

Figure S1.
UniFrac distance based hierarchical clustering (UPGMA) of total microbial communities (**bold**) and cultured microbial communities (*italicized*) from various habitats during the months of May (M) and July (J).

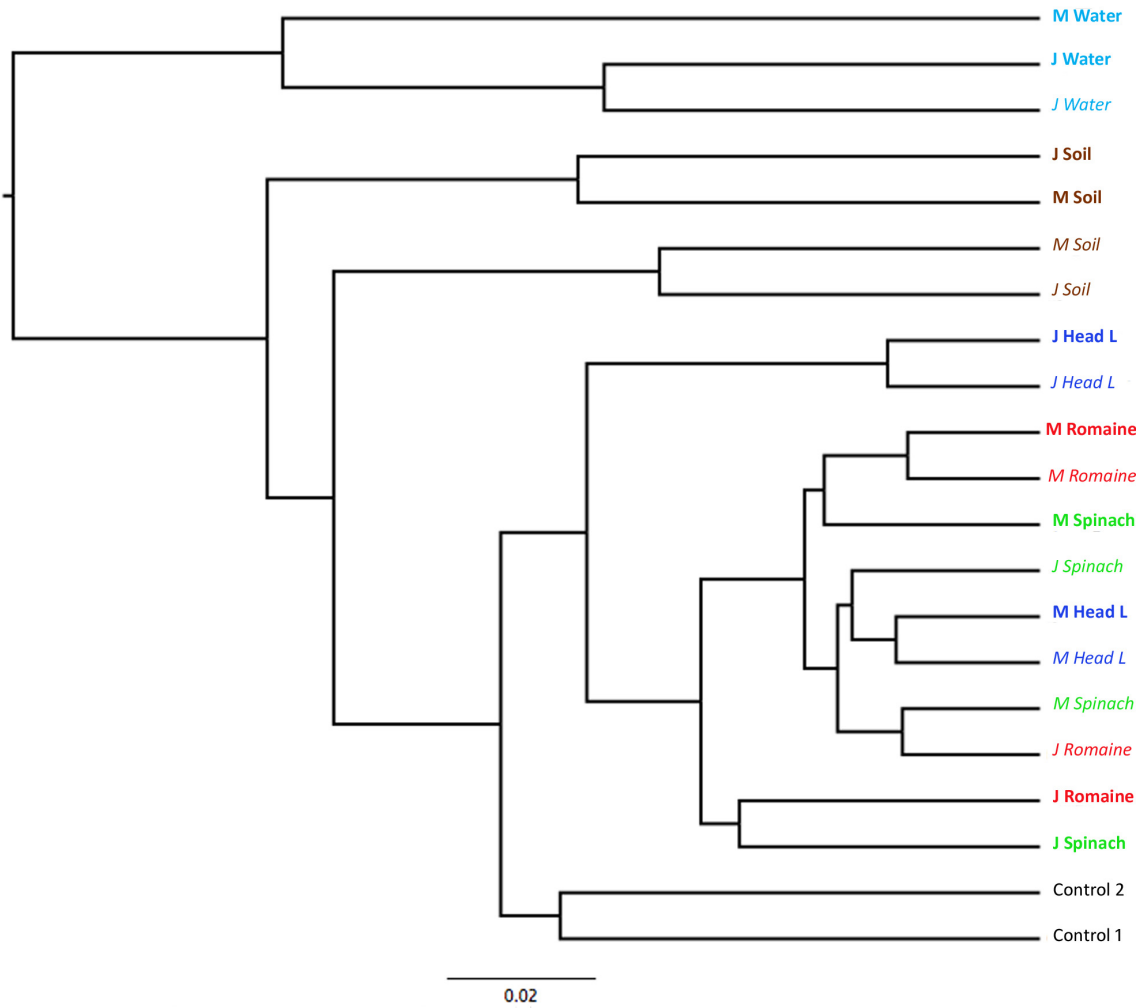


Figure S2.

UniFrac distance based hierarchical clustering (UPGMA) of culture-independent microbial communities from individual leaf samples of head lettuce, romaine and spinach during the months of May (M) and July (J). Colors denote the proportion of surfactant producers observed from the samples when cultured (blue 0-15%, green 16-30%, yellow 31-50%, red 51-100%). One sample (J Head L) did not yield isolates when cultured and thus is not color-coded.

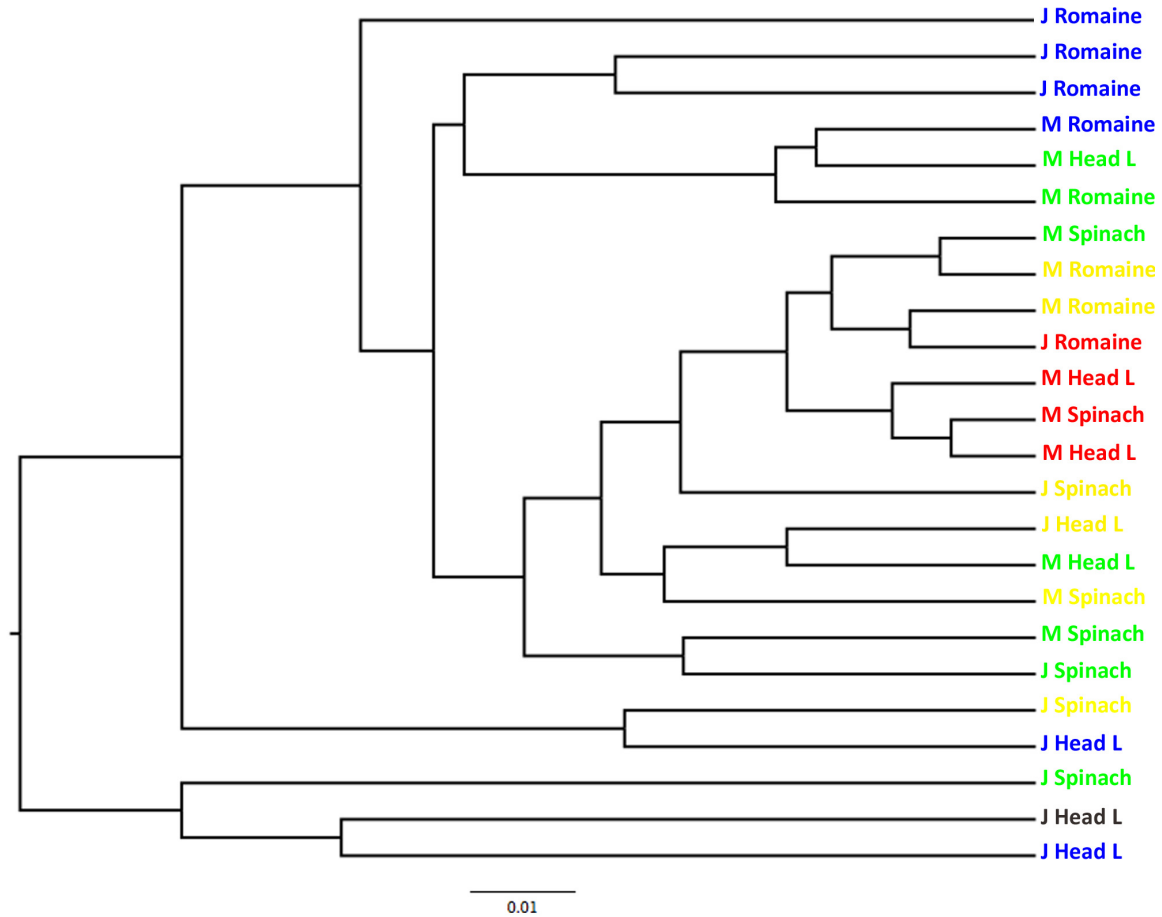


Table S1.

List of the OTUs that were most prevalent (>0.2% total reads) in plant samples (top) and soil samples (bottom). OTUs without cultured representatives are in red.

% Plant reads	Taxonomy
29.54	o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas
13.84	o__Enterobacteriales; f__Enterobacteriaceae
13.13	o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__viridiflava
7.38	o__Burkholderiales; f__Oxalobacteraceae; g__Janthinobacterium; s__
3.12	o__Burkholderiales; f__Oxalobacteraceae; g__Janthinobacterium; s__
2.87	o__Enterobacteriales; f__Enterobacteriaceae; g__Erwinia; s__
1.62	o__Rhizobiales; f__Rhizobiaceae; g__Agrobacterium; s__
1.41	o__Enterobacteriales; f__Enterobacteriaceae
1.25	o__Xanthomonadales; f__Xanthomonadaceae
1.13	o__Enterobacteriales; f__Enterobacteriaceae; g__Buchnera; s__
1.05	o__Enterobacteriales; f__Enterobacteriaceae; g__Erwinia; s__
0.94	o__Pseudomonadales; f__Pseudomonadaceae
0.90	o__Pseudomonadales; f__Moraxellaceae; g__Alkanindiges; s__
0.86	o__Bacillales; f__Bacillaceae; g__Bacillus; s__flexus
0.84	o__Enterobacteriales; f__Enterobacteriaceae
0.78	o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__succinicans
0.70	o__Pseudomonadales; f__Pseudomonadaceae
0.67	o__Burkholderiales; f__Oxalobacteraceae; g__Janthinobacterium; s__
0.61	c__Gammaproteobacteria
0.45	c__Gammaproteobacteria
0.44	o__Burkholderiales; f__Oxalobacteraceae
0.42	o__Enterobacteriales; f__Enterobacteriaceae; g__Erwinia
0.38	o__Actinomycetales; f__Micrococcaceae; g__; s__
0.35	o__Flavobacteriales; f__Flavobacteriaceae; g__Chryseobacterium; s__
0.34	o__Exiguobacteriales; f__Exiguobacteraceae; g__Exiguobacterium; s__indicum
0.34	o__Burkholderiales; f__Oxalobacteraceae; g__; s__
0.31	o__Xanthomonadales; f__Xanthomonadaceae; g__Stenotrophomonas
0.29	o__Flavobacteriales; f__Flavobacteriaceae; g__Chryseobacterium; s__
0.28	o__Burkholderiales; f__Comamonadaceae; g__Limnohabitans; s__
0.27	o__Burkholderiales; f__Comamonadaceae
0.27	o__Sphingobacteriales; f__Sphingobacteriaceae; g__Sphingobacterium; s__multivorum
0.25	o__Methylophilales; f__Methylophilaceae; g__Methylotenera; s__
0.25	o__Enterobacteriales; f__Enterobacteriaceae; g__Erwinia; s__
0.24	o__Exiguobacteriales; f__Exiguobacteraceae; g__Exiguobacterium; s__indicum
0.24	o__Pseudomonadales; f__Pseudomonadaceae
0.24	c__Gammaproteobacteria
0.22	o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas

0.22 o__Actinomycetales; f__Microbacteriaceae; g__Microbacterium; s__
0.21 o__Burkholderiales; f__Alcaligenaceae; g__Achromobacter; s__
0.21 o__Aeromonadales; f__; g__; s__

% Soil
reads

Taxonomy

8.65 o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas
8.05 o__Bacillales; f__Bacillaceae; g__Bacillus; s__flexus
1.70 o__Rubrobacterales; f__Rubrobacteraceae; g__Rubrobacter; s__
1.65 o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__succinicans
1.63 o__Xanthomonadales; f__Xanthomonadaceae
1.63 o__Xanthomonadales; f__Xanthomonadaceae; g__Thermomonas; s__
1.48 o__Sphingobacteriales; f__Chitinophagaceae; g__Flavisolibacter; s__
1.45 o__Bacillales
1.28 o__Nitrosomonadales; f__Nitrosomonadaceae; g__; s__
1.03 o__Actinomycetales; f__Micrococcaceae
1.00 o__Sphingomonadales; f__Sphingomonadaceae; g__Kaistobacter; s__
0.93 o__Bacillales; f__Bacillaceae
0.93 o__N1423WL; f__; g__; s__
0.90 o__Burkholderiales; f__Oxalobacteraceae
0.88 o__Pseudomonadales; f__Pseudomonadaceae
0.88 o__Sphingobacteriales; f__Chitinophagaceae; g__Flavisolibacter; s__
0.78 o__Xanthomonadales; f__Xanthomonadaceae; g__Thermomonas; s__
0.73 o__Flavobacteriales; f__Flavobacteriaceae; g__Gillisia; s__
0.73 o__Burkholderiales; f__Oxalobacteraceae; g__Janthinobacterium; s__
0.73 o__Rhodospirillales; f__Rhodospirillaceae; g__Skermanella; s__
0.70 o__Xanthomonadales; f__Xanthomonadaceae; g__Lysobacter; s__
0.70 o__Bacillales; f__Bacillaceae
0.63 o__Methylophilales; f__Methylophilaceae
0.60 o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__stutzeri
0.58 o__Rhodobacterales; f__Rhodobacteraceae; g__Rhodobacter; s__
0.58 o__Burkholderiales; f__Comamonadaceae; g__Ramlibacter; s__
0.55 o__Xanthomonadales; f__Xanthomonadaceae; g__Lysobacter; s__
0.55 o__[Pedosphaerales]; f__Ellin517; g__; s__
0.55 c__Gemmatimonadetes; o__; f__; g__; s__
0.55 c__JL-ETNP-Z39; o__; f__; g__; s__
0.53 o__Burkholderiales; f__Alcaligenaceae; g__Achromobacter; s__
0.53 o__Sphingobacteriales; f__Flexibacteraceae; g__Pontibacter; s__
0.53 o__Nitrospirales; f__Nitrospiraceae; g__Nitrospira; s__
0.50 o__Rhizobiales; f__Phyllobacteriaceae
0.48 o__Xanthomonadales; f__Xanthomonadaceae; g__Stenotrophomonas
0.45 o__Sphingobacteriales; f__Flexibacteraceae; g__Adhaeribacter; s__
0.45 o__Sphingobacteriales; f__Flammeovirgaceae; g__A4; s__

0.45 o__Syntrophobacterales; f__Syntrophobacteraceae; g__ ; s__
0.45 o__Actinomycetales; f__Micrococcaceae; g__ ; s__
0.45 o__Myxococcales; f__Myxococcaceae
0.43 o__Rhodospirillales; f__Rhodospirillaceae; g__Skermanella; s__
0.43 o__Sphingobacteriales; f__Chitinophagaceae
0.43 c__Gemm-5; o__ ; f__ ; g__ ; s__
0.43 o__Thiotrichales; f__Piscirickettsiaceae; g__Methylophaga; s__
0.40 o__Sphingomonadales; f__Erythrobacteraceae; g__ ; s__
0.40 p__Chloroflexi; c__TK17; o__S085; f__ ; g__ ; s__
0.38 o__Sphingobacteriales; f__Chitinophagaceae; g__Segetibacter; s__
0.38 o__Solibacterales; f__Solibacteraceae; g__Candidatus Solibacter; s__
0.38 o__Myxococcales; f__Cystobacteraceae; g__ ; s__
0.35 o__Burkholderiales; f__Oxalobacteraceae; g__Janthinobacterium; s__
0.33 o__Solirubrobacterales; f__Solirubrobacteraceae
0.33 o__Sphingobacteriales; f__Saprosiraceae; g__ ; s__
0.33 c__Gemmatimonadetes
0.33 o__Gemmatimonadales; f__Ellin5301; g__ ; s__
0.30 o__Sphingobacteriales; f__Flexibacteraceae; g__ ; s__
0.30 o__Rhodospirillales; f__Rhodospirillaceae; g__Skermanella; s__
0.30 o__Solirubrobacterales; f__ ; g__ ; s__
0.30 c__Gemmatimonadetes; o__ ; f__ ; g__ ; s__
0.30 c__Betaproteobacteria; o__SC-I-84; f__ ; g__ ; s__
0.30 o__Myxococcales; f__Nannocystaceae; g__Nannocystis; s__
0.28 o__Caulobacterales; f__Caulobacteraceae
0.28 o__Gaiellales; f__Gaiellaceae; g__ ; s__
0.28 o__Burkholderiales; f__Comamonadaceae; g__Methylibium; s__
0.28 k__Bacteria
0.28 o__Hydrogenophilales; f__Hydrogenophilaceae; g__Thiobacillus; s__
0.28 o__Xanthomonadales; f__Xanthomonadaceae
0.28 o__[Pedosphaerales]; f__ ; g__ ; s__
0.25 o__Actinomycetales; f__Nocardiodaceae; g__ ; s__
0.25 o__Actinomycetales; f__Nocardiodaceae; g__Aeromicrobium; s__
0.25 o__Nitrospirales; f__Nitrospiraceae; g__Nitrospira; s__
0.25 o__Bacillales; f__Bacillaceae
0.23 o__Xanthomonadales; f__Sinobacteraceae; g__ ; s__
0.23 o__Xanthomonadales; f__Xanthomonadaceae; g__Thermomonas; s__
0.20 o__Burkholderiales; f__Oxalobacteraceae
0.20 o__Xanthomonadales; f__Sinobacteraceae; g__Steroidobacter; s__
0.20 o__Sphingomonadales; f__Sphingomonadaceae; g__ ; s__

Table S2. Culturability, prevalence, and surfactant production of OTUs.

Culturability	% of total	% surfactant	Taxonomy
0.00	0.08		o__Solibacterales; f__Solibacteraceae; g__Candidatus Solibacter; s__
0.00	0.05		o__Actinomycetales; f__Geodermatophilaceae
0.00	0.04		o__Actinomycetales; f__Intrasporangiaceae
0.00	0.05		o__Actinomycetales; f__Intrasporangiaceae; g__; s__
0.00	0.16		o__Actinomycetales; f__Microbacteriaceae; g__Microbacterium; s__
0.08	0.28	0.00	o__Actinomycetales; f__Micrococcaceae
0.11	0.37	0.00	o__Actinomycetales; f__Micrococcaceae; g__; s__
0.00	0.05		o__Actinomycetales; f__Nocardiaceae; g__Rhodococcus; s__
0.00	0.06		o__Actinomycetales; f__Nocardioidaceae; g__; s__
0.00	0.06		o__Actinomycetales; f__Nocardioidaceae; g__; s__
0.00	0.05		o__Actinomycetales; f__Nocardioidaceae; g__Aeromicrobium; s__
0.00	0.06		o__Actinomycetales; f__Sporichthyaceae; g__; s__
0.00	0.39		o__Rubrobacterales; f__Rubrobacteraceae; g__Rubrobacter; s__
0.00	0.06		o__Gaiellales; f__Gaiellaceae; g__; s__
0.00	0.06		o__Solirubrobacterales; f__; g__; s__
0.00	0.08		o__Solirubrobacterales; f__Solirubrobacteraceae
2.95	0.09	0.00	o__Flavobacteriales; f__Flavobacteriaceae
0.00	0.08		o__Flavobacteriales; f__Flavobacteriaceae
4.64	0.21	0.80	o__Flavobacteriales; f__Flavobacteriaceae; g__Chryseobacterium; s__
3.23	0.26	0.72	o__Flavobacteriales; f__Flavobacteriaceae; g__Chryseobacterium; s__
0.00	0.11		o__Flavobacteriales; f__Flavobacteriaceae; g__Chryseobacterium; s__joostei
1.96	0.16	0.00	o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium
2.45	0.07	0.00	o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium
0.64	0.09	0.00	o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium
0.00	0.10		o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__
0.68	1.07	0.00	o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__succinicans
0.00	0.04		o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__succinicans
0.00	0.17		o__Flavobacteriales; f__Flavobacteriaceae; g__Gillisia; s__
0.00	0.11		o__Sphingobacteriales; f__Chitinophagaceae
0.00	0.11		o__Sphingobacteriales; f__Chitinophagaceae
0.00	0.04		o__Sphingobacteriales; f__Chitinophagaceae; g__; s__
0.00	0.23		o__Sphingobacteriales; f__Chitinophagaceae; g__Flavisolibacter; s__
0.00	0.36		o__Sphingobacteriales; f__Chitinophagaceae; g__Flavisolibacter; s__
0.00	0.08		o__Sphingobacteriales; f__Chitinophagaceae; g__Segetibacter; s__
0.00	0.10		o__Sphingobacteriales; f__Flammeovirgaceae; g__A4; s__
0.95	1.85	0.00	o__Sphingobacteriales; f__Flexibacteraceae
0.00	0.08		o__Sphingobacteriales; f__Flexibacteraceae; g__; s__
0.00	0.06		o__Sphingobacteriales; f__Flexibacteraceae; g__Adhaeribacter; s__
0.00	0.11		o__Sphingobacteriales; f__Flexibacteraceae; g__Adhaeribacter; s__
0.00	0.11		o__Sphingobacteriales; f__Flexibacteraceae; g__Pontibacter; s__

0.00	0.06		o__Sphingobacteriales; f__Flexibacteraceae; g__Pontibacter; s__korkensis
0.00	0.07		o__Sphingobacteriales; f__Saprospiraceae; g__; s__
3.93	0.05	0.00	o__Sphingobacteriales; f__Sphingobacteriaceae; g__; s__
0.10	0.51	0.00	o__Sphingobacteriales; f__Sphingobacteriaceae; g__; s__
0.00	0.05		o__Sphingobacteriales; f__Sphingobacteriaceae; g__; s__
0.00	0.12		o__Sphingobacteriales; f__Sphingobacteriaceae; g__Pedobacter; s__
0.25	0.19	0.67	o__Sphingobacteriales; f__Sphingobacteriaceae; g__Sphingobacterium; s__multivorum
0.00	0.09		p__Chloroflexi; c__TK17; o__S085; f__; g__; s__
3.14	0.01	0.00	o__Bacillales
0.00	0.40		o__Bacillales
0.51	0.32	0.00	o__Bacillales; f__Bacillaceae
0.00	0.05		o__Bacillales; f__Bacillaceae
0.00	0.16		o__Bacillales; f__Bacillaceae
14.76	0.02	0.00	o__Bacillales; f__Bacillaceae; g__Bacillus
4.54	0.03	0.00	o__Bacillales; f__Bacillaceae; g__Bacillus
4.00	0.01	1.00	o__Bacillales; f__Bacillaceae; g__Bacillus; s__
8.89	0.02	0.00	o__Bacillales; f__Bacillaceae; g__Bacillus; s__firmus
5.94	2.34	0.02	o__Bacillales; f__Bacillaceae; g__Bacillus; s__flexus
9.00	0.01	1.00	o__Bacillales; f__Paenibacillaceae; g__Paenibacillus
2.54	0.07	0.00	o__Bacillales; f__Planococcaceae
0.68	0.25	1.00	o__Exiguobacteriales; f__Exiguobacteraceae; g__Exiguobacterium; s__indicum
0.00	0.17		o__Exiguobacteriales; f__Exiguobacteraceae; g__Exiguobacterium; s__indicum
0.00	0.09		p__Gemmatimonadetes; c__Gemm-5; o__; f__; g__; s__
0.00	0.07		c__Gemmatimonadetes
0.00	0.06		c__Gemmatimonadetes; o__; f__; g__; s__
0.00	0.12		c__Gemmatimonadetes; o__; f__; g__; s__
0.00	0.07		o__Gemmatimonadales; f__Ellin5301; g__; s__
0.00	0.20		c__Gemmatimonadetes; o__N1423WL; f__; g__; s__
0.00	0.12		p__Gemmatimonadetes; c__JL-ETNP-Z39; o__; f__; g__; s__
0.00	0.05		o__Nitrospirales; f__Nitrospiraceae; g__Nitrospira; s__
0.00	0.11		o__Nitrospirales; f__Nitrospiraceae; g__Nitrospira; s__
4.50	0.01	0.00	p__Proteobacteria
0.00	0.04		p__Proteobacteria
0.00	0.05		p__Proteobacteria
0.00	0.06		p__Proteobacteria
0.08	0.10	0.00	o__Caulobacteriales; f__Caulobacteraceae
0.00	0.08		o__Rhizobiales; f__Methylobacteriaceae; g__Methylobacterium; s__adhaesivum
0.00	0.11		o__Rhizobiales; f__Phyllobacteriaceae
0.39	1.15	0.17	o__Rhizobiales; f__Rhizobiaceae; g__Agrobacterium; s__
0.00	0.08		o__Rhodobacteriales; f__Rhodobacteraceae; g__Paracoccus; s__marcusii
0.00	0.12		o__Rhodobacteriales; f__Rhodobacteraceae; g__Rhodobacter; s__
0.00	0.11		o__Rhodobacteriales; f__Rhodobacteraceae; g__Rhodobacter; s__
0.00	0.08		o__Rhodospirillales; f__Rhodospirillaceae; g__Skermanella; s__

0.00	0.15		o__Rhodospirillales; f__Rhodospirillaceae; g__Skermanella; s__
0.00	0.18		o__Rhodospirillales; f__Rhodospirillaceae; g__Skermanella; s__
0.00	0.10		o__Sphingomonadales; f__Erythrobacteraceae; g__; s__
0.00	0.05		o__Sphingomonadales; f__Sphingomonadaceae; g__; s__
0.00	0.22		o__Sphingomonadales; f__Sphingomonadaceae; g__Kaistobacter; s__
0.00	0.05		o__Sphingomonadales; f__Sphingomonadaceae; g__Novosphingobium
0.00	0.05		o__Sphingomonadales; f__Sphingomonadaceae; g__Novosphingobium; s__
5.00	0.02	0.00	c__Betaproteobacteria
0.00	0.06		c__Betaproteobacteria
0.00	0.06		o__Burkholderiales
0.46	0.26	0.00	o__Burkholderiales; f__Alcaligenaceae; g__Achromobacter; s__
0.74	0.07	0.75	o__Burkholderiales; f__Comamonadaceae
0.20	0.13	0.00	o__Burkholderiales; f__Comamonadaceae
0.00	0.04		o__Burkholderiales; f__Comamonadaceae
0.00	0.06		o__Burkholderiales; f__Comamonadaceae
0.00	0.10		o__Burkholderiales; f__Comamonadaceae
0.00	0.22		o__Burkholderiales; f__Comamonadaceae
0.29	3.04	0.00	o__Burkholderiales; f__Comamonadaceae; g__Limnohabitans; s__
0.00	0.06		o__Burkholderiales; f__Comamonadaceae; g__Methylibium; s__
0.06	0.12	0.00	o__Burkholderiales; f__Comamonadaceae; g__Ramlibacter; s__
4.63	0.03	0.00	o__Burkholderiales; f__Oxalobacteraceae
0.67	0.02	0.00	o__Burkholderiales; f__Oxalobacteraceae
0.45	0.36	0.00	o__Burkholderiales; f__Oxalobacteraceae
0.00	0.15		o__Burkholderiales; f__Oxalobacteraceae
0.00	0.29		o__Burkholderiales; f__Oxalobacteraceae
0.00	0.25		o__Burkholderiales; f__Oxalobacteraceae; g__; s__
0.92	0.48	0.01	o__Burkholderiales; f__Oxalobacteraceae; g__Janthinobacterium; s__
0.59	5.34	0.00	o__Burkholderiales; f__Oxalobacteraceae; g__Janthinobacterium; s__
0.30	2.38	0.00	o__Burkholderiales; f__Oxalobacteraceae; g__Janthinobacterium; s__
0.00	0.06		o__Hydrogenophilales; f__Hydrogenophilaceae; g__Thiobacillus; s__
0.00	0.18		o__Methylophilales; f__Methylophilaceae
2.12	0.18	0.00	o__Methylophilales; f__Methylophilaceae; g__Methylotenera; s__
0.00	0.32		o__Nitrosomonadales; f__Nitrosomonadaceae; g__; s__
0.00	0.06		c__Betaproteobacteria; o__SC-l-84; f__; g__; s__
0.00	0.08		o__Myxococcales; f__Cystobacteraceae; g__; s__
0.00	0.10		o__Myxococcales; f__Myxococcaceae
0.00	0.06		o__Myxococcales; f__Nannocystaceae; g__Nannocystis; s__
0.00	0.10		o__Syntrophobacterales; f__Syntrophobacteraceae; g__; s__
32.00	0.00	0.00	c__Gammaproteobacteria
18.00	0.01	0.00	c__Gammaproteobacteria
6.00	0.01	0.00	c__Gammaproteobacteria
2.13	0.06	0.00	c__Gammaproteobacteria
1.87	0.11	0.00	c__Gammaproteobacteria

1.33	0.43	0.01	c__Gammaproteobacteria
0.22	0.17	0.00	c__Gammaproteobacteria
0.00	0.04		c__Gammaproteobacteria
0.00	0.10		c__Gammaproteobacteria
2.24	0.15	0.00	o__Aeromonadales; f__g__; s__
0.11	0.06	0.00	o__Aeromonadales; f__g__; s__
3.43	0.30	0.00	o__Alteromonadales; f__[Chromatiaceae]; g__; s__
129.00	0.01	0.00	o__Alteromonadales; f__[Chromatiaceae]; g__Rheinheimera; s__
5.45	0.02	0.00	o__Alteromonadales; f__[Chromatiaceae]; g__Rheinheimera; s__
0.00	0.06		o__Alteromonadales; f__Alteromonadaceae; g__Cellvibrio; s__
51.00	0.00	0.00	o__Enterobacteriales; f__Enterobacteriaceae
4.40	0.04	0.00	o__Enterobacteriales; f__Enterobacteriaceae
4.00	0.01	0.00	o__Enterobacteriales; f__Enterobacteriaceae
1.73	0.04	0.00	o__Enterobacteriales; f__Enterobacteriaceae
1.45	9.88	0.00	o__Enterobacteriales; f__Enterobacteriaceae
0.73	1.00	0.00	o__Enterobacteriales; f__Enterobacteriaceae
0.37	0.60	0.00	o__Enterobacteriales; f__Enterobacteriaceae
0.00	0.06		o__Enterobacteriales; f__Enterobacteriaceae
0.00	0.12		o__Enterobacteriales; f__Enterobacteriaceae
0.00	0.81		o__Enterobacteriales; f__Enterobacteriaceae; g__Buchnera; s__
0.19	0.30	0.00	o__Enterobacteriales; f__Enterobacteriaceae; g__Erwinia
1.62	0.18	0.00	o__Enterobacteriales; f__Enterobacteriaceae; g__Erwinia; s__
0.66	0.75	0.00	o__Enterobacteriales; f__Enterobacteriaceae; g__Erwinia; s__
0.57	2.05	0.14	o__Enterobacteriales; f__Enterobacteriaceae; g__Erwinia; s__
0.00	0.13		o__Pseudomonadales; f__Moraxellaceae; g__Alkanindiges; s__
0.00	0.64		o__Pseudomonadales; f__Moraxellaceae; g__Alkanindiges; s__
40.00	0.00	0.01	o__Pseudomonadales; f__Pseudomonadaceae
9.72	0.05	0.02	o__Pseudomonadales; f__Pseudomonadaceae
2.18	0.10	0.03	o__Pseudomonadales; f__Pseudomonadaceae
1.64	0.03	0.00	o__Pseudomonadales; f__Pseudomonadaceae
1.15	0.17	0.17	o__Pseudomonadales; f__Pseudomonadaceae
0.71	0.50	0.32	o__Pseudomonadales; f__Pseudomonadaceae
0.18	0.86	0.28	o__Pseudomonadales; f__Pseudomonadaceae
6.34	0.05	0.05	o__Pseudomonadales; f__Pseudomonadaceae; g__; s__
3.30	0.02	0.00	o__Pseudomonadales; f__Pseudomonadaceae; g__; s__
1.94	0.04	0.00	o__Pseudomonadales; f__Pseudomonadaceae; g__; s__
0.16	0.07	0.00	o__Pseudomonadales; f__Pseudomonadaceae; g__; s__
0.00	0.09		o__Pseudomonadales; f__Pseudomonadaceae; g__; s__
1.67	22.98	0.44	o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas
0.25	0.16	0.63	o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas
0.00	0.05		o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas
0.00	0.10		o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas
0.03	0.13	1.00	o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__stutzeri

0.48	9.38	0.98	o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__viridiflava
0.00	0.08		o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__viridiflava
0.00	0.09		o__Thiotrichales; f__Piscirickettsiaceae; g__Methylophaga; s__
0.00	0.05		o__Xanthomonadales; f__Sinobacteraceae; g__; s__
0.00	0.06		o__Xanthomonadales; f__Sinobacteraceae; g__Steriodobacter; s__
1.01	1.25	0.23	o__Xanthomonadales; f__Xanthomonadaceae
0.00	0.06		o__Xanthomonadales; f__Xanthomonadaceae
0.00	0.15		o__Xanthomonadales; f__Xanthomonadaceae; g__Lysobacter; s__
0.00	0.16		o__Xanthomonadales; f__Xanthomonadaceae; g__Lysobacter; s__
0.22	0.15	1.00	o__Xanthomonadales; f__Xanthomonadaceae; g__Rhodanobacter; s__
3.23	0.32	0.01	o__Xanthomonadales; f__Xanthomonadaceae; g__Stenotrophomonas
0.00	0.07		o__Xanthomonadales; f__Xanthomonadaceae; g__Thermomonas; s__
0.00	0.17		o__Xanthomonadales; f__Xanthomonadaceae; g__Thermomonas; s__
0.00	0.36		o__Xanthomonadales; f__Xanthomonadaceae; g__Thermomonas; s__
0.00	0.06		o__[Pedosphaerales]; f__; g__; s__
0.00	0.12		o__[Pedosphaerales]; f__Ellin517; g__; s__

This table includes all OTUs that were observed as 1% or more of the reads from at least one individual sample of total bacteria from plants, soil, or water.

Samples were excluded from this analysis when there were insufficient HTS reads (fewer than 200) from the corresponding cultured reads, since an estimate of culturability would be unreliable without these measurements; this excluded June romaine samples and April water samples.

“Culturability” values were color-coded: Orange for OTUs that were never observed in culture, and a white-green gradient for those that were observed.

“% of total” is the observation frequency of any culture-independent OTU in relation to all OTU reads from culture-independent samples combined at rarefied proportions equal to their proportions in the culture library (8 spinach: 4 romaine [April only]: 8 head lettuce: 2 irrigation water [June only]: and 6 soil), and calculates. We utilize a red gradient color-coding of “% total” for more rapid visual inspection.

“% surfactant” was calculated as the estimated # of colonies of that OTU that were classified as surfactant producers divided by the total estimated # of colonies of that OTU that were cultured (see materials and methods for estimation calculations.) No numbers are recorded for OTUs that were not cultured, and a blue color-coding captures OTUs with higher likelihoods of having been characterized as surfactant producers.