

Table 3.3:  $^{13}\text{C}$ -cellulose responders in the complex treatment

OTU ID	Fold change <sup>a</sup>	Top BLAST hits <sup>b</sup>	BLAST %ID <sup>b</sup>	Phylum;Class;Order <sup>c</sup>
OTU.465	2.32	No hits of at least 95% identity	92.73	<i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>
OTU.4322	2.48	No hits of at least 95% identity	89.14	<i>Chloroflexi</i> <i>Herpetosiphonales</i> <i>Herpetosiphonaceae</i>
OTU.98	2.32	No hits of at least 95% identity	88.18	<i>Chloroflexi</i> <i>Herpetosiphonales</i> <i>Herpetosiphonaceae</i>
OTU.64	2.08	No hits of at least 95% identity	89.5	<i>Chloroflexi</i> <i>Herpetosiphonales</i> <i>Herpetosiphonaceae</i>
OTU.120	1.92	No hits of at least 95% identity	94.52	<i>Cyanobacteria</i> <i>SM1D11</i> <i>uncultured-bacterium</i>
OTU.204	2.31	No hits of at least 95% identity	nan	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.484	2.15	No hits of at least 95% identity	89.09	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.285	1.91	No hits of at least 95% identity	90.87	<i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i>
OTU.119	2.0	<i>Brevundimonas alba</i>	100.0	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Caulobacteriales</i>
OTU.766	2.04	<i>Devosia insulae</i>	99.54	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.1087	1.9	<i>Devosia soli</i> , <i>Devosia crocina</i> , <i>Devosia riboflavina</i>	99.09	<i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i>
OTU.633	1.95	No hits of at least 95% identity	89.5	<i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i>
OTU.185	2.45	No hits of at least 95% identity	85.14	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacteriales</i>
OTU.266	2.16	No hits of at least 95% identity	83.64	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacteriales</i>
OTU.541	2.15	No hits of at least 95% identity	84.23	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacteriales</i>
OTU.1023	2.0	No hits of at least 95% identity	80.54	<i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacteriales</i>
OTU.83	2.45	<i>Luteolibacter</i> sp. <i>CCTCC AB 2010415</i>	97.72	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>
OTU.638	2.09	No hits of at least 95% identity	93.61	<i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i>

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