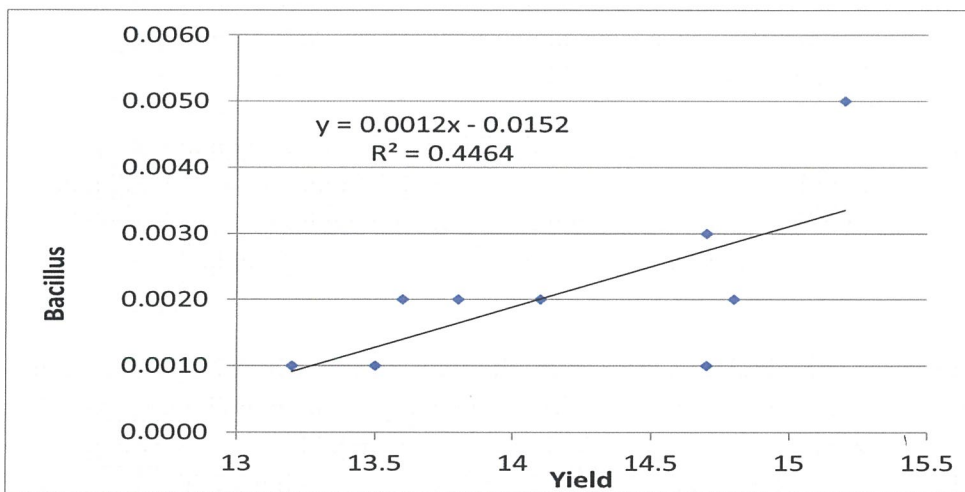


Figure 12: Soil Bacteria: genera Bacillus and Yield from Hamono

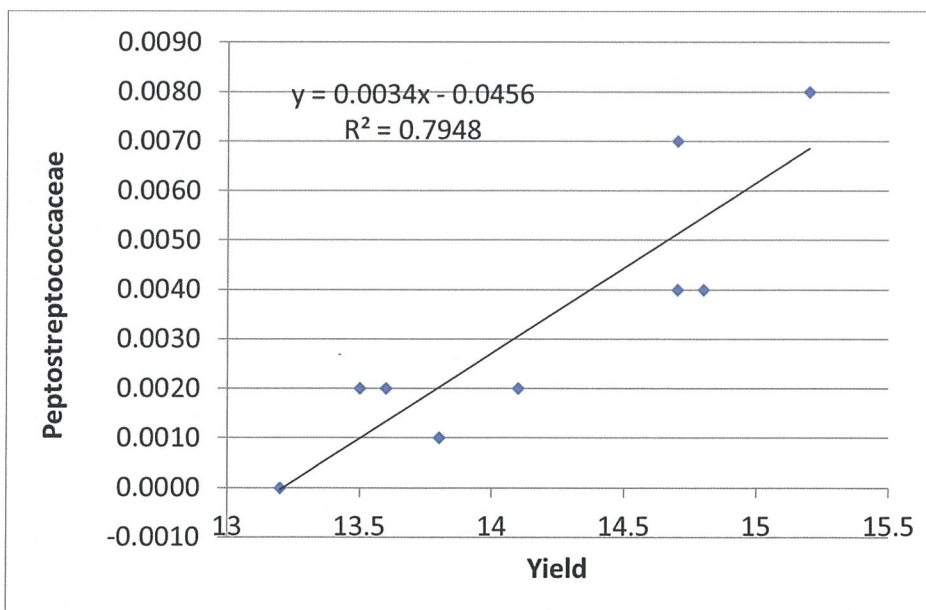


Figure 13: Soil Bacteria family Peptostreptococcaceae and Yield from Hamono

Discussion

Very little correlation was found between soil chemistry properties at the 10-30cm level and yield or NDVI, hence all analysis was focused on the 0-10cm depth. Based on this the strongest relationship at the Hamono site was with the Organic Carbon levels, with yield shown to increase as the level of organic carbon increased ($R^2=0.3758$) (Figure 4).

Soil Carbon is involved in binding soil particles together into larger aggregates. Aggregation is important for good soil structure, aeration, water infiltration and resistance to erosion and crusting. Soil carbon is also an important source of nutrition for the crop. These relationship between maize yield and soil organic carbon at Hamono's is not surprising given that Research by Zhang et al (2008) has indicated that both wheat and corn grain yields were significantly correlated with soil organic carbon, total and available nitrogen and phosphorus.

At the Kennedy site the strongest relationship was with the Colwell Phosphorus levels, with NDVI shown to decrease as the level of Collwell P increased ($R^2=0.253$) (Figure 5). This is the reverse of what might be expected with phosphorus being essential for plant growth and involved in photosynthesis, respiration and other metabolic processes, including energy metabolism within the plant (Salisbury & Ross, 1992).

A cone penetrometer was used to measure soil strength and gives an indication of how hard plant roots have to work to explore the soil. As penetrometer resistance increases, measured in kilopascals, the soil is becoming stronger and more difficult of root to grow through. Penetrometer resistance is influenced by soil water content, soil type and management practices.

Soil strength were measured at both sites, with results shown in Figure 6 and 7. There was no significant variation between any of the treatments for soil strength. In general, crop root growth starts to be restricted when the penetration resistance exceeds 1500 kPa and is severely restricted at 2500 kPa or more (Cotching and Davies). Based on this, and the results shown in Figure 7, it is possible that maize root growth may have been impeded at depths at Kennedy's site across all NDVI levels. At the Hamono site there appears to be variation in soil strength between the high, medium and low yielding areas., with the low yielding region hitting 1500kPa at the 5-10cm depth, the medium yielding region at the 15-20cm depth and the high yielding area at the 20-25cm depth.

The strongest relationship between yield and soil fungi was evident for *Chlorophyta*, $R^2=0.3332$ (Figure 9). *Chlorophyta* are also know as green algae, and may occur in damp soil. Green algae have been found to form water-stable soil aggregates that have important ecological roles in nutrient cycling, water retention, and stabilization of soils (Evans and Johansen, 1999)

The strongest relationship between yield and soil bacteria was evident for the phyla *Firmicutes* (Figure 11). The regression analysis the showed the strongest relationship was evident for the following:

- Phyla: *Firmicutes*; class: *Bacilli*; order: *Bacillales*; family: *Bacillaceae*; genera: *Bacillus* $R^2= 0.4464$ (Figure 12)
- Phyla: *Firmicutes*; class: *Clostridia*; order: *Clostridiales*; family: *Peptostreptococcaceae* $R^2=0.7948$ (Figure 13)

Bacillus spores are very resistant to many adverse conditions and may be Gram-positive, or Gram-positive only in early stages of growth, or Gram-negative (Schleifer, 2009). Research by Paton and Innes (1991) has shown that there are some symbiotic associations between L-form *Bacillus* bacteria and plants.

Peptostreptococcaceae are non-spore-forming obligately anaerobic Gram-stain-positive cocci. The optimum temperature for growth is 37°C, and they are involved in the metabolization of peptone and amino acids to acetic, butyric, isobutyric, caproic, and isocaproic acid (Holdeman et al., 1986). *Peptostreptococcaceae* is also common bacteria in cattle manure or livestock waste. They are typically in higher abundances in organically managed plots (Hartman et al 2018).

Soil samples were taken over 8 months after the crop for which we had yield maps. Hence the soil had been cultivated for the summer crop which had already been planted when the soil testing was conducted. Therefore, some of the soil properties that may have impacted on yield in the previous season may have been ameliorated through management (i.e. cultivation and addition of lime and fertiliser).

Conclusion

Unfortunately yield maps were not available for the Kennedy location, hence it was not possible to determine if there was a relationship between NDVI and yield.

Based on the soil penetrometer results from the Hamono site there appears to be a relationship between soil compaction and maize yield. Hence soil practices that reduce compaction may result in increased yield.

Soil organic carbon and phosphorus were found to correlate with crop yield (Hamono) and NDVI or plant growth (Kennedy).

Green algae is considered to be important in nutrient cycling, water retention, and stabilization of soils (Evans and Johansen, 1999) Further studies on *Chlorophyta* should be conducted to determine if their presence does in fact increase crop yield.

The strongest relationship between yield and soil fungi was evident for the phyla *Firmicutes*, in particular Phyla: *Firmicutes*; class: *Bacilli*; order: *Bacillales*; family: *Bacillaceae*; genera: *Bacillus* and Phyla: *Firmicutes*; class: *Clostridia*; order: *Clostridiales*; family: *Peptostreptococcaceae*. As *Bacillus* has been associated with plants in a symbiotic relationship some species of this bacteria are already commercially available. Further research is required through to determine if applying these bacteria result in increased crop yield.

As previous research has suggested that manure application to soil may introduce beneficial bacterial from the family *Peptostreptococcaceae* to the root microbiome (Hartman et al. 2018). Hence, the introduction of microbes from manure and their influence on maize yield should be further investigated.

References

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Appendix 1



Run ID	Zient	Sample Name	Yr no	Field range	Yield 30	Yield 70	NDVI	Rep	Depth	Lab Number	PH/EC	EC:1.5	Chloride	Boron	K	Cu	Mg	Na	N	MS	Ammonium	Organic Carbon	Colwell P	PH	NO3 Salinity	Each Al	Each K	Each Ca	Each Mg	Each Fe	Each Mn	Each Zn	Each Pb	Each Cd	Each Cr	Each Ni	Each Cu	Each Mn	Each Zn	Each Pb	Each Cd	Each Cr	Each Ni	ratio
3200	Pinet	P1-0-0	1	L	12.8	13	13.2	1	0-0	T065	6.78	6.21	0.12		494.7	1765.9	694.4	88.4	27.9	3.1	4.8	1.83	33	88.3	8.3	0.01	1.055	8.512	5.139	0.388	15.09	6.86	56.43	34.07	2.59	0.00	0.07	100	1.66					
3200	Pinet	P2-0-0	1	L	13.5	13.4	13.6	2	0-0	T065	6.13	5.65	0.18		451.4	1582.7	399.7	47.5	61.7	9.1	5.6	2.65	46	116.8	13.4	0.02	0.01	1.154	7.798	3.290	0.207	12.47	9.26	62.54	26.38	1.66	0.08	0.08	100	2.37				
3200	Pinet	P3-0-0	1	L	13.3	13.6	13.8	3	0-0	T067	6.17	5.63	0.15		302.1	1592.1	349.1	59.7	52.8	3.5	3.9	2.46	40	93.9	9.2	0.02	0.01	0.839	7.845	2.873	0.260	11.62	7.05	65.81	24.73	2.24	0.09	0.09	100	2.66				
3200	Pinet	P4-0-0	1	L	13.8	13.6	13.5	4	0-0	T069	6.1	5.58	0.16		433.3	1597.5	345.3	46.1	46.6	3.7	4.8	2.22	76	81	13.5	0.03	0.01	1.108	7.822	2.842	0.201	12.00	9.23	65.17	23.68	1.67	0.17	0.08	100	2.75				
3200	Pinet	P5-0-0	3	H	15.5	15.4	15.2	1	0-0	T094	6.1	5.58	0.17		406.8	1747.5	588.5	68.5	58.8	3.1	4.1	2.97	56	94	11.6	0.03	0.01	1.040	8.720	4.679	0.298	14.77	7.05	59.05	31.68	2.02	0.14	0.07	100	1.86				
3200	Pinet	P6-0-0	3	H	14.7	14.7	14.7	2	0-0	T093	6.36	5.92	0.19		422.5	1663.3	351.9	53.7	62.8	3.3	4.4	2.29	42	83	8.8	0.01	0.01	1.061	8.165	2.896	0.234	12.39	8.72	65.92	23.38	1.89	0.00	0.00	100	2.82				
3200	Pinet	P7-0-0	3	H	14.7	14.9	14.8	3	0-0	T095	6.1	5.79	0.27		451.4	1746.8	694.9	88.8	103.2	3.7	5.0	2.7	46	126.4	14.1	0.02	0.01	1.154	8.717	4.979	0.386	15.26	7.57	57.14	32.63	2.53	0.07	0.00	100	1.75				
3200	Pinet	P8-0-0	3	H	15.2	15	14.7	4	0-0	T097	6.44	6.01	0.18		481.2	1988.1	681.5	79	58.1	3.9	7.9	2.6	40	116.3	12.3	0.01	0.01	1.231	9.521	5.609	0.344	16.21	7.36	56.56	33.55	2.06	0.00	0.06	100	1.70				
3200	Pinet	P9-0-0	2	M	14	14.1	14.1	1	0-0	T061	6.31	5.98	0.26		538	2052.3	624.3	81.6	107.5	3.5	5.6	2.81	54	133.2	11.7	0.01	0.01	1.376	10.241	5.138	0.355	17.72	8.04	59.82	30.01	2.07	0.00	0.06	100	1.99				
3200	Pinet	P10-0-0	2	M	14.2	14.1	14.1	2	0-0	T063	5.89	5.35	0.17		282.3	1753.9	572.9	108.1	93.5	4.1	2.6	2.9	70	130.1	12.4	0.04	0.02	0.722	8.792	4.715	0.448	14.68	4.92	59.63	32.13	3.06	0.14	0.14	100	1.86				
3200	Kennedy	K1-0-0	4	H				1	0-0	T065	6.4	5.62	0.12		477.2	1950.6	792.6	124.1	104	2.5	3.9	1.08	124	149.2	15.1	0.02	0.01	1.220	9.794	6.523	0.540	18.04	6.77	53.96	36.17	2.99	0.06	0.06	100	1.49				
3200	Kennedy	K2-0-0	4	H				2	0-0	T067	6.19	5.71	0.18		588.5	1838.5	820.8	160.3	8	3.2	6.4	1.27	117	157	22.8	0.02	0.01	1.595	9.174	6.756	0.627	18.15	8.29	50.54	37.22	3.84	0.06	0.06	100	1.36				
3200	Kennedy	K3-0-0	4	H				3	0-0	T069	5.88	5.41	0.16		614.4	1492.7	642	121	17.7	3.2	5.2	1.45	127	154.4	24.5	0.07	0.03	1.571	7.449	5.284	0.526	14.90	10.55	48.99	35.46	3.53	0.27	0.20	100	1.41				
3200	Kennedy	K4-0-0	4	H				4	0-0	T061	6.38	5.82	0.11		573.6	1814.9	808.2	165.3	9.2	2.6	4.8	1.06	128	138.4	14.2	0.02	0.01	1.324	9.056	6.652	0.659	17.51	7.56	51.72	37.99	2.62	0.06	0.06	100	1.36				
3200	Kennedy	K5-0-0	3	A				1	0-0	T063	5.94	5.3	0.13		531.6	1647	621	121.7	8.9	3.1	4.8	1.3	142	151.4	19	0.09	0.04	1.360	8.219	6.596	0.529	15.56	8.74	52.81	34.48	3.40	0.22	0.26	100	1.53				
3200	Kennedy	K6-0-0	3	A				2	0-0	T065	6.76	6.11	0.15		462	1956.8	1027.7	187.5	16.7	2.2	3.6	0.79	86	146.4	17.7	0.01	0.01	1.182	9.665	8.458	0.616	20.13	5.87	48.01	42.02	4.05	0.00	0.05	100	1.14				
3200	Kennedy	K7-0-0	3	A				3	0-0	T067	6.59	5.66	0.1		536.4	1868.2	844.8	101.5	5.3	2.7	4.7	1.09	113	144.8	13.1	0.03	0.01	1.372	9.322	6.953	0.441	18.12	7.57	51.45	38.37	2.44	0.11	0.06	100	1.34				
3200	Kennedy	K8-0-0	3	A				4	0-0	T069	6.15	5.55	0.13		541.9	1707.2	843.5	119.1	6	3.5	4.2	1.28	127	146.5	17.9	0.03	0.01	1.366	8.519	6.942	0.518	17.40	7.97	48.97	39.91	2.98	0.11	0.06	100	1.23				
3200	Kennedy	K9-0-0	2	M				1	0-0	T071	5.92	5.28	0.11		484.7	1683.6	653.8	124.6	11.6	3.1	3.72	1.24	135	149.9	15.7	0.09	0.04	1.240	8.202	6.151	0.542	15.22	8.14	53.87	33.89	3.56	0.33	0.26	100	1.59				
3200	Kennedy	K10-0-0	2	M				2	0-0	T093	6.84	6.1	0.12		476.7	2002.2	1177	185.7	7.7	3.9	3.88	0.88	93	145.3	15.2	0.01	0.01	1.219	9.991	9.687	0.808	21.72	5.61	46.01	44.61	3.72	0.00	0.05	100	1.09				
3200	Kennedy	K11-0-0	2	M				3	0-0	T095	6.33	5.66	0.14		530.2	1856.1	826.6	142.7	8.4	2.5	4.0	1.01	126	144.9	17.3	0.02	0.01	1.355	9.362	6.803	0.621	18.06	7.51	51.28	37.67	3.44	0.06	0.06	100	1.36				
3200	Kennedy	K12-0-0	2	M				4	0-0	T097	6.15	5.43	0.11		484.5	1765.1	654.2	128.2	5.9	2.8	4.79	1.27	119	154.4	17.2	0.05	0.02	1.265	8.906	7.050	0.559	17.41	7.26	48.87	40.38	3.20	0.17	0.11	100	1.21				
3200	Kennedy	L1-0-0	1	L				1	0-0	T099	6.1	5.62	0.18		673.6	1844.7	712.6	148.1	9.2	3.6	5.7	1.31	176	170.8	22.2	0.03	0.01	1.590	9.055	5.865	0.622	17.30	9.13	53.20	35.90	3.60	0.12	0.06	100	1.57				
3200	Kennedy	L2-0-0	1	L				2	0-0	T081	5.86	5.33	0.15		425.8	1821.2	633.7	129.9	6.8	2.7	3.40	1.32	180	132	15.8	0.07	0.04	1.068	9.068	5.051	0.555	15.86	6.87	57.29	31.84	3.56	0.19	0.25	100	1.80				

Appendix 2

	L1	L2	L3	L4	H1	H2	H3	H4	M1	M2
k_Fungi;p_Ascomycota	0.16%	1.76%	0.58%	0.83%	0.58%	1.24%	1.64%	16.06%	1.26%	0.59%
k_Fungi;p_Basidiomycota	10.98%	42.39%	60.86%	52.93%	42.11%	33.47%	43.15%	23.82%	27.07%	43.08%
k_Fungi;p_Chytridiomycota	82.38%	11.97%	13.00%	14.24%	5.62%	15.54%	9.76%	11.45%	11.50%	8.69%
k_Fungi;p_Glomeromycota	0.05%	0.13%	0.07%	0.47%	0.04%	0.16%	0.40%	0.02%	0.58%	0.23%
k_Fungi;p_Zygomycota	5.63%	37.14%	17.44%	25.38%	47.60%	27.78%	28.15%	40.94%	56.09%	26.91%
k_Fungi;p_unclassified_Fungi	0.79%	5.98%	7.92%	6.10%	3.58%	21.13%	16.47%	7.40%	3.19%	20.40%
k_Plantae;p_Chlorophyta	0.00%	0.63%	0.11%	0.04%	0.49%	0.67%	0.43%	0.31%	0.31%	0.07%
k_Protista;p_Cercozoa	0.00%	0.00%	0.02%	0.02%	0.00%	0.02%	0.00%	0.02%	0.00%	0.02%

Appendix 3

taxonomy	L1	L2	L3	L4	H1	H2	H3	H4	M2
Unassigned;Other;Other;Other;Other	%	%	%	%	%	%	%	%	%
k_Archaea;p_Crenarchaeota;c_Thaumarchaeota;o_Nitrososphaerales;f_Nitrososphaerales;g_Candidatus Nitrososphaera	0.20%	0.30%	0.40%	0.30%	0.40%	0.50%	0.30%	0.20%	0.50%
k_Bacteria;p_Actinobacteria;c_Acidobacteria-5;p_if_jg	0.00%	0.50%	1.30%	1.10%	0.90%	0.90%	0.60%	0.60%	0.80%
k_Bacteria;p_Actinobacteria;c_Acidobacteria-6;o_CCU21;f_jg	0.40%	0.10%	0.10%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Acidobacteria-6;o_iii-15;f_jg	5.90%	2.40%	5.90%	4.60%	3.20%	2.70%	2.90%	2.60%	1.90%
k_Bacteria;p_Actinobacteria;c_Acidobacteria-6;o_iii-15;f_RB40;g	0.30%	0.30%	0.40%	0.30%	0.50%	0.20%	0.60%	0.90%	0.40%
k_Bacteria;p_Actinobacteria;c_Acidobacteria-6;o_iii-15;f_mh24;g	0.90%	0.50%	0.60%	0.40%	0.50%	0.50%	0.40%	0.60%	0.10%
k_Bacteria;p_Actinobacteria;c_Acidobacteria;o_Acidobacteriales;f_Acidobacteriaceae;g	0.10%	0.20%	0.10%	0.70%	0.80%	0.10%	0.20%	0.00%	0.80%
k_Bacteria;p_Actinobacteria;c_Acidobacteria;o_Acidobacteriales;f_Acidobacteriaceae;g_Edaphobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Acidobacteria;o_Acidobacteriales;f_Koribacteraceae;g	0.30%	0.60%	1.70%	1.00%	0.80%	0.40%	0.70%	0.20%	1.10%
k_Bacteria;p_Actinobacteria;c_Acidobacteria;o_Acidobacteriales;f_Koribacteraceae;g_Candidatus Koribacter	0.00%	0.30%	0.70%	0.50%	0.80%	0.30%	0.70%	0.20%	0.80%
k_Bacteria;p_Actinobacteria;c_EC113;o_if_jg	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Solibacteres;o_Solibacterales;f_jg	0.20%	0.20%	0.10%	0.10%	0.10%	0.20%	0.30%	0.20%	0.20%
k_Bacteria;p_Actinobacteria;c_Solibacteres;o_Solibacterales;f_Solibacteraceae;g	0.10%	0.10%	0.10%	0.10%	0.10%	0.10%	0.00%	0.00%	0.20%
k_Bacteria;p_Actinobacteria;c_Solibacteres;o_Solibacterales;f_Solibacteraceae;g_Candidatus Solibacter	0.00%	0.10%	0.10%	0.20%	0.10%	0.10%	0.30%	0.10%	0.20%
k_Bacteria;p_Actinobacteria;c_Solibacteres;o_Solibacterales;f_Ibrubacteraceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Sva0725;o_Sva0725;f_jg	0.20%	0.00%	0.00%	0.00%	0.10%	0.20%	0.20%	1.80%	0.30%
k_Bacteria;p_Actinobacteria;c_[Chloracidobacteria];o_11-24;f_jg	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_[Chloracidobacteria];o_DS-100;f_jg	0.10%	0.00%	0.10%	0.00%	0.30%	0.00%	0.20%	0.50%	0.10%
k_Bacteria;p_Actinobacteria;c_[Chloracidobacteria];o_RB41;f_jg	0.40%	0.00%	0.20%	0.00%	0.10%	0.00%	0.20%	0.20%	0.10%
k_Bacteria;p_Actinobacteria;c_[Chloracidobacteria];o_RB41;f_Elli n6075;g	1.40%	0.60%	1.10%	1.00%	0.30%	0.60%	0.70%	1.10%	0.20%
k_Bacteria;p_Actinobacteria;c_iii-8;o_32-20;f_jg	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%
k_Bacteria;p_Actinobacteria;c_iii-8;o_DS-18;f_jg	0.40%	0.30%	0.80%	0.30%	0.60%	0.30%	0.80%	0.20%	0.30%
k_Bacteria;p_Actinobacteria;c_Acidimicrobia;o_Acidimicrobiales;f_jg	0.10%	0.00%	0.10%	0.20%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Acidimicrobia;o_Acidimicrobiales;f_EB1017;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;Other;Other	0.20%	0.30%	0.20%	0.10%	0.10%	0.20%	0.30%	0.20%	0.20%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_jg	2.40%	3.10%	2.70%	2.50%	7.00%	4.20%	4.80%	5.10%	5.60%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae;g_Actinosynnemataceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinosynnemataceae;g_Lentzea	0.30%	0.00%	0.10%	0.10%	0.00%	0.50%	0.20%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Bogoriellaceae;g_Geopelia	0.20%	0.10%	0.00%	0.10%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;Other	1.00%	10.80%	0.10%	0.60%	0.20%	1.10%	0.10%	0.40%	0.20%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Cellulomonas	0.30%	0.30%	0.10%	0.20%	0.10%	0.40%	0.10%	0.20%	0.20%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Cellulomonadaceae;g_Demouza	0.20%	0.10%	0.10%	0.10%	0.00%	0.20%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Frankiaceae;g	0.20%	0.40%	0.40%	0.40%	0.60%	0.30%	0.30%	0.80%	0.60%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;Other	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;g	0.40%	0.60%	0.60%	0.90%	1.00%	0.80%	0.50%	0.90%	1.30%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;g_Geodermatophilus	1.60%	2.00%	2.20%	2.20%	1.40%	2.50%	1.40%	1.50%	2.20%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Geodermatophilaceae;g_Modesobacter	0.20%	0.20%	0.10%	0.30%	0.20%	0.20%	0.20%	0.20%	0.30%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Glycomycetaceae;g_Glycomyces	0.00%	0.20%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;Other	0.10%	0.20%	0.20%	0.10%	0.20%	0.10%	0.00%	0.10%	0.50%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Phycococcus	0.90%	0.40%	0.40%	0.40%	0.30%	0.60%	0.30%	0.50%	0.60%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Intrasporangiaceae;g_Terracoccus	0.20%	0.30%	0.10%	0.30%	0.30%	0.40%	0.20%	0.30%	0.20%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Kinosporiaceae;g	0.20%	0.10%	0.10%	0.20%	0.30%	0.40%	0.10%	0.10%	0.20%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Leucobacter	0.00%	0.10%	0.00%	0.10%	0.00%	0.10%	0.00%	0.10%	0.10%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Atromyces	0.10%	0.40%	0.00%	0.10%	0.10%	0.00%	0.00%	0.10%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Rathayabacter	0.20%	5.70%	0.00%	0.10%	0.10%	0.00%	0.00%	0.00%	0.10%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Microbacteriaceae;g_Salinibacterium	0.40%	0.30%	0.10%	0.50%	0.70%	0.70%	0.40%	0.70%	0.50%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococaceae;g	0.20%	0.10%	0.10%	0.20%	0.40%	0.30%	0.20%	0.30%	0.10%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococaceae;g_Arthrobacter	0.00%	0.10%	0.00%	0.00%	0.00%	0.10%	0.00%	0.10%	0.10%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;Other	1.20%	1.00%	1.80%	1.90%	2.30%	1.70%	3.50%	5.00%	3.80%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g	1.70%	1.30%	1.50%	1.10%	2.00%	2.50%	1.80%	4.50%	1.70%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Actinoplanes	0.20%	0.10%	0.10%	0.20%	0.30%	0.20%	0.10%	0.20%	1.10%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Catellatospora	0.20%	0.20%	0.20%	0.20%	0.40%	0.10%	0.20%	0.70%	0.30%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Dactylosporangium	0.30%	0.30%	0.10%	0.10%	0.10%	0.00%	0.10%	0.20%	0.20%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Pilmelia	0.10%	0.00%	0.10%	0.10%	0.10%	0.10%	0.20%	0.20%	0.20%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micromonosporaceae;g_Vigorsporangium	0.30%	0.10%	0.10%	0.00%	0.00%	0.10%	0.10%	0.70%	0.10%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Mycobacteriaceae;g_Mycobacterium	0.90%	1.00%	0.70%	0.50%	1.00%	1.10%	1.20%	1.80%	1.10%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nakamurellaceae;g	0.10%	0.20%	0.10%	0.10%	0.00%	0.10%	0.10%	0.20%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiaceae;Other	0.10%	0.20%	0.00%	0.10%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardiaceae;g_Rhodococcus	0.00%	0.10%	0.00%	0.00%	0.10%	0.00%	0.10%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g	1.30%	0.90%	1.20%	1.80%	0.80%	1.80%	0.70%	1.60%	0.70%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g_Aeromicrobium	0.10%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.10%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g_Kribella	1.50%	0.90%	0.40%	0.40%	0.60%	0.80%	0.70%	1.10%	1.10%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Nocardioidaceae;g_Nocardioides	0.50%	0.80%	0.40%	0.70%	1.00%	0.90%	0.70%	1.40%	1.30%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Promicromonosporaceae;g_Promicromonospora	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Promicromonosporaceae;g_Xylomicrobium	0.10%	7.40%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Pseudonocardiaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%

Taxonomy	L1 %	L2 %	L3 %	L4 %	H1 %	H2 %	H3 %	H4 %	M2 %
k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Chlorophyta;f_jg	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Stramenopiles;f_jg	0.20%	0.10%	0.10%	0.20%	0.10%	0.10%	0.20%	0.20%	0.10%
k_Bacteria;p_Cyanobacteria;c_Chloroplast;o_Streptophyta;f_jg	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Cyanobacteria;c_ML6351-21;o_f_jg	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Elusimicrobia;c_Elusimicrobia;o_FAC88;f_jg	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.10%	0.00%
k_Bacteria;p_Elusimicrobia;c_Elusimicrobia;o_IIbf_jg	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Elusimicrobia;c_Elusimicrobia;o_MVP-88;f_jg	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Fibrobacteres;c_Fibrobacteria;o_258ds10;f_jg	0.00%	0.00%	0.00%	0.20%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Fibrobacteres;c_Fibrobacteria;o_258ds10;f_jg	0.10%	0.10%	0.20%	0.10%	0.10%	0.10%	0.10%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_jg	0.30%	0.60%	0.50%	0.30%	1.50%	0.30%	0.40%	0.40%	0.90%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Allycyclobacillaceae;g_Allycyclobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;g_Bacillus	0.10%	0.20%	0.20%	0.10%	0.50%	0.30%	0.20%	0.10%	0.20%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Ammoniphilus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Paenibacillaceae;g_Paenibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;Other	0.10%	0.20%	0.10%	0.20%	0.50%	0.10%	0.40%	0.20%	0.30%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Bacillales;f_Planococcaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Bacilli;o_Turicibacterales;f_Turicibacteraceae;g_Turicibacter	0.00%	0.00%	0.00%	0.00%	0.10%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Alkaliphilus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.10%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coproccocus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptostreptococcaceae;g	0.00%	0.20%	0.10%	0.20%	0.80%	0.40%	0.40%	0.70%	0.20%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_f_jg	0.30%	0.10%	0.40%	0.20%	0.30%	0.20%	0.20%	0.40%	0.20%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_f_jg	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_f_jg	0.00%	0.10%	0.10%	0.10%	0.10%	0.00%	0.00%	0.10%	0.00%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_f_jg	0.20%	0.30%	1.10%	0.60%	0.90%	0.30%	0.40%	0.20%	0.50%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Ellin5290;f_jg	0.70%	1.00%	1.40%	2.30%	2.00%	0.50%	1.00%	0.90%	1.70%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_jg	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.10%	0.00%	0.10%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_Ellin5301;g	0.60%	0.50%	0.60%	0.70%	0.40%	0.40%	0.80%	0.50%	0.90%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_Gemmatimonadales;f_Gemmatimonadaceae;g_Gemmatimonas	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_KD8-87;f_jg	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Gemmatimonadetes;c_Gemmatimonadetes;o_N1423;f_jg	0.60%	0.80%	1.80%	1.40%	0.50%	0.30%	0.50%	0.70%	0.60%
k_Bacteria;p_Nitrospirae;c_Nitrospira;o_Nitrospirales;f_0319-6A21;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Nitrospirae;c_Nitrospira;o_Nitrospirales;f_Nitrospiraceae;g	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Nitrospirae;c_Nitrospira;o_Nitrospirales;f_Nitrospiraceae;g_Nitrospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_OD1;c_ZB2;o_f_jg	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Planctomycetes;c_BD7-11;o_f_jg	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%
k_Bacteria;p_Planctomycetes;c_OM130;o_CL500-15;f_jg	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%
k_Bacteria;p_Planctomycetes;c_OM190;o_egg2;f_jg	0.40%	0.10%	0.20%	0.10%	0.40%	0.00%	0.10%	0.40%	0.00%
k_Bacteria;p_Planctomycetes;c_Phycisphaerae;o_CPA-3;f_jg	0.10%	0.20%	0.20%	0.10%	0.30%	0.10%	0.20%	0.20%	0.10%
k_Bacteria;p_Planctomycetes;c_Phycisphaerae;o_Phycisphaerales;f_jg	0.00%	0.00%	0.10%	0.00%	0.10%	0.00%	0.00%	0.10%	0.00%
k_Bacteria;p_Planctomycetes;c_Phycisphaerae;o_WD2101;f_jg	2.80%	2.00%	4.30%	4.60%	2.80%	2.90%	3.60%	3.20%	3.40%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g	0.30%	0.20%	0.60%	0.90%	0.50%	0.60%	0.70%	0.70%	0.50%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Gemmatales;f_Gemmataceae;g_Gemmata	1.00%	0.40%	0.70%	0.80%	0.40%	0.80%	0.50%	0.60%	0.40%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g	0.50%	0.60%	0.50%	0.30%	0.80%	0.60%	0.60%	0.80%	0.40%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_A17	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.10%	0.10%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Pirellulales;f_Pirellulaceae;g_Pirellula	0.20%	0.10%	0.10%	0.00%	0.10%	0.20%	0.10%	0.10%	0.20%
k_Bacteria;p_Planctomycetes;c_Planctomycetia;o_Planctomycetiales;f_Planctomycetaceae;g_Planctomyces	0.40%	0.10%	0.10%	0.10%	0.20%	0.30%	0.20%	0.30%	0.10%
k_Bacteria;p_Planctomycetes;c_vadinHA49;o_DH61;f_jg	0.10%	0.00%	0.10%	0.00%	0.20%	0.10%	0.10%	0.10%	0.10%
k_Bacteria;p_Proteobacteria;c_jg	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.10%	0.10%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_f_jg	0.00%	0.00%	0.10%	0.00%	0.10%	0.10%	0.10%	0.10%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g	0.20%	0.30%	0.30%	0.30%	0.70%	0.20%	0.40%	0.60%	0.50%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Asticcacaulis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Caulobacter	0.20%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Mycoplana	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae;g_Phenylobacterium	0.30%	0.10%	0.20%	0.30%	0.40%	0.40%	0.30%	0.20%	0.30%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Ellin329;f_jg	0.80%	0.70%	0.80%	1.10%	1.60%	0.80%	1.10%	0.70%	1.40%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_jg	0.50%	0.40%	0.20%	0.30%	0.30%	0.50%	0.60%	0.30%	0.50%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Aurantimonadales;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bejerinckiaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiales;g	1.20%	1.10%	1.30%	0.90%	1.20%	1.40%	1.20%	0.80%	1.50%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiales;g_Balneimonas	0.10%	0.10%	0.10%	0.10%	0.00%	0.10%	0.10%	0.10%	0.10%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Bradyrhizobiales;g_Bradyrhizobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Brucellaceae;g_Ochrobactrum	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiales;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiales;g_Devosia	0.40%	0.50%	0.40%	0.20%	0.50%	0.50%	0.50%	0.50%	0.30%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiales;g_Hyphomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiales;g_Pedomicrobium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Hyphomicrobiales;g_Rhodolanes	1.40%	0.90%	1.60%	1.90%	1.50%	1.30%	1.70%	1.80%	1.70%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales;f_Methylobacteriaceae;g_Methylobacterium	0.10%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.10%

Taxonomy	L1 %	L2 %	L3 %	L4 %	H1 %	H2 %	H3 %	H4 %	M2 %
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Methylocystaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Phyllobacteriaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Phyllobacteriaceae;g_Mesorhizobium	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Phyllobacteriaceae;g_Phyllobacterium	0.10%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Rhizobiaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Rhizobiaceae;g_Agrobacterium	0.20%	0.00%	0.10%	0.10%	0.10%	0.40%	0.20%	0.10%	0.10%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Rhizobiaceae;g_Kaistia	0.00%	0.10%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Rhizobiaceae;g_Rhizobium	0.10%	0.00%	0.10%	0.20%	0.00%	0.20%	0.00%	0.10%	0.10%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Rhodobiaceae;g_Aififella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhizobiales f_Xanthobacteraceae;g_Labrys	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobact erales;f_Hyphomonadaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobact erales;f_Rhodobacteraceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobact erales;f_Rhodobacteraceae;g_Amaricoccus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodobact erales;f_Rhodobacteraceae;g_Rhodobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirill ales;f ;g	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirill ales;f_Acetobacteraceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirill ales;f_Acetobacteraceae;g	0.40%	0.40%	0.30%	0.60%	0.60%	0.50%	0.60%	0.30%	0.70%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirill ales;f_Acetobacteraceae;g_Acidiphilium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirill ales;f_Rhodospirillaceae;g	1.20%	0.60%	0.80%	0.90%	1.20%	0.60%	1.10%	0.90%	1.10%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirill ales;f_Rhodospirillaceae;g_Inquillinus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rhodospirill ales;f_Rhodospirillaceae;g_Skermanella	0.90%	0.20%	0.20%	0.20%	0.10%	0.50%	0.20%	0.20%	0.20%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiale s;f ;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Rickettsiale s;f_mitochondria;g_Vermamoeba	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomo nadales;f_Erythrobacteraceae;Other	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.10%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomo nadales;f_Erythrobacteraceae;g	1.10%	1.50%	1.00%	1.40%	0.80%	0.50%	1.10%	0.60%	1.10%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomo nadales;f_Sphingomonadaceae;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomo nadales;f_Sphingomonadaceae;g	0.20%	0.10%	0.20%	0.10%	0.40%	0.20%	0.70%	0.30%	0.30%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomo nadales;f_Sphingomonadaceae;g_Kaistobacter	1.50%	1.00%	1.20%	1.70%	1.30%	1.30%	1.70%	0.80%	2.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomo nadales;f_Sphingomonadaceae;g_Novosphingobium	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomo nadales;f_Sphingomonadaceae;g_Sphingobium	0.10%	0.00%	0.00%	0.00%	0.00%	0.10%	0.20%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomo nadales;f_Sphingomonadaceae;g_Sphingomonas	0.40%	0.20%	0.30%	0.20%	0.20%	0.60%	0.40%	0.30%	0.50%
k_Bacteria;p_Proteobacteria;c_Alphaproteobacteria;o_Sphingomo nadales;f_Sphingomonadaceae;g_Sphingopyxis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o ;f ;g	0.20%	0.10%	0.20%	0.40%	0.40%	0.30%	0.30%	0.10%	0.10%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_A21b;f_EB 1003;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_A21b;f_UD S;g	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Alcaligenaceae;g_Achromobacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Burkholderiaceae;g_Burkholderia	0.10%	0.10%	0.10%	0.10%	0.20%	0.10%	0.20%	0.00%	0.10%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Burkholderiaceae;g_Salinispora	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Comamonadaceae;Other	0.00%	0.00%	0.00%	0.10%	0.00%	0.10%	0.10%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Comamonadaceae;g	0.40%	0.20%	0.20%	0.30%	0.20%	0.60%	0.20%	0.10%	0.20%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Comamonadaceae;g_Hylemonella	0.20%	0.20%	0.20%	0.20%	0.20%	0.30%	0.30%	0.10%	0.30%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Comamonadaceae;g_Methylibium	1.10%	0.60%	0.70%	1.40%	0.80%	0.90%	0.90%	0.40%	0.40%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Comamonadaceae;g_Polaromonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Oxalobacteraceae;g	0.40%	0.20%	0.20%	0.20%	0.10%	0.60%	0.20%	0.10%	0.20%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderia les;f_Oxalobacteraceae;g_Janthinobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.20%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Ellin6067;f_ ;g	0.90%	0.70%	0.90%	1.50%	0.60%	0.60%	0.70%	0.20%	0.70%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_MND1;f ;g	0.30%	0.30%	0.80%	0.60%	0.40%	0.10%	0.00%	0.10%	0.10%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Methylophil ales;f_Methylophilaceae;g	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Methylophil ales;f_Methylophilaceae;g_Methylotenera	0.10%	0.00%	0.00%	0.10%	0.10%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Nitrosomon adales;f_Nitrosomonadaceae;g_Nitrosovibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocycla es;f_Rhodocyclaceae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

Taxonomy	L1 %	L2 %	L3 %	L4 %	H1 %	H2 %	H3 %	H4 %	M2 %
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Dechloromonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Rhodocyclales;f_Rhodocyclaceae;g_Propionivibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_SC-I-84;f_g	0.10%	0.10%	0.20%	0.30%	0.10%	0.10%	0.30%	0.10%	0.10%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_f_g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bacteriovoraceae;g	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Bdellovibrionales;f_Bdellovibrionaceae;g_Bdellovibrio	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfobacterales;f_Desulfobulbaceae;g_Desulfobulbus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Desulfuromonadales;f_Geobacteraceae;g_Geobacter	0.10%	0.10%	0.20%	0.20%	0.10%	0.20%	0.10%	0.00%	0.20%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_MIZ46;f_g	0.10%	0.10%	0.10%	0.10%	0.10%	0.10%	0.10%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;Other;Other	0.10%	0.10%	0.20%	0.00%	0.10%	0.10%	0.30%	0.20%	0.20%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_g	4.00%	2.10%	2.80%	2.50%	2.50%	3.10%	2.00%	2.50%	1.70%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Cystobacterineae;g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Haliangiaceae;g	1.20%	0.80%	1.20%	0.90%	1.00%	0.50%	0.80%	0.70%	0.70%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Myxococcaceae;g	0.00%	0.10%	0.40%	0.30%	0.00%	0.10%	0.10%	0.00%	0.20%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Myxococcaceae;g_Anaeromyxobacter	0.10%	0.00%	0.10%	0.00%	0.00%	0.10%	0.30%	0.20%	0.10%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Nannocystaceae;g_Nannocystis	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Nannocystaceae;g_Plesiocystis	0.40%	0.00%	0.20%	0.00%	0.20%	0.10%	0.10%	0.30%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_OM27;g	0.10%	0.10%	0.10%	0.00%	0.10%	0.00%	0.10%	0.10%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Polyangiaceae;g	0.10%	0.00%	0.10%	0.10%	0.10%	0.10%	0.10%	0.00%	0.10%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Myxococcales;f_Polyangiaceae;g_Sorangium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.20%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Spirochallales;f_g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Deltaproteobacteria;o_Syntrophobacterales;f_Syntrophobacteraceae;g	0.00%	0.10%	0.00%	0.00%	0.10%	0.10%	0.00%	0.20%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;Other;Other;Other	0.00%	0.10%	0.00%	0.00%	0.20%	0.00%	0.00%	0.00%	0.10%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_f_g	0.10%	0.10%	0.20%	0.10%	0.00%	0.20%	0.00%	0.20%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_211ds20;g	0.10%	0.10%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Alteromonadales;f_Alteromonadaceae;g_Cellvibrio	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacterales;f_Enterobacteriaceae;g	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Coxiellaceae;g_Aquicella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Legionellales;f_Legionellaceae;g_Legionella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Pseudomonadaceae;g_Pseudomonas	0.10%	0.10%	0.00%	0.10%	0.10%	0.60%	0.40%	0.10%	0.10%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Thiotrichales;f_Piscirickettsiaceae;g	0.30%	0.20%	0.00%	0.10%	0.40%	0.10%	0.00%	0.20%	0.10%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Sinobacteraceae;g	2.10%	1.50%	1.20%	1.80%	2.40%	1.20%	2.00%	2.00%	1.10%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Sinobacteraceae;g_Steroidobacter	0.40%	0.20%	0.30%	0.10%	0.50%	0.30%	0.40%	0.40%	0.20%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g	1.50%	1.20%	1.60%	2.30%	2.20%	1.30%	1.40%	0.60%	1.10%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Arenimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Dokdonella	0.20%	0.40%	0.50%	0.30%	0.50%	0.40%	0.70%	0.20%	0.60%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Luteibacter	0.10%	0.00%	0.00%	0.10%	0.00%	0.10%	0.00%	0.00%	0.10%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Luteimonas	0.30%	0.30%	0.60%	0.90%	1.40%	0.40%	0.80%	0.50%	0.90%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Lysobacter	0.10%	0.00%	0.00%	0.00%	0.10%	0.10%	0.10%	0.10%	0.00%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Xanthomonadales;f_Xanthomonadaceae;g_Rhodanobacter	0.00%	0.00%	0.00%	0.10%	0.20%	0.00%	0.10%	0.10%	0.10%
k_Bacteria;p_Spirochaetes;c_Spirochaetes;o_Spirochaetales;f_Spirochaetaceae;g_Spirochaeta	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_TM7;c_SC3;o_f_g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%
k_Bacteria;p_Verrucomicrobia;c_Opitutae;o_Opitutales;f_Opitutaceae;g	0.20%	0.20%	0.10%	0.20%	0.40%	0.20%	0.20%	0.20%	0.20%
k_Bacteria;p_Verrucomicrobia;c_Opitutae;o_Opitutales;f_Opitutaceae;g_Opitutus	1.10%	0.30%	0.40%	0.40%	0.90%	0.80%	0.70%	0.70%	0.60%
k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g	0.20%	0.10%	0.00%	0.10%	0.00%	0.30%	0.20%	0.10%	0.00%
k_Bacteria;p_Verrucomicrobia;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Verrucomicrobiaceae;g_Luteolibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%
k_Bacteria;p_Verrucomicrobia;c_Pedospaerae;o_Pedospaerales;Other;Other	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
k_Bacteria;p_Verrucomicrobia;c_Pedospaerae;o_Pedospaerales;f_g	0.50%	0.50%	0.80%	0.80%	1.10%	0.60%	0.90%	1.20%	0.70%
k_Bacteria;p_Verrucomicrobia;c_Pedospaerae;o_Pedospaerales;f_Ellin515;g	0.10%	0.10%	0.20%	0.20%	0.20%	0.20%	0.30%	0.10%	0.10%
k_Bacteria;p_Verrucomicrobia;c_Pedospaerae;o_Pedospaerales;f_Ellin517;g	0.50%	0.40%	0.70%	0.60%	0.60%	0.50%	0.40%	0.70%	0.40%
k_Bacteria;p_Verrucomicrobia;c_Pedospaerae;o_Pedospaerales;f_auto67_4W;g	0.10%	0.40%	0.20%	0.30%	0.50%	0.20%	0.10%	0.20%	0.20%
k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacterales;f_Chthoniobacteraceae;g	1.10%	0.20%	0.20%	1.00%	0.30%	0.50%	0.10%	0.20%	0.20%
k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacterales;f_Chthoniobacteraceae;g_Candidatus_Xiphinematobacter	0.10%	0.00%	0.10%	0.10%	0.10%	0.00%	0.00%	0.00%	0.10%
k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacterales;f_Chthoniobacteraceae;g_Chthoniobacter	0.00%	0.00%	0.10%	0.10%	0.20%	0.20%	0.10%	0.10%	0.10%
k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacterales;f_Chthoniobacteraceae;g_DA101	1.10%	0.50%	1.80%	1.70%	0.50%	1.20%	2.10%	1.00%	1.20%
k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacterales;f_Chthoniobacteraceae;g_Ellin506	0.20%	0.00%	0.10%	0.10%	0.10%	0.10%	0.00%	0.00%	0.10%
k_Bacteria;p_Verrucomicrobia;c_Spartobacteria;o_Chthoniobacterales;f_Chthoniobacteraceae;g_OR-59	0.60%	0.10%	0.20%	0.20%	0.10%	0.30%	0.10%	0.00%	0.00%
k_Bacteria;p_WS2;c_SHA-109;o_f_g	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%