

Table 3.2: ¹³C-cellulose responders in the simple treatment

OTU ID	Fold change ^a	Top BLAST hits ^b	BLAST %ID ^b	Phylum;Class;Order ^c
OTU.569	2.15	No hits of at least 95% identity	84.16	<i>Acidobacteria Candidatus-Solibacter uncultured-bacterium</i>
OTU.382	2.98	No hits of at least 95% identity	89.19	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.525	1.9	<i>Cytophaga hutchinsonii ATCC 33406</i>	98.63	<i>Bacteroidetes Cytophagia Cytophagales</i>
OTU.64	2.78	No hits of at least 95% identity	89.5	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.98	2.56	No hits of at least 95% identity	88.18	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.4322	2.26	No hits of at least 95% identity	89.14	<i>Chloroflexi Herpetosiphonales Herpetosiphonaceae</i>
OTU.285	2.52	No hits of at least 95% identity	90.87	<i>Planctomycetes Planctomycetacia Planctomycetales</i>
OTU.766	2.36	<i>Devosia insulae</i>	99.54	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.206	2.31	<i>Andersenella baltica</i>	95.89	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.73	1.95	<i>Mesorhizobium temperatum</i> , <i>Mesorhizobium caraganae</i> , <i>Mesorhizobium robiniae</i> , <i>Mesorhizobium gobiense</i> , <i>Mesorhizobium sp. Ala-3</i> , <i>Mesorhizobium tarimense</i> , <i>Mesorhizobium tianshanense</i> , <i>Mesorhizobium metallidurans</i> , <i>Mesorhizobium mediterraneum</i>	100.0	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.19	1.86	<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 Alphaproteobacteria Rhizobiales</i>
OTU.263	1.77	No hits of at least 95% identity	94.06	<i>Proteobacteria Alphaproteobacteria Rhizobiales</i>
OTU.89	2.62	<i>Sphingomonas trueperi</i> , <i>Sphingomonas sp.</i> , <i>Sphingomonas pituitosa</i> , <i>Caulobacter leidyia</i>	100.0	<i>Proteobacteria Alphaproteobacteria Sphingomonadales</i>
OTU.1414	1.87	<i>Sphingomonas kaistensis</i>	97.72	<i>Proteobacteria Alphaproteobacteria Sphingomonadales</i>
OTU.38	1.82	<i>Kaistobacter terrae</i>	100.0	<i>Proteobacteria Alphaproteobacteria Sphingomonadales</i>
OTU.17	1.79	<i>Sphingomonas sp. 382</i>	97.72	<i>Proteobacteria Alphaproteobacteria Sphingomonadales</i>
OTU.20	1.66	<i>Sphingomonas jaspsi</i>	98.17	<i>Proteobacteria Alphaproteobacteria Sphingomonadales</i>
OTU.2294	1.65	<i>Kaistobacter sp. Gsoil 634</i>	97.26	<i>Proteobacteria Alphaproteobacteria Sphingomonadales</i>

Table 3.2 – continued from previous page

OTU ID	Fold change	Top BLAST hits	BLAST %ID	Phylum;Class;Order
OTU.114	3.01	<i>Herbaspirillum</i> sp. <i>SUEMI03</i> , <i>Herbaspirillum</i> sp. <i>SUEMI10</i> , <i>Oxalicibacterium solurbis</i> , <i>Hermiimonas fonticola</i> , <i>Oxalicibacterium horti</i>	100.0	<i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i>
OTU.5680	2.83	No hits of at least 95% identity	90.05	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.169	2.39	No hits of at least 95% identity	92.27	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.442	1.85	No hits of at least 95% identity	92.24	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.6	2.78	<i>Cellvibrio fulvus</i>	100.0	<i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Pseudomonadales</i>
OTU.945	1.71	<i>Turneriella parva</i>	99.54	<i>Spirochaetes</i> <i>Spirochaetales</i> <i>Leptospiraceae</i>
OTU.400	2.76	No hits of at least 95% identity	83.64	<i>Verrucomicrobia</i> <i>Candidatus-Methylacidiphilum</i> <i>uncultured-bacterium</i>
OTU.185	3.26	No hits of at least 95% identity	85.14	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.266	3.14	No hits of at least 95% identity	83.64	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.2192	3.12	No hits of at least 95% identity	83.56	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>
OTU.541	2.85	No hits of at least 95% identity	84.23	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i>

^a Maximum observed \log_2 of fold change.^b Against Living Tree Project database.^c Annotation from Silva database assigned during OTU binning (see methods).