

Table 4.4: ¹³C-cellulose responders in the pulse root exudate treatment

OTU ID	Fold change ^a	Day ^b	Top BLAST hits ^c	BLAST %ID ^c	Phylum;Class;Order ^d
OTU.1341	4.77	14	No hits of at least 97% identity	86.02	<i>Acidobacteria</i> 11-24 <i>uncultured-bacterium</i>
OTU.2288	3.64	45	No hits of at least 97% identity	82.7	<i>Acidobacteria</i> 11-24 <i>uncultured-bacterium</i>
OTU.1197	2.41	45	No hits of at least 97% identity	83.02	<i>Acidobacteria</i> 11-24 <i>uncultured-bacterium</i>
OTU.1507	3.24	45	No hits of at least 97% identity	82.24	<i>Acidobacteria</i> <i>Candidatus-Chloracidobacterium</i> <i>uncultured-Acidobacteria-bacterium</i>
OTU.3817	2.44	28	No hits of at least 97% identity	86.36	<i>Acidobacteria</i> DA023 <i>uncultured-bacterium</i>
OTU.12188	6.09	45	No hits of at least 97% identity	86.44	<i>Acidobacteria</i> Holophagae CA002
OTU.1016	4.18	14	No hits of at least 97% identity	85.18	<i>Acidobacteria</i> RB25 <i>uncultured-bacterium</i>
OTU.370	4.37	28	<i>Gordonia sputi</i>	100.0	<i>Actinobacteria</i> <i>Corynebacteriales</i> Nocardiaceae
OTU.1181	4.79	14	No hits of at least 97% identity	92.27	<i>Armatimonadetes</i> <i>Armatimonadia</i> <i>Armatimonadales</i>
OTU.1303	4.57	45	No hits of at least 97% identity	82.34	<i>Armatimonadetes</i> <i>uncultured-bacterium</i>
OTU.1664	7.31	14	<i>Sporocytophaga myxococcoides</i>	99.19	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.1026	4.75	14	No hits of at least 97% identity	94.32	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.2905	4.2	45	No hits of at least 97% identity	91.85	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.7868	3.58	14	No hits of at least 97% identity	96.94	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.331	3.32	14	<i>Ohtaekwangia kribbensis</i>	97.04	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.10192	3.07	14	<i>Adhaeribacter terreus</i>	97.57	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.6036	3.02	14	<i>Ohtaekwangia kribbensis</i>	100.0	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.598	2.94	14	<i>Sphingobacteria bacterium RYG</i>	97.31	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.152	2.53	14	<i>Adhaeribacter terreus</i>	98.11	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.155	2.09	14	No hits of at least 97% identity	92.7	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.44	2.04	14	No hits of at least 97% identity	95.14	<i>Bacteroidetes</i> Cytophagia Cytophagales
OTU.2099	4.99	45	<i>Chryseobacterium</i> sp. THG 15, <i>Chryseobacterium formosense</i>	100.0	<i>Bacteroidetes</i> Flavobacteria Flavobacteriales
OTU.1330	4.7	14	<i>Flavobacterium fluvii</i>	99.73	<i>Bacteroidetes</i> Flavobacteria Flavobacteriales

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.7315	2.72	14	<i>Flavobacterium columnare</i>	98.84	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.2082	6.2	28	No hits of at least 97% identity	86.7	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1414	4.85	14	No hits of at least 97% identity	89.49	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1929	4.8	14	No hits of at least 97% identity	96.49	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.4996	4.2	14	No hits of at least 97% identity	96.22	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.283	4.11	14	No hits of at least 97% identity	94.32	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.873	3.95	14	<i>Segetibacter aerophilus</i>	97.03	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.140	3.89	14	No hits of at least 97% identity	95.14	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1969	3.67	14	No hits of at least 97% identity	96.76	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.325	3.59	14	<i>Flavisolibacter ginsengisoli</i>	98.38	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.490	3.5	14	No hits of at least 97% identity	95.41	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.425	3.38	14	No hits of at least 97% identity	88.44	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.3332	3.38	14	No hits of at least 97% identity	96.76	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.343	3.33	14	No hits of at least 97% identity	92.45	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.3380	3.28	14	No hits of at least 97% identity	96.22	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.717	3.24	14	No hits of at least 97% identity	89.62	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.7661	3.17	14	No hits of at least 97% identity	95.69	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.7953	3.07	14	No hits of at least 97% identity	94.59	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.178	3.07	14	No hits of at least 97% identity	94.86	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.145	3.02	14	No hits of at least 97% identity	90.84	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.718	3.02	14	No hits of at least 97% identity	88.56	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.7103	3.0	14	No hits of at least 97% identity	87.87	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.215	2.93	14	No hits of at least 97% identity	96.49	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.7560	2.91	14	<i>Pedobacter africanus</i> , <i>Pedobacter steynii</i> , <i>Pedobacter caeni</i>	98.65	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.12538	2.83	14	No hits of at least 97% identity	93.5	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.523	2.83	14	No hits of at least 97% identity	88.65	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.103	2.83	14	No hits of at least 97% identity	95.95	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.9220	2.8	14	No hits of at least 97% identity	94.86	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.3730	2.74	14	No hits of at least 97% identity	95.41	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.498	2.72	14	No hits of at least 97% identity	88.38	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.570	2.66	14	No hits of at least 97% identity	92.18	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.5218	2.6	14	No hits of at least 97% identity	95.14	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.431	2.6	14	No hits of at least 97% identity	93.55	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.916	2.6	28	<i>Chitinophaga niabensis</i>	97.57	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.75	2.54	14	<i>Flavisolibacter ginsengisoli</i>	97.84	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.45	2.51	14	<i>Flavitalea populi</i>	98.92	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.228	2.5	14	No hits of at least 97% identity	94.59	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.3841	2.43	14	No hits of at least 97% identity	93.24	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.133	2.36	14	No hits of at least 97% identity	95.41	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.725	2.34	14	No hits of at least 97% identity	95.95	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.225	2.33	14	No hits of at least 97% identity	96.49	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.8100	2.13	14	No hits of at least 97% identity	95.52	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.2351	5.22	14	No hits of at least 97% identity	88.59	<i>Bacteroidetes VC2.1-Bac22 uncultured-bacterium</i>
OTU.3465	4.28	45	No hits of at least 97% identity	75.53	<i>Candidate-division-OP11 uncultured-bacterium</i>
OTU.1980	3.97	14	No hits of at least 97% identity	85.91	<i>Candidate-division-WS3 uncultured-bacterium</i>
OTU.3682	2.63	14	No hits of at least 97% identity	83.96	<i>Candidate-division-WS3 uncultured-bacterium</i>
OTU.509	2.24	14	No hits of at least 97% identity	85.98	<i>Candidate-division-WS3 uncultured-bacterium</i>
OTU.958	4.72	14	No hits of at least 97% identity	82.61	<i>Chlorobi Chlorobia Chlorobiales</i>

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.1217	3.2	45	No hits of at least 97% identity	80.48	<i>Chloroflexi</i> <i>Anaerolineae</i> <i>Anaerolineales</i>
OTU.907	2.83	14	No hits of at least 97% identity	83.68	<i>Chloroflexi</i> <i>Anaerolineae</i> <i>Anaerolineales</i>
OTU.3983	6.24	45	No hits of at least 97% identity	80.31	<i>Chloroflexi</i> <i>Chloroflexales</i> <i>Chloroflexaceae</i>
OTU.3585	5.14	45	No hits of at least 97% identity	96.22	<i>Cyanobacteria</i> <i>SM1D11</i>
OTU.640	3.86	28	<i>Streptococcus tigurinus</i> , <i>Streptococcus mitis</i> , <i>Streptococcus infantis</i> , <i>Streptococcus pseudopneumoniae</i> , <i>Streptococcus oralis</i>	99.73	<i>Firmicutes</i> <i>Bacilli</i> <i>Lactobacillales</i>
OTU.1115	3.0	28	No hits of at least 97% identity	80.59	<i>Planctomycetes</i> <i>Phycisphaerae</i> <i>WD2101-soil-group</i>
OTU.5726	5.13	14	No hits of at least 97% identity	90.4	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.6106	4.63	45	No hits of at least 97% identity	92.27	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.3395	3.53	45	No hits of at least 97% identity	85.25	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.7980	3.39	45	No hits of at least 97% identity	94.13	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.1073	2.93	45	No hits of at least 97% identity	89.63	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.6068	2.83	14	No hits of at least 97% identity	85.79	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.345	2.04	14	No hits of at least 97% identity	89.52	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.3431	3.78	28	No hits of at least 97% identity	87.17	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>DB1-14</i>
OTU.7792	5.13	14	No hits of at least 97% identity	90.35	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>OCS116-clade</i>
OTU.6486	3.97	45	<i>Kaistia</i> sp. <i>B1-1</i>	98.92	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.991	3.21	14	<i>Kaistia</i> sp. <i>5YN7-3</i> , <i>Kaistia</i> sp. <i>B6-12</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.517	2.66	14	No hits of at least 97% identity	94.1	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.1627	5.95	45	No hits of at least 97% identity	91.76	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i>

Table 4.4 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.187	4.08	28	<i>Roseomonas gilardii</i> subsp. <i>gilardii</i> , <i>Roseomonas mucosa</i> , <i>Roseomonas gilardii</i> subsp. <i>rosea</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i>
OTU.482	2.22	14	No hits of at least 97% identity	90.45	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i>
OTU.7443	2.07	28	No hits of at least 97% identity	95.38	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i>
OTU.2141	5.38	14	No hits of at least 97% identity	84.49	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i>
OTU.486	5.31	14	No hits of at least 97% identity	90.03	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i>
OTU.1930	4.67	14	No hits of at least 97% identity	87.77	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i>
OTU.1165	3.99	14	No hits of at least 97% identity	88.47	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i>
OTU.2814	5.28	14	No hits of at least 97% identity	96.26	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.289	2.61	14	No hits of at least 97% identity	96.78	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.141	4.69	14	No hits of at least 97% identity	94.65	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.5640	3.4	45	<i>Paucimonas lemoignei</i>	98.12	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.2239	4.22	45	No hits of at least 97% identity	94.12	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Hydrogenophila</i>
OTU.3811	4.57	14	No hits of at least 97% identity	89.49	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Desulfobacterales</i>
OTU.2036	4.69	45	No hits of at least 97% identity	87.09	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.696	2.34	45	No hits of at least 97% identity	93.85	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.6577	5.83	45	No hits of at least 97% identity	95.72	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.1190	4.28	45	No hits of at least 97% identity	96.27	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>

Table 4.4 – continued from previous page

OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.475	2.28	45	<i>Aquicella siphonis</i>	97.31	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.433	5.63	45	No hits of at least 97% identity	87.47	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>NKB5</i>
OTU.2651	4.31	45	No hits of at least 97% identity	87.4	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>NKB5</i>
OTU.10253	4.48	14	No hits of at least 97% identity	93.26	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Pseudomonadales</i>
OTU.1332	4.12	14	<i>Panacagrimonas perspica</i>	97.86	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.273	2.16	14	No hits of at least 97% identity	94.88	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.465	2.15	14	No hits of at least 97% identity	94.34	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.5114	6.24	14	No hits of at least 97% identity	92.78	<i>Verrucomicrobia</i> <i>Opitutae</i> <i>Opitales</i>
OTU.4224	5.35	45	No hits of at least 97% identity	88.1	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.1993	3.77	45	No hits of at least 97% identity	88.1	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.10213	4.65	28	<i>Prostheco bacter fusiformis</i>	98.4	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.3003	4.31	45	<i>Prostheco bacter fluviatilis</i>	97.33	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.1705	3.06	45	No hits of at least 97% identity	84.76	

^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).