

Different bacterial communities in ectomycorrhizae and surrounding soil.

Vik, Unni¹ Logares, Ramiro² Błaalid, Rakel² Halvorsen, Rune² Carlsen, Tor² Bakke, Ingrid² Kolstø, Anne-Brit Økstad, Ole Andreas² Kausrud, Håvard²

Supplementary information.

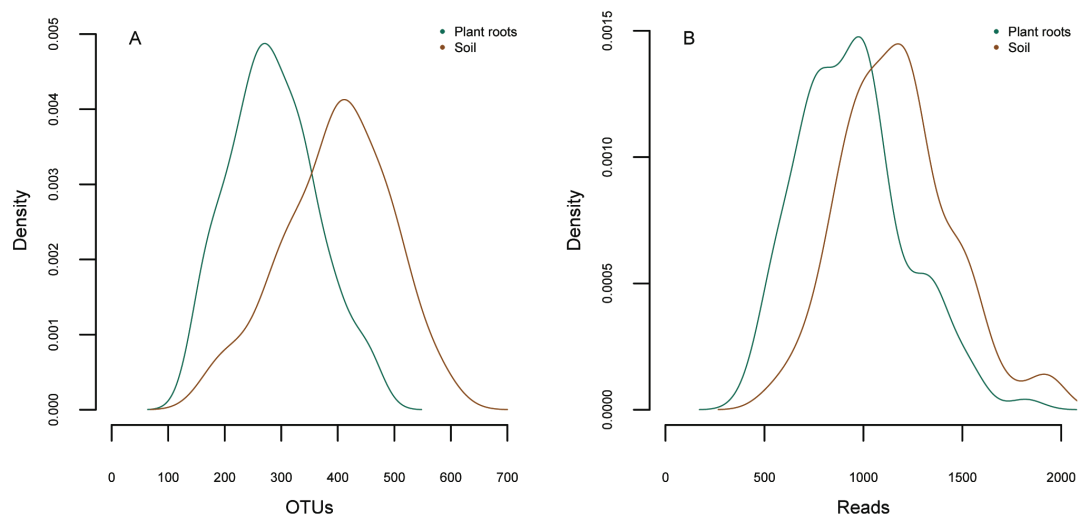


Figure S1. Density plot of distribution of bacterial A) OTUs and B) reads in the 115 plant root systems of *B. vivipara* (green) and the 63 adjacent soil samples (brown).

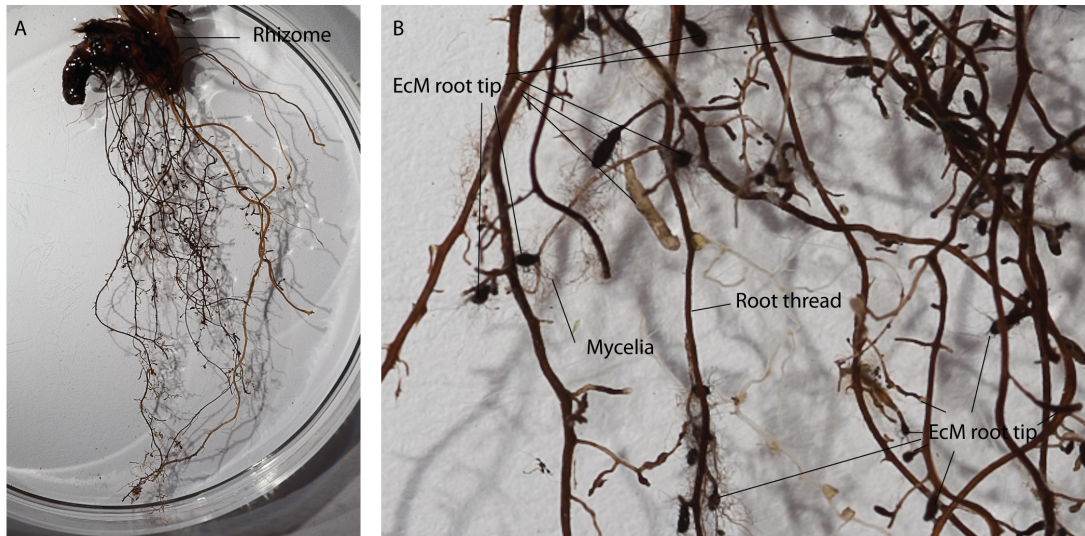


Figure S2. A shows a typical *Bistorta vivipara* root system attached to the rhizome. B shows a magnified part of A, where the root thread, EcM tips and mycelia are highlighted.

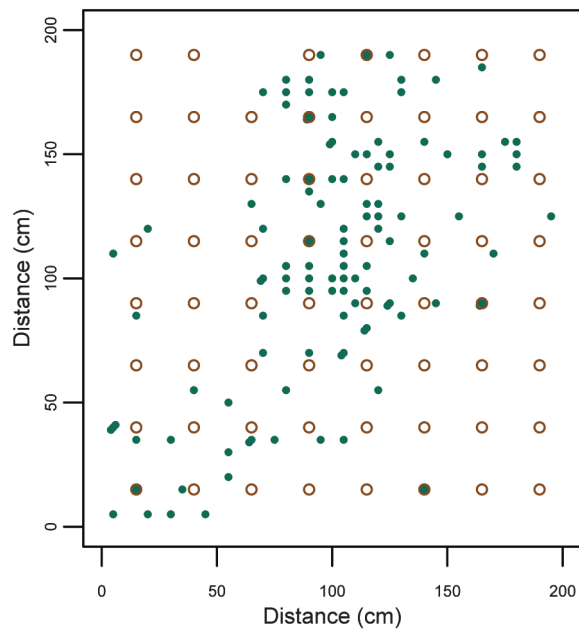


Figure S3. The sampled plot of *Bistorta vivipara* root systems (green filled circles) and soil samples (brown open circles). Certain places, there was an overlap between the plant samples and soil samples. Samples that were not included in downstream analyses are removed from the plot.

Table S1. G-test of independence of the bacterial OTUs appearing in the 115 *Bistorta vivipara* plant root samples and 63 soil samples.

OTU	g_prob	Bonferroni corrected probability	Pla nt_ ob s	Plant _est	Percent of obs	soil _o bs	soil_est	Percent of obs	Phyla	Class	Order	Family
2911	6.74E-12	1.35E-09	51	32.95	154.78	0	18.05	0.00	AD3	JG37-AG-4	Unknown	Unknown
6114	6.74E-12	1.35E-09	51	32.95	154.78	0	18.05	0.00	Chloroflexi	Anaerolineae	Unknown	Unknown
7763	6.74E-12	1.35E-09	51	32.95	154.78	0	18.05	0.00	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
9113	2.52E-15	5.05E-13	62	40.06	154.78	0	21.94	0.00	Chloroflexi	Unknown	Unknown	Unknown
4988	4.86E-11	9.73E-09	48	31.01	154.78	0	16.99	0.00	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae
491	3.77E-18	7.54E-16	70	45.22	154.78	0	24.78	0.00	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae
638	1.74E-12	3.48E-10	53	34.24	154.78	0	18.76	0.00	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae
3139	5.26E-25	1.05E-22	86	55.56	154.78	0	30.44	0.00	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
1232	8.86E-18	1.77E-15	69	44.58	154.78	0	24.42	0.00	Unknown	Unknown	Unknown	Unknown
8523	9.26E-11	1.85E-08	47	30.37	154.78	0	16.63	0.00	Unknown	Unknown	Unknown	Unknown
606	5.05E-14	1.01E-11	58	37.47	154.78	0	20.53	0.00	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
4680	1.66E-25	3.32E-23	87	56.21	154.78	0	30.79	0.00	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
1686	9.07E-22	1.81E-19	79	51.04	154.78	0	27.96	0.00	Acidobacteria	Acidobacteria	Acidobacteriales	Koribacteraceae
8581	2.54E-11	5.07E-09	49	31.66	154.78	0	17.34	0.00	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
6952	2.54E-11	5.07E-09	49	31.66	154.78	0	17.34	0.00	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Thermogemmatisporaceae
1256	1.04E-13	2.09E-11	57	36.83	154.78	0	20.17	0.00	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Thermogemmatisporaceae
9042	1.75E-10	3.50E-08	46	29.72	154.78	0	16.28	0.00	Unknown	Unknown	Unknown	Unknown
8079	8.71E-13	1.74E-10	54	34.89	154.78	0	19.11	0.00	Unknown	Unknown	Unknown	Unknown
7662	7.08E-17	1.42E-14	72	47.16	152.66	1	25.84	3.87	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
1018	1.01E-13	2.01E-11	63	41.35	152.36	1	22.65	4.41	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
7767	1.54E-11	3.07E-09	56	36.83	152.07	1	20.17	4.96	TM7	TM7-1	Unknown	Unknown
5493	2.21E-10	4.43E-08	52	34.24	151.86	1	18.76	5.33	TM7	TM7-1	Unknown	Unknown
1573	2.79E-09	5.58E-07	48	31.66	151.62	1	17.34	5.77	Unknown	Unknown	Unknown	Unknown

2629	5.15E-09	1.03E-06	47	31.01	151.56	1	16.99	5.89	Unknown	Unknown	Unknown	Unknown
2928	3.10E-08	6.20E-06	44	29.07	151.34	1	15.93	6.28	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
926	4.56E-16	9.12E-14	77	51.69	148.98	3	28.31	10.60	Unknown	Unknown	Unknown	Unknown
7449	6.84E-09	1.37E-06	51	34.24	148.94	2	18.76	10.66	Actinobacteria	Actinobacteria	Actinomycetales	Unknown
5693	1.26E-08	2.52E-06	50	33.60	148.83	2	18.40	10.87	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Thermogemmatisporaceae
5564	1.26E-08	2.52E-06	50	33.60	148.83	2	18.40	10.87	Acidobacteria	Acidobacteria	Acidobacteriales	Koribacteraceae
7770	7.66E-13	1.53E-10	68	45.87	148.24	3	25.13	11.94	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae
8371	6.02E-11	1.20E-08	62	41.99	147.64	3	23.01	13.04	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae
7390	1.64E-16	3.28E-14	81	54.92	147.50	4	30.08	13.30	Acidobacteria	Unknown	Unknown	Unknown
4092	8.33E-12	1.67E-09	68	46.52	146.18	4	25.48	15.70	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae
1578	3.50E-22	6.99E-20	99	68.48	144.56	7	37.52	18.66	TM7	TM7-1	Unknown	Unknown
3490	4.69E-08	9.39E-06	55	38.12	144.29	4	20.88	19.16	Actinobacteria	Actinobacteria	Actinomycetales	Kineosporiaceae
1339	2.42E-06	0.00048345	48	33.60	142.88	4	18.40	21.73	Actinobacteria	Actinobacteria	Actinomycetales	Micromonosporaceae
1069	3.52E-20	7.05E-18	99	69.78	141.88	9	38.22	23.54	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Thermogemmatisporaceae
8948	3.08E-05	0.00616465	43	30.37	141.61	4	16.63	24.05	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae
3278	2.75E-07	5.49E-05	58	41.35	140.27	6	22.65	26.49	Bacteroidetes	Sphingobacteria	Sphingobacteriales	Chitinophagaceae
7759	1.23E-05	0.0024663	48	34.24	140.18	5	18.76	26.65	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae
3911	4.86E-07	9.71E-05	57	40.70	140.04	6	22.30	26.91	Actinobacteria	Actinobacteria	Actinomycetales	Unknown
8656	2.03E-05	0.00405981	47	33.60	139.90	5	18.40	27.17	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Thermogemmatisporaceae
4117	2.52E-10	5.04E-08	74	52.98	139.68	8	29.02	27.56	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae
4201	4.19E-07	8.38E-05	60	43.29	138.61	7	23.71	29.52	Actinobacteria	Actinobacteria	Actinomycetales	Actinospicaceae
4530	0.00021384	0.04276867	42	30.37	138.32	5	16.63	30.06	Unknown	Unknown	Unknown	Unknown
9428	5.88E-07	0.00011757	62	45.22	137.09	8	24.78	32.29	Planctomycetes	Phycisphaerae	Unknown	Unknown
7342	1.25E-08	2.50E-06	73	53.62	136.13	10	29.38	34.04	TM7	TM7-1	Unknown	Unknown
5660	3.93E-05	0.00786747	54	40.06	134.81	8	21.94	36.46	Unknown	Unknown	Unknown	Unknown
6129	4.06E-22	8.11E-20	111	82.70	134.23	17	45.30	37.52	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae
6597	4.41E-14	8.83E-12	101	76.88	131.37	18	42.12	42.74	Armatimonadetes	Armatimonadia	Armatimonadales	Armatimonadaceae

8727	0.00015693	0.03138575	56	42.64	131.33	10	23.36	42.81	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae
1618	1.99E-14	3.99E-12	104	80.11	129.82	20	43.89	45.57	Chloroflexi	Ktedonobacteria	Thermogemmatissporales	Unknown
1669	3.36E-18	6.71E-16	113	89.16	126.74	25	48.84	51.18	Chloroflexi	Ktedonobacteria	Thermogemmatissporales	Thermogemmatissporaceae
3484	2.25E-14	4.50E-12	108	85.28	126.64	24	46.72	51.37	Actinobacteria	Actinobacteria	Actinomycetales	Unknown
7230	1.62E-06	0.00032341	83	65.90	125.95	19	36.10	52.63	AD3	JG37-AG-4	Unknown	Unknown
9553	2.30E-08	4.60E-06	99	80.76	122.59	26	44.24	58.77	WPS-2	Unknown	Unknown	Unknown
5354	1.02E-10	2.04E-08	108	89.16	121.13	30	48.84	61.42	Chloroflexi	Ktedonobacteria	Thermogemmatissporales	Thermogemmatissporaceae
5212	1.09E-05	0.00217694	106	93.03	113.94	38	50.97	74.56	Actinobacteria	Actinobacteria	Actinomycetales	Streptomycetaceae
262	5.00E-05	0.0099923	73	85.28	85.60	59	46.72	126.29	Verrucomicrobia	Spartobacteria	Chthoniobacterales	Chthoniobacteraceae
7445	6.34E-05	0.01267464	62	75.59	82.02	55	41.41	132.82	Planctomycetes	Planctomycetia	Planctomycetales	Planctomycetaceae
7712	0.00014433	0.02886601	52	65.90	78.91	50	36.10	138.50	Proteobacteria	Betaproteobacteria	Ellin6067	Unknown
7540	5.73E-10	1.15E-07	50	69.78	71.66	58	38.22	151.73	Acidobacteria	Chloracidobacteria	Unknown	Unknown
3746	2.97E-09	5.93E-07	47	66.54	70.63	56	36.46	153.61	Unknown	Unknown	Unknown	Unknown
1078	4.64E-05	0.00927623	36	51.04	70.53	43	27.96	153.79	Planctomycetes	Phycisphaerae	Unknown	Unknown
1475	2.15E-07	4.29E-05	40	58.15	68.79	50	31.85	156.97	Planctomycetes	Planctomycetia	Gemmatales	Isosphaeraceae
4908	1.63E-12	3.27E-10	48	69.78	68.79	60	38.22	156.97	Acidobacteria	iii1-8	DS-18	Unknown
4631	3.19E-09	6.38E-07	40	60.08	66.57	53	32.92	161.02	Verrucomicrobia	Spartobacteria	Chthoniobacterales	Chthoniobacteraceae
5180	8.34E-06	0.00166788	28	43.93	63.73	40	24.07	166.20	Planctomycetes	Phycisphaerae	Unknown	Unknown
2266	1.33E-06	0.00026539	30	47.16	63.61	43	25.84	166.43	Planctomycetes	Phycisphaerae	Unknown	Unknown
7762	4.35E-07	8.71E-05	30	47.81	62.75	44	26.19	168.00	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae
1240	7.91E-07	0.00015821	23	40.06	57.42	39	21.94	177.73	Actinobacteria	Actinobacteria	Actinomycetales	Intrasporangiaceae
5483	2.81E-12	5.62E-10	29	52.33	55.42	52	28.67	181.38	Planctomycetes	Phycisphaerae	Unknown	Unknown
7087	7.91E-10	1.58E-07	25	45.87	54.50	46	25.13	183.05	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae
5257	2.45E-11	4.89E-09	26	48.46	53.66	49	26.54	184.59	Actinobacteria	Acidimicrobiia	Acidimicrobiales	Unknown
3792	5.45E-08	1.09E-05	21	39.41	53.29	40	21.59	185.27	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae
1392	1.13E-08	2.27E-06	22	41.35	53.21	42	22.65	185.42	Planctomycetes	Phycisphaerae	Unknown	Unknown
443	1.19E-06	0.00023874	18	34.24	52.57	35	18.76	186.58	Fusobacteria	Fusobacteria	Unknown	Unknown

524	1.38E-10	2.75E-08	20	41.35	48.37	44	22.65	194.25	Acidobacteria	Chloracidobacteria	Unknown	Unknown
7197	2.07E-10	4.14E-08	19	40.06	47.43	43	21.94	195.95	Acidobacteria	Chloracidobacteria	Unknown	Unknown
4616	1.27E-07	2.54E-05	13	29.72	43.74	33	16.28	202.69	Proteobacteria	Betaproteobacteria	IS-44	Unknown
7513	9.41E-12	1.88E-09	16	38.12	41.97	43	20.88	205.92	Acidobacteria	Acidobacteria-6	iii1-15	Unknown
7740	9.20E-10	1.84E-07	14	33.60	41.67	38	18.40	206.47	Planctomycetes	Phycisphaerae	Unknown	Unknown
564	3.06E-14	6.13E-12	15	39.41	38.06	46	21.59	213.06	WPS-2	Unknown	Unknown	Unknown
2890	4.88E-09	9.75E-07	11	29.07	37.84	34	15.93	213.47	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae
9005	1.11E-10	2.21E-08	11	31.01	35.47	37	16.99	217.79	Planctomycetes	Planctomycetia	Gemmatales	Isosphaeraceae
9272	8.04E-12	1.61E-09	10	31.01	32.25	38	16.99	223.68	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae
7349	5.49E-18	1.10E-15	10	36.83	27.15	47	20.17	232.97	Acidobacteria	iii1-8	DS-18	Unknown
7597	1.33E-19	2.65E-17	10	38.12	26.23	49	20.88	234.65	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae
5870	3.44E-21	6.88E-19	9	38.12	23.61	50	20.88	239.44	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae
8137	7.18E-23	1.44E-20	8	38.12	20.99	51	20.88	244.23	Planctomycetes	Phycisphaerae	Unknown	Unknown
6768	1.72E-16	3.45E-14	6	30.37	19.76	41	16.63	246.47	Planctomycetes	Planctomycetia	Gemmatales	Gemmataceae
8870	9.00E-23	1.80E-20	6	35.53	16.89	49	19.47	251.72	Acidobacteria	Unknown	Unknown	Unknown
2262	1.14E-23	2.29E-21	6	36.18	16.58	50	19.82	252.27	Nitrospirae	Nitrospira	Nitrospirales	Unknown
3873	6.09E-22	1.22E-19	2	29.07	6.88	43	15.93	269.98	Acidobacteria	Acidobacteria-6	Unknown	Unknown
4263	1.53E-28	3.05E-26	1	32.30	3.10	49	17.70	276.89	AD3	JG37-AG-4	Unknown	Unknown

Table S2. Accession numbers and species names for sequences used in primer design

Species name	Group	Accession number
Uncultured acidobacterium	Acidobacterium	Z95734
<i>Corynebacterium bovis</i>	Actinobacteria	AF311417
<i>Rhizobium</i> sp.	Alphaproteobacteria	AF345540
<i>Bacteroides fragilis</i>	Bacteroidetes	X83950
<i>Burkholderia gladioli</i>	Betaproteobacteria	S55001
<i>Kouleothrix aurantiaca</i>	Chloroflexi	AB079638
<i>Enterococcus</i> sp.	Firmicutes	AM884197
Verrucomicrobia bacterium	Verrucomicrobia	S 002445559
<i>Auxis rochei</i>	Vertebrate	AB193568
<i>Arabidopsis thaliana</i>	Flowering plant	X16077
<i>Pfiesteria piscicida</i>	Protist	AF330617
<i>Leucostoma personii</i>	Sac fungi	M83259

Table S3. The OTUs that appeared in the negative control, and were removed in the downstream analyses. OTU gives the OTU ID, RS gives the average number of reads in each root sample, S gives the average number of reads in each soil sample. Neg gives the observed number of reads in the negative control. Phyla, class, order and family gives the taxonomic annotation of the OTU removed.

OTU	RS	S	Neg.	Phyla	Class	Order	Family
6820	1.07	0.86	1	Acidobacteria	Acidobacteria-6	iii1-15	Unknown
3642	14.71	0.32	7	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae
3925	0.04	0.00	1	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae
7946	0.10	0.05	3	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae
3449	0.47	0.00	1	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae
6222	0.11	4.21	2	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae
7498	0.14	0.38	3	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae
7642	0.05	0.11	2	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae
8460	3.92	2.29	32	Actinobacteria	Actinobacteria	Actinomycetales	Propionibacteriaceae
2328	0.10	0.00	1	Actinobacteria	Actinobacteria	Actinomycetales	Unknown
7930	2.68	0.00	3	Actinobacteria	Actinobacteria	Actinomycetales	Unknown
4188	0.00	0.21	1	Actinobacteria	Actinobacteria	Actinomycetales	Yaniellaceae
739	0.09	0.05	16	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae
1082	0.02	0.02	6	Armatimonadetes	Chthonomonadetes	Chthonomonadales	Chthonomonadaceae
8893	0.02	0.08	80	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
5441	2.09	46.00	1	Chloroflexi	Ellin6529	Unknown	Unknown
1887	0.08	0.00	3	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
6146	11.20	0.29	29	Chloroflexi	Ktedonobacteria	Thermogemmatisporales	Unknown
8492	0.03	0.00	2	Firmicutes	Bacilli	Bacillales	Staphylococcaceae
1273	0.02	0.17	41	Firmicutes	Bacilli	Bacillales	Unknown
7579	0.00	1.40	17	Firmicutes	Bacilli	Bacillales	Unknown
9017	0.01	25.94	488	Firmicutes	Bacilli	Bacillales	Unknown
9497	0.00	0.13	11	Firmicutes	Bacilli	Bacillales	Unknown
8731	0.04	2.41	26	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae
1451	0.00	0.17	2	Firmicutes	Bacilli	Unknown	Unknown
2108	0.00	0.19	2	Firmicutes	Bacilli	Unknown	Unknown
4091	0.02	8.46	23	Firmicutes	Bacilli	Unknown	Unknown
5391	0.00	0.02	18	Firmicutes	Bacilli	Unknown	Unknown
5556	0.00	0.05	5	Firmicutes	Bacilli	Unknown	Unknown
5711	0.00	0.17	3	Firmicutes	Bacilli	Unknown	Unknown
9103	0.00	0.27	1	Firmicutes	Bacilli	Unknown	Unknown
9298	0.01	7.17	59	Firmicutes	Bacilli	Unknown	Unknown
9487	0.01	0.00	14	Planctomycetes	Planctomycetia	Pirellulales	Pirellulaceae
703	0.00	0.03	46	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae
665	0.03	0.00	4	Proteobacteria	Alphaproteobacteria	Caulobacterales	Unknown
2363	0.33	0.33	167	Proteobacteria	Alphaproteobacteria	Caulobacterales	Unknown

3965	5.68	3.62	12	Proteobacteria	Alphaproteobacteria	Rhizobiales	Bradyrhizobiaceae
357	0.45	0.10	2	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae
733	1.19	3.59	108	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unknown
7348	0.00	0.32	3	Proteobacteria	Alphaproteobacteria	Rhizobiales	Unknown
3802	0.01	0.00	30	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae
4539	0.20	0.02	4	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae
3315	0.52	0.44	55	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae
6789	0.05	0.17	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae
7365	0.15	0.22	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiaceae
104	0.68	0.19	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae
7510	0.12	0.05	1	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae
8366	0.02	0.16	11	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae
9169	0.06	0.19	17	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae
792	0.05	0.00	1	Proteobacteria	Betaproteobacteria	Unknown	Unknown
890	1.23	6.43	12	Proteobacteria	Betaproteobacteria	Unknown	Unknown
1031	0.13	0.00	1	Proteobacteria	Betaproteobacteria	Unknown	Unknown
3634	0.26	0.00	1	Proteobacteria	Betaproteobacteria	Unknown	Unknown
3869	8.07	0.44	524	Proteobacteria	Betaproteobacteria	Unknown	Unknown
4549	0.09	0.00	1	Proteobacteria	Betaproteobacteria	Unknown	Unknown
7326	0.12	0.00	1	Proteobacteria	Betaproteobacteria	Unknown	Unknown
9417	0.03	0.02	1	Proteobacteria	Betaproteobacteria	Unknown	Unknown
614	0.03	0.06	25	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae
9385	0.51	4.03	1	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae
6837	0.00	0.44	7	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae
3817	0.03	0.03	3	Proteobacteria	Unknown	Unknown	Unknown
8958	0.30	0.49	29	Proteobacteria	Unknown	Unknown	Unknown
1499	35.98	0.19	122	TM7	TM7-1	Unknown	Unknown
5317	0.08	0.00	2	TM7	TM7-1	Unknown	Unknown
5388	0.24	0.00	1	TM7	TM7-1	Unknown	Unknown
223	107.75	0.10	11	Unknown	Unknown	Unknown	Unknown
3273	0.12	0.00	1	Unknown	Unknown	Unknown	Unknown
4298	0.00	0.02	9	Unknown	Unknown	Unknown	Unknown
4834	0.10	0.00	2	Unknown	Unknown	Unknown	Unknown
5662	24.96	0.03	2	Unknown	Unknown	Unknown	Unknown
9264	0.05	0.32	1	Unknown	Unknown	Unknown	Unknown
3666	0.01	0.08	4	Verrucomicrobia	Spartobacteria	Chthoniobacterales	Chthoniobacteraceae
5571	0.45	3.84	1	Verrucomicrobia	Spartobacteria	Chthoniobacterales	Chthoniobacteraceae
8804	0.05	0.05	2	Verrucomicrobia	Spartobacteria	Chthoniobacterales	Chthoniobacteraceae
