

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

OTU ID	Fold change	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.862	5.87	<i>Allokutzneria albata</i>	100.0	Actinobacteria Pseudonocardiales Pseudonocardiaceae
OTU.257	2.94	<i>Lentzea waywayandensis</i> , <i>Lentzea flaviverrucosa</i>	100.0	Actinobacteria Pseudonocardiales Pseudonocardiaceae
OTU.132	2.81	<i>Streptomyces</i> spp.	100.0	Actinobacteria Streptomycetales Streptomycetaceae
OTU.465	3.79	<i>Ohtaekwangia kribbensis</i>	92.73	Bacteroidetes Cytophagia Cytophagales
OTU.1094	3.69	<i>Sporocytophaga myxococcoides</i>	99.55	Bacteroidetes Cytophagia Cytophagales
OTU.669	3.34	<i>Ohtaekwangia koreensis</i>	92.69	Bacteroidetes Cytophagia Cytophagales
OTU.573	3.03	<i>Adhaeribacter aerophilus</i>	92.76	Bacteroidetes Cytophagia Cytophagales
OTU.670	2.87	<i>Adhaeribacter aerophilus</i>	91.78	Bacteroidetes Cytophagia Cytophagales
OTU.971	3.68	No hits of at least 90% identity	78.57	Chloroflexi Anaerolineae Anaerolineales
OTU.64	4.31	No hits of at least 90% identity	89.5	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.4322	4.19	No hits of at least 90% identity	89.14	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.98	3.68	No hits of at least 90% identity	88.18	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.5190	3.6	No hits of at least 90% identity	88.13	Chloroflexi Herpetosiphonales Herpetosiphonaceae
OTU.120	4.76	<i>Vampirovibrio chlorellavorus</i>	94.52	Cyanobacteria SM1D11 uncultured-bacterium
OTU.1065	5.31	No hits of at least 90% identity	84.55	Planctomycetes Planctomycetacia Planctomycetales
OTU.484	4.92	No hits of at least 90% identity	89.09	Planctomycetes Planctomycetacia Planctomycetales
OTU.1204	4.32	<i>Planctomyces limnophilus</i>	91.78	Planctomycetes Planctomycetacia Planctomycetales
OTU.150	4.06	No hits of at least 90% identity	86.76	Planctomycetes Planctomycetacia Planctomycetales
OTU.663	3.63	<i>Pirellula staleyi</i> DSM 6068	90.87	Planctomycetes Planctomycetacia Planctomycetales
OTU.473	3.58	<i>Pirellula staleyi</i> DSM 6068	90.91	Planctomycetes Planctomycetacia Planctomycetales
OTU.285	3.55	<i>Blastopirellula marina</i>	90.87	Planctomycetes Planctomycetacia Planctomycetales
OTU.351	3.54	<i>Pirellula staleyi</i> DSM 6068	91.86	Planctomycetes Planctomycetacia Planctomycetales
OTU.600	3.48	No hits of at least 90% identity	80.37	Planctomycetes Planctomycetacia Planctomycetales
OTU.900	4.87	<i>Brevundimonas vesicularis</i> , <i>Brevundimonas nasdae</i>	100.0	Proteobacteria Alphaproteobacteria Caulobacteriales
OTU.1754	4.48	<i>Asticcacaulis biprosthecium</i> , <i>Asticcacaulis benevestitus</i>	96.8	Proteobacteria Alphaproteobacteria Caulobacteriales

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OTU.119	3.31	<i>Brevundimonas alba</i>	100.0	<i>Proteobacteria Alphaproteobacteria Caulobacteriales</i>
OTU.327	2.99	<i>Asticcacaulis biprosthecium</i> , <i>Asticcacaulis benevestitus</i>	98.63	<i>Proteobacteria Alphaproteobacteria Caulobacteriales</i>
OTU.982	4.47	<i>Devosia neptuniae</i>	100.0	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.1087	4.32	<i>Devosia soli</i> , <i>Devosia crocina</i> , <i>Devosia riboflavina</i>	99.09	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.5539	4.01	<i>Devosia subaequoris</i>	98.17	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.3775	3.88	<i>Devosia glacialis</i> , <i>Devosia chinhatensis</i> , <i>Devosia geojensis</i> , <i>Devosia yakushimensis</i>	98.63	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.429	3.7	<i>Devosia limi</i> , <i>Devosia psychrophila</i>	97.72	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.766	3.21	<i>Devosia insulae</i>	99.54	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.165	3.1	<i>Rhizobium spp.</i>	100.0	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.28	2.59	<i>Rhizobium giardinii</i> , <i>Rhizobium tubonense</i> , <i>Rhizobium tibeticum</i> , <i>Rhizobium mesoamericanum</i> CCGE 501, <i>Rhizobium herbae</i> , <i>Rhizobium endophyticum</i>	99.54	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.19	2.44	<i>Rhizobium spp.</i> , <i>Arthrobacter spp.</i>	99.54	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.90	2.94	<i>Sphingopyxis panaciterrae</i> , <i>Sphingopyxis chilensis</i> , <i>Sphingopyxis sp. BZ30</i> , <i>Sphingomonas sp.</i>	100.0	<i>Proteobacteria Alphaproteobacteria Sphingomonadales</i>
OTU.518	4.8	<i>Hydrogenophaga intermedia</i>	100.0	<i>Proteobacteria Betaproteobacteria Burkholderiales</i>
OTU.1312	4.07	<i>Paucimonas lemoignei</i>	99.54	<i>Proteobacteria Betaproteobacteria Burkholderiales</i>
OTU.5	3.69	<i>Delftia tsuruhatensis</i> , <i>Delftia lacustris</i>	100.0	<i>Proteobacteria Betaproteobacteria Burkholderiales</i>
OTU.114	2.78	<i>Herbaspirillum sp. SUEMI03</i> , <i>Herbaspirillum sp. SUEMI10</i> , <i>Oxalicibacterium solurbis</i> , <i>Hermiimonas fonticola</i> , <i>Oxalicibacterium horti</i>	100.0	<i>Proteobacteria Betaproteobacteria Burkholderiales</i>
OTU.633	3.84	No hits of at least 90% identity	89.5	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>
OTU.3594	3.83	<i>Chondromyces robustus</i>	90.41	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>
OTU.442	3.05	<i>Chondromyces robustus</i>	92.24	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>

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OTU.32	3.0	<i>Sandaracinus amylolyticus</i>	94.98	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>
OTU.228	2.54	<i>Sorangium cellulosum</i>	98.17	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>
OTU.899	2.28	<i>Enhygromyxa salina</i>	97.72	<i>Proteobacteria Deltaproteobacteria Myxococcales</i>
OTU.6	3.62	<i>Cellvibrio fulvus</i>	100.0	<i>Proteobacteria Gammaproteobacteria Pseudomonadales</i>
OTU.11	5.25	<i>Stenotrophomonas pavanii</i> , <i>Stenotrophomonas maltophilia</i> , <i>Pseudomonas geniculata</i>	99.54	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.6062	4.83	<i>Dokdonella sp. DC-3</i> , <i>Luteibacter rhizovicinus</i>	97.26	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.154	3.24	<i>Pseudoxanthomonas mexicana</i> , <i>Pseudoxanthomonas japonensis</i>	100.0	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.100	2.66	<i>Pseudoxanthomonas sacheonensis</i> , <i>Pseudoxanthomonas dokdonensis</i>	100.0	<i>Proteobacteria Gammaproteobacteria Xanthomonadales</i>
OTU.1023	4.61	No hits of at least 90% identity	80.54	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.266	4.54	No hits of at least 90% identity	83.64	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.541	4.49	No hits of at least 90% identity	84.23	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.185	4.37	No hits of at least 90% identity	85.14	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.2192	3.49	No hits of at least 90% identity	83.56	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.1533	3.43	No hits of at least 90% identity	82.27	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.241	3.38	No hits of at least 90% identity	87.73	<i>Verrucomicrobia Spartobacteria Chthoniobacterales</i>
OTU.83	5.61	<i>Luteolibacter sp. CCTCC AB 2010415</i>	97.72	<i>Verrucomicrobia Verrucomicrobiae Verrucomicrobiales</i>
OTU.627	4.43	<i>Verrucomicrobiaceae bacterium DC2a-G7</i>	100.0	<i>Verrucomicrobia Verrucomicrobiae Verrucomicrobiales</i>
OTU.638	4.0	<i>Luteolibacter sp. CCTCC AB 2010415</i> , <i>Luteolibacter algae</i>	93.61	<i>Verrucomicrobia Verrucomicrobiae Verrucomicrobiales</i>