

Supplementary Table 2: Overview of the taxonomic classification of 16S rRNA and 16S rRNA gene sequences derived by Sanger and 454 amplicon sequencing. Reads were analyzed with the RDP Classifier (Wang *et al.*, 2007) (<http://rdp.cme.msu.edu/classifier/classifier.jsp>). Numbers depict relative sequence abundances (%). Sanger 1 and 2 are two biological replicates, the same applies to 454 amplicon 1 and 2.

| Phyla | DNA samples | | | | | | | | cDNA samples | | | | | | | |
|----------------------------|--------------------|--------------------|---------|-------|-----------------|-----------------|---------|-------|--------------------|--------------------|---------|-------|-----------------|-----------------|---------|-------|
| | Sanger replicate 1 | Sanger replicate 2 | average | STDEV | 454 replicate 1 | 454 replicate 2 | average | STDEV | Sanger replicate 1 | Sanger replicate 2 | average | STDEV | 454 replicate 1 | 454 replicate 2 | average | STDEV |
| Actinobacteria | 0.00 | 0.00 | 0.00 | 0.00 | 0.18 | 0.25 | 0.21 | 0.05 | 0.65 | 0.60 | 0.63 | 0.04 | 0.34 | 0.26 | 0.30 | 0.06 |
| Armatimonadetes | 0.00 | 0.00 | 0.00 | 0.00 | 0.08 | 0.01 | 0.04 | 0.05 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 |
| Bacteroidetes | 32.81 | 17.42 | 25.12 | 10.88 | 10.53 | 10.97 | 10.75 | 0.32 | 6.54 | 8.43 | 7.48 | 1.34 | 2.94 | 3.51 | 3.22 | 0.40 |
| Chlorobi | 0.00 | 0.00 | 0.00 | 0.00 | 0.10 | 0.05 | 0.08 | 0.04 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.02 | 0.01 | 0.01 |
| Chloroflexi | 11.72 | 6.06 | 8.89 | 4.00 | 28.10 | 13.33 | 20.72 | 10.45 | 8.50 | 6.02 | 7.26 | 1.75 | 2.04 | 2.66 | 2.35 | 0.44 |
| Cyanobacteria | 4.69 | 9.47 | 7.08 | 3.38 | 13.18 | 11.91 | 12.55 | 0.90 | 56.86 | 62.05 | 59.46 | 3.67 | 77.13 | 69.76 | 73.45 | 5.22 |
| Deinococcus-Thermus | 0.78 | 2.27 | 1.53 | 1.05 | 0.26 | 0.53 | 0.40 | 0.19 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.01 | 0.01 | 0.00 |
| Firmicutes | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | 0.01 | 0.02 | 0.02 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.02 | 0.01 | 0.02 |
| Lentisphaerae | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | 0.00 | 0.02 | 0.02 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 |
| Planctomycetes | 1.95 | 4.17 | 3.06 | 1.57 | 2.38 | 3.51 | 2.95 | 0.80 | 1.31 | 0.60 | 0.95 | 0.50 | 0.32 | 0.61 | 0.46 | 0.20 |
| Proteobacteria | 30.08 | 36.36 | 33.22 | 4.44 | 20.18 | 34.20 | 27.19 | 9.91 | 19.61 | 15.66 | 17.64 | 2.79 | 7.17 | 8.40 | 7.78 | 0.87 |
| Cand. Division SR1 | 0.78 | 0.00 | 0.39 | 0.55 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Spirochaetes | 0.39 | 3.03 | 1.71 | 1.87 | 1.92 | 2.14 | 2.03 | 0.15 | 0.65 | 0.00 | 0.33 | 0.46 | 0.08 | 0.11 | 0.10 | 0.02 |
| TM7 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Verrucomicrobia | 0.78 | 9.47 | 5.13 | 6.14 | 1.82 | 2.49 | 2.16 | 0.48 | 0.65 | 1.81 | 1.23 | 0.82 | 0.38 | 0.32 | 0.35 | 0.04 |
| Euryarchaeota | 0.00 | 0.00 | 0.00 | 0.00 | 0.04 | 0.02 | 0.03 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.01 | 0.01 | 0.00 |
| not assigned | 16.02 | 11.74 | 13.88 | 3.02 | 21.17 | 20.58 | 20.88 | 0.41 | 5.23 | 4.82 | 5.02 | 0.29 | 9.56 | 14.30 | 11.93 | 3.35 |