

Table 4.4: ¹³C-cellulose responders in the pulse root exudate treatment

| OTU ID | Fold change ^a | Day ^b | Top BLAST hits ^c | BLAST %ID ^c | Phylum;Class;Order ^d |
|-----------|--------------------------|------------------|---|------------------------|--|
| OTU.1341 | 4.77 | 14 | No hits of at least 97% identity | 86.02 | <i>Acidobacteria</i> 11-24 <i>uncultured-bacterium</i> |
| OTU.2288 | 3.64 | 45 | No hits of at least 97% identity | 82.7 | <i>Acidobacteria</i> 11-24 <i>uncultured-bacterium</i> |
| OTU.1197 | 2.41 | 45 | No hits of at least 97% identity | 83.02 | <i>Acidobacteria</i> 11-24 <i>uncultured-bacterium</i> |
| OTU.1507 | 3.24 | 45 | No hits of at least 97% identity | 82.24 | <i>Acidobacteria</i> <i>Candidatus-Chloracidobacterium</i> <i>uncultured-Acidobacteria-bacterium</i> |
| OTU.3817 | 2.44 | 28 | No hits of at least 97% identity | 86.36 | <i>Acidobacteria</i> DA023 <i>uncultured-bacterium</i> |
| OTU.12188 | 6.09 | 45 | No hits of at least 97% identity | 86.44 | <i>Acidobacteria</i> Holophagae CA002 |
| OTU.1016 | 4.18 | 14 | No hits of at least 97% identity | 85.18 | <i>Acidobacteria</i> RB25 <i>uncultured-bacterium</i> |
| OTU.370 | 4.37 | 28 | <i>Gordonia sputi</i> | 100.0 | <i>Actinobacteria</i> <i>Corynebacteriales</i> Nocardiaceae |
| OTU.1181 | 4.79 | 14 | No hits of at least 97% identity | 92.27 | <i>Armatimonadetes</i> <i>Armatimonadia</i> <i>Armatimonadales</i> |
| OTU.1303 | 4.57 | 45 | No hits of at least 97% identity | 82.34 | <i>Armatimonadetes</i> <i>uncultured-bacterium</i> |
| OTU.1664 | 7.31 | 14 | <i>Sporocytophaga myxococcoides</i> | 99.19 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.1026 | 4.75 | 14 | No hits of at least 97% identity | 94.32 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.2905 | 4.2 | 45 | No hits of at least 97% identity | 91.85 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.7868 | 3.58 | 14 | No hits of at least 97% identity | 96.94 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.331 | 3.32 | 14 | <i>Ohtaekwangia kribbensis</i> | 97.04 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.10192 | 3.07 | 14 | <i>Adhaeribacter terreus</i> | 97.57 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.6036 | 3.02 | 14 | <i>Ohtaekwangia kribbensis</i> | 100.0 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.598 | 2.94 | 14 | <i>Sphingobacteria bacterium RYG</i> | 97.31 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.152 | 2.53 | 14 | <i>Adhaeribacter terreus</i> | 98.11 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.155 | 2.09 | 14 | No hits of at least 97% identity | 92.7 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.44 | 2.04 | 14 | No hits of at least 97% identity | 95.14 | <i>Bacteroidetes</i> Cytophagia Cytophagales |
| OTU.2099 | 4.99 | 45 | <i>Chryseobacterium</i> sp. THG 15, <i>Chryseobacterium formosense</i> | 100.0 | <i>Bacteroidetes</i> Flavobacteria Flavobacteriales |
| OTU.1330 | 4.7 | 14 | <i>Flavobacterium fluvii</i> | 99.73 | <i>Bacteroidetes</i> Flavobacteria Flavobacteriales |

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| OTU ID | Fold change | Day | Top BLAST hits | BLAST %ID | Phylum;Class;Order |
|----------|-------------|-----|---|-----------|--|
| OTU.7315 | 2.72 | 14 | <i>Flavobacterium columnare</i> | 98.84 | <i>Bacteroidetes Flavobacteria Flavobacteriales</i> |
| OTU.2082 | 6.2 | 28 | No hits of at least 97% identity | 86.7 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.1414 | 4.85 | 14 | No hits of at least 97% identity | 89.49 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.1929 | 4.8 | 14 | No hits of at least 97% identity | 96.49 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.4996 | 4.2 | 14 | No hits of at least 97% identity | 96.22 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.283 | 4.11 | 14 | No hits of at least 97% identity | 94.32 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.873 | 3.95 | 14 | <i>Segetibacter aerophilus</i> | 97.03 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.140 | 3.89 | 14 | No hits of at least 97% identity | 95.14 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.1969 | 3.67 | 14 | No hits of at least 97% identity | 96.76 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.325 | 3.59 | 14 | <i>Flavisolibacter ginsengisoli</i> | 98.38 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.490 | 3.5 | 14 | No hits of at least 97% identity | 95.41 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.425 | 3.38 | 14 | No hits of at least 97% identity | 88.44 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.3332 | 3.38 | 14 | No hits of at least 97% identity | 96.76 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.343 | 3.33 | 14 | No hits of at least 97% identity | 92.45 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.3380 | 3.28 | 14 | No hits of at least 97% identity | 96.22 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.717 | 3.24 | 14 | No hits of at least 97% identity | 89.62 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.7661 | 3.17 | 14 | No hits of at least 97% identity | 95.69 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.7953 | 3.07 | 14 | No hits of at least 97% identity | 94.59 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.178 | 3.07 | 14 | No hits of at least 97% identity | 94.86 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.145 | 3.02 | 14 | No hits of at least 97% identity | 90.84 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.718 | 3.02 | 14 | No hits of at least 97% identity | 88.56 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.7103 | 3.0 | 14 | No hits of at least 97% identity | 87.87 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.215 | 2.93 | 14 | No hits of at least 97% identity | 96.49 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.7560 | 2.91 | 14 | <i>Pedobacter africanus</i> , <i>Pedobacter steynii</i> , <i>Pedobacter caeni</i> | 98.65 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |

Table 4.4 – continued from previous page

| OTU ID | Fold change | Day | Top BLAST hits | BLAST %ID | Phylum;Class;Order |
|-----------|-------------|-----|-------------------------------------|-----------|--|
| OTU.12538 | 2.83 | 14 | No hits of at least 97% identity | 93.5 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.523 | 2.83 | 14 | No hits of at least 97% identity | 88.65 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.103 | 2.83 | 14 | No hits of at least 97% identity | 95.95 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.9220 | 2.8 | 14 | No hits of at least 97% identity | 94.86 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.3730 | 2.74 | 14 | No hits of at least 97% identity | 95.41 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.498 | 2.72 | 14 | No hits of at least 97% identity | 88.38 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.570 | 2.66 | 14 | No hits of at least 97% identity | 92.18 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.5218 | 2.6 | 14 | No hits of at least 97% identity | 95.14 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.431 | 2.6 | 14 | No hits of at least 97% identity | 93.55 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.916 | 2.6 | 28 | <i>Chitinophaga niabensis</i> | 97.57 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.75 | 2.54 | 14 | <i>Flavisolibacter ginsengisoli</i> | 97.84 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.45 | 2.51 | 14 | <i>Flavitalea populi</i> | 98.92 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.228 | 2.5 | 14 | No hits of at least 97% identity | 94.59 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.3841 | 2.43 | 14 | No hits of at least 97% identity | 93.24 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.133 | 2.36 | 14 | No hits of at least 97% identity | 95.41 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.725 | 2.34 | 14 | No hits of at least 97% identity | 95.95 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.225 | 2.33 | 14 | No hits of at least 97% identity | 96.49 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.8100 | 2.13 | 14 | No hits of at least 97% identity | 95.52 | <i>Bacteroidetes Sphingobacteriia Sphingobacteriales</i> |
| OTU.2351 | 5.22 | 14 | No hits of at least 97% identity | 88.59 | <i>Bacteroidetes VC2.1-Bac22 uncultured-bacterium</i> |
| OTU.3465 | 4.28 | 45 | No hits of at least 97% identity | 75.53 | <i>Candidate-division-OP11 uncultured-bacterium</i> |
| OTU.1980 | 3.97 | 14 | No hits of at least 97% identity | 85.91 | <i>Candidate-division-WS3 uncultured-bacterium</i> |
| OTU.3682 | 2.63 | 14 | No hits of at least 97% identity | 83.96 | <i>Candidate-division-WS3 uncultured-bacterium</i> |
| OTU.509 | 2.24 | 14 | No hits of at least 97% identity | 85.98 | <i>Candidate-division-WS3 uncultured-bacterium</i> |
| OTU.958 | 4.72 | 14 | No hits of at least 97% identity | 82.61 | <i>Chlorobi Chlorobia Chlorobiales</i> |

Table 4.4 – continued from previous page

| OTU ID | Fold change | Day | Top BLAST hits | BLAST %ID | Phylum;Class;Order |
|----------|-------------|-----|---|-----------|--|
| OTU.1217 | 3.2 | 45 | No hits of at least 97% identity | 80.48 | <i>Chloroflexi</i> <i>Anaerolineae</i> <i>Anaerolineales</i> |
| OTU.907 | 2.83 | 14 | No hits of at least 97% identity | 83.68 | <i>Chloroflexi</i> <i>Anaerolineae</i> <i>Anaerolineales</i> |
| OTU.3983 | 6.24 | 45 | No hits of at least 97% identity | 80.31 | <i>Chloroflexi</i> <i>Chloroflexales</i> <i>Chloroflexaceae</i> |
| OTU.3585 | 5.14 | 45 | No hits of at least 97% identity | 96.22 | <i>Cyanobacteria</i> <i>SM1D11</i> |
| OTU.640 | 3.86 | 28 | <i>Streptococcus tigurinus</i> , <i>Streptococcus mitis</i> , <i>Streptococcus infantis</i> , <i>Streptococcus pseudopneumoniae</i> , <i>Streptococcus oralis</i> | 99.73 | <i>Firmicutes</i> <i>Bacilli</i> <i>Lactobacillales</i> |
| OTU.1115 | 3.0 | 28 | No hits of at least 97% identity | 80.59 | <i>Planctomycetes</i> <i>Phycisphaerae</i> <i>WD2101-soil-group</i> |
| OTU.5726 | 5.13 | 14 | No hits of at least 97% identity | 90.4 | <i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i> |
| OTU.6106 | 4.63 | 45 | No hits of at least 97% identity | 92.27 | <i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i> |
| OTU.3395 | 3.53 | 45 | No hits of at least 97% identity | 85.25 | <i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i> |
| OTU.7980 | 3.39 | 45 | No hits of at least 97% identity | 94.13 | <i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i> |
| OTU.1073 | 2.93 | 45 | No hits of at least 97% identity | 89.63 | <i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i> |
| OTU.6068 | 2.83 | 14 | No hits of at least 97% identity | 85.79 | <i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i> |
| OTU.345 | 2.04 | 14 | No hits of at least 97% identity | 89.52 | <i>Planctomycetes</i> <i>Planctomycetacia</i> <i>Planctomycetales</i> |
| OTU.3431 | 3.78 | 28 | No hits of at least 97% identity | 87.17 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>DB1-14</i> |
| OTU.7792 | 5.13 | 14 | No hits of at least 97% identity | 90.35 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>OCS116-clade</i> |
| OTU.6486 | 3.97 | 45 | <i>Kaistia</i> sp. <i>B1-1</i> | 98.92 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i> |
| OTU.991 | 3.21 | 14 | <i>Kaistia</i> sp. <i>5YN7-3</i> , <i>Kaistia</i> sp. <i>B6-12</i> | 100.0 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i> |
| OTU.517 | 2.66 | 14 | No hits of at least 97% identity | 94.1 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhizobiales</i> |
| OTU.1627 | 5.95 | 45 | No hits of at least 97% identity | 91.76 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i> |

Table 4.4 – continued from previous page

| OTU ID | Fold change | Day | Top BLAST hits | BLAST %ID | Phylum;Class;Order |
|----------|-------------|-----|---|-----------|---|
| OTU.187 | 4.08 | 28 | <i>Roseomonas gilardii</i> subsp. <i>gilardii</i> , <i>Roseomonas mucosa</i> , <i>Roseomonas gilardii</i> subsp. <i>rosea</i> | 100.0 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i> |
| OTU.482 | 2.22 | 14 | No hits of at least 97% identity | 90.45 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i> |
| OTU.7443 | 2.07 | 28 | No hits of at least 97% identity | 95.38 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rhodospirillales</i> |
| OTU.2141 | 5.38 | 14 | No hits of at least 97% identity | 84.49 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i> |
| OTU.486 | 5.31 | 14 | No hits of at least 97% identity | 90.03 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i> |
| OTU.1930 | 4.67 | 14 | No hits of at least 97% identity | 87.77 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i> |
| OTU.1165 | 3.99 | 14 | No hits of at least 97% identity | 88.47 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Rickettsiales</i> |
| OTU.2814 | 5.28 | 14 | No hits of at least 97% identity | 96.26 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i> |
| OTU.289 | 2.61 | 14 | No hits of at least 97% identity | 96.78 | <i>Proteobacteria</i> <i>Alphaproteobacteria</i> <i>Sphingomonadales</i> |
| OTU.141 | 4.69 | 14 | No hits of at least 97% identity | 94.65 | <i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i> |
| OTU.5640 | 3.4 | 45 | <i>Paucimonas lemoignei</i> | 98.12 | <i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Burkholderiales</i> |
| OTU.2239 | 4.22 | 45 | No hits of at least 97% identity | 94.12 | <i>Proteobacteria</i> <i>Betaproteobacteria</i> <i>Hydrogenophila</i> |
| OTU.3811 | 4.57 | 14 | No hits of at least 97% identity | 89.49 | <i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Desulfobacterales</i> |
| OTU.2036 | 4.69 | 45 | No hits of at least 97% identity | 87.09 | <i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i> |
| OTU.696 | 2.34 | 45 | No hits of at least 97% identity | 93.85 | <i>Proteobacteria</i> <i>Deltaproteobacteria</i> <i>Myxococcales</i> |
| OTU.6577 | 5.83 | 45 | No hits of at least 97% identity | 95.72 | <i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i> |
| OTU.1190 | 4.28 | 45 | No hits of at least 97% identity | 96.27 | <i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i> |

Table 4.4 – continued from previous page

| OTU ID | Fold change | Day | Top BLAST hits | BLAST %ID | Phylum;Class;Order |
|-----------|-------------|-----|-------------------------------------|-----------|--|
| OTU.475 | 2.28 | 45 | <i>Aquicella siphonis</i> | 97.31 | <i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Legionellales</i> |
| OTU.433 | 5.63 | 45 | No hits of at least 97% identity | 87.47 | <i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>NKB5</i> |
| OTU.2651 | 4.31 | 45 | No hits of at least 97% identity | 87.4 | <i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>NKB5</i> |
| OTU.10253 | 4.48 | 14 | No hits of at least 97% identity | 93.26 | <i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Pseudomonadales</i> |
| OTU.1332 | 4.12 | 14 | <i>Panacagrimonas perspica</i> | 97.86 | <i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i> |
| OTU.273 | 2.16 | 14 | No hits of at least 97% identity | 94.88 | <i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i> |
| OTU.465 | 2.15 | 14 | No hits of at least 97% identity | 94.34 | <i>Proteobacteria</i> <i>Gammaproteobacteria</i> <i>Xanthomonadales</i> |
| OTU.5114 | 6.24 | 14 | No hits of at least 97% identity | 92.78 | <i>Verrucomicrobia</i> <i>Opitutae</i> <i>Opitales</i> |
| OTU.4224 | 5.35 | 45 | No hits of at least 97% identity | 88.1 | <i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i> |
| OTU.1993 | 3.77 | 45 | No hits of at least 97% identity | 88.1 | <i>Verrucomicrobia</i> <i>Spartobacteria</i> <i>Chthoniobacterales</i> |
| OTU.10213 | 4.65 | 28 | <i>Prostheco bacter fusiformis</i> | 98.4 | <i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i> |
| OTU.3003 | 4.31 | 45 | <i>Prostheco bacter fluviatilis</i> | 97.33 | <i>Verrucomicrobia</i> <i>Verrucomicrobiae</i> <i>Verrucomicrobiales</i> |
| OTU.1705 | 3.06 | 45 | No hits of at least 97% identity | 84.76 | |

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