

Table 4.2: ¹³C-cellulose responders in the cellulose only treatment

OTU ID	Fold change ^a	Day ^b	Top BLAST hits ^c	BLAST %ID ^c	Phylum;Class;Order ^d
OTU.10167	3.86	45	No hits of at least 97% identity	80.65	<i>Acidobacteria</i> <i>Candidatus-Chloracidobacterium</i> <i>uncultured-Acidobacteria-bacterium</i>
OTU.1236	5.07	45	No hits of at least 97% identity	82.02	<i>Acidobacteria</i> <i>Candidatus-Chloracidobacterium</i> <i>uncultured-bacterium</i>
OTU.7198	4.42	14	No hits of at least 97% identity	82.16	<i>Acidobacteria</i> <i>Candidatus-Chloracidobacterium</i> <i>uncultured-soil-bacterium</i>
OTU.3445	4.31	45	No hits of at least 97% identity	92.74	<i>Acidobacteria</i> <i>Candidatus-Solibacter</i> <i>uncultured-bacterium</i>
OTU.1707	2.89	45	No hits of at least 97% identity	86.97	<i>Acidobacteria</i> <i>Holophagae</i> <i>CA002</i>
OTU.7337	2.48	14	No hits of at least 97% identity	87.77	<i>Acidobacteria</i> <i>Holophagae</i> <i>iii1-8</i>
OTU.1576	4.87	14	No hits of at least 97% identity	90.59	<i>Acidobacteria</i> <i>Order-Incertae-Sedis</i> <i>Family-Incertae-Sedis</i>
OTU.1274	3.75	45	<i>Bryobacter aggregatus</i>	97.31	<i>Acidobacteria</i> <i>Order-Incertae-Sedis</i> <i>Family-Incertae-Sedis</i>
OTU.446	2.3	14	No hits of at least 97% identity	92.74	<i>Acidobacteria</i> <i>SJA-149</i> <i>uncultured-bacterium</i>
OTU.1	2.53	14	<i>Arthrobacter spp.</i>	100.0	<i>Actinobacteria</i> <i>Micrococcales</i> <i>Micrococcaceae</i>
OTU.2360	3.62	45	<i>Micromonospora halophytica</i> , <i>Micromonospora lupini</i> , <i>Micromonospora chokoriensis</i> , <i>Micromonospora saelicesensis</i> , <i>Actinoplanes brasiliensis</i> , <i>Actinoplanes sp. A4029</i> , <i>Micromonospora carbonacea</i>	97.07	<i>Actinobacteria</i> <i>Micromonosporales</i> <i>Micromonosporaceae</i>
OTU.347	3.5	45	<i>Catellatospora coxensis</i> , <i>Catellatospora methionotrophica</i> , <i>Catellatospora chokoriensis</i> , <i>Catellatospora citrea</i> subsp. <i>citrea</i>	100.0	<i>Actinobacteria</i> <i>Micromonosporales</i> <i>Micromonosporaceae</i>
OTU.1598	2.82	45	<i>Aeromicrobium ponti</i>	98.66	<i>Actinobacteria</i> <i>Propionibacteriales</i> <i>Nocardiodaceae</i>
OTU.11083	4.05	14	<i>Saccharothrix sp. SA181</i> , <i>Saccharothrix longispora</i> , <i>Saccharothrix texasensis</i>	98.66	<i>Actinobacteria</i> <i>Pseudonocardiales</i> <i>Pseudonocardiaceae</i>
OTU.567	3.6	45	<i>Lentzea kentuckyensis</i>	100.0	<i>Actinobacteria</i> <i>Pseudonocardiales</i> <i>Pseudonocardiaceae</i>
OTU.101	3.31	45	<i>Streptomyces spp.</i> , <i>Kitasatospora spp.</i>	100.0	<i>Actinobacteria</i> <i>Streptomycetales</i> <i>Streptomycetaceae</i>
OTU.13276	5.23	45	No hits of at least 97% identity	90.91	<i>Actinobacteria</i> <i>Thermoleophilia</i> <i>Solirubrobacterales</i>
OTU.224	5.07	45	No hits of at least 97% identity	92.25	<i>Actinobacteria</i> <i>Thermoleophilia</i> <i>Solirubrobacterales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.720	3.73	14	No hits of at least 97% identity	94.67	<i>Armatimonadetes</i> <i>Armatimonadia</i> <i>Armatimonadales</i>
OTU.385	7.03	14	No hits of at least 97% identity	96.27	<i>Armatimonadetes</i> <i>uncultured-bacterium</i>
OTU.1219	2.95	14	No hits of at least 97% identity	85.83	<i>Armatimonadetes</i> <i>uncultured-bacterium</i>
OTU.519	2.58	14	No hits of at least 97% identity	91.8	<i>Armatimonadetes</i> <i>uncultured-bacterium</i>
OTU.1411	5.29	45	No hits of at least 97% identity	75.62	<i>BD1-5 uncultured-bacterium</i>
OTU.5258	4.94	45	No hits of at least 97% identity	75.27	<i>BD1-5 uncultured-bacterium</i>
OTU.1647	7.38	14	<i>Hymenobacter ocellatus</i>	97.3	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.879	5.42	14	No hits of at least 97% identity	94.09	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.1269	5.29	14	<i>Dyadobacter hamtensis</i>	98.38	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.802	4.77	14	No hits of at least 97% identity	90.59	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.10789	4.66	14	No hits of at least 97% identity	95.95	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.10228	4.57	14	No hits of at least 97% identity	91.39	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.1512	4.51	14	No hits of at least 97% identity	90.19	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.2730	4.47	14	No hits of at least 97% identity	95.42	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.1120	4.41	14	No hits of at least 97% identity	96.76	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.259	4.37	14	<i>Dyadobacter beijingensis</i>	97.57	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.389	4.29	14	No hits of at least 97% identity	94.35	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.500	4.23	14	No hits of at least 97% identity	90.59	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.1498	4.21	45	No hits of at least 97% identity	92.1	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.1847	4.06	45	No hits of at least 97% identity	85.71	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.814	3.49	14	No hits of at least 97% identity	95.42	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.1419	5.74	14	<i>Flavobacterium glycines</i>	98.37	<i>Bacteroidetes</i> <i>Flavobacteria</i> <i>Flavobacteriales</i>
OTU.336	5.07	14	<i>Flavobacterium banpakuense</i>	99.46	<i>Bacteroidetes</i> <i>Flavobacteria</i> <i>Flavobacteriales</i>
OTU.1448	4.8	14	<i>Flavobacterium beibuense</i>	98.38	<i>Bacteroidetes</i> <i>Flavobacteria</i> <i>Flavobacteriales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.783	4.73	14	<i>Flavobacterium johnsoniae</i>	98.35	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.3141	4.13	14	<i>Flavobacterium chungnamense</i>	97.55	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.3519	3.78	14	<i>Flavobacterium spp.</i>	97.28	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.237	3.48	14	<i>Flavobacterium columnare</i>	98.08	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.6303	3.34	14	No hits of at least 97% identity	96.47	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.580	3.32	45	No hits of at least 97% identity	87.06	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.7456	3.16	14	<i>Flavobacterium granuli</i>	98.88	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.1171	2.26	14	<i>Flavobacterium granuli</i> , <i>Flavobacterium frigidimaris</i>	97.57	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.2004	6.98	14	<i>Pedobacter borealis</i> , <i>Pedobacter agri PB92</i>	100.0	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1862	6.25	45	No hits of at least 97% identity	93.51	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1470	5.97	14	<i>Mucilaginibacter sp. DRP28</i> , <i>Mucilaginibacter gossypiiicola</i> , <i>Mucilaginibacter gossypii</i>	100.0	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.142	5.09	14	No hits of at least 97% identity	96.22	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.577	5.04	45	<i>Chitinophaga japonensis</i>	98.38	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1032	5.03	45	No hits of at least 97% identity	92.37	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.102	4.75	28	<i>Niastella koreensis</i>	99.19	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.2157	4.71	45	<i>Sphingobacterium detergens</i>	100.0	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.12560	4.31	14	<i>Chitinophaga niabensis</i>	98.64	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.5424	4.2	45	<i>Niastella populi</i>	97.84	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.659	4.08	14	No hits of at least 97% identity	87.98	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.877	3.85	45	No hits of at least 97% identity	88.92	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.534	3.78	28	<i>Chitinophaga filiformis</i> , <i>Chitinophaga ginsengisoli</i>	98.38	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.7770	3.76	14	<i>Niabella yanshanensis</i>	97.3	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.4278	3.52	14	<i>Terrimonas lutea</i>	97.57	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.170	3.42	14	No hits of at least 97% identity	95.41	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.1916	3.31	14	No hits of at least 97% identity	95.68	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1009	3.15	14	<i>Lacibacter cauensis</i>	98.38	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.7805	2.81	14	<i>Terrimonas lutea</i>	97.77	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.12647	2.73	14	<i>Flavisolibacter ginsengisoli</i>	97.28	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.428	2.69	14	<i>Terrimonas ferruginea</i>	97.84	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.4	2.2	14	No hits of at least 97% identity	95.95	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.378	2.13	14	<i>Pedobacter oryzae DSM 19973</i>	98.65	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.694	2.59	14	No hits of at least 97% identity	82.23	<i>Candidate-division-BRC1 uncultured-bacterium</i>
OTU.2028	5.74	45	No hits of at least 97% identity	80.33	<i>Candidate-division-OD1 uncultured-bacterium</i>
OTU.1342	4.84	14	No hits of at least 97% identity	83.52	<i>Chlorobi Chlorobia Chlorobiales</i>
OTU.941	3.25	14	No hits of at least 97% identity	82.45	<i>Chlorobi Chlorobia Chlorobiales</i>
OTU.1546	5.6	28	No hits of at least 97% identity	80.95	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.2440	5.45	45	No hits of at least 97% identity	80.9	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.1506	5.39	45	No hits of at least 97% identity	91.06	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.8564	4.76	45	No hits of at least 97% identity	80.5	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.1551	4.62	45	No hits of at least 97% identity	80.11	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.553	4.62	14	No hits of at least 97% identity	84.54	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.468	4.51	14	No hits of at least 97% identity	79.95	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.3038	4.2	45	No hits of at least 97% identity	81.7	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.535	3.98	45	No hits of at least 97% identity	75.07	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.2050	3.78	45	No hits of at least 97% identity	89.23	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.1703	3.17	14	No hits of at least 97% identity	80.32	<i>Chloroflexi Anaerolineae Anaerolineales</i>
OTU.1307	6.98	45	No hits of at least 97% identity	88.65	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.245	5.68	45	No hits of at least 97% identity	89.68	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.5834	5.54	45	No hits of at least 97% identity	88.62	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.6853	5.26	45	No hits of at least 97% identity	88.89	<i>Chloroflexi</i> <i>Herpetosiphonales</i> <i>Herpetosiphonaceae</i>
OTU.6205	4.9	45	No hits of at least 97% identity	88.42	<i>Chloroflexi</i> <i>Herpetosiphonales</i> <i>Herpetosiphonaceae</i>
OTU.50	5.58	14	No hits of at least 97% identity	84.91	<i>Chloroflexi</i> <i>Ktedonobacteria</i> <i>C0119</i>
OTU.1629	3.36	45	No hits of at least 97% identity	86.33	<i>Cyanobacteria</i> <i>MLE1-12</i> <i>uncultured-bacterium</i>
OTU.1155	6.39	28	No hits of at least 97% identity	94.86	<i>Cyanobacteria</i> <i>SM1D11</i> <i>uncultured-bacterium</i>
OTU.5011	4.84	14	No hits of at least 97% identity	93.78	<i>Cyanobacteria</i> <i>SM1D11</i> <i>uncultured-bacterium</i>
OTU.3573	5.22	45	No hits of at least 97% identity	83.29	<i>Elusimicrobia</i> <i>Lineage-IV</i> <i>uncultured-bacterium</i>
OTU.2537	5.12	45	No hits of at least 97% identity	83.02	<i>Elusimicrobia</i> <i>Lineage-IV</i>
OTU.6775	4.7	45	No hits of at least 97% identity	84.89	<i>Elusimicrobia</i> <i>MVP-88</i>
OTU.3241	5.46	45	No hits of at least 97% identity	80.55	<i>Fibrobacteres</i> <i>Fibrobacteria</i> <i>Fibrobacterales</i>
OTU.1639	3.46	45	No hits of at least 97% identity	81.27	<i>Fibrobacteres</i> <i>Fibrobacteria</i> <i>Fibrobacterales</i>
OTU.1102	4.69	45	No hits of at least 97% identity	85.19	<i>Gemmatimonadetes</i> <i>AT425-EubC11-terrestrial-group</i> <i>uncultured-bacterium</i>
OTU.2772	4.69	28	No hits of at least 97% identity	92.27	<i>Gemmatimonadetes</i> <i>Gemmatimonadales</i> <i>Gemmatimonadaceae</i>
OTU.763	2.21	14	No hits of at least 97% identity	84.59	<i>Nitrospirae</i> <i>Nitrospira</i> <i>Nitrospirales</i>
OTU.4075	4.65	14	No hits of at least 97% identity	83.38	<i>Planctomycetes</i> <i>OM190</i> <i>uncultured-bacterium</i>
OTU.6795	4.59	14	No hits of at least 97% identity	83.52	<i>Planctomycetes</i> <i>OM190</i> <i>uncultured-bacterium</i>
OTU.549	3.92	28	No hits of at least 97% identity	81.32	<i>Planctomycetes</i> <i>OM190</i> <i>uncultured-bacterium</i>
OTU.8807	3.47	45	No hits of at least 97% identity	81.87	<i>Planctomycetes</i> <i>OM190</i> <i>uncultured-bacterium</i>
OTU.1029	3.42	28	No hits of at least 97% identity	82.57	<i>Planctomycetes</i> <i>OM190</i> <i>uncultured-bacterium</i>
OTU.312	2.79	14	No hits of at least 97% identity	82.88	<i>Planctomycetes</i> <i>OM190</i> <i>uncultured-bacterium</i>
OTU.3216	4.01	28	No hits of at least 97% identity	81.75	<i>Planctomycetes</i> <i>OM190</i>
OTU.595	2.91	28	No hits of at least 97% identity	83.33	<i>Planctomycetes</i> <i>OM190</i>
OTU.494	2.4	14	No hits of at least 97% identity	81.62	<i>Planctomycetes</i> <i>OM190</i>
OTU.3073	5.15	45	No hits of at least 97% identity	79.58	<i>Planctomycetes</i> <i>Phycisphaerae</i> <i>Phycisphaerales</i>
OTU.1068	4.22	45	No hits of at least 97% identity	77.89	<i>Planctomycetes</i> <i>Phycisphaerae</i> <i>Phycisphaerales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.1152	3.93	45	No hits of at least 97% identity	83.03	<i>Planctomycetes Phycisphaerae Phycisphaerales</i>
OTU.1077	3.81	45	No hits of at least 97% identity	84.39	<i>Planctomycetes Phycisphaerae Phycisphaerales</i>
OTU.1334	3.11	45	No hits of at least 97% identity	77.93	<i>Planctomycetes Phycisphaerae Phycisphaerales</i>
OTU.678	4.8	45	No hits of at least 97% identity	78.59	<i>Planctomycetes Phycisphaerae WD2101-soil-group</i>
OTU.3000	4.5	45	No hits of at least 97% identity	79.17	<i>Planctomycetes Phycisphaerae WD2101-soil-group</i>
OTU.1324	3.5	45	No hits of at least 97% identity	80.82	<i>Planctomycetes Phycisphaerae WD2101-soil-group</i>
OTU.307	2.62	28	No hits of at least 97% identity	80.06	<i>Planctomycetes Phycisphaerae WD2101-soil-group</i>
OTU.266	6.73	45	No hits of at least 97% identity	85.07	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.2901	5.98	45	No hits of at least 97% identity	92.53	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.3667	5.88	45	No hits of at least 97% identity	83.99	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.9627	5.7	45	<i>Schlesneria paludicola</i>	97.04	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.1702	5.46	45	No hits of at least 97% identity	86.67	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.2880	5.3	45	No hits of at least 97% identity	86.98	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.1650	4.84	45	No hits of at least 97% identity	88.8	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.3091	4.81	45	No hits of at least 97% identity	89.63	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.1294	4.7	45	No hits of at least 97% identity	91.44	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.701	4.64	45	No hits of at least 97% identity	86.46	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.2441	4.64	45	No hits of at least 97% identity	89.36	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.10699	4.44	14	No hits of at least 97% identity	84.17	<i>Planctomycetes Planctomycetacia Planctomycetales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.1816	4.37	45	No hits of at least 97% identity	91.71	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.667	4.27	45	No hits of at least 97% identity	89.3	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.1869	4.26	45	No hits of at least 97% identity	86.13	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.521	4.18	45	No hits of at least 97% identity	87.97	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.559	3.91	45	No hits of at least 97% identity	86.74	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.2586	3.86	45	No hits of at least 97% identity	85.08	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.3835	3.81	14	No hits of at least 97% identity	86.86	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.600	3.77	45	No hits of at least 97% identity	93.57	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.1370	3.67	45	No hits of at least 97% identity	87.85	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.633	3.67	45	No hits of at least 97% identity	92.25	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.1174	3.52	45	No hits of at least 97% identity	92.03	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.4923	3.48	45	No hits of at least 97% identity	88.06	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.2151	3.38	28	No hits of at least 97% identity	88.53	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.80	3.35	45	No hits of at least 97% identity	90.93	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.8906	3.35	28	No hits of at least 97% identity	89.92	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.2102	3.34	45	No hits of at least 97% identity	89.04	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.404	3.29	45	No hits of at least 97% identity	90.05	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.438	3.21	45	No hits of at least 97% identity	92.25	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.1338	3.14	45	No hits of at least 97% identity	90.08	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.445	3.09	45	No hits of at least 97% identity	89.25	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.1239	3.04	45	No hits of at least 97% identity	90.43	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.513	3.03	45	No hits of at least 97% identity	95.16	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.6443	3.03	45	No hits of at least 97% identity	92.09	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.202	2.84	45	No hits of at least 97% identity	86.74	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.8826	2.82	45	No hits of at least 97% identity	86.1	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.685	2.77	28	No hits of at least 97% identity	87.8	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.368	2.74	45	No hits of at least 97% identity	89.52	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.238	2.74	45	No hits of at least 97% identity	88.03	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.7136	2.3	28	No hits of at least 97% identity	90.3	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.825	1.97	14	No hits of at least 97% identity	93.63	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.213	1.85	28	No hits of at least 97% identity	91.44	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.623	5.09	45	No hits of at least 97% identity	85.56	<i>Planctomycetes vadinHA49</i> <i>uncultured-Planctomycetales-bacterium</i>
OTU.1329	5.23	45	No hits of at least 97% identity	81.47	<i>Planctomycetes vadinHA49</i> <i>uncultured-bacterium</i>
OTU.2136	4.68	45	No hits of at least 97% identity	85.05	<i>Planctomycetes vadinHA49</i> <i>uncultured-bacterium</i>
OTU.690	6.93	14	<i>Brevundimonas variabilis</i>	99.46	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacteriales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.2416	6.22	14	<i>Brevundimonas vesicularis</i> , <i>Brevundimonas nasdae</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.3062	6.09	14	<i>Caulobacter vibrioides</i> , <i>Caulobacter segnis</i>	99.46	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.184	5.8	14	<i>Brevundimonas alba</i>	99.19	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.10	5.26	14	<i>Caulobacter henricii</i>	99.46	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.232	4.88	14	<i>Asticcacaulis taihuensis</i>	98.13	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.3030	4.86	28	<i>Asticcacaulis excentricus</i>	98.66	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.402	4.26	14	<i>Caulobacter fusiformis</i>	99.46	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.12989	3.94	14	<i>Brevundimonas terrae</i>	99.46	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.121	3.33	14	<i>Phenylobacterium sp. A8</i>	98.66	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.566	3.29	14	<i>Phenylobacterium lituiforme</i>	97.31	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.12754	3.09	14	<i>Phenylobacterium sp. A8</i>	98.61	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.3134	5.24	45	No hits of at least 97% identity	85.03	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> DB1-14
OTU.371	4.83	45	No hits of at least 97% identity	88.27	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> DB1-14
OTU.1248	4.87	14	<i>Ferrovibrio denitrificans</i>	98.92	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> MNG3
OTU.277	6.31	45	No hits of at least 97% identity	94.09	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> Rhizobiales
OTU.34	4.68	45	<i>Ensifer adhaerens</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> Rhizobiales
OTU.111	4.44	45	No hits of at least 97% identity	92.23	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> Rhizobiales
OTU.472	4.39	45	No hits of at least 97% identity	92.23	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> Rhizobiales
OTU.3911	4.38	45	<i>Rhizobium spp.</i> , <i>Arthrobacter spp.</i>	97.83	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> Rhizobiales

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.7	4.25	45	<i>Bradyrhizobium</i> spp.	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.5106	4.24	45	<i>Afipia massiliensis</i>	98.12	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.73	4.12	14	<i>Bosea</i> sp. R-46060	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.10638	4.11	14	<i>Aminobacter</i> sp. STM 4645	98.37	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.16	4.11	45	<i>Mesorhizobium caraganae</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.9449	3.98	14	No hits of at least 97% identity	96.47	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.49	3.95	45	<i>Rhizobium herbae</i>	99.73	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.27	3.82	28	<i>Devosia insulae</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.5674	3.77	45	<i>Bosea</i> sp. R-46070	99.73	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.844	3.76	45	<i>Devosia limi</i>	98.12	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.86	3.72	45	No hits of at least 97% identity	94.62	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.6165	3.69	45	<i>Rhizobium cellulosilyticum</i>	98.92	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.1098	3.49	14	<i>Vasilyevaea enhydra</i>	98.66	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.1759	3.28	45	<i>Shinella yambaruensis</i>	99.18	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.264	2.8	45	<i>Aminobacter aminovorans</i> , <i>Mesorhizobium loti</i> , <i>Mesorhizobium australicum</i> WSM2073, <i>Mesorhizobium shangrilense</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.3368	2.72	45	<i>Rhodopseudomonas</i> sp. R-45977	98.66	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.512	2.65	45	No hits of at least 97% identity	94.64	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.6819	2.56	14	No hits of at least 97% identity	96.74	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.11661	2.49	14	No hits of at least 97% identity	94.59	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.107	2.18	45	<i>Rhodoplanes roseus</i>	97.31	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.6217	1.86	14	No hits of at least 97% identity	95.65	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.1057	3.53	14	<i>Catellibacterium nectariphilum</i>	98.39	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodobacterales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.338	7.96	45	No hits of at least 97% identity	89.84	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i>
OTU.2418	6.66	14	No hits of at least 97% identity	86.74	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i>
OTU.766	4.65	14	No hits of at least 97% identity	91.91	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i>
OTU.1480	4.1	14	No hits of at least 97% identity	91.67	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i>
OTU.3165	6.61	14	No hits of at least 97% identity	96.78	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.31	6.56	14	<i>Sphingomonas trueperi</i> , <i>Sphingomonas pituitosa</i>	98.66	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.169	5.7	45	<i>Sphingopyxis panaciterrae</i> , <i>Sphingopyxis chilensis</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.7891	5.38	45	<i>Sphingomonas haloaromaticamans</i> , <i>Sphingomonas wittichii</i>	97.86	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.4687	5.37	45	<i>Sphingomonas asaccharolytica</i>	97.86	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.380	5.3	14	No hits of at least 97% identity	95.98	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.9193	4.95	14	No hits of at least 97% identity	96.51	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.10665	4.93	14	No hits of at least 97% identity	94.72	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.8290	4.66	14	<i>Sphingomonas koreensis</i>	97.59	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.2256	4.61	45	<i>Sphingomonas sp. 382</i> , <i>Sphingomonas wittichii</i> , <i>Sphingomonas sp. UM2</i>	98.39	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.456	3.69	45	<i>Novosphingobium nitrogenifigens</i>	98.39	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.426	3.48	28	<i>Altererythrobacter sp. S3-63</i>	97.86	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.8359	3.45	45	<i>Kaistobacter terrae</i>	98.12	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.8167	2.99	14	No hits of at least 97% identity	92.8	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.4714	2.94	45	<i>Erythrobacter aquimaris</i>	98.39	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.740	2.75	28	<i>Novosphingobium lentum</i>	98.93	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.23	2.67	28	<i>Sphingomonas</i> sp. YC6722	97.32	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.420	2.66	28	<i>Kaistobacter terrae</i>	98.12	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.6783	2.52	28	No hits of at least 97% identity	96.94	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.13	2.36	28	<i>Sphingomonas jaspsi</i>	98.93	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.9664	2.06	28	No hits of at least 97% identity	96.27	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.3156	2.03	28	<i>Kaistobacter terrae</i>	97.32	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.5320	1.72	14	<i>Kaistobacter terrae</i>	97.06	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.151	6.44	14	<i>Polaromonas aquatica</i> , <i>Polaromonas jejuensis</i> , <i>Polaromonas vacuolata</i>	99.46	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.4112	5.56	45	<i>Ralstonia insidiosa</i>	97.06	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.1666	5.19	45	<i>Cupriavidus necator</i> , <i>Wautersia numazuensis</i> , <i>Cupriavidus basilensis</i>	99.73	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.5544	4.93	45	<i>Herminiimonas aquatilis</i>	97.58	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.5575	4.91	14	<i>Paucibacter toxinivorans</i>	98.66	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.72	4.87	14	<i>Rhizobacter dauci</i>	100.0	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.54	4.27	14	<i>Pseudoduganella violaceinigra</i>	99.73	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.815	4.16	45	No hits of at least 97% identity	94.89	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.11076	4.11	14	<i>Variovorax ginsengisoli</i> , <i>Variovorax boronicumulans</i>	97.3	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.5105	3.87	14	<i>Variovorax paradoxus</i>	98.12	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.159	3.81	14	<i>Massilia suwonensis</i> , <i>Massilia alkalitolerans</i> , <i>Massilia jejuensis</i> , <i>Massilia varians</i> , <i>Massilia niabensis</i>	100.0	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.7831	3.28	14	<i>Massilia tieshanensis</i> , <i>Massilia aerilata</i>	98.92	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.139	3.21	45	<i>Pelomonas puraquae</i>	98.66	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.441	3.17	45	No hits of at least 97% identity	93.82	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.2645	2.78	45	<i>Herbaspirillum sp. SUEMI08</i>	97.85	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.40	2.56	14	<i>Acidovorax sp. NF1078</i>	99.73	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.5914	2.35	14	<i>Comamonas thiooxydans</i> , <i>Comamonas testosteroni</i>	98.39	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.2176	1.71	14	<i>Piscinibacter aquaticus</i>	98.91	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.2161	4.73	45	No hits of at least 97% identity	90.11	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Hydrogenophilales</i>
OTU.357	5.59	45	No hits of at least 97% identity	94.93	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Nitrosomonadales</i>
OTU.965	3.58	45	No hits of at least 97% identity	93.03	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Nitrosomonadales</i>
OTU.1967	6.29	14	No hits of at least 97% identity	91.18	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Rhodocyclales</i>
OTU.2276	6.33	45	No hits of at least 97% identity	91.71	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Bdellovibrionales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.6149	5.66	45	No hits of at least 97% identity	93.32	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Bdellovibrionales</i>
OTU.913	5.43	45	No hits of at least 97% identity	94.12	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Bdellovibrionales</i>
OTU.4322	4.62	45	No hits of at least 97% identity	89.57	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Bdellovibrionales</i>
OTU.699	3.73	14	No hits of at least 97% identity	93.32	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Bdellovibrionales</i>
OTU.2525	3.43	45	No hits of at least 97% identity	86.17	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Bdellovibrionales</i>
OTU.4156	4.63	45	No hits of at least 97% identity	86.03	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>GR-WP33-30</i>
OTU.686	6.89	45	No hits of at least 97% identity	92.27	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.1041	6.09	45	No hits of at least 97% identity	84.0	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.3831	5.86	45	No hits of at least 97% identity	90.91	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.706	5.65	45	No hits of at least 97% identity	96.52	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.649	5.27	45	No hits of at least 97% identity	92.51	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.461	5.01	45	No hits of at least 97% identity	91.71	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.6791	5.01	45	No hits of at least 97% identity	91.33	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.947	4.89	45	No hits of at least 97% identity	90.67	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.2624	4.88	45	No hits of at least 97% identity	89.07	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.269	4.88	45	No hits of at least 97% identity	89.25	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.883	4.65	45	No hits of at least 97% identity	90.93	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.2610	4.58	45	No hits of at least 97% identity	83.96	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.1097	4.56	45	<i>Cystobacter violaceus</i> , <i>Archangium gephyra</i>	97.59	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.2576	4.28	45	No hits of at least 97% identity	85.94	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.1889	4.22	45	No hits of at least 97% identity	95.21	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.5612	4.15	45	No hits of at least 97% identity	95.99	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.2628	4.11	45	No hits of at least 97% identity	90.11	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.10767	4.08	45	No hits of at least 97% identity	91.06	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.2179	3.98	45	No hits of at least 97% identity	90.16	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.3805	3.76	45	No hits of at least 97% identity	89.7	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.722	3.67	45	No hits of at least 97% identity	90.64	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.1900	3.65	45	No hits of at least 97% identity	92.51	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.2493	3.52	45	No hits of at least 97% identity	84.95	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.6077	3.5	28	No hits of at least 97% identity	92.78	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.1573	3.48	45	No hits of at least 97% identity	89.28	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.3842	3.3	45	No hits of at least 97% identity	90.4	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.1736	3.28	45	No hits of at least 97% identity	82.62	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.927	2.95	45	<i>Enhygromyxa salina</i>	97.05	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.1398	4.56	45	No hits of at least 97% identity	87.5	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Sh765B-TzT-29</i>
OTU.2212	7.35	45	No hits of at least 97% identity	90.11	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.537	6.34	14	No hits of at least 97% identity	93.01	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.1223	6.25	45	No hits of at least 97% identity	96.79	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.2386	4.74	45	No hits of at least 97% identity	87.23	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.4746	4.66	45	No hits of at least 97% identity	92.51	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.2329	4.62	45	No hits of at least 97% identity	93.85	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.1318	4.55	45	No hits of at least 97% identity	91.98	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.584	4.49	45	No hits of at least 97% identity	89.3	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.2213	4.43	45	No hits of at least 97% identity	95.99	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.3661	3.96	45	No hits of at least 97% identity	95.99	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.3267	3.78	14	No hits of at least 97% identity	95.43	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.811	3.59	45	No hits of at least 97% identity	93.85	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.1083	3.18	45	<i>Legionella sp. LegA</i>	97.86	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.1648	4.55	45	No hits of at least 97% identity	87.98	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>NKB5</i>
OTU.131	6.7	14	<i>Cellvibrio ostraviensis</i> , <i>Cellvibrio fibrivorans</i> , <i>Cellvibrio mixtus</i> subsp. <i>mixtus</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Pseudomonadales</i>
OTU.1590	6.6	14	<i>Cellvibrio gandavensis</i>	97.59	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Pseudomonadales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.11032	5.14	14	<i>Cellvibrio gandavensis</i>	99.46	Proteobacteria Gammaproteobacteria Pseudomonadales
OTU.3310	4.36	45	No hits of at least 97% identity	92.25	Proteobacteria Gammaproteobacteria Pseudomonadales
OTU.6689	3.83	45	<i>Sphingomonas sp. S8-3</i>	99.46	Proteobacteria Gammaproteobacteria Pseudomonadales
OTU.7738	3.71	14	<i>Pseudomonas brassicacearum</i> subsp. <i>neaurantidis</i> , <i>Pseudomonas frederiksbergensis</i>	98.64	Proteobacteria Gammaproteobacteria Pseudomonadales
OTU.1214	3.22	14	<i>Pseudomonas alcaligenes</i>	99.18	Proteobacteria Gammaproteobacteria Pseudomonadales
OTU.32	2.81	14	<i>Pseudomonas kilonensis</i> , <i>Pseudomonas jessenii</i> , <i>Pseudomonas mohnii</i> , <i>Pseudomonas corrugata</i> , <i>Pseudomonas vancouverensis</i> , <i>Pseudomonas moorei</i>	100.0	Proteobacteria Gammaproteobacteria Pseudomonadales
OTU.886	6.19	45	No hits of at least 97% identity	94.15	Proteobacteria Gammaproteobacteria WN-HWB-116
OTU.77	5.4	45	<i>Pseudoxanthomonas dokdonensis</i>	100.0	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.144	4.69	14	No hits of at least 97% identity	95.72	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.499	4.61	28	No hits of at least 97% identity	94.65	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.1178	3.93	28	<i>Dokdonella sp. KIS28-6</i>	100.0	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.3336	3.83	45	No hits of at least 97% identity	92.78	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.230	3.83	45	No hits of at least 97% identity	96.79	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.769	3.82	14	<i>Arenimonas sp. CH15-1</i>	97.33	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.109	3.8	28	No hits of at least 97% identity	96.26	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.1574	3.74	45	No hits of at least 97% identity	91.67	Proteobacteria Gammaproteobacteria Xanthomonadales

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.7596	3.63	14	No hits of at least 97% identity	96.42	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.6983	3.61	14	<i>Dyella koreensis</i> , <i>Dyella soli</i>	97.3	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.51	3.6	28	<i>Lysobacter gummosus</i> , <i>Lysobacter antibioticus</i>	99.47	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.413	3.5	14	No hits of at least 97% identity	96.52	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.695	3.38	14	<i>Lysobacter niabensis</i>	98.4	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.514	3.13	28	No hits of at least 97% identity	96.79	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.8067	2.83	45	No hits of at least 97% identity	88.5	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.79	2.72	45	No hits of at least 97% identity	90.11	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.28	2.61	14	<i>Lysobacter oryzae</i>	99.47	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.24	2.15	45	<i>Arenimonas sp. CH15-1</i>	98.66	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.1306	5.2	45	No hits of at least 97% identity	85.11	<i>Verrucomicrobia</i> <i>Candidatus-Methylocidiphilum</i> <i>uncultured-bacterium</i>
OTU.1632	4.85	45	No hits of at least 97% identity	85.09	<i>Verrucomicrobia</i> <i>OPB35-soil-group</i> <i>uncultured-bacterium</i>
OTU.620	4.33	45	No hits of at least 97% identity	83.78	<i>Verrucomicrobia</i> <i>OPB35-soil-group</i> <i>uncultured-bacterium</i>
OTU.9695	3.41	45	No hits of at least 97% identity	86.02	<i>Verrucomicrobia</i> <i>OPB35-soil-group</i> <i>uncultured-bacterium</i>
OTU.308	3.17	14	No hits of at least 97% identity	84.8	<i>Verrucomicrobia</i> <i>OPB35-soil-group</i> <i>uncultured-bacterium</i>
OTU.875	5.71	45	No hits of at least 97% identity	88.06	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.554	5.65	45	No hits of at least 97% identity	85.56	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.1237	5.16	45	No hits of at least 97% identity	88.53	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.805	5.0	45	No hits of at least 97% identity	89.12	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.752	4.87	45	No hits of at least 97% identity	88.83	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.1544	4.8	45	No hits of at least 97% identity	89.66	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.7170	4.48	45	No hits of at least 97% identity	89.52	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.2863	4.38	45	No hits of at least 97% identity	85.16	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.4740	4.37	45	No hits of at least 97% identity	82.38	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.1150	4.12	45	No hits of at least 97% identity	85.94	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.473	4.11	45	No hits of at least 97% identity	89.84	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.3106	3.97	28	No hits of at least 97% identity	87.23	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.799	3.9	45	No hits of at least 97% identity	87.57	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.7396	3.54	45	No hits of at least 97% identity	89.34	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.13967	3.4	45	No hits of at least 97% identity	87.36	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.405	3.33	45	No hits of at least 97% identity	87.83	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.327	3.31	45	No hits of at least 97% identity	89.66	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.867	2.54	45	No hits of at least 97% identity	86.1	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.950	7.65	45	<i>Verrucomicrobiaceae</i> bacterium <i>DC2a-G7</i>	100.0	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.11380	6.28	45	<i>Verrucomicrobiaceae</i> bacterium <i>DC2a-G7</i>	97.28	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.2818	6.25	45	No hits of at least 97% identity	85.56	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.1787	5.59	45	<i>Luteolibacter pohnpeiensis</i> , <i>Luteolibacter</i> sp. <i>CCTCC AB 2010415</i>	97.59	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.903	5.51	45	No hits of at least 97% identity	94.92	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.5545	5.29	45	<i>Verrucomicrobium spinosum</i>	97.84	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>

Table 4.2 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.866	5.13	45	<i>Verrucomicrobium spinosum</i>	98.93	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.5228	2.65	14	No hits of at least 97% identity	89.73	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>

^a Maximum observed \log_2 of fold change.
^b Day of maximum fold change.
^c Against Living Tree Project database.
^d Annotation from Silva database assigned during OTU binning (see methods).