Table 1: $^{13}\mathrm{C}\text{-}\mathrm{cellulose}$ responders BLAST against Living Tree Project

OTU ID	Fold change ^a	Day b	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.862	5.87	14	Allokutzneria albata	100.0	Actinobacteria Pseudonocardiales Pseudonocardiaceae
OTU.257	2.94	14	Lentzea waywayandensis, Lentzea flaviverrucosa	100.0	Actinobacteria Pseudonocardiales Pseudonocardiaceae
OTU.132	2.81	14	Streptomyces spp.	100.0	Actinobacteria Streptomycetales Streptomycetaceae
OTU.465	3.79	30	Ohtaekwangia kribbensis	92.73	Bacteroidetes Cytophagia Cytophagales
OTU.1094	3.69	30	$Sporocytophaga\ myxococcoides$	99.55	Bacteroidetes Cytophagia Cytophagales
OTU.669	3.34	30	Ohtaekwangia koreensis	92.69	Bacteroidetes Cytophagia Cytophagales
OTU.573	3.03	30	$Adhaeri bacter\ aerophilus$	92.76	Bacteroidetes Cytophagia Cytophagales
OTU.670	2.87	30	Adhaeribacter aerophilus	91.78	Bacteroidetes Cytophagia Cytophagales
OTU.971	3.68	30	No hits of at least 90% identity	78.57	Chloroflexi Anaerolineae Anaerolineales
OTU.64	4.31	14	No hits of at least 90% identity	89.5	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.4322	4.19	14	No hits of at least 90% identity	89.14	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.98	3.68	14	No hits of at least 90% identity	88.18	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.5190	3.6	30	No hits of at least 90% identity	88.13	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.120	4.76	14	Vampirovibrio chlorellavorus	94.52	Cyanobacteria SM1D11 uncultured-bacterium
OTU.1065	5.31	14	No hits of at least 90% identity	84.55	Planctomycetes Planctomycetacia Planctomycetales
OTU.484	4.92	14	No hits of at least 90% identity	89.09	Planctomycetes Planctomycetacia Planctomycetales
OTU.1204	4.32	30	Planctomyces limnophilus	91.78	Planctomycetes Planctomycetacia Planctomycetales
OTU.150	4.06	14	No hits of at least 90% identity	86.76	Planctomycetes Planctomycetacia Planctomycetales
OTU.663	3.63	30	Pirellula staleyi DSM 6068	90.87	Planctomycetes Planctomycetacia Planctomycetales
OTU.473	3.58	14	Pirellula staleyi DSM 6068	90.91	Planctomycetes Planctomycetacia Planctomycetales

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OTU ID	Fold change	Day	Top BLAST hits B	BLAST %ID	Phylum;Class;Order
OTU.285	3.55	30	Blastopirellula marina	90.87	Planctomycetes Planctomycetacia Planctomycetales
OTU.351	3.54	14	Pirellula staleyi DSM 6068	91.86	Planctomycetes Planctomycetacia Planctomycetales
OTU.600	3.48	30	No hits of at least 90% identity	80.37	Planctomycetes Planctomycetacia Planctomycetales
OTU.900	4.87	14	Brevundimonas vesicularis, Brevundimonas nasdae	100.0	$Proteobacteria \ Alphaproteobacteria \ Caulobacterales$
OTU.1754	4.48	14	Asticcacaulis biprosthecium, Asticcacaulis benevestitus	96.8	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.119	3.31	14	Brevundimonas alba	100.0	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.327	2.99	14	Asticcacaulis biprosthecium, Asticcacaulis benevestitus	98.63	Proteobacteria Alphaproteobacteria Caulobacterales
OTU.982	4.47	14	Devosia neptuniae	100.0	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.1087	4.32	14	Devosia soli, Devosia crocina, Devosia riboflavina	99.09	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.5539	4.01	14	Devosia subaequoris	98.17	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.3775	3.88	14	Devosia glacialis, Devosia chinhatensis, Devosia geojensis, Devosia yakushimensis	98.63	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.429	3.7	30	Devosia limi, Devosia psychrophila	97.72	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.766	3.21	14	Devosia insulae	99.54	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.165	3.1	14	Rhizobium skierniewicense, Rhizobium vignae, Rhizobium larrymoorei, Rhizobium alkalisoli, Rhizobium galegae, Rhizobium huautlense	100.0	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.28	2.59	14	Rhizobium giardinii, Rhizobium tubonense, Rhizobium tibeticum, Rhizobium mesoamericanum CCGE Rhizobium herbae, Rhizobium endophyticum	99.54 501,	Proteobacteria Alphaproteobacteria Rhizobiales

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OTU ID	Fold change	Day	Top BLAST hits	BLAST %ID	Phylum; Class; Order
OTU.19	2.44	14	Rhizobium alamii, Rhizobium mesosinicum, Rhizobium mongolense, Arthrobacter viscosus, Rhizobium sullae, Rhizobium yanglingense, Rhizobium loessense	99.54	Proteobacteria Alphaproteobacteria Rhizobiales
OTU.90	2.94	14	Sphingopyxis panaciterrae, Sphingopyxis chilensis, Sphingopyxis sp. BZ30, Sphingomonas sp.	100.0	$Proteobacteria \ Alphaproteobacteria \ Sphingomonadales$
OTU.518	4.8	14	$Hydrogenophaga\ intermedia$	100.0	Proteobacteria Betaproteobacteria Burkholderiales
OTU.1312	4.07	30	Paucimonas lemoignei	99.54	Proteobacteria Betaproteobacteria Burkholderiales
OTU.114	2.78	14	Herbaspirillum sp. SUEMI03, Herbaspirillum sp. SUEMI10, Oxalicibacterium solurbis, Herminiimonas fonticola, Oxalicibacterium horti	100.0	Proteobacteria Betaproteobacteria Burkholderiales
OTU.633	3.84	30	No hits of at least 90% identity	89.5	Proteobacteria Deltaproteobacteria Myxococcales
OTU.3594	3.83	30	Chondromyces robustus	90.41	Proteobacteria Deltaproteobacteria Myxococcales
OTU.442	3.05	30	Chondromyces robustus	92.24	Proteobacteria Deltaproteobacteria Myxococcales
OTU.228	2.54	30	Sorangium cellulosum	98.17	Proteobacteria Deltaproteobacteria Myxococcales
OTU.899	2.28	30	Enhygromyxa salina	97.72	Proteobacteria Deltaproteobacteria Myxococcales
OTU.6	3.62	7	Cellvibrio fulvus	100.0	Proteobacteria Gammaproteobacteria Pseudomonadales
OTU.6062	4.83	30	Dokdonella sp. DC-3, Luteibacter rhizovicinus	97.26	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.154	3.24	14	Pseudoxanthomonas mexicana, Pseudoxanthomonas japonensis	100.0	$Proteobacteria \ Gamma proteobacteria \ Xanthomonadales$
OTU.100	2.66	14	Pseudoxanthomonas sacheonensis. Pseudoxanthomonas dokdonensis	, 100.0	Proteobacteria Gammaproteobacteria Xanthomonadales
OTU.1023	4.61	30	No hits of at least 90% identity	80.54	Verrucomicrobia Spartobacteria Chthoniobacterales

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OTU ID	Fold change	Day	Top BLAST hits B	BLAST %ID	Phylum;Class;Order
OTU.266	4.54	30	No hits of at least 90% identity	83.64	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.541	4.49	30	No hits of at least 90% identity	84.23	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.185	4.37	14	No hits of at least 90% identity	85.14	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.2192	3.49	30	No hits of at least 90% identity	83.56	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.1533	3.43	30	No hits of at least 90% identity	82.27	Verrucomicrobia Spartobacteria Chthoniobacterales
OTU.83	5.61	14	Luteolibacter sp. CCTCC AB 20104	15 97.72	Verrucomicrobia Verrucomicrobiae Verrucomicrobiales
OTU.627	4.43	14	Verrucomicrobiaceae bacterium DC2	a-G7 100.0	Verrucomicrobia Verrucomicrobiae Verrucomicrobiales
OTU.638	4.0	30	Luteolibacter sp. CCTCC AB 20104. Luteolibacter algae	15, 93.61	Verrucomicrobia Verrucomicrobiae Verrucomicrobiales

^a Maximum observed log_2 of fold change. ^b Day of maximum fold change.