

Figure S1. Alpha diversity indices (Observed, Shannon, InvSimpson) for (a) prokaryotic, based on 16S rRNA gene libraries, and (b) fungal data, based on ITS2 fragment libraries. Days of the experiment are on the X-axis. Significant differences were assessed by ANOVA: (**) p-value ≤ 0.01 ; (***) p-value ≤ 0.001 ; (****) p-value ≤ 0.0001

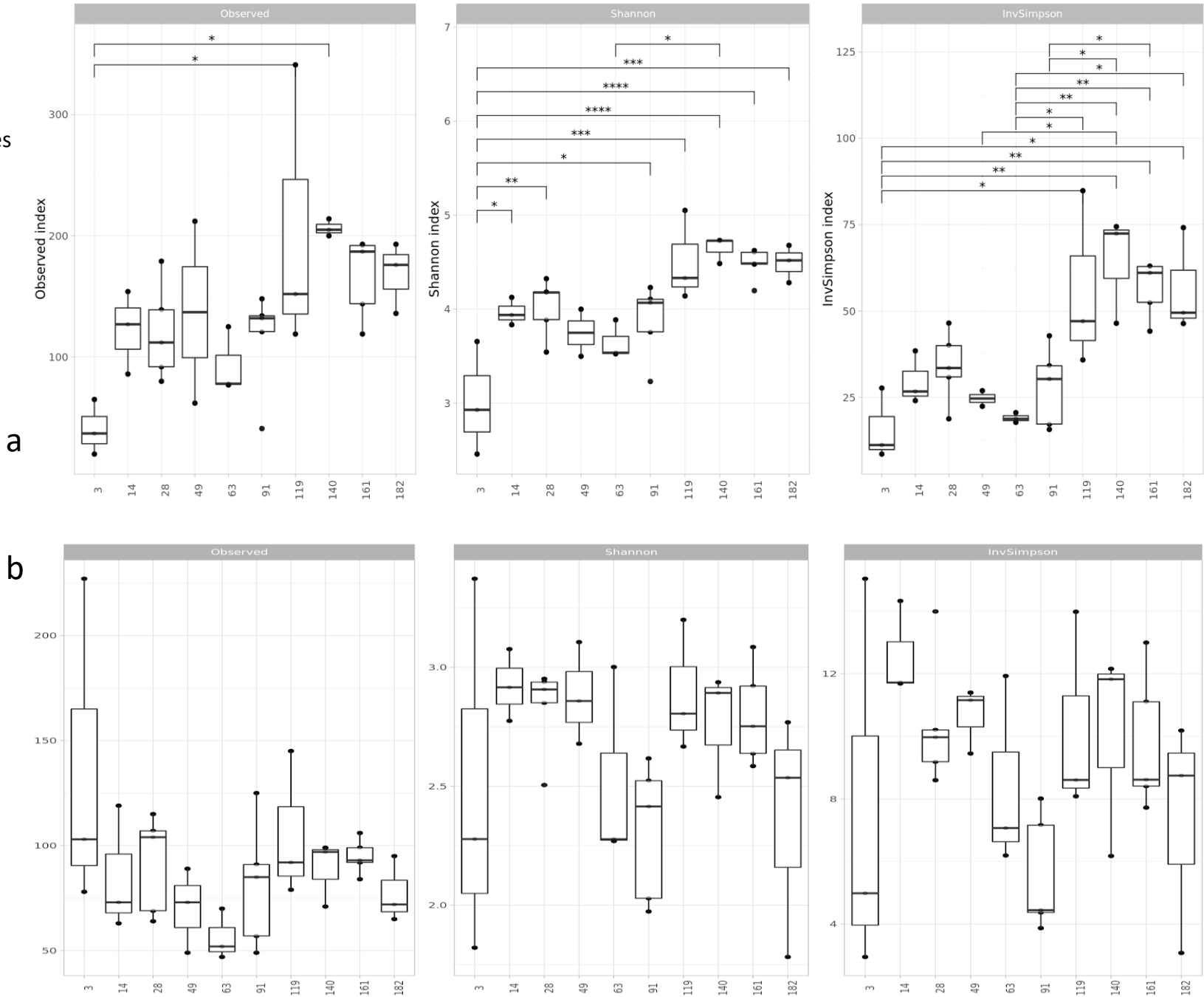


Figure S2. Z-scaled values of Alpha diversity indices (Observed, Shannon, InvSimpson) and SR data. On the X-axis are bag ID: 1 – day 3, 3 – day 14, 5 – day 28, 7 – day 49, 8 – day 63, 10 – day 91, 12 – day 119, 13 – day 140, 14 – day 161, 15 – day 181

bag_id	day	week
1	3	0,428571
2	7	1
3	14	2
4	21	3
5	28	4
6	35	5
7	49	7
8	63	9
9	77	11
10	91	13
11	105	15
12	119	17
13	140	20
14	161	23
15	182	26

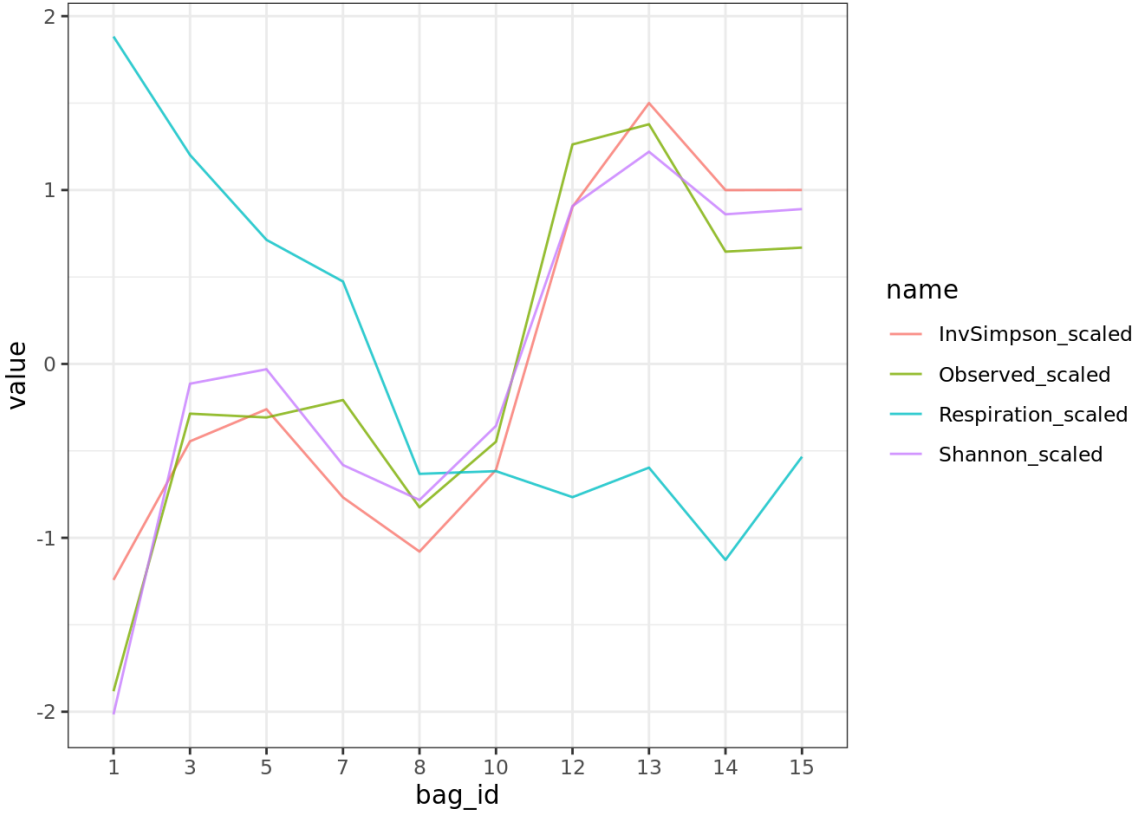


Figure S3. Stepwise comparison of beta diversity between the first sample with the others On the X-axis are bag ID: D03 – day 14, D05 – day 28, D07 – day 49, D08 – day 63, D10 – day 91, D12 – day 119, D14 – day 140, 9 – day 161, D15 – day 181

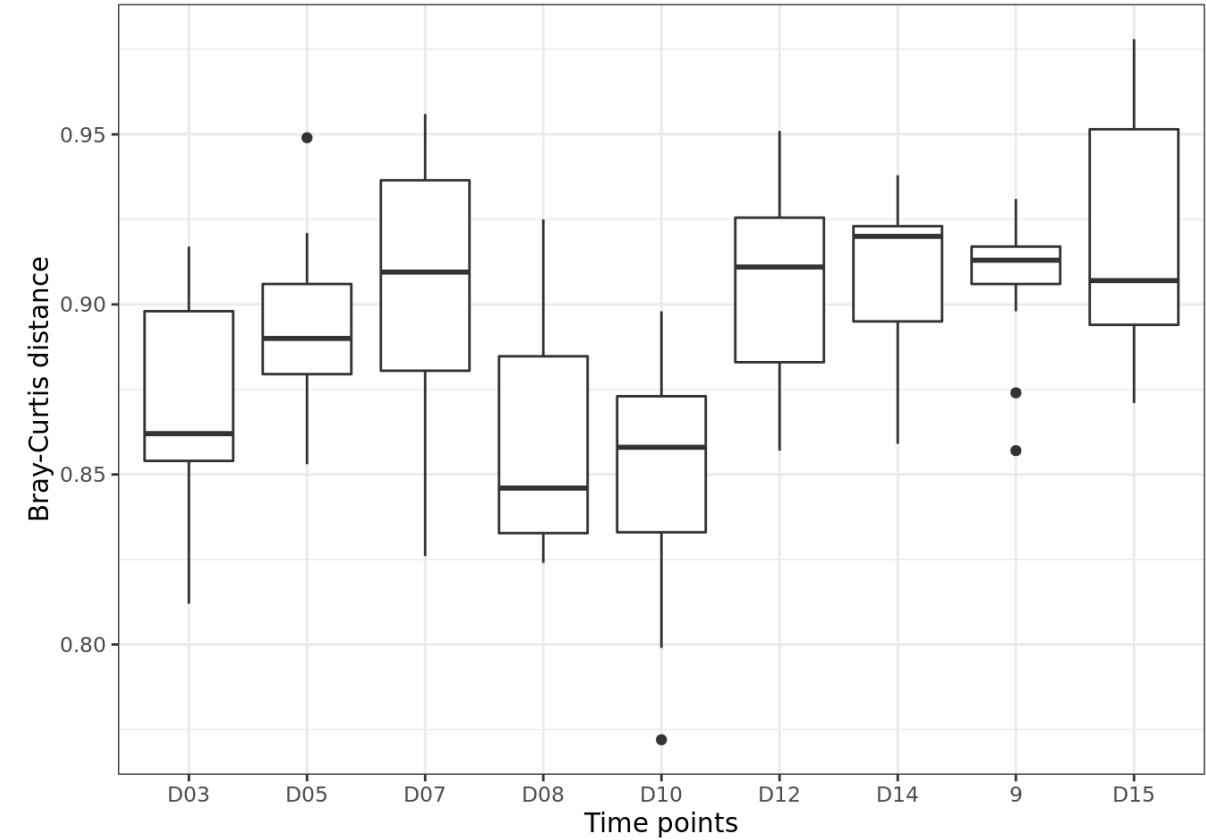


Figure S4. Heatmap of the most abundant phylotypes on the genus level in the microbial straw decomposing community from ten sampling points, based on (a) prokaryotic and (b) fungal amplicon sequencing data. The relative abundance is given in % of the read count of each sampling day, orange for maximal, and blue for minimal values.

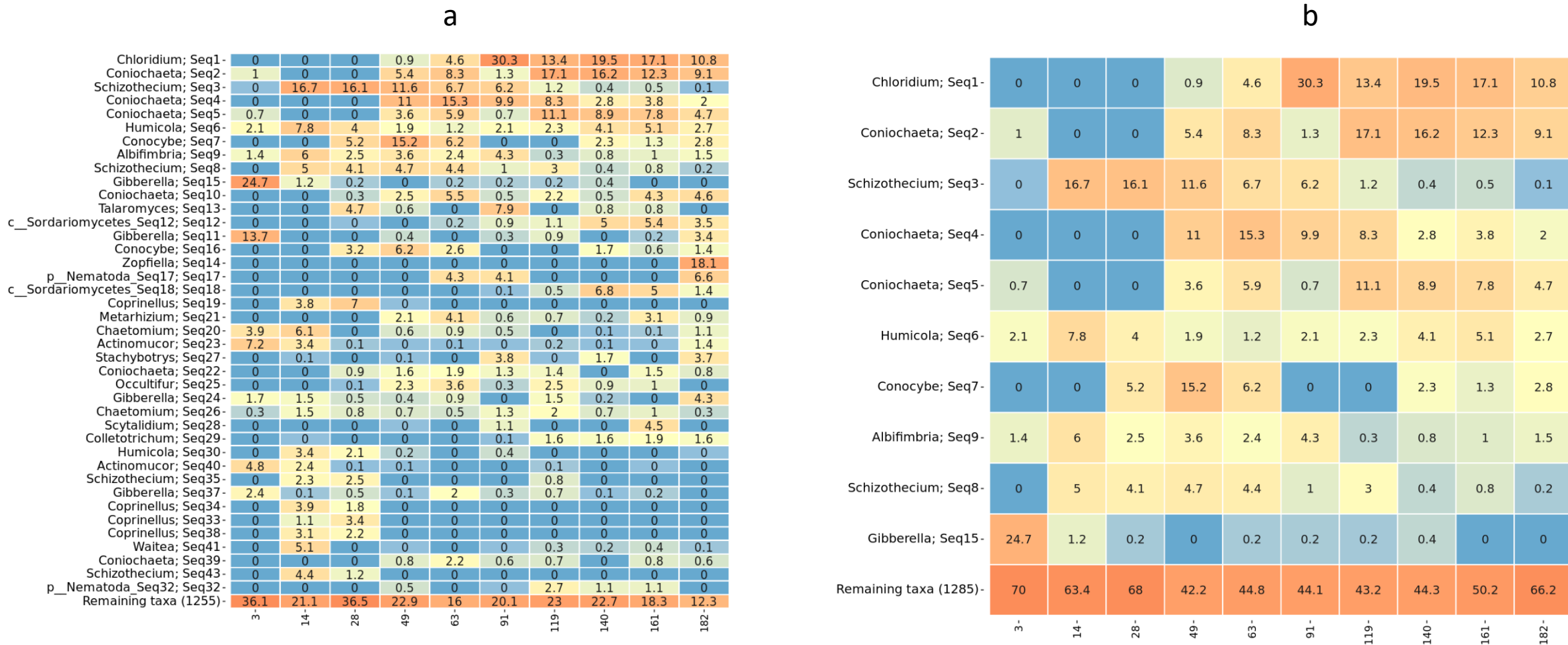


Figure S5. Dispersion of outlier phylotypes between days. D01 – day 3, D03 – day 14, D05 – day 28, D07 – day 49, D08 – day 63, D10 – day 91, D12 – day 119, D13 – day 140, D014 – day 161, D15 – day 181

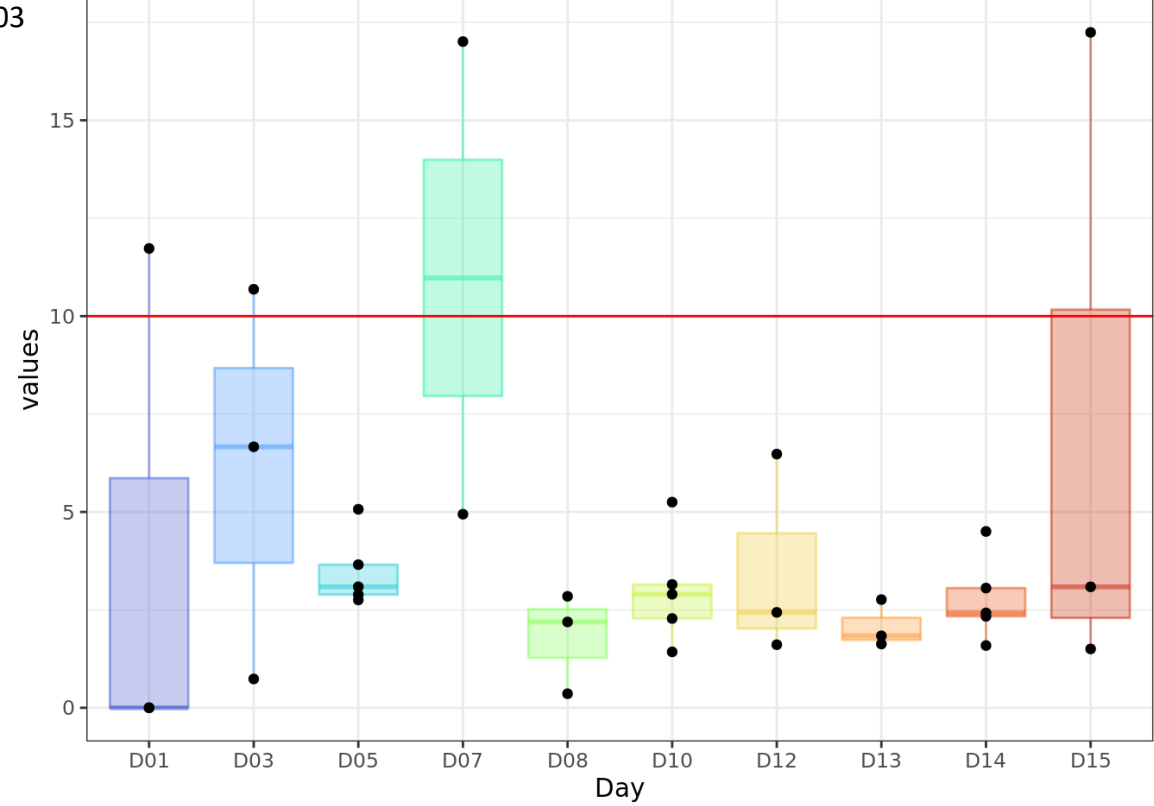


Figure S6. Heatmap of the outlier phylotypes on the genus level in the microbial straw decomposing community from ten sampling points, based on prokaryotic amplicon sequencing data. The relative abundance is given in % of the read count of each sampling day, orange for maximal, and blue for minimal values.

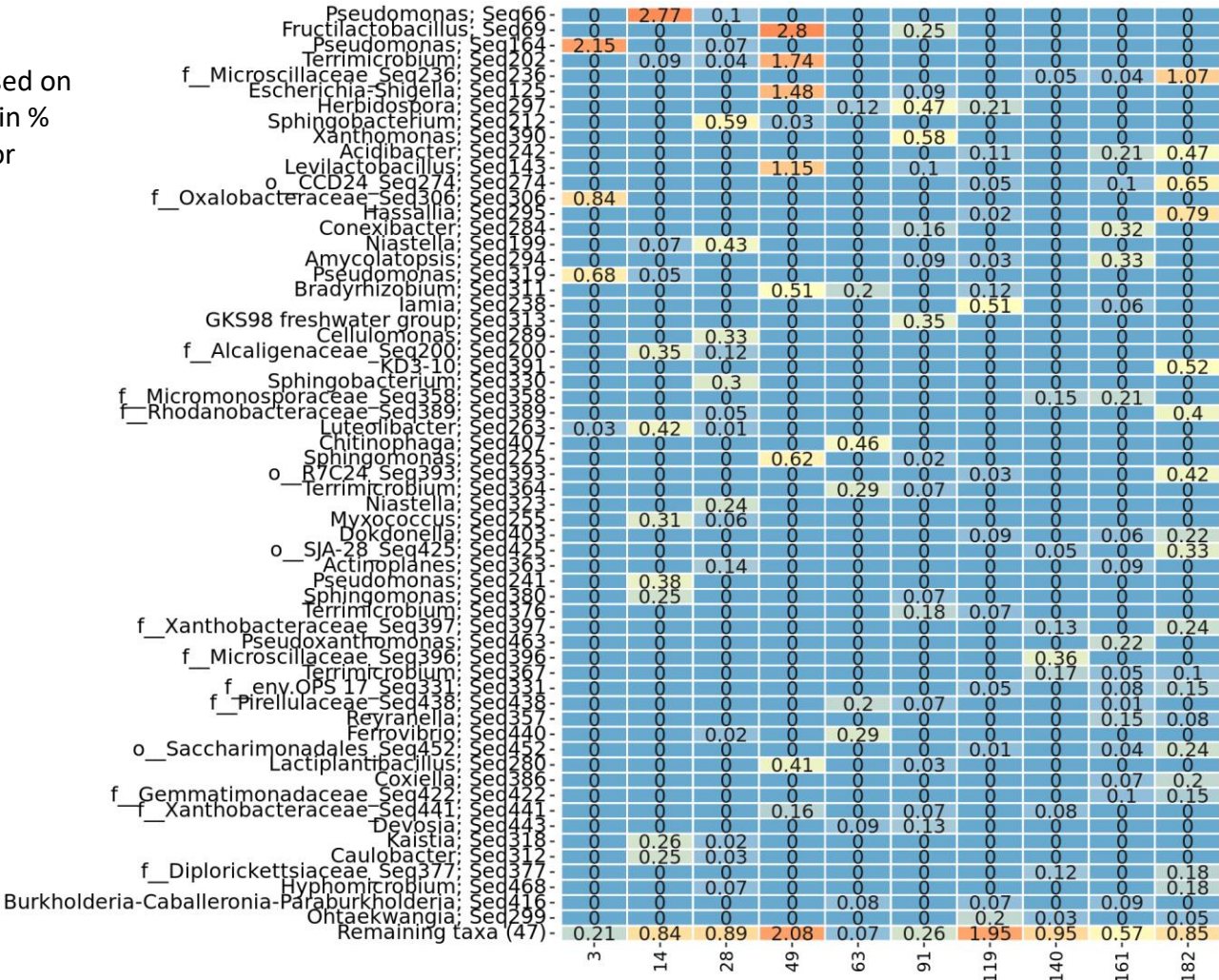


Figure S7b. Heatmap of the middle group (cyan) phylotypes on the genus level in the microbial straw decomposing community from ten sampling points, based on prokaryotic amplicon sequencing data. The relative abundance is given in % of the read count of each sampling day, orange for maximal, and blue for minimal values.

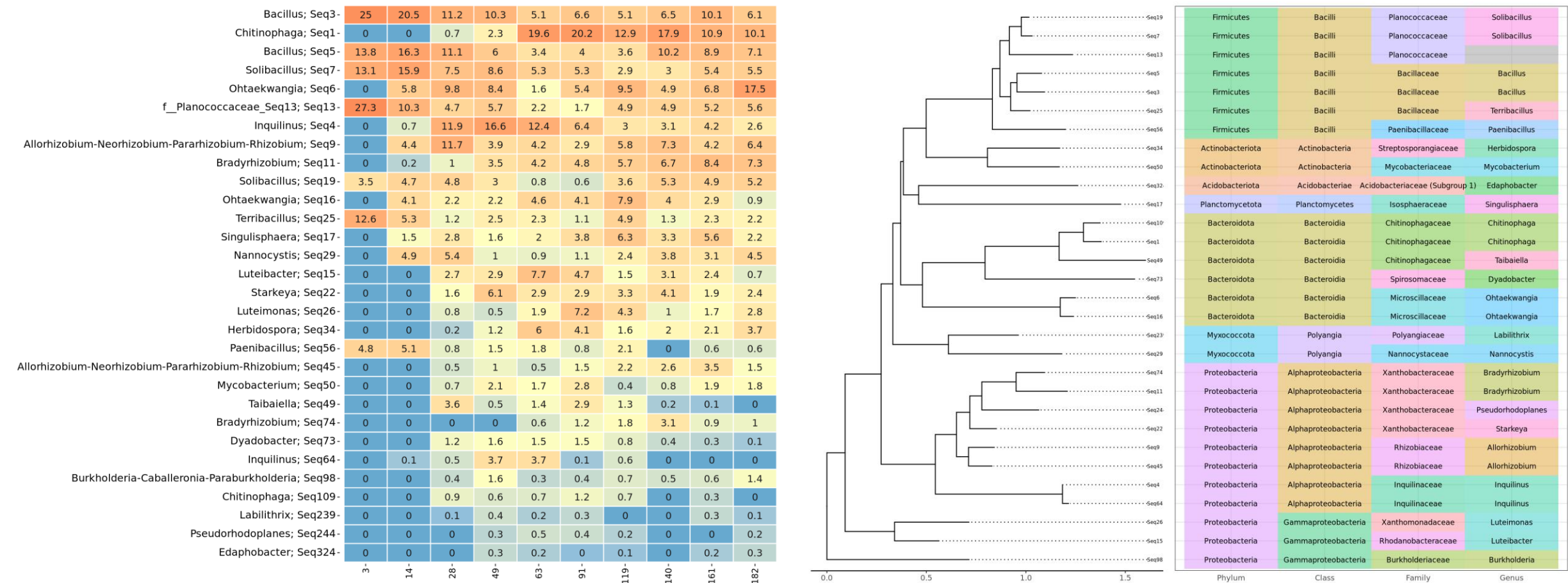


Figure S7c. Heatmap of the late group (blue) phylotypes on the genus level in the microbial straw decomposing community from ten sampling points, based on prokaryotic amplicon sequencing data. The relative abundance is given in % of the read count of each sampling day, orange for maximal, and blue for minimal values.

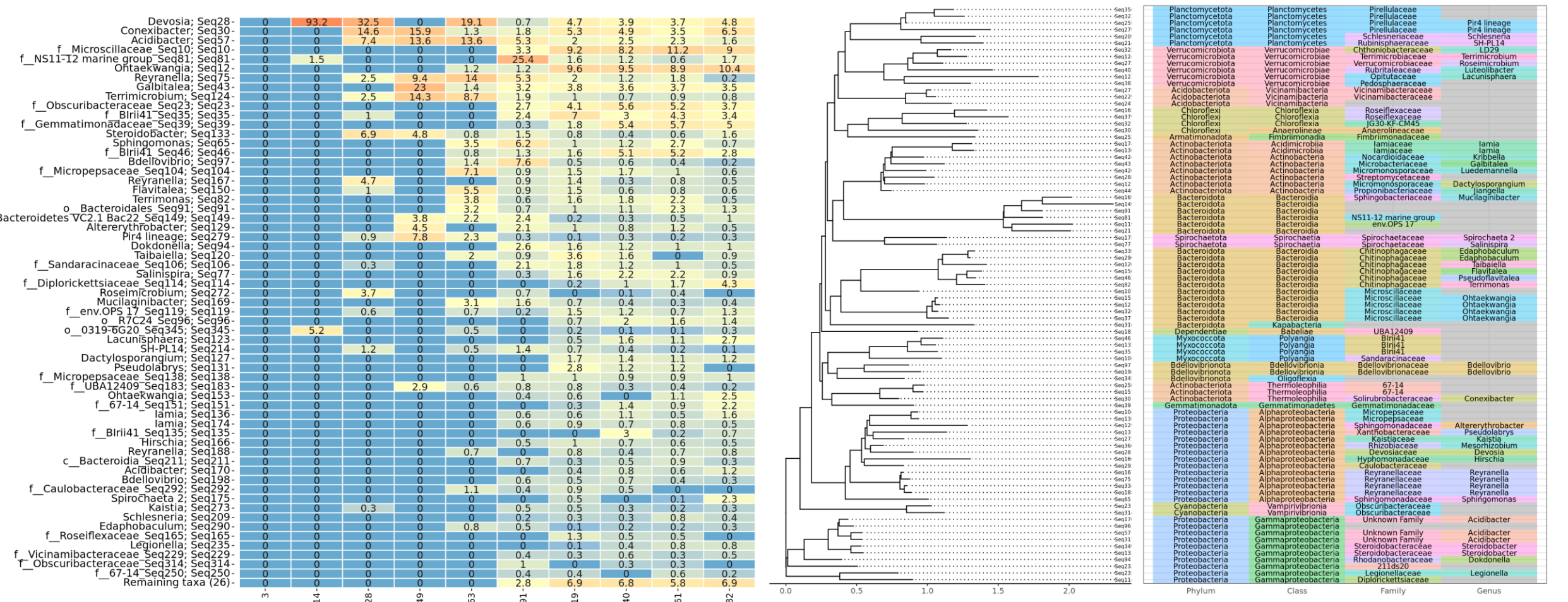


Figure S7d. Heatmap of the late group (green) phylotypes on the genus level in the microbial straw decomposing community from ten sampling points, based on prokaryotic amplicon sequencing data. The relative abundance is given in % of the read count of each sampling day, orange for maximal, and blue for minimal values.

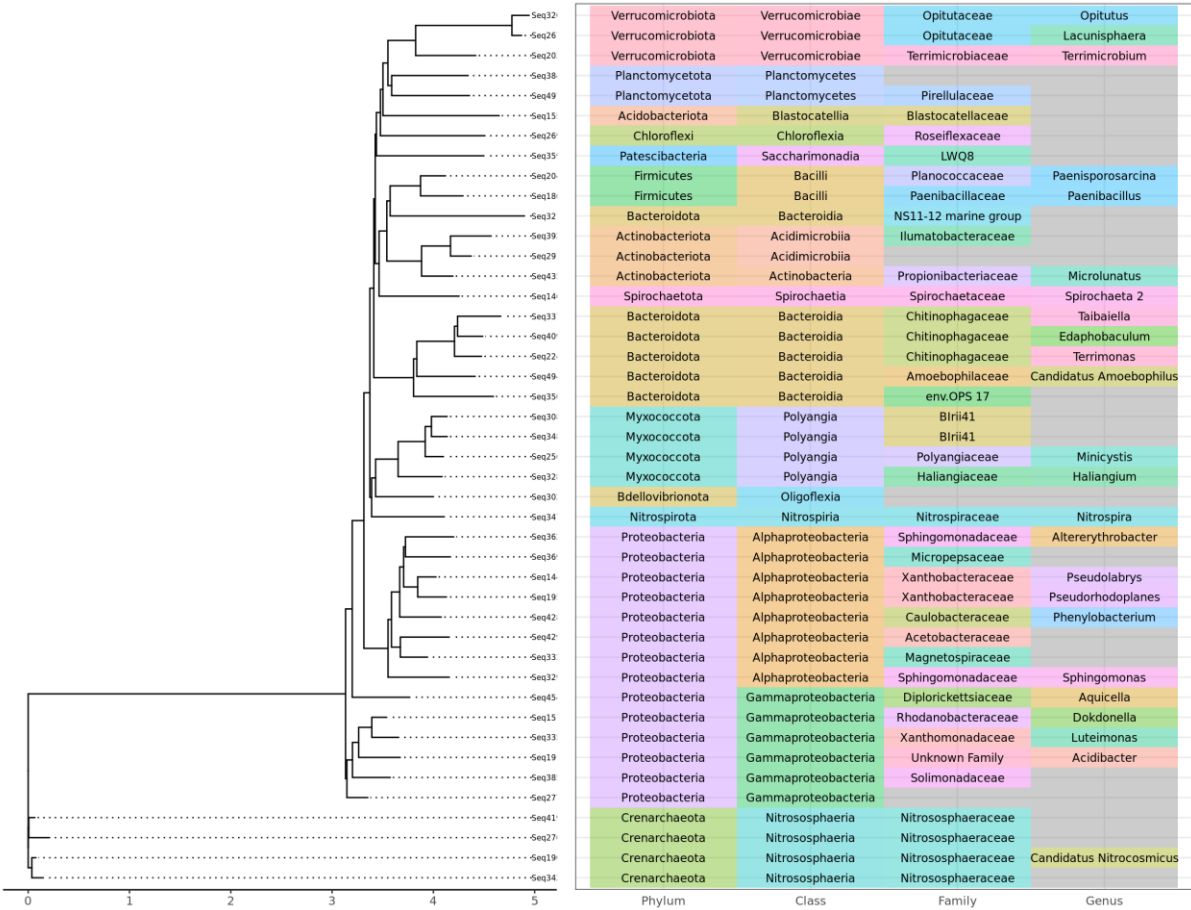
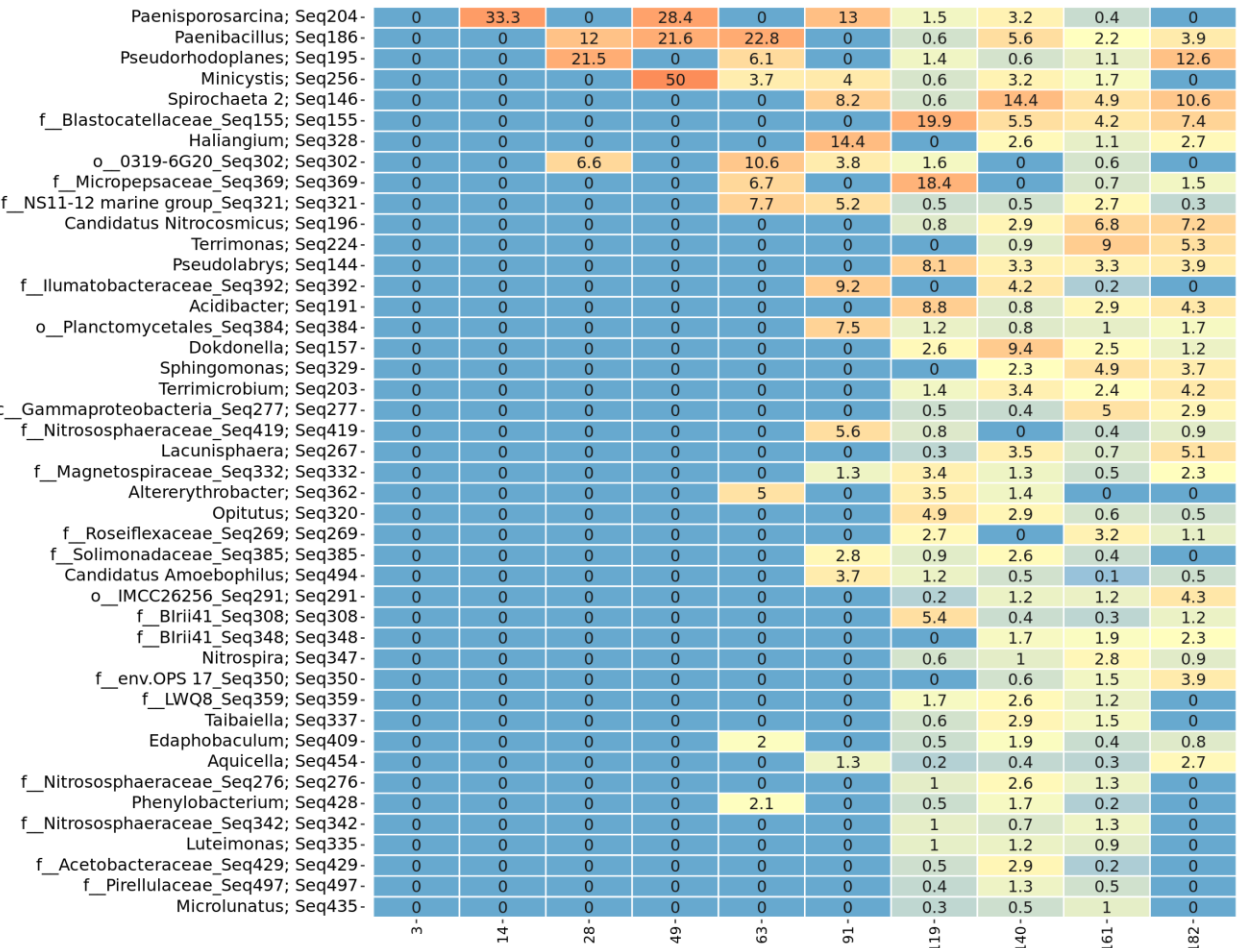


Figure S7e. Heatmap of the late group (plum) phylotypes on the genus level in the microbial straw decomposing community from ten sampling points, based on prokaryotic amplicon sequencing data. The relative abundance is given in % of the read count of each sampling day, orange for maximal, and blue for minimal values.

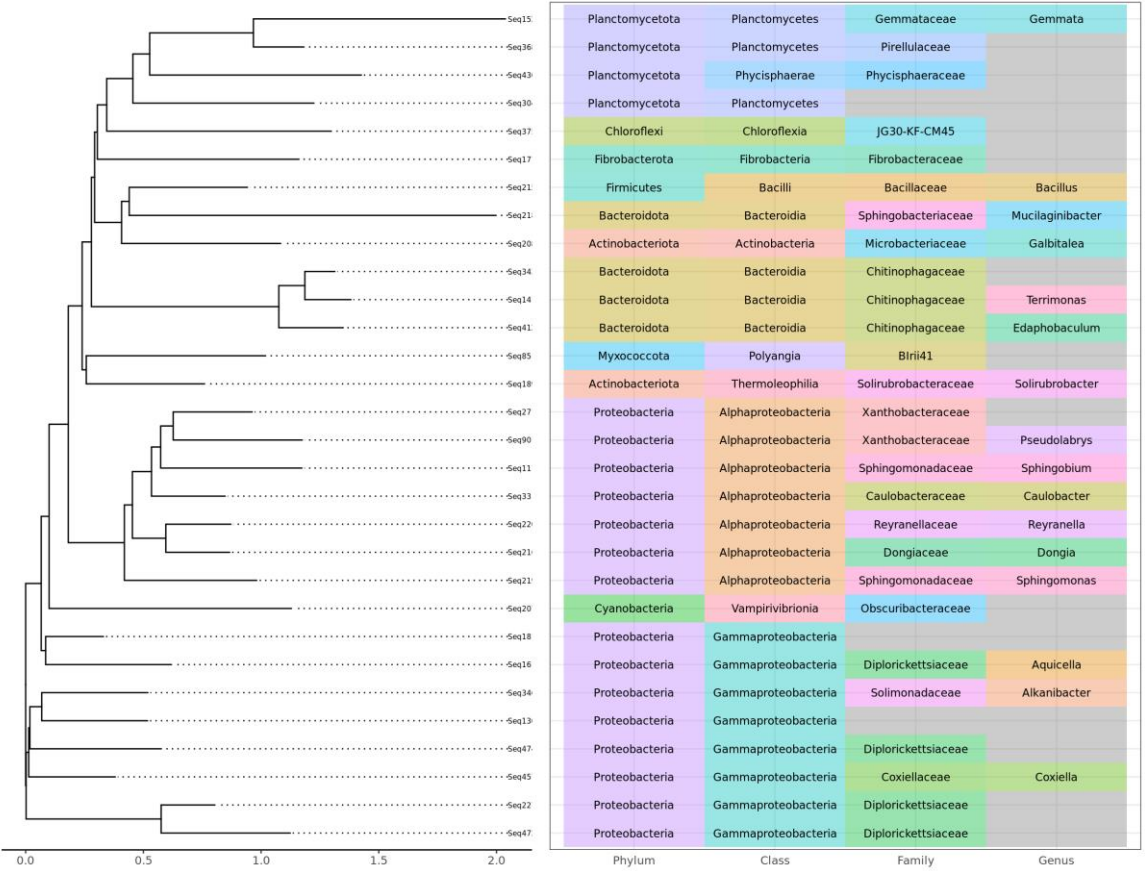
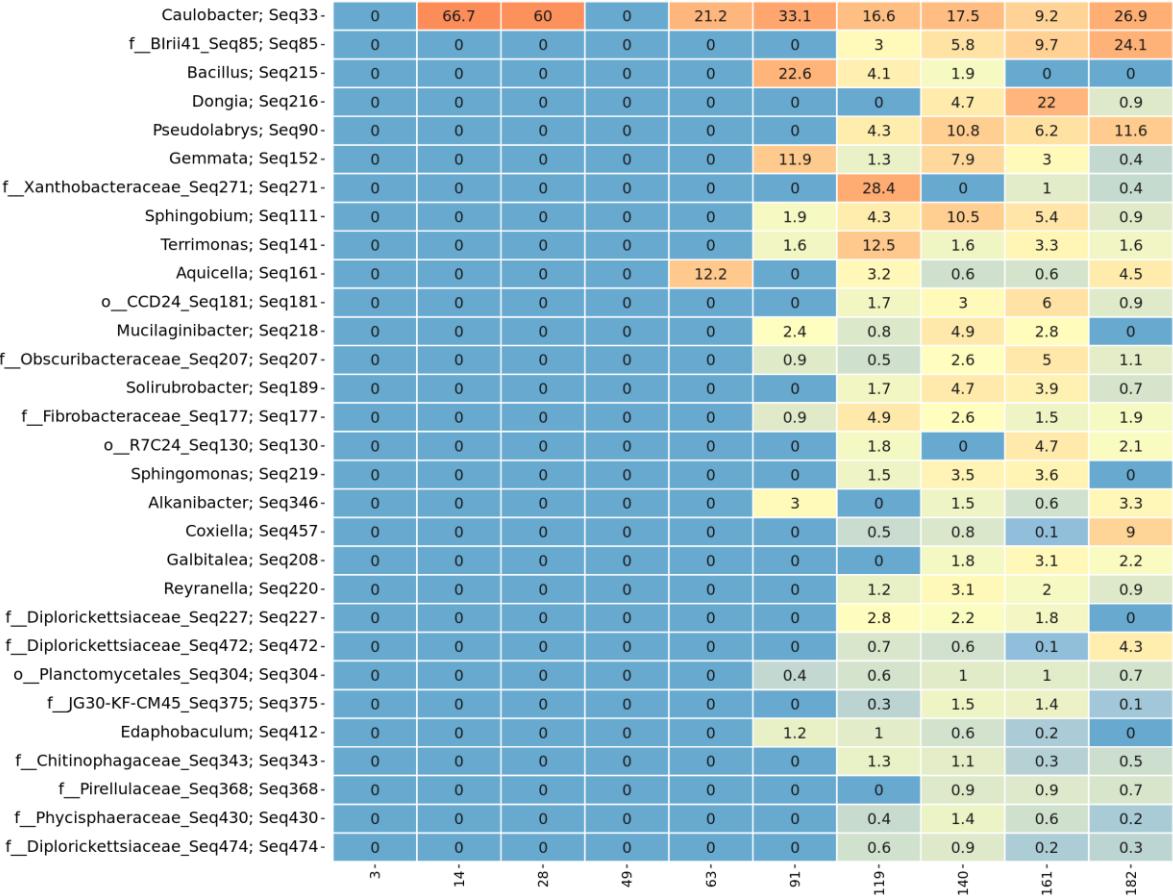


Figure S8a. Heatmap of the early group (salmon) phylotypes on the genus level in the microbial straw decomposing community from ten sampling points, based on eukaryotic amplicon sequencing data. The relative abundance is given in % of the read count of each sampling day, orange for maximal, and blue for minimal values.

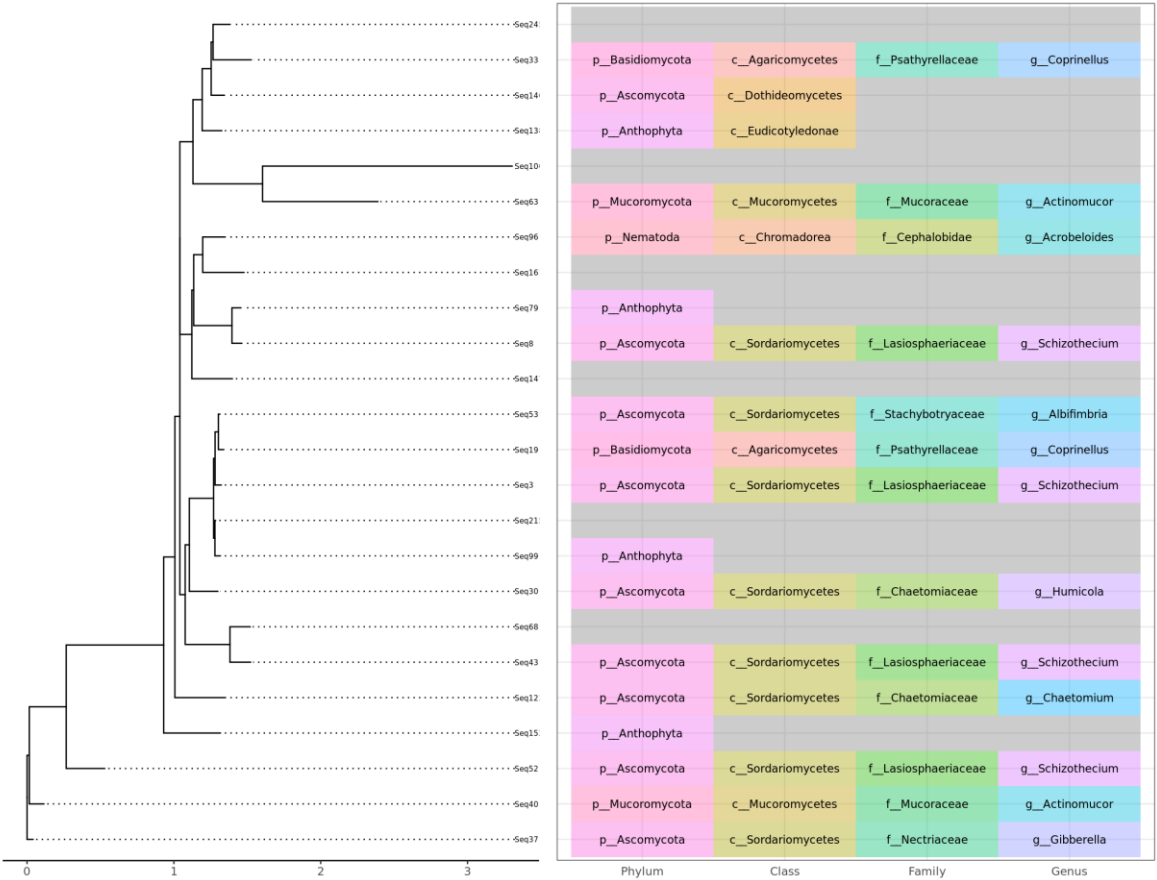
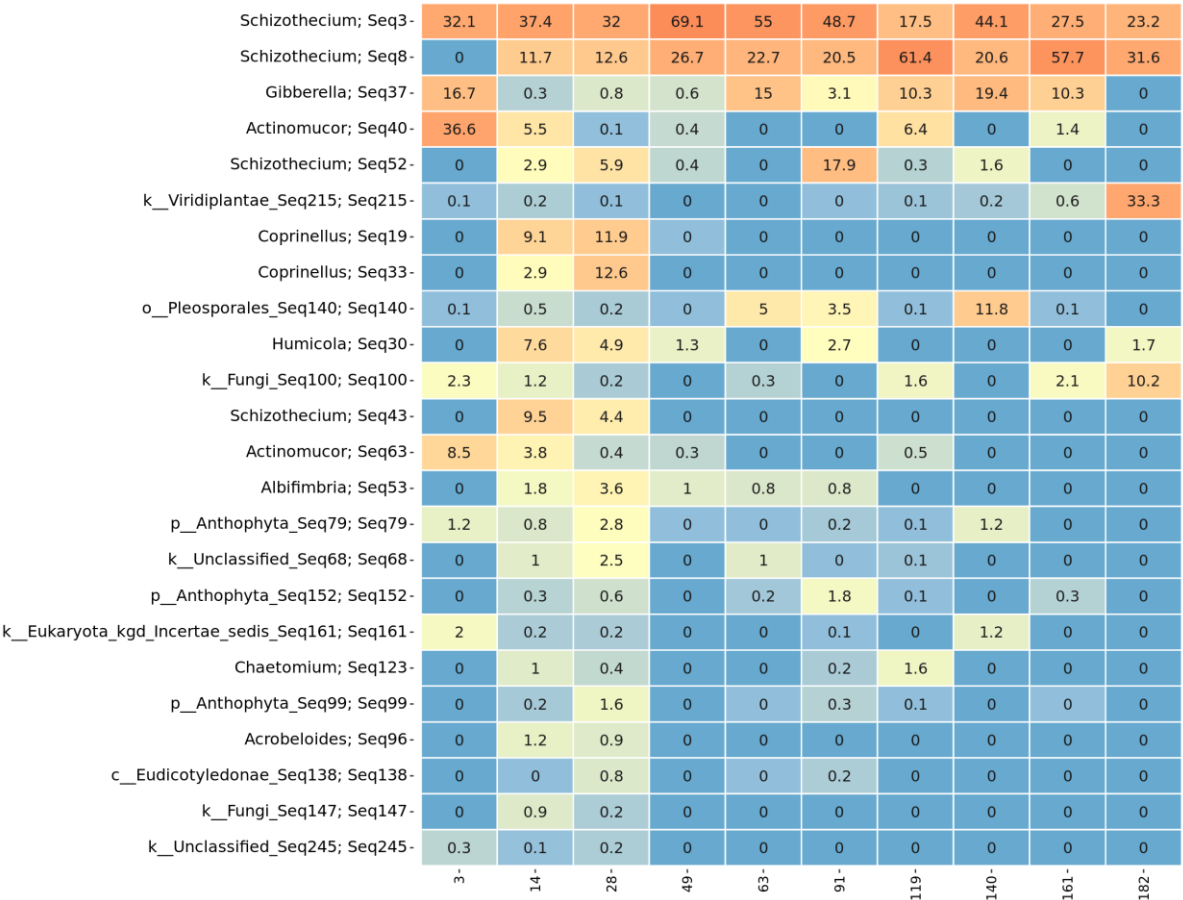


Figure S8c. Heatmap of the universal group (green) phylotypes on the genus level in the microbial straw decomposing community from ten sampling points, based on eukaryotic amplicon sequencing data. The relative abundance is given in % of the read count of each sampling day, orange for maximal, and blue for minimal values.

