

Table 4.3: ¹³C-cellulose responders in the continuous root exudate treatment

OTU ID	Fold change ^a	Day ^b	Top BLAST hits ^c	BLAST %ID ^c	Phylum;Class;Order ^d
OTU.406	2.02	45	No hits of at least 97% identity	85.83	<i>Acidobacteria DA023 uncultured-bacterium</i>
OTU.205	1.91	45	No hits of at least 97% identity	91.94	<i>Acidobacteria Order-Incertae-Sedis Family-Incertae-Sedis</i>
OTU.7984	4.42	14	No hits of at least 97% identity	89.1	<i>Actinobacteria Corynebacteriales uncultured</i>
OTU.8951	5.76	14	No hits of at least 97% identity	93.83	<i>Actinobacteria Micrococcales Micrococcaceae</i>
OTU.9722	4.82	14	No hits of at least 97% identity	95.7	<i>Actinobacteria Streptomycetales Streptomycetaceae</i>
OTU.1811	4.72	28	No hits of at least 97% identity	92.29	<i>Armatimonadetes Armatimonadia Armatimonadales</i>
OTU.998	4.14	28	No hits of at least 97% identity	92.53	<i>Armatimonadetes Armatimonadia Armatimonadales</i>
OTU.2526	4.45	28	No hits of at least 97% identity	88.53	<i>Armatimonadetes Chthonomonadetes Chthonomonadales</i>
OTU.982	2.53	28	No hits of at least 97% identity	84.8	<i>Armatimonadetes Chthonomonadetes Chthonomonadales</i>
OTU.782	5.47	28	No hits of at least 97% identity	94.86	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.7433	4.79	14	No hits of at least 97% identity	93.52	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.3926	4.74	28	No hits of at least 97% identity	95.41	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.774	4.49	45	No hits of at least 97% identity	93.19	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.911	3.96	14	No hits of at least 97% identity	93.51	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.645	2.54	28	No hits of at least 97% identity	89.76	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.13290	5.16	28	<i>Flavobacterium sp. FCS-5</i>	98.38	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.750	3.58	28	No hits of at least 97% identity	88.65	<i>Bacteroidetes Flavobacteria Flavobacteriales</i>
OTU.2137	5.98	28	No hits of at least 97% identity	95.95	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.2215	4.66	28	No hits of at least 97% identity	94.88	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1119	4.56	45	<i>Flavihumibacter petaseus</i>	97.84	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1837	4.53	45	No hits of at least 97% identity	93.5	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.838	3.91	45	No hits of at least 97% identity	94.91	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.632	2.8	45	No hits of at least 97% identity	96.76	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.6354	2.79	45	No hits of at least 97% identity	88.65	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.403	2.6	28	No hits of at least 97% identity	96.76	<i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i>
OTU.1784	3.83	14	No hits of at least 97% identity	83.24	<i>Candidate-division-BRC1 uncultured-bacterium</i>
OTU.1783	3.81	14	No hits of at least 97% identity	83.82	<i>Candidate-division-BRC1 uncultured-bacterium</i>
OTU.692	3.23	14	No hits of at least 97% identity	85.91	<i>Chlorobi Chlorobia Chlorobiales</i>
OTU.597	2.28	28	No hits of at least 97% identity	86.96	<i>Chlorobi Chlorobia Chlorobiales</i>
OTU.848	3.83	45	No hits of at least 97% identity	83.65	<i>Cyanobacteria MLE1-12 uncultured-bacterium</i>
OTU.1992	7.28	14	No hits of at least 97% identity	93.24	<i>Cyanobacteria SM1D11 uncultured-bacterium</i>
OTU.1776	2.87	28	No hits of at least 97% identity	80.76	<i>Firmicutes Erysipelotrichi Erysipelotrichales</i>
OTU.2568	4.16	28	No hits of at least 97% identity	86.6	<i>Gemmatimonadetes Gemmatimonadales Gemmatimonadaceae</i>
OTU.8775	3.78	28	No hits of at least 97% identity	81.92	<i>Planctomycetes OM190 uncultured-bacterium</i>
OTU.1312	3.36	14	No hits of at least 97% identity	81.82	<i>Planctomycetes OM190 uncultured-bacterium</i>
OTU.2087	4.51	28	No hits of at least 97% identity	91.15	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.1667	4.46	45	No hits of at least 97% identity	88.17	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.12128	4.26	28	No hits of at least 97% identity	93.46	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.6253	4.02	14	No hits of at least 97% identity	85.83	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.5851	3.98	14	No hits of at least 97% identity	88.3	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.2023	3.04	45	No hits of at least 97% identity	90.32	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.1310	2.82	28	No hits of at least 97% identity	91.2	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.1586	2.67	28	No hits of at least 97% identity	90.62	<i>Planctomycetes Planctomycetacia Planctomycetales</i>

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.3271	2.66	28	No hits of at least 97% identity	91.14	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.252	2.46	28	No hits of at least 97% identity	90.08	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.209	2.09	28	No hits of at least 97% identity	93.32	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.10671	4.78	28	No hits of at least 97% identity	94.74	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.7576	4.63	14	No hits of at least 97% identity	91.67	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.1850	4.59	28	No hits of at least 97% identity	92.29	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.787	3.62	45	<i>Starkeya koreensis</i>	98.12	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.4411	3.02	45	No hits of at least 97% identity	92.47	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.223	1.88	45	<i>Reyranella massiliensis</i>	97.85	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i>
OTU.6520	5.18	28	No hits of at least 97% identity	84.76	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i>
OTU.1125	3.94	14	No hits of at least 97% identity	84.72	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i>
OTU.1708	5.89	14	No hits of at least 97% identity	94.64	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.6552	5.45	28	<i>Sphingobium</i> sp. 301, <i>Sphingobium amiense</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.9555	4.9	45	<i>Sphingomonas</i> sp. LNB2	97.05	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.1196	4.12	45	<i>Sphingopyxis taejonensis</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.4255	5.59	14	No hits of at least 97% identity	92.76	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.8266	3.53	14	No hits of at least 97% identity	93.22	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.2243	2.83	28	<i>Comamonas koreensis</i>	98.66	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.5915	3.19	14	No hits of at least 97% identity	90.32	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Nitrosomonadales</i>
OTU.4552	3.24	14	No hits of at least 97% identity	89.67	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>SC-I-84</i>
OTU.491	3.71	45	No hits of at least 97% identity	89.54	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Bdellovibrionales</i>
OTU.1960	3.25	45	No hits of at least 97% identity	90.59	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Bdellovibrionales</i>
OTU.2140	3.97	45	No hits of at least 97% identity	83.29	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.5550	4.05	45	No hits of at least 97% identity	92.76	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Alteromonadales</i>
OTU.1987	5.72	45	No hits of at least 97% identity	92.78	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.2059	4.84	28	No hits of at least 97% identity	94.64	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i>
OTU.3050	4.78	28	No hits of at least 97% identity	88.8	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>NKB5</i>
OTU.1212	4.41	14	No hits of at least 97% identity	87.94	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>NKB5</i>
OTU.3534	4.2	14	No hits of at least 97% identity	86.74	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>NKB5</i>
OTU.610	7.21	45	<i>Pseudoxanthomonas mexicana</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.1774	5.37	14	No hits of at least 97% identity	94.09	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.6017	3.82	14	No hits of at least 97% identity	93.55	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.6823	3.5	45	<i>Lysobacter</i> <i>sp.</i> <i>DCY21T</i>	97.83	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.11115	2.88	14	No hits of at least 97% identity	94.92	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.193	2.81	28	<i>Lysobacter ginsengisoli</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.4934	2.45	14	<i>Xanthomonas</i> <i>sp.</i> <i>T7-07</i>	99.47	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.414	2.18	45	<i>Stenotrophomonas pavanii</i> , <i>Stenotrophomonas maltophilia</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.303	2.15	14	<i>Arenimonas sp. CH15-1</i>	98.13	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.5763	2.09	45	<i>Thermomonas dokdonensis</i>	98.92	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.5454	2.09	14	<i>Arenimonas sp. CH15-1</i>	97.59	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.8860	3.96	28	No hits of at least 97% identity	88.15	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.1553	5.34	45	No hits of at least 97% identity	96.79	<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).