

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

| OTU ID   | Fold change | Top BLAST hits   | BLAST %ID | Phylum;Class;Order  |
|----------|-------------|--|-----------|---|
| OTU.465  | 2.32        | <i>Ohtaekwangia kribbensis</i>   | 92.73     | <i>Bacteroidetes</i> <i>Cytophagia</i> <i>Cytophagales</i>                  |
| OTU.4322 | 2.48        | No hits of at least 90% identity   | 89.14     | <i>Chloroflexi</i> <i>Herpetosiphonales</i><br><i>Herpetosiphonaceae</i>    |
| OTU.98   | 2.32        | No hits of at least 90% identity   | 88.18     | <i>Chloroflexi</i> <i>Herpetosiphonales</i><br><i>Herpetosiphonaceae</i>    |
| OTU.64   | 2.08        | No hits of at least 90% identity   | 89.5      | <i>Chloroflexi</i> <i>Herpetosiphonales</i><br><i>Herpetosiphonaceae</i>    |
| OTU.120  | 1.92        | <i>Vampirovibrio chlorellavorus</i>  | 94.52     | <i>Cyanobacteria</i> <i>SM1D11</i><br><i>uncultured-bacterium</i>           |
| OTU.484  | 2.15        | No hits of at least 90% identity   | 89.09     | <i>Planctomycetes</i> <i>Planctomycetacia</i><br><i>Planctomycetales</i>    |
| OTU.285  | 1.91        | <i>Blastopirellula marina</i>  | 90.87     | <i>Planctomycetes</i> <i>Planctomycetacia</i><br><i>Planctomycetales</i>    |
| OTU.119  | 2.0         | <i>Brevundimonas alba</i>  | 100.0     | <i>Proteobacteria</i> <i>Alphaproteobacteria</i><br><i>Caulobacteriales</i> |
| OTU.766  | 2.04        | <i>Devosia insulae</i>   | 99.54     | <i>Proteobacteria</i> <i>Alphaproteobacteria</i><br><i>Rhizobiales</i>      |
| OTU.1087 | 1.9         | <i>Devosia soli</i> , <i>Devosia crocina</i> ,<br><i>Devosia riboflavina</i>     | 99.09     | <i>Proteobacteria</i> <i>Alphaproteobacteria</i><br><i>Rhizobiales</i>      |
| OTU.633  | 1.95        | No hits of at least 90% identity   | 89.5      | <i>Proteobacteria</i> <i>Deltaproteobacteria</i><br><i>Myxococcales</i>     |
| OTU.185  | 2.45        | No hits of at least 90% identity   | 85.14     | <i>Verrucomicrobia</i> <i>Spartobacteria</i><br><i>Chthoniobacteriales</i>  |
| OTU.266  | 2.16        | No hits of at least 90% identity   | 83.64     | <i>Verrucomicrobia</i> <i>Spartobacteria</i><br><i>Chthoniobacteriales</i>  |
| OTU.541  | 2.15        | No hits of at least 90% identity   | 84.23     | <i>Verrucomicrobia</i> <i>Spartobacteria</i><br><i>Chthoniobacteriales</i>  |
| OTU.1023 | 2.0         | No hits of at least 90% identity   | 80.54     | <i>Verrucomicrobia</i> <i>Spartobacteria</i><br><i>Chthoniobacteriales</i>  |
| OTU.83   | 2.45        | <i>Luteolibacter</i> sp. <i>CCTCC AB 2010415</i>                                 | 97.72     | <i>Verrucomicrobia</i> <i>Verrucomicrobiae</i><br><i>Verrucomicrobiales</i> |
| OTU.638  | 2.09        | <i>Luteolibacter</i> sp. <i>CCTCC AB 2010415</i> ,<br><i>Luteolibacter algae</i> | 93.61     | <i>Verrucomicrobia</i> <i>Verrucomicrobiae</i><br><i>Verrucomicrobiales</i> |