

Table 1: <sup>13</sup>C-cellulose responders BLAST against Living Tree Project

OTU ID	Fold change <sup>a</sup>	Day <sup>b</sup>	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.100	2.66	14	<i>Pseudoxanthomonas sacheonensis</i> , <i>Pseudoxanthomonas dokdonensis</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.1023	4.61	30	No hits of at least 90% identity	80.54	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.1065	5.31	14	No hits of at least 90% identity	84.55	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.1087	4.32	14	<i>Devosia soli</i> , <i>Devosia crocina</i> , <i>Devosia riboflavina</i>	99.09	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.1094	3.69	30	<i>Sporocytophaga myxococcoides</i>	99.55	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.11	3.41	14	<i>Stenotrophomonas pavanii</i> , <i>Stenotrophomonas maltophilia</i> , <i>Pseudomonas geniculata</i>	99.54	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.114	2.78	14	<i>Herbaspirillum</i> sp. <i>SUEMI03</i> , <i>Herbaspirillum</i> sp. <i>SUEMI10</i> , <i>Oxalicibacterium solurbis</i> , <i>Herminiimonas fonticola</i> , <i>Oxalicibacterium horti</i>	100.0	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.119	3.31	14	<i>Brevundimonas alba</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.120	4.76	14	<i>Vampirovibrio chlorellavorus</i>	94.52	<i>Cyanobacteria</i> <i>SM1D11</i> <i>uncultured-bacterium</i>
OTU.1204	4.32	30	<i>Planctomyces limnophilus</i>	91.78	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.1312	4.07	30	<i>Paucimonas lemoignei</i>	99.54	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.132	2.81	14	<i>Streptomyces</i> spp.	100.0	<i>Actinobacteria</i> <i>Streptomycetales</i> <i>Streptomycetaceae</i>
OTU.150	4.06	14	No hits of at least 90% identity	86.76	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.1533	3.43	30	No hits of at least 90% identity	82.27	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.154	3.24	14	<i>Pseudoxanthomonas mexicana</i> , <i>Pseudoxanthomonas japonensis</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.165	3.1	14	<i>Rhizobium skierniewicense</i> , <i>Rhizobium vignae</i> , <i>Rhizobium larrymoorei</i> , <i>Rhizobium alkalisoli</i> , <i>Rhizobium galegae</i> , <i>Rhizobium huautlense</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.1754	4.48	14	<i>Asticcacaulis biprosthecium</i> , <i>Asticcacaulis benevestitus</i>	96.8	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.185	4.37	14	No hits of at least 90% identity	85.14	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.19	2.44	14	<i>Rhizobium alarii</i> , <i>Rhizobium mesosinicum</i> , <i>Rhizobium mongolense</i> , <i>Arthrobacter viscosus</i> , <i>Rhizobium sullae</i> , <i>Rhizobium yanglingense</i> , <i>Rhizobium loessense</i>	99.54	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.204	3.81	14	No hits of at least 90% identity	nan	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.2192	3.49	30	No hits of at least 90% identity	83.56	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.228	2.54	30	<i>Sorangium cellulosum</i>	98.17	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.241	2.66	14	No hits of at least 90% identity	87.73	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.257	2.94	14	<i>Lentzea waywayandensis</i> , <i>Lentzea flaviverrucosa</i>	100.0	<i>Actinobacteria</i> <i>Pseudonocardiales</i> <i>Pseudonocardiaceae</i>
OTU.266	4.54	30	No hits of at least 90% identity	83.64	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.28	2.59	14	<i>Rhizobium giardinii</i> , <i>Rhizobium tubonense</i> , <i>Rhizobium tibeticum</i> , <i>Rhizobium mesoamericanum</i> <i>CCGE 501</i> , <i>Rhizobium herbae</i> , <i>Rhizobium endophyticum</i>	99.54	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.285	3.55	30	<i>Blastopirellula marina</i>	90.87	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.32	2.34	3	<i>Sandaracinus amylolyticus</i>	94.98	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.327	2.99	14	<i>Asticcacaulis biprosthecium</i> , <i>Asticcacaulis benevestitus</i>	98.63	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.351	3.54	14	<i>Pirellula staleyi</i> <i>DSM 6068</i>	91.86	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.3594	3.83	30	<i>Chondromyces robustus</i>	90.41	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.3775	3.88	14	<i>Devosia glacialis</i> , <i>Devosia chinhatensis</i> , <i>Devosia geojensis</i> , <i>Devosia yakushimensis</i>	98.63	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.429	3.7	30	<i>Devosia limi</i> , <i>Devosia psychrophila</i>	97.72	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.4322	4.19	14	No hits of at least 90% identity	89.14	<i>Chloroflexi</i> <i>Herpetosiphonales</i> <i>Herpetosiphonaceae</i>
OTU.442	3.05	30	<i>Chondromyces robustus</i>	92.24	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.465	3.79	30	<i>Ohtaekwangia kribbensis</i>	92.73	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.473	3.58	14	<i>Pirellula staleyi</i> DSM 6068	90.91	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.484	4.92	14	No hits of at least 90% identity	89.09	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.5	2.69	14	<i>Delftia tsuruhatensis</i> , <i>Delftia lacustris</i>	100.0	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.518	4.8	14	<i>Hydrogenophaga intermedia</i>	100.0	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.5190	3.6	30	No hits of at least 90% identity	88.13	<i>Chloroflexi</i> <i>Herpetosiphonales</i> <i>Herpetosiphonaceae</i>
OTU.541	4.49	30	No hits of at least 90% identity	84.23	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.5539	4.01	14	<i>Devosia subaequoris</i>	98.17	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.573	3.03	30	<i>Adhaeribacter aerophilus</i>	92.76	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.6	3.62	7	<i>Cellvibrio fulvus</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Pseudomonadales</i>
OTU.600	3.48	30	No hits of at least 90% identity	80.37	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.6062	4.83	30	<i>Dokdonella</i> sp. DC-3, <i>Luteibacter rhizovicinus</i>	97.26	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i>
OTU.627	4.43	14	<i>Verrucomicrobiaceae</i> bacterium DC2a-G7	100.0	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.633	3.84	30	No hits of at least 90% identity	89.5	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.638	4.0	30	<i>Luteolibacter</i> sp. CCTCC AB 2010415, <i>Luteolibacter algae</i>	93.61	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.64	4.31	14	No hits of at least 90% identity	89.5	<i>Chloroflexi</i> <i>Herpetosiphonales</i> <i>Herpetosiphonaceae</i>
OTU.663	3.63	30	<i>Pirellula staleyi</i> DSM 6068	90.87	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.669	3.34	30	<i>Ohtaekwangia koreensis</i>	92.69	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.670	2.87	30	<i>Adhaeribacter aerophilus</i>	91.78	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.766	3.21	14	<i>Devosia insulae</i>	99.54	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.83	5.61	14	<i>Luteolibacter</i> sp. CCTCC AB 2010415	97.72	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.862	5.87	14	<i>Allokutzneria albata</i>	100.0	<i>Actinobacteria</i> <i>Pseudonocardiales</i> <i>Pseudonocardiaceae</i>
OTU.899	2.28	30	<i>Enhygromyxa salina</i>	97.72	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.90	2.94	14	<i>Sphingopyxis panaciterrae</i> , <i>Sphingopyxis chilensis</i> , <i>Sphingopyxis</i> sp. BZ30, <i>Sphingomonas</i> sp.	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i>
OTU.900	4.87	14	<i>Brevundimonas vesicularis</i> , <i>Brevundimonas nasdae</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacterales</i>
OTU.971	3.68	30	No hits of at least 90% identity	78.57	<i>Chloroflexi</i> <i>Anaerolineae</i> <i>Anaerolineales</i>
OTU.98	3.68	14	No hits of at least 90% identity	88.18	<i>Chloroflexi</i> <i>Herpetosiphonales</i> <i>Herpetosiphonaceae</i>
OTU.982	4.47	14	<i>Devosia neptuniae</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>

<sup>a</sup> Maximum observed  $\log_2$  of fold change.<sup>b</sup> Day of maximum fold change.