Table 1: $^{13}$C-cellulose responders BLAST against Living Tree Project

| OTU ID | Fold change | Top BLAST hits | BLAST %ID | Phylum;Class;Order |
|---|---|---|---|---|
| OTU.4446 | 3.49 | *Catenuloplanes niger*, *Catenuloplanes castaneus*, *Catenuloplanes atrovinosus*, *Catenuloplanes crispus*, *Catenuloplanes nepalensis*, *Catenuloplanes japonicus* | 97.72 | *Actinobacteria Frankiales Nakamurellaceae* |
| OTU.62 | 2.57 | *Nakamurella flavida* | 100.0 | *Actinobacteria Frankiales Nakamurellaceae* |
| OTU.24 | 2.81 | *Cellulomonas aerilata*, *Cellulomonas humilata*, *Cellulomonas terrae*, *Cellulomonas soli*, *Cellulomonas xylanilytica* | 100.0 | *Actinobacteria Micrococcales Cellulomonadaceae* |
| OTU.4 | 2.84 | *Agromyces ramosus* | 100.0 | *Actinobacteria Micrococcales Microbacteriaceae* |
| OTU.37 | 2.68 | *Phycicola gilvus*, *Microterricola viridarii*, *Frigoribacterium faeni*, *Frondihabitans sp. RS-15*, *Frondihabitans australicus* | 100.0 | *Actinobacteria Micrococcales Microbacteriaceae* |
| OTU.5284 | 3.56 | *Isoptericola nanjingensis*, *Isoptericola hypogeus*, *Isoptericola variabilis* | 98.63 | *Actinobacteria Micrococcales Promicromonosporaceae* |
| OTU.252 | 3.34 | *Promicromonospora thailandica* | 100.0 | *Actinobacteria Micrococcales Promicromonosporaceae* |
| OTU.244 | 3.08 | *Cellulosimicrobium funkei*, *Cellulosimicrobium terreum* | 100.0 | *Actinobacteria Micrococcales Promicromonosporaceae* |
| OTU.760 | 2.89 | *Dyadobacter hamtensis* | 98.63 | *Bacteroidetes Cytophagia Cytophagales* |
| OTU.14 | 3.92 | *Flavobacterium oncorhynchi*, *Flavobacterium glycines*, *Flavobacterium succinicans* | 99.09 | *Bacteroidetes Flavobacteria Flavobacteriales* |
| OTU.6203 | 3.32 | *Flavobacterium granuli*, *Flavobacterium glaciei* | 100.0 | *Bacteroidetes Flavobacteria Flavobacteriales* |
| OTU.159 | 3.16 | *Flavobacterium hibernum* | 98.17 | *Bacteroidetes Flavobacteria Flavobacteriales* |
| OTU.2379 | 3.1 | *Flavobacterium pectinovorum*, *Flavobacterium sp. CS100* | 97.72 | *Bacteroidetes Flavobacteria Flavobacteriales* |
| OTU.131 | 3.07 | *Flavobacterium fluvii*, *Flavobacteria bacterium HMD1033*, *Flavobacterium sp. HMD1001* | 100.0 | *Bacteroidetes Flavobacteria Flavobacteriales* |
| OTU.3540 | 2.52 | *Flavobacterium terrigena* | 99.54 | *Bacteroidetes Flavobacteria Flavobacteriales* |
| OTU.107 | 2.25 | *Flavobacterium sp. 15C3*, *Flavobacterium banpakuense* | 99.54 | *Bacteroidetes Flavobacteria Flavobacteriales* |
| OTU.277 | 3.52 | *Solibius ginsengiterrae* | 95.43 | *Bacteroidetes Sphingobacteriia Sphingobacteriales* |
| OTU.183 | 3.31 | No hits of at least 90% identity | 89.5 | *Bacteroidetes Sphingobacteriia Sphingobacteriales* |
| OTU.5906 | 3.16 | *Terrimonas sp. M-8* | 96.8 | *Bacteroidetes Sphingobacteriia Sphingobacteriales* |

Table 1 – continued from previous page

| OTU ID | Fold change | Top BLAST hits | BLAST %ID | Phylum;Class;Order |
|---|---|---|---|---|
| OTU.360 | 2.98 | *Flavisolibacter ginsengisoli* | 95.0 | *Bacteroidetes Sphingobacteriia Sphingobacteriales* |
| OTU.369 | 5.05 | *Paenibacillus sp. D75*, *Paenibacillus glycanilyticus* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.267 | 4.97 | *Paenibacillus pabuli*, *Paenibacillus tundrae*, *Paenibacillus taichungensis*, *Paenibacillus xylanexedens*, *Paenibacillus xylanilyticus* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.1040 | 4.78 | *Paenibacillus daejeonensis* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.57 | 4.39 | *Paenibacillus castaneae* | 98.62 | *Firmicutes Bacilli Bacillales* |
| OTU.394 | 4.06 | *Paenibacillus pocheonensis* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.319 | 3.98 | *Paenibacillus xinjiangensis* | 97.25 | *Firmicutes Bacilli Bacillales* |
| OTU.5603 | 3.96 | *Paenibacillus uliginis* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.1069 | 3.85 | *Paenibacillus terrigena* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.843 | 3.62 | *Paenibacillus agarexedens* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.2040 | 2.91 | *Paenibacillus pectinilyticus* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.3 | 2.61 | *[Brevibacterium] frigoritolerans*, *Bacillus sp. LMG 20238*, *Bacillus coahuilensis m4-4*, *Bacillus simplex* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.335 | 2.53 | *Paenibacillus thailandensis* | 98.17 | *Firmicutes Bacilli Bacillales* |
| OTU.3507 | 2.36 | Bacillus spp. | 98.63 | *Firmicutes Bacilli Bacillales* |
| OTU.8 | 2.26 | *Bacillus niacini* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.4743 | 2.24 | *Lysinibacillus fusiformis*, *Lysinibacillus sphaericus* | 99.09 | *Firmicutes Bacilli Bacillales* |
| OTU.9 | 2.04 | *Bacillus megaterium*, *Bacillus flexus* | 100.0 | *Firmicutes Bacilli Bacillales* |
| OTU.22 | 2.8 | *Paracoccus sp. NB88* | 99.09 | *Proteobacteria Alphaproteobacteria Rhodobacterales* |
| OTU.346 | 3.44 | *Pseudoduganella violaceinigra* | 99.54 | *Proteobacteria Betaproteobacteria Burkholderiales* |
| OTU.68 | 3.74 | *Shigella flexneri*, *Escherichia fergusonii*, *Escherichia coli*, *Shigella sonnei* | 100.0 | *Proteobacteria Gammaproteobacteria Enterobacteriales* |
| OTU.290 | 3.59 | Pantoea spp., Kluyvera spp., Klebsiella spp., Erwinia spp., Enterobacter spp., Buttiauxella spp. | 100.0 | *Proteobacteria Gammaproteobacteria Enterobacteriales* |
| OTU.48 | 2.99 | Aeromonas spp. | 100.0 | *Proteobacteria Gammaproteobacteria aaa34a10* |