

Table S5. Phylogenetic classification of identified SSU rRNA sequence tags (pyrosequencing) based on phylum level. Values indicate “**evenness**” (number of sequence tags identified for each phylum) given as percentage. Phyla contributing  $\geq 10\%$  are in bold. Average values are from n=4 beads. n.d. = not detected.

	T1		T2		T3		T4	
	no lignin	lignin	no lignin	lignin	no lignin	lignin	no lignin	lignin
Archaea	n.d.	0.1 $\pm$ 0.1	n.d.	n.d.	0.0 $\pm$ 0.1	0.0 $\pm$ 0.1	0.1 $\pm$ 0.0	0.5 $\pm$ 0.3
ABY1 OD1	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	0.1 $\pm$ 0.1	0.1 $\pm$ 0.1
<u>Acidobacteria</u>	2.6 $\pm$ 1.7	4.3 $\pm$ 3.0	0.8 $\pm$ 0.4	2.5 $\pm$ 2.8	3.1 $\pm$ 3.0	6.2 $\pm$ 3.7	3.5 $\pm$ 2.8	<b>10.6 <math>\pm</math>1.1</b>
<u>Actinobacteria</u>	5.7 $\pm$ 4.5	<b>10.6 <math>\pm</math>6.5</b>	3.3 $\pm$ 1.6	6.0 $\pm$ 1.9	5.5 $\pm$ 2.1	7.8 $\pm$ 3.2	6.1 $\pm$ 3.4	<b>10.4 <math>\pm</math>2.5</b>
AD3	n.d.	0.1 $\pm$ 0.1	n.d.	n.d.	n.d.	0.1 $\pm$ 0.0	n.d.	0.1 $\pm$ 0.1
Bacteroidetes	2.3 $\pm$ 2.3	2.2 $\pm$ 1.8	5.3 $\pm$ 4.9	3.6 $\pm$ 2.1	4.0 $\pm$ 0.8	4.4 $\pm$ 2.7	4.3 $\pm$ 2.1	2.6 $\pm$ 0.6
BRC1	n.d.	n.d.	0.0 $\pm$ 0.1	n.d.	n.d.	0.1 $\pm$ 0.1	0.0 $\pm$ 0.1	0.0 $\pm$ 0.1
Caldithrix	n.d.	n.d.	n.d.	n.d.	n.d.	0.0 $\pm$ 0.1	n.d.	n.d.
Chlamydiae	0.1 $\pm$ 0.0	0.3 $\pm$ 0.2	0.1 $\pm$ 0.2	1.0 $\pm$ 0.8	4.5 $\pm$ 1.8	0.8 $\pm$ 0.5	7.2 $\pm$ 6.9	1.7 $\pm$ 1.2
Chlorobi	n.d.	n.d.	1.5 $\pm$ 1.8	0.1 $\pm$ 0.1	0.1 $\pm$ 0.1	0.6 $\pm$ 0.8	0.1 $\pm$ 0.1	0.2 $\pm$ 0.1
Chloroflexi	1.3 $\pm$ 0.5	6.4 $\pm$ 4.8	0.4 $\pm$ 0.3	1.7 $\pm$ 1.7	2.3 $\pm$ 2.6	5.0 $\pm$ 3.0	2.5 $\pm$ 2.3	8.8 $\pm$ 2.8
Cyanobacteria	n.d.	n.d.	n.d.	0.1 $\pm$ 0.1	0.4 $\pm$ 0.2	0.2 $\pm$ 0.2	0.5 $\pm$ 0.3	0.1 $\pm$ 0.1
Elusimicrobia	n.d.	n.d.	n.d.	0.2 $\pm$ 0.3	0.0 $\pm$ 0.1	0.2 $\pm$ 0.3	0.1 $\pm$ 0.1	0.3 $\pm$ 0.2
Entotheonella	n.d.	0.1 $\pm$ 0.1	0.0 $\pm$ 0.1	0.1 $\pm$ 0.1	n.d.	0.1 $\pm$ 0.1	n.d.	0.1 $\pm$ 0.0
FCPS706	n.d.	0.1 $\pm$ 0.1	n.d.	n.d.	n.d.	n.d.	n.d.	0.1 $\pm$ 0.0
Firmicutes	7.0 $\pm$ 7.8	4.2 $\pm$ 3.4	1.2 $\pm$ 1.3	1.7 $\pm$ 1.6	1.0 $\pm$ 0.6	1.7 $\pm$ 0.3	1.4 $\pm$ 0.8	1.8 $\pm$ 0.3
GAL15	0.1 $\pm$ 0.1	0.3 $\pm$ 0.3	n.d.	0.1 $\pm$ 0.1	0.1 $\pm$ 0.1	0.1 $\pm$ 0.1	0.1 $\pm$ 0.1	0.1 $\pm$ 0.1
Gemmatimonadetes	0.2 $\pm$ 0.1	0.1 $\pm$ 0.1	0.2 $\pm$ 0.1	0.3 $\pm$ 0.3	0.9 $\pm$ 0.3	0.8 $\pm$ 0.3	1.3 $\pm$ 0.8	0.7 $\pm$ 0.3
GN02	n.d.	n.d.	n.d.	n.d.	n.d.	0.0 $\pm$ 0.1	n.d.	n.d.
NC10	n.d.	0.1 $\pm$ 0.1	n.d.	n.d.	0.0 $\pm$ 0.1	0.2 $\pm$ 0.1	n.d.	0.5 $\pm$ 0.4
Nitrospirae	n.d.	0.2 $\pm$ 0.3	0.0 $\pm$ 0.1	0.2 $\pm$ 0.2	0.1 $\pm$ 0.1	0.3 $\pm$ 0.2	0.1 $\pm$ 0.1	0.7 $\pm$ 0.2
OP10	0.1 $\pm$ 0.1	0.1 $\pm$ 0.0	n.d.	0.2 $\pm$ 0.2	0.0 $\pm$ 0.1	0.4 $\pm$ 0.2	0.1 $\pm$ 0.1	0.2 $\pm$ 0.1
OP11	n.d.	n.d.	n.d.	n.d.	0.0 $\pm$ 0.1	0.3 $\pm$ 0.3	0.1 $\pm$ 0.1	0.6 $\pm$ 0.3
Planctomycetes	0.8 $\pm$ 0.3	1.4 $\pm$ 1.1	1.2 $\pm$ 1.0	1.2 $\pm$ 0.6	4.0 $\pm$ 0.7	2.8 $\pm$ 0.6	4.7 $\pm$ 0.4	4.8 $\pm$ 0.8
<u>Alphaproteobacteria</u>	<b>13.2 <math>\pm</math>7.5</b>	<b>12.4 <math>\pm</math>8.3</b>	<b>29.8 <math>\pm</math>11.1</b>	<b>22.9 <math>\pm</math>11.0</b>	<b>40.2 <math>\pm</math>16.8</b>	<b>26.0 <math>\pm</math>9.5</b>	<b>34.5 <math>\pm</math>4.0</b>	<b>26.1 <math>\pm</math>3.9</b>
<u>Betaproteobacteria</u>	<b>38.4 <math>\pm</math>6.2</b>	<b>36.6 <math>\pm</math>19.4</b>	<b>28.1 <math>\pm</math>6.7</b>	<b>36.9 <math>\pm</math>13.9</b>	<b>13.7 <math>\pm</math>8.5</b>	<b>21.0 <math>\pm</math>7.6</b>	7.5 $\pm$ 3.2	<b>10.7 <math>\pm</math>1.9</b>

Table S5, cont'd	T1		T2		T3		T4	
	no lignin	lignin	no lignin	lignin	no lignin	lignin	no lignin	lignin
<u>Gammaproteobacteria</u>	18.3 ±18.6	14.2 ±11.4	8.4 ±6.6	5.5 ±3.0	4.6 ±1.1	3.2 ±1.6	6.4 ±2.1	4.1 ±1.4
Deltaproteobacteria	0.7 ±0.6	1.1 ±0.8	1.7 ±1.7	2.6 ±1.6	2.0 ±1.1	5.8 ±3.2	2.4 ±1.7	5.1 ±2.1
SC3	n.d.	n.d.	n.d.	0.1 ±0.1	n.d.	n.d.	n.d.	0.1 ±0.1
SM2F11	n.d.	n.d.	n.d.	n.d.	n.d.	0.1 ±0.1	0.0 ±0.1	0.1 ±0.0
SPAM	0.1 ±0.1	0.2 ±0.1	n.d.	0.1 ±0.2	0.2 ±0.2	0.4 ±0.3	0.1 ±0.0	0.8 ±0.2
Spirochaetes	n.d.	n.d.	0.1 ±0.1	0.1 ±0.1	0.1 ±0.1	0.1 ±0.0	0.1 ±0.0	0.1 ±0.1
SR1	n.d.	n.d.	n.d.	0.0 ±0.1	n.d.	n.d.	n.d.	n.d.
Thermi	0.2 ±0.3	0.1 ±0.1	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
TM6	0.1 ±0.1	0.1 ±0.1	1.0 ±2.0	0.3 ±0.2	1.4 ±1.1	0.4 ±0.3	2.0 ±1.9	0.6 ±0.3
TM7	n.d.	0.1 ±0.1	0.1 ±0.1	0.3 ±0.1	0.1 ±0.0	0.1 ±0.1	0.1 ±0.1	0.1 ±0.1
Verrucomicrobia	0.6 ±0.4	0.6 ±0.4	0.6 ±0.3	1.0 ±1.0	0.8 ±0.6	1.7 ±0.8	1.7 ±0.6	2.7 ±0.2
WCHB1-27	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	0.1 ±0.0
WPS-2	0.1 ±0.1	0.1 ±0.0	n.d.	n.d.	n.d.	0.1 ±0.0	n.d.	0.1 ±0.1
WS3	n.d.	n.d.	n.d.	n.d.	0.0 ±0.1	0.1 ±0.1	n.d.	0.1 ±0.1
ZB2	n.d.	n.d.	n.d.	n.d.	0.0 ±0.1	0.2 ±0.1	0.4 ±0.4	0.2 ±0.3
Fungi	5.8 ±10.4	0.7 ±0.4	3.0 ±2.4	3.7 ±4.0	5.3 ±4.3	1.6 ±1.2	3.6 ±0.9	1.4 ±0.9
Alveolata	0.3 ±0.2	0.6 ±0.1	3.4 ±3.9	0.6 ±0.8	0.4 ±0.2	2.5 ±3.8	1.3 ±0.7	0.3 ±0.2
Cercozoa	0.3 ±0.1	0.5 ±0.7	2.8 ±2.8	3.0 ±2.9	1.3 ±0.4	2.5 ±2.9	2.2 ±0.8	0.8 ±0.8
Euglenozoa	0.1 ±0.1	1.2 ±2.0	0.2 ±0.2	0.5 ±0.9	0.2 ±0.1	0.1 ±0.1	0.7 ±1.2	0.1 ±0.2
Heterolobosea	n.d.	n.d.	0.7 ±1.3	0.3 ±0.3	0.3 ±0.2	0.0 ±0.1	0.3 ±0.3	0.1 ±0.1
Eukaryota (others)	0.6 ±0.6	0.4 ±0.4	1.0 ±0.7	1.9 ±0.9	1.8 ±0.6	1.2 ±0.9	3.4 ±1.9	1.1 ±0.5
Chloroplasts	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	0.0 ±0.1	n.d.
Unclassified	0.7 ±0.4	0.4 ±0.4	4.6 ±3.2	1.0 ±0.5	1.1 ±0.5	0.6 ±0.8	0.6 ±0.3	0.4 ±0.1