Supplementary:

The impact of immigration on microbial community composition in full-scale anaerobic digesters

Rasmus H. Kirkegaard, Simon J. McIlroy, Jannie M. Kristensen, Marta Nierychlo, Søren M. Karst, Morten S. Dueholm, Mads Albertsen and Per H. Nielsen.

Centre for Microbial Communities, Department of Chemistry and Bioscience, Aalborg University, Fredrik Bajers Vej 7H, DK-9220 Aalborg, Denmark.

*Correspondence to phn@bio.aau.dk

| | Mesophilic | | | | | | | | | | | | | | Т | THP | | | | |
|---|------------|-------------|-------------|---------------|----------|-------------|--------|-------------|----------|---------------|------------|----------|---------|------|---------------|---------------|--------------|-----------|-------------|-----------|
| Euryarchaeota; Methanosaeta; OTU_1 | 25.6 | 31.4 | 32.6 | 33.4 | 31.9 | 33.3 | 31.4 | 27.7 | 30.3 | 29.4 | 32.1 | 31.3 | 30.2 | 0.6 | 0.9 | 0.3 | 0.3 | 0.4 | 38.6 | 38.2 |
| Euryarchaeota; Methanothermobacter; OTU_2 - | 0 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 43.2 | 46.7 | 37.3 | 42 | 47.9 | 0.5 | 0 |
| Euryarchaeota; Methanosaeta; OTU_705 - | 11.7 | 11.6 | 11.4 | 15.1 | 11.9 | 11.7 | 11.8 | 9.3 | 10.6 | 9.2 | 11 | 10.9 | 11.1 | 0.2 | 0.2 | 0.1 | 0.1 | 0.2 | 15.3 | 14.1 |
| Euryarchaeota; Methanosaeta; OTU_498 - | 8.8 | 9.9 | 9.9 | 11.8 | 10.3 | 10.3 | 10.2 | 8.4 | 9.4 | 9 | 9.8 | 9.5 | 9.5 | 0.2 | 0.3 | 0.1 | 0.1 | 0.1 | 12.6 | 12.1 |
| Euryarchaeota; Methanosarcina; OTU_4 - | 0 | 0.1 | 0.1 | 0 | 0.2 | 0.2 | 0.1 | 0 | 0.1 | 0.3 | 0.1 | 0.2 | 0.1 | 19.2 | 17.2 | 16.9 | 24.5 | 9.9 | 0.1 | 1.3 |
| Euryarchaeota; Methanothermobacter; OTU_730 - | 0 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 17.2 | 17.9 | 6 | 15.8 | 19.2 | 0.2 | 0 |
| Euryarchaeota; Methanosaeta; OTU_945 - | 5.5 | 4.8 | 5 | 6.9 | 4.9 | 4.6 | 4.9 | 3.8 | 4.3 | 3.5 | 4.5 | 4.5 | 4.5 | 0.1 | 0.1 | 0.1 | 0 | 0.1 | 6.7 | 5.7 |
| Euryarchaeota; Methanolinea; OTU_3 - | 15 | 4.6 | 0.8 | 0.3 | 0.2 | 0.5 | 0 | 14 | 9.2 | 10 | 2 | 0 | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Euryarchaeota; Methanosaeta; OTU_695 - | 3.4 | 3.8 | 3.8 | 3.8 | 3.6 | 3.8 | 3.7 | 3.2 | 3.9 | 3.9 | 3.8 | 3.6 | 3.8 | 0.1 | 0.1 | 0 | 0 | 0.1 | 4.3 | 4.4 |
| Euryarchaeota; Methanobrevibacter; OTU_5 - | 0.9 | 1.8 | 1.5 | 0.9 | 4.1 | 3.1 | 7.2 | 3.2 | 1.3 | 2 | 1.6 | 4.6 | 3.3 | 1.1 | 2.2 | 1.4 | 0.7 | 2.2 | 0.1 | 0 |
| Euryarchaeota; WCHA1-57; OTU_8 - | 1.4 | 2.4 | 2.6 | 1.6 | 5.7 | 1.8 | 4.2 | 3.8 | 1.1 | 1.6 | 3.5 | 3.7 | 1.6 | 0 | 0 | 0 | 0 | 0 | 0.5 | 1.8 |
| Euryarchaeota; Methanospirillum; OTU_6 - | - 4 | 4.1 | 2 | 3.1 | 1.1 | 2.6 | 0.2 | 2.1 | 6.1 | 3.5 | 2.6 | 0.3 | 3.8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Euryarchaeota; Methanothermobacter; OTU_552 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2.3 | 3.3 | 19.5 | 4.7 | 2.5 | 0 | 0 |
| Euryarchaeota; Methanosaeta; OTU_868 - | 1.6 | 2 | 2 | 2.1 | 2.1 | 2.1 | 2.1 | 1.7 | 1.9 | 2 | 2 | 2 | 2 | 0.1 | 0 | 0 | 0 | 0 | 2.5 | 2.4 |
| Euryarchaeota; Methanosaeta; OTU_527 - | 1.7 | 2 | 1.9 | 2.3 | 2 | 2.1 | 2 | 1.8 | 1.9 | 1.9 | 2 | 2 | 1.9 | 0 | 0.1 | 0 | 0 | 0 | 2.5 | 2.4 |
| Euryarchaeota; Methanolinea; OTU_622 - | 4.9 | 3.6 | 0.9 | 0.5 | 0.1 | 0.8 | 0 | 3.9 | 4.4 | 3.4 | 3.3 | 0 | 3.9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Euryarchaeota; Methanospirillum; OTU_98 - | 0.1 | 0.1 | 3.4 | 0.7 | 1.9 | 0.6 | 5.7 | 0.4 | 0.3 | 0.2 | 1.4 | 9.7 | 0.4 | 0 | 0 | 0 | 0 | 0 | 0 | 0.2 |
| Woesearchaeota (DHVEG-6); OTU_7; OTU_7 - | 1.9 | 2.6 | 2 | 0 | 1.8 | 2.9 | 0.6 | 2.3 | 2.1 | 4.8 | 2.7 | 0.2 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Euryarchaeota; Methanosarcina; OTU_746 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 4.9 | 4.3 | 4.1 | 7.3 | 2.9 | 0 | 0.2 |
| Euryarchaeota; Methanolinea; OTU_297 · | 4 | 3 | 0.9 | 0.7 | 0 | 0.6 | 0 | 2.7 | 3.2 | 2.5 | 2.8 | O | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | AVEDOERE - | DAMHUSAAEN- | EBY_MOELLE- | ESBJERG_WEST- | FORNAES- | HJOERRING - | HOBRO- | LUNDTOFTE - | RANDERS- | RINGKOEBING - | SLAGELSE - | SOEHOLT- | VIBORG- | ABY | AALBORG_EAST- | VALBORG_WEST- | BJERGMARKEN- | HERNING - | FREDERICIA- | NAESTVED- |

Figure S1| Heatmap of the 20 most abundant archaeal OTUs. Phylum and genus level classifications of the OTUs are shown, when no classification is available OTU number is given. The wastewater treatment plants had a total of 32 AD reactors (1-4 per plant) and they were analysed 2-23 times. The mean read abundance is shown for each plant. The taxa are sorted by mean read abundance across the plants.



Figure S2| Alpha diversity indices. A) Shannon index for bacteria, B) Shannon index for archaea, C) Simpson index for bacteria, D) Simpson index for archaea.

|] | Mesophilic | | | | | | | | | | | | | | Thermophilic | | |
|---|------------|------------|------------|-----------|------------|---------|------------|-----------|------------|------------|-----------|----------|------------|-----------|--------------|-------------|------------|
| Actinobacteria; Tetrasphaera; OTU_4 - | 1.2 | 0.6 | 2.4 | 7.1 | 2.4 | 0.7 | 1.1 | 0.3 | 1.7 | 1.1 | 4.3 | 1.3 | 3.7 | 1.7 | 11.6 | 0 | 0 |
| Bacteroidetes; KD1-22; OTU_5 - | 0 | 1 | 3.9 | 1.1 | 5.9 | 1 | 2.3 | 2.6 | 1.1 | 3.8 | 0.8 | 2.7 | 0 | 0 | 0 | 0 | 0 |
| Firmicutes; B55_F; OTU_10 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.1 | 0.1 | 0 | 0 | 0 | 2.2 | 0.2 | D | 12.8 | 11.2 |
| Chloroflexi; A6; OTU_7 - | 0 | 0 | 2.1 | 1.9 | 0 | 0 | 0.6 | 0 | 0 | 4.8 | 7.6 | 0 | 0 | 0 | 0.2 | 4.2 | 0.6 |
| Synergistetes; Thermovirga; OTU_51 - | 0.7 | 1.1 | 3.2 | 1.7 | 0.5 | 0.9 | 2 | 3.8 | 0.1 | 1.3 | 0.7 | 2.3 | 0 | 0 | 0 | 0.9 | 0 |
| Firmicutes; ; OTU_37 - | 0 | 0 | 0 | 0 | 0.1 | 0 | 0 | 0.1 | 0 | 0 | 0.1 | 0 | 4.1 | 3 | 3 | 9.4 | 1.7 |
| Bacteroidetes; SHA-94; OTU_9 - | 1.8 | 1.2 | 2.5 | 1.4 | 0.8 | 2.9 | 1.8 | 1.8 | 0.7 | 3.4 | 0.9 | 1.7 | 0 | 0 | O | O | 0.4 |
| Bacteroidetes; G35_D8; OTU_11 - | D | 0 | 0 | D | 0.1 | 0 | 0 | 0 | 0 | 0 | 0.1 | 0 | 8 | 6.4 | 0.8 | 3.6 | 0 |
| Chloroflexi; T78; OTU_24 - | 1.5 | 0.6 | 3.4 | 0.3 | 0.6 | 4.1 | 1.9 | 3 | 3.8 | 1.9 | 0.1 | 2.1 | 0 | 0 | 0.7 | 0 | 0.1 |
| Bacteroidetes; vadinBC27 wastewater-sludge group; OTU_19- | 1.8 | 2.1 | 0.7 | 0.7 | 1.8 | 1.6 | 1.6 | 2.7 | 1.5 | 1 | 0 | 2.1 | 0 | 0 | 0 | 0 | 0 |
| Firmicutes; Fastidiosipila; OTU_30 - | 0 | 0 | 0 | 0 | 0.1 | 6.2 | 0 | 0 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 | 4.9 | 19.8 |
| Firmicutes; Romboutsia; OTU_12 - | 1 | 1.2 | 1.7 | 1.5 | 0.8 | 1.7 | 1.7 | 2 | 1.8 | 1 | 1.4 | 1.8 | 0.8 | 1.6 | 1.1 | 0 | 0 |
| Fermentibacteria; Candidatus Fermentibacter; OTU_18 - | 1 | 2.9 | 1.7 | 0.1 | 1.5 | 0.2 | 3.2 | 1.6 | 0.5 | 1.4 | 0 | 1.2 | 0 | 0 | 0 | 0 | 0 |
| Chloroflexi; T78; OTU_63 - | 2.1 | 2.5 | 0.9 | O | 2.4 | 0.3 | 1.8 | 2.1 | 0.9 | 0.2 | 0 | 0.9 | 0 | 0 | O | 0 | 0 |
| Chloroflexi; Leptolinea; OTU_13 - | 1.7 | 0.8 | 1.9 | 0.9 | 0.3 | 0.2 | 1.4 | 12 | 1.3 | 1.8 | 0.2 | 2.6 | 0 | 0 | 0 | 0 | 0 |
| Actinobacteria; Candidatus Microthrix; OTU_1 - | 0.8 | 1.1 | 1 | 0.4 | 1.1 | 0 | 2.4 | 1 | 0.5 | 0.5 | 1.8 | 0.9 | 1.7 | 1 | 1.7 | 0 | 0 |
| Chloroflexi; T78; OTU_26 - | 1.4 | 0.7 | 2 | 0.8 | 0.6 | 0.6 | 1 | 0.7 | 0.7 | 1.8 | 1.1 | 2.4 | 0 | 0 | 0.1 | 0 | 0 |
| Chloroflexi; Candidatus Amarilinum; OTU_3 - | 0.3 | 0.9 | 0.5 | 0 | 0 | 0 | 0.2 | 0.3 | 0 | 0.9 | 0.1 | 0 | 5.9 | 0 | 0.2 | O | 0 |
| Firmicutes; Coprothermobacter; OTU_16 - | D | 0.1 | 0 | 0.1 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 5.5 | 4.6 | 5.4 | D | 0 |
| Actinobacteria; Candidatus Microthrix; OTU_8 - | 1.2 | 0.5 | 0.4 | 2.4 | 1.3 | 0 | 0.5 | 1.2 | 0.7 | 0.3 | 1 | 1 | 0.4 | 0.6 | 3.2 | O | 0 |
| · · · · · | AVEDOERE - | MHUSAAEN - | - WOETLE - | FORNAES - | HOERRING - | HOBRO - | UNDTOFTE - | RANDERS - | GKOEBING - | SLAGELSE - | SOEHOLT - | VIBORG - | RGMARKEN - | HERNING - | - YAABY - | REDERICIA - | NAESTVED - |

Figure S3| Heatmap of the 20 most abundant bacterial OTUs. Phylum and genus level classifications of the OTUs are shown, when no classification is available the field is empty. The wastewater treatment plants had a total of 32 AD reactors (1-4 per plant) and they were analysed 3-30 times. The mean read abundance is shown for each plant. The taxa are sorted by mean read abundance across the plants.





Figure S4| Heatmap of the 100 most abundant bacterial OTUs. The wastewater treatment plants had a total of 32 AD reactors (1-4 per plant) and they were analysed 3-30 times. The mean read abundance is shown for each plant. The taxa are sorted by mean read abundance across the plants. The right panel indicates whether the digester to influent read abundance ratio was above 10 (\bullet) and likely actively growing, between 1 and 10 (\bullet), or below 1 (\bullet), indicating no growth.



Figure S5| Rank abundance curve indicating the number of OTUs needed to account for a certain fraction of the cumulative reads for mesophilic (\blacksquare), thermophilic (\blacksquare) and mesophilic with THP (\blacksquare) samples. Those constituting 80% are often defined as the abundant core community.



Figure S6| Principal component analysis of the bacterial communities analysed in this study highlighting samples by process type information. Mesophilic (•), thermophilic (•), and mesophilic with thermal hydrolysis pre-treatment (• THP), primary sludge (•) and surplus sludge (•).

| Figure S7 | | | | | | | | | | | | | | |
|---|--------------|-------------|-------------|-------------|--------------|-------------|-------------|-------------|-------------|-------------|------------|----------|---------|---------|
| Firmicutes; Streptococcus | 2.3 | 9.1 | 4.1 | 3.4 | 5.2 | 33.2 | 1.2 | 0.6 | 1.2 | 1.9 | 2.6 | 3 | 1.3 | 3.1 |
| Proteobacteria; Arcobacter - | 4.4 | 16.6 | 6.1 | 1.8 | 3.6 | 4.4 | 3 | 5.3 | 6.7 | 1.3 | 2.6 | 3.7 | 7.5 | 3.2 |
| Firmicutes; Trichococcus - | 2.8 | 1.2 | 3.5 | 6.7 | 3.4 | 0.5 | 4.5 | 12.3 | 5 | 7.3 | 5 | 2.8 | 1.2 | 3.4 |
| Firmicutes; Blautia - | 2 | 3 | 5 | 4.7 | 4 | 0.6 | 2.6 | 0.9 | 3.7 | 7.1 | 7.2 | 4.5 | 2.7 | 6 |
| Firmicutes; Lactococcus - | 0.8 | 0.8 | 2.4 | 3.1 | 4.2 | 4.9 | 6.3 | 16 | 4.7 | 0.9 | 0.9 | 1.3 | 0.8 | 2.4 |
| Proteobacteria; Acidovorax - | 9 | 1.9 | 2.3 | 1.3 | 1.4 | 0.6 | 4.3 | 3.5 | 5.9 | 1.5 | 0.8 | 5.2 | 7.5 | 2.8 |
| Firmicutes; Subdoligranulum - | 1.3 | 1.5 | 2.6 | 3.9 | 2.8 | 0.4 | 1.5 | 0.7 | 1.9 | 4.1 | 3.6 | 2.3 | 1.4 | 2.9 |
| Firmicutes; Faecalibacterium - | 1.9 | 2.3 | 3.8 | 1.9 | 2.3 | 0.6 | 1.1 | 0.9 | 2.2 | 2 | 1.2 | 2.3 | 2 | 2.6 |
| Firmicutes; Enterococcus - | 1.6 | 0.7 | 1.6 | 2.6 | 1.6 | 2.2 | 1.7 | 0.8 | 1.6 | 1.9 | 2.3 | 2.5 | 0.8 | 2.5 |
| Firmicutes; Pseudobutyrivibrio - | 1.1 | 1.3 | 2.1 | 1.3 | 1.4 | 0.3 | 1 | 0.3 | 1.4 | 3 | 2.4 | 1.9 | 1.5 | 2 |
| Firmicutes; Ruminococcus 2 - | 1 | 0.8 | 1.8 | 1.8 | 1.3 | 0.2 | 1 | 0.5 | 1.2 | 2.8 | 2.4 | 1.5 | 0.9 | 1.1 |
| Fusobacteria; Leptotrichia - | 1.3 | 0.6 | 1.7 | 1.7 | 0.5 | 0.5 | 1.6 | 1 | 1.7 | 0.9 | 0.5 | 1.4 | 1.1 | 2.1 |
| Firmicutes; Fusicatenibacter- | 0.9 | 0.7 | 1.4 | 1.4 | 1.2 | 0.2 | 0.9 | 0.5 | 1.2 | 2.1 | 1.8 | 1.5 | 1.1 | 1.6 |
| Firmicutes; Dorea - | 0.8 | 0.8 | 1.9 | 1.2 | 1.2 | 0.2 | 0.8 | 0.3 | 1 | 2.2 | 2 | 1.4 | 0.8 | 1.6 |
| Proteobacteria; Comamonas - | 2.3 | 2.6 | 0.5 | 0.1 | 1 | 0.7 | 1 | 0.8 | 1.8 | 0.2 | 0.2 | 1.7 | 2.1 | 1.2 |
| Firmicutes; Clostridium sensu stricto 1 - | 1 | 0.5 | 1.3 | 1.8 | 0.9 | 0.5 | 0.9 | 0.6 | 1.1 | 1.3 | 1.3 | 1.4 | 0.8 | 1.8 |
| Bacteroidetes; Flavobacterium - | 1.1 | 1.1 | 0.9 | 0.2 | 0.2 | 0.3 | 0.7 | 2.7 | 1.5 | 0.2 | 0.2 | 0.6 | 5.1 | 0.3 |
| Firmicutes; Anaerostipes - | 0.7 | 0.6 | 1.3 | 1.6 | 0.9 | 0.1 | 0.8 | 0.3 | 1 | 2.1 | 1.9 | 1.2 | 0.8 | 1.5 |
| Actinobacteria; Collinsella - | 0.2 | 0.3 | 0.5 | 3.7 | 0.3 | 0 | 0.3 | 0 | 0.1 | 4.2 | 3.2 | 1.5 | 0 | 0.3 |
| Firmicutes; Romboutsia - | 0.7 | 0.6 | 1.1 | 1.7 | 1.3 | 0.2 | 0.9 | 0.4 | 1.1 | 1.3 | 1.3 | 1.3 | 0.8 | 1.5 |
| - | ALBORG_EAST- | LBORG_WEST- | JERGMARKEN- | EBY_MOELLE- | SBJERG_WEST- | FREDERICIA- | HADERSLEV - | HIRTSHALS - | HJOERRING - | ODENSE_NE - | ODENSE_NW- | RANDERS- | SKIVE - | VIBORG- |

Figure S7 | Heatmap of the 20 most abundant genera in the primary sludge. Phylum level classifications are shown. The mean read abundances are shown for each plant (3-23 samples per plant). The taxa are sorted by mean read abundance across the plants.

| Actinobacteria; Tetrasphaera - | 5.2 | 2.1 | 1.9 | 5.3 | 2.6 | 7.2 | 6.7 | 6.2 | 19.4 | 7.5 | 2.5 | 3.7 | 2 | 2.8 | 0.6 | 2.6 | 5.1 | 1.7 | 5 | 1.3 | 8.5 | 6.2 | 6.6 |
|---|-------|------------|------------|------------|------------|--------------|-------------|------------|----------|-------------|------------|----------|------------|------------|-----------|------------|------------|----------|-------|-------|------------|----------|--------|
| Actinobacteria; Candidatus Microthrix - | 4.3 | 1.5 | 7.6 | 3.3 | 8.2 | 2.6 | 2.3 | 5.7 | 3.1 | 0.5 | 1.1 | 0.8 | 0.2 | 0.7 | 5.5 | 2.9 | 7.6 | 7 | 0.4 | 2.1 | 2.1 | 7.9 | 2.9 |
| Chloroflexi; Candidatus Amarilinum - | 0.1 | 0.2 | 2.1 | 21.7 | 0.8 | 16.8 | 0 | 0 | 0 | 0 | 1.2 | 0.1 | 0 | 0.2 | 15.6 | 7 | 0 | 1.3 | 0 | 0.5 | 1.5 | 0.2 | 0 |
| Proteobacteria; Rhodoferax - | 5.8 | 3 | 2.7 | 0.6 | 2 | 0.4 | 1.4 | 0.8 | 4 | 0 | 1.2 | 4.8 | 1.1 | 1 | 3.7 | 2.2 | 1.6 | 0.9 | 2 | 2.7 | 2.4 | 3.2 | 2 |
| Acidobacteria; Blastocatella - | 0.4 | 0.5 | 1 | 0.6 | 0.6 | 0.7 | 1 | 2.1 | 0.3 | 22.3 | 2 | 0.5 | 1.7 | 1 | 0.5 | 0.8 | 0.9 | 1.7 | 0.8 | 1.6 | 1 | 0.8 | 1.1 |
| Proteobacteria; Dechloromonas - | 1.1 | 0.7 | 3.1 | 0.7 | 2.1 | 1.2 | 2.7 | 2 | 1.2 | 0 | 0.3 | 3.6 | 3.2 | 3.2 | 1.3 | 0.1 | 0 | 1.9 | 2.7 | 1.8 | 6.3 | 1.1 | 1.4 |
| Bacteroidetes; QEDR3BF09 - | 1.8 | 2.8 | 2.9 | 0.4 | 2.2 | 0.4 | 1 | 4.6 | 0.5 | 0 | 0.7 | 1.2 | 2.2 | 2.6 | 0.8 | 0.6 | 0.5 | 3 | 2.6 | 2.6 | 1.6 | 2.2 | 0.6 |
| Proteobacteria; Rhodobacter - | 1.2 | 1.5 | 1.4 | 0.5 | 1.7 | 0.7 | 2.6 | 2.9 | 1.9 | 0.1 | 1.7 | 1.3 | 1.5 | 1.8 | 0.8 | 2.1 | 2.3 | 1.8 | 1 | 1.5 | 1.1 | 1.8 | 2.9 |
| Chloroflexi; Candidatus Villogracilis - | 0.6 | 2.5 | 1.7 | 0.1 | 0.7 | 0.5 | 6.6 | 1.2 | 0.5 | 0.1 | 1.3 | 0.6 | 1 | 2.6 | 1.2 | 1.5 | 0.4 | 1.8 | 0.5 | 2.3 | 0.5 | 2.9 | 0.5 |
| Bacteroidetes; Candidatus Epiflobacter- | 0.3 | 0.7 | 1.7 | 0.2 | 0.9 | 0.3 | 2.8 | 0.9 | 0.4 | 1.3 | 0.7 | 0.6 | 2.5 | 3.2 | 0.2 | 0.5 | 1.8 | 1.1 | 1.2 | 1.1 | 0.6 | 0.3 | 1.7 |
| Bacteroidetes; Ferruginibacter - | 0.7 | 0.9 | 0.6 | 0.6 | 1 | 0.5 | 0.6 | 1.3 | 1 | 0 | 1.3 | 0.4 | 1.1 | 1.3 | 0.5 | 0.5 | 0.1 | 1.4 | 2.7 | 1.6 | 0.7 | 1.9 | 3.2 |
| Bacteroidetes; CYCU-0281 - | 1.9 | 2 | 3 | 0.4 | 1.7 | 0.4 | 0.6 | 1.3 | 1 | 0.5 | 0.7 | 0.4 | 0.9 | 0.7 | 1 | 0.7 | 0.4 | 0.6 | 0.3 | 2.4 | 1.4 | 0.7 | 0.4 |
| Bacteroidetes; MK04 - | 0.6 | 3.8 | 1.7 | 0.1 | 1.1 | 0.1 | 1.3 | 0.9 | 0.6 | 0 | 0 | 4.7 | 0.2 | 0.2 | 0.4 | 0.1 | 0.6 | 0.2 | 0.4 | 2.3 | 0.9 | 0.9 | 2.1 |
| Proteobacteria; Hyphomicrobium - | 0.5 | 0.7 | 0.5 | 1 | 0.8 | 0.7 | 0.5 | 1.3 | 0.6 | 3.9 | 1.6 | 0.3 | 1.1 | 0.5 | 0.7 | 1.5 | 1.4 | 0.9 | 0.8 | 0.7 | 1 | 1 | 1.5 |
| Nitrospirae; Nitrospira - | 0.3 | 0.2 | 0.2 | 0.1 | 0.8 | 0.2 | 0.5 | 0.8 | 0.2 | 0.4 | 0.8 | 1 | 2.1 | 1.6 | 0.2 | 0.1 | 0 | 0.7 | 6.1 | 1.2 | 0.9 | 1.2 | 2.1 |
| Bacteroidetes; PHOS-HE28 - | 1.8 | 0.5 | 2.3 | 0.3 | 1.1 | 0.6 | 1.8 | 0.8 | 1.1 | 1 | 0.3 | 0.8 | 1.5 | 0.4 | 0.9 | 0.3 | 0.1 | 0.6 | 1.3 | 1.3 | 1.9 | 0.7 | 0.2 |
| Chloroflexi; Candidatus Defluviifilum - | 1.1 | 1 | 1.4 | 1 | 1.3 | 1.7 | 0.4 | 1.1 | 0.8 | 1.3 | 0.6 | 0.3 | 1.1 | 0.4 | 1.1 | 1.2 | 0.9 | 0.7 | 0.5 | 0.5 | 0.8 | 0.9 | 0.7 |
| Bacteroidetes; Terrimonas - | 0.9 | 0.9 | 1.7 | 0.6 | 0.8 | 0.4 | 0.8 | 0.9 | 0.8 | 0.3 | 0.8 | 0.5 | 0.6 | 1.7 | 0.6 | 0.5 | 0.6 | 1.1 | 1.1 | 1.4 | 1.1 | 0.5 | 1.7 |
| Chloroflexi; Candidatus Promineofilum - | 1.4 | 0.5 | 1.7 | 0.3 | 1.3 | 3.1 | 0.4 | 0.3 | 0.3 | 0 | 0.7 | 0.3 | 0.8 | 0.7 | 0.4 | 0.4 | 2.3 | 0.5 | 0.2 | 0.6 | 1 | 0.7 | 0.2 |
| Chlorobi; oca15 - | 0.4 | 0.3 | 1.6 | 0.8 | 0.6 | 0.7 | 0.2 | 0.3 | 0.7 | 0 | 0 | 0.5 | 2.6 | 2.8 | 0.5 | 0.2 | 0 | 1.5 | 0 | 0.7 | 0.7 | 0.2 | 0.2 |
| | AABY- | BORG_EAST- | BORG_WEST- | ERGMARKEN- | AMHUSAAEN- | - DEV_MOELLE | BJERG_EAST- | UERG_WEST- | FORNAES- | FREDERICIA- | HADERSLEV- | HERNING- | HIRTSHALS- | HJOERRING- | NAESTVED- | ODENSE_NE- | ODENSE_NW- | RANDERS- | RIBE- | SKNE- | SLAGELSE - | SOEHOLT- | VBORG- |

Figure S8 Heatmap of the 20 most abundant genera in the surplus sludge. Phylum level classifications are shown. The mean read abundance is shown for plants with more than 1 sample (1-24 samples per plant). The taxa are sorted by mean read abundance across the plants.



Figure S9| Density plot for ratios between OTU read abundance in the anaerobic digesters and the influent streams (primary and surplus sludge) weighted by the read abundance in the anaerobic digesters. Frederica has thermal hydrolysis pre-treatment.

| Δ | Chloroflexi: T78 - | 22 | 12.7 | 10.6 | 5.5 | 4.6 | 5.8 | 12.4 | 15 | 9.7 | 5.8 | 4. | 26 | 5.7 | 4.2 | 6.5 |
|---|---|---|---|--|---|---|--|---|---|--|--|--|--|---|---|---|
| ~ | Acidobacteria: OTU 33- | 0 | 0 | 0 | 0.4 | 0.1 | 1.4 | 4.1 | 1.1 | 7.1 | 17.5 | 5 8. | 4 6 | 5.9 | 7.8 | 1.6 |
| | Chloroflexi; Leptolinea - | 3.7 | 6.6 | 6.2 | 1.7 | 0.6 | 2.3 | 4.6 | 3 | 4.2 | 5.8 | 2 | 3 | 3.2 | 1.8 | 3.3 |
| | Synergistetes: Thermovirga - | 0.2 | 0.6 | 0.4 | 0.9 | 1.6 | 1.5 | 5.1 | 8.4 | 3.7 | 6.8 | 3. | 3 3 | 3.5 | 3.5 | 4 |
| | Bacteroidetes: KD1-22- | 0.4 | 5.9 | 1.4 | 2.5 | 2.9 | 4.3 | 0.4 | 3.7 | 1.9 | 3 | 7. | 8 2 | 2.2 | 0.1 | 2.5 |
| | Bacteroidetes; vadinBC27 wastewater-sludge group- | 5.5 | 1.1 | 15.4 | 2.4 | 3.6 | 1.7 | 1.1 | 2.2 | 0.5 | 0 | 2 | 5 0 |).3 | 0.1 | 2.7 |
| | Actinobacteria: Candidatus Microthrix - | 2.3 | 2.9 | 5.1 | 2.5 | 6.6 | 2 | 1 | 0.8 | 0.7 | 0.6 | 0. | 7 1 | .6 | 1.3 | 1.2 |
| | Firmicutes: Clostridium sensu stricto 1 - | 1.6 | 3.3 | 2 | 1.6 | 2.4 | 1.9 | 2 | 1.7 | 2.9 | 1.7 | 2 | 2 1 | .9 | 2.4 | 1.6 |
| | Firmicutes: Romboutsia - | 1.7 | 3.6 | 2 | 1.6 | 1.9 | 2 | 2 | 1.8 | 2.6 | 1.9 | 1. | 9 | 2 | 2 | 1.4 |
| | Bacteroidetes: SHA-94 - | 0.8 | 3.5 | 3.6 | 1.6 | 1 | 1.5 | 1.3 | 1.8 | 1.7 | 0.5 | 2 | 4 (| .8 | 1 | 2 |
| | Proteobacteria: Smithella - | 0.9 | 1 | 1.5 | 0.8 | 1.6 | 1.7 | 3 | 2.6 | 2.5 | 2.1 | 1. | 9 1 | .9 | 1.4 | 1.8 |
| | Actinobacteria: Tetrasphaera - | 1.2 | 1.3 | 0.2 | 1.1 | 1.4 | 1.6 | 1.5 | 0.8 | 0.9 | 1 | 2 | 4 2 | 2.5 | 2.7 | 1.6 |
| | Proteobacteria: Dechloromonas - | 0.1 | 0.1 | 0.1 | 2.8 | 3.1 | 2.4 | 1.6 | 1 | 0.7 | 0.7 | 1. | 2 1 | .3 | 2.8 | 2 |
| | Actinobacteria: Gordonia - | 1.9 | 2 | 1.1 | 44 | 4.7 | 2 | 0.4 | 0.1 | 0.1 | 0.1 | 0 | 1 0 | 13 | 0.4 | 0.1 |
| | Fermentibacteria: Candidatus Fermentibacter - | 12 | 0.5 | 2 | 12 | 02 | 24 | 0 | 4.1 | 1 | 1 | 1 | 3 0 | 12 | 0 | 21 |
| | Firmicutes: Christensenellaceae R-7 group - | 2.8 | 13 | 16 | 15 | 21 | 1 | 0.5 | 11 | 0.5 | 0.8 | 1 | 1 0 | 15 | 0.6 | 13 |
| | Firmicutes: Ruminococcus 1 - | 0.3 | 0 | 0 | 0.1 | 0 | 0.4 | 0.2 | 0.6 | 1 | 2.4 | 1 | 7 6 | 5.7 | 1.1 | 0.5 |
| | Proteobacteria: Rhodobacter - | 0.8 | 1 | 0.5 | 2.6 | 32 | 0.9 | 0.6 | 1.3 | 0.4 | 0.6 | 0 | 5 0 | 12 | 0.6 | 1 |
| | Firmicutes: Gelria - | 0.3 | 0.1 | 0.2 | 0.3 | 0.5 | 0.4 | 0.6 | 0.5 | 1 | 1.4 | 1 | 1 | .4 | 0.8 | 5 |
| | Thermotogae; SC103 - | 0.3 | 0.5 | 0.3 | 0.9 | 0.4 | 0.7 | 1.3 | 0.3 | 0.4 | 0.4 | 0. | 9 1 | 1.3 | 1.5 | 1.8 |
| | | ģ | 6 | 4 | - | - | 8 | - | - <u>0</u> | - | + | ģ | , | ģ | | 7- |
| | | ¥ | 8 | 5 | 33 | 8 | 82 | 3 | ğ | 5 | 8 | 250 | į. | 8 | 5 | 8 |
| | | 7 | ÷ | ÷ | 130 | 13 | 13 | 9 | 4 | 4 | 15 | 15 | 2 | 15 | 42 | 10 |
| | | 2 | 2 | 8 | 3 | 2 | 8 | 3 | 3 | 3 | 3 | 00 | 1 | 3 | 3 | 3 |
| | | | | | | | S | ampl | le da | te | | | | | | |
| | | | | | | | () | vvvn | nmd | d) | | | | | | |
| | | | | | | | | ,,,, | | | | | | | | |
| D | Firmicutes: Conrothermohacter- | 14 | 97 | 98 7 | 6 4 | 10 | 6 10 6 | 4.6 | Q | 13.5 | 69 | 17.6 | 13.6 | 69 | 12.8 | 14.7 |
| в | Firmicutes; Coprothermobacter - Firmicutes: A55, D21 - | 14 | 9.7 | 9.8 7 | 7.6 4 8.2 6 | 10. | 6 10.6 | 4.6 | 9 | 13.5 | 6.9 | 17.6 10 1 | 13.6 | 6.9 1 9 | 12.8 | 14.7 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes: G35_D8 - | 14 9.3 4.6 | 9.7 8.8 7 | 9.8 7 5.4 8 9.4 5 | 7.6 4 3.2 6.3 | 10. 2 5 4 3.3 | 6 10.6 8.3 | 4.6 7.3 | 9 5.9 5.5 | 13.5 6.3 3.9 | 6.9 9.3 | 17.6 10.1 4.6 | 13.6 5.7 9.4 | 6.9 1.9 2.3 | 12.8 5.4 9.6 | 14.7 5.8 5.3 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria: Candidatus Microthrix - | 14 9.3 4.6 7.1 | 9.7 8.8 7 3.6 | 9.8 7 5.4 8 9.4 5 12.3 3 | 7.6 4 3.2 6.2 5.7 14 3.7 5.2 | 10. 2 5 4 3.3 7 6.6 | 6 10.6 8.3 3 2.1 5 6.8 | 4.6 7.3 10.5 2.8 | 9 5.9 5.5 6.7 | 13.5 6.3 3.9 3.7 | 6.9 9.3 6.3 3.7 | 17.6 10.1 4.6 4 | 13.6 5.7 9.4 8.5 | 6.9 1.9 2.3 7.5 | 12.8 5.4 9.6 5.2 | 14.7 5.8 5.3 8.4 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes: OTU 37 - | 14 9.3 4.6 7.1 3.7 | 9.7 8.8 7 3.6 4.8 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 | 7.6 4 8.2 6.2 6.7 14 8.7 5.2 8.9 6.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 | 6 10.6 8.3 3 2.1 5 6.8 5 3.5 | 4.6 7.3 10.5 2.8 4.1 | 9 5.9 5.5 6.7 5.3 | 13.5 6.3 3.9 3.7 3.8 | 6.9 9.3 6.3 3.7 5.3 | 17.6 10.1 4.6 4 5.6 | 13.6 5.7 9.4 8.5 5 | 6.9 1.9 2.3 7.5 4.6 | 12.8 5.4 9.6 5.2 4.5 | 14.7 5.8 5.3 8.4 4.3 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi: RB349 - | 14 9.3 4.6 7.1 3.7 4.7 | 9.7 8.8 7 3.6 4.8 2 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 | 7.6 4 8.2 6.2 5.7 14 8.7 5.2 8.9 6.2 5 1.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 | 6 10.6 8.3 3 2.1 5 6.8 5 3.5 3 3.5 | 4.6 7.3 10.5 2.8 4.1 8.4 | 9 5.9 5.5 6.7 5.3 3 | 13.5 6.3 3.9 3.7 3.8 1.7 | 6.9 9.3 6.3 3.7 5.3 4.2 | 17.6 10.1 4.6 4 5.6 6.1 | 13.6 5.7 9.4 8.5 5 5.2 | 6.9 1.9 2.3 7.5 4.6 6.5 | 12.8 5.4 9.6 5.2 4.5 7 | 14.7 5.8 5.3 8.4 4.3 4.1 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Svnergistetes: Anaerobaculum - | 14 9.3 4.6 7.1 3.7 4.7 3.6 | 9.7 8.8 7 3.6 4.8 2 2.8 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2 2 | 1.6 4 3.2 6.1 5.7 14 3.7 5.1 3.9 6.1 5 1.1 2.5 5.1 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 | 6 10.6 8.3 3 2.1 5 6.8 5 3.5 3 3.5 5 3.8 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 | 9 5.9 5.5 6.7 5.3 3 3.7 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 | 17.6 10.1 4.6 4 5.6 6.1 2.5 | 13.6 5.7 9.4 8.5 5 5.2 2.5 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 | 12.8 5.4 9.6 5.2 4.5 7 2.8 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes: Gelria - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 | 1.6 4 3.2 6.1 5.7 14 3.7 5.1 3.9 6.1 5 1.1 2.5 5.1 2.5 3.1 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.9 | 6 10.6 8.3 2.1 5 6.8 5 3.5 3 3.5 5 3.8 9 2.2 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 | 9 5.9 5.5 6.7 5.3 3 3.7 2 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 | 17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 | 13.6 5.7 9.4 8.5 5 5.2 2.5 2.1 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; B55 F - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 | 1.6 4 3.2 6.1 5.7 14 3.7 5.1 3.9 6.1 5.5 1.1 2.5 5.1 2.5 3.1 1 1.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.9 4 2.7 | 6 10.6 8.3 3 2.1 5 6.8 5 3.5 3 3.5 5 3.8 9 2.2 7 1.8 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 | 9 5.9 5.5 6.7 5.3 3.7 2 2 2 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 2.4 | 17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 2 | 13.6 5.7 9.4 8.5 5 5.2 2.5 2.1 2.4 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; B55_F - Thermotogae; Fervidobacterium - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1.7 2 | 7.6 4 3.2 6.1 5.7 14 3.7 5.1 3.9 6.1 5.5 1.2 2.5 5.2 1 1.2 2.4 3.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.9 4 2.7 4 1.9 4 1.9 | 6 10.6 8.3 3 2.1 5 6.8 5 3.5 3 3.5 5 3.8 9 2.2 7 1.8 9 1.6 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 | 9 5.9 5.5 6.7 5.3 3.7 2 2 2 1.4 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.9 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 2.4 1.6 | 17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 2 2.3 | 13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; B65_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1.7 2.8 3 | 7.6 4 3.2 6.1 5.7 14 3.7 5.1 3.9 6.1 5.5 3.2 5.5 3.2 1 1.2 2.4 3.3 2.5 2.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.9 4 2.7 4 1.9 2 3.6 | 6 10.6 8.3 2.1 5 6.8 5 3.5 3 3.5 5 3.8 9 2.2 7 1.8 9 1.6 5 4.4 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.9 1.9 1 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 2.4 1.6 1.4 | 17.6 10.1 4.6 5.6 6.1 2.5 1.9 2 2.3 0.8 | 13.6 5.7 9.4 8.5 5 5.2 2.5 2.1 2.4 1.8 0.6 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Propionicimonas - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1.7 2 2.8 3 0.7 2 | 7.6 4 3.2 6.3 5.7 14 3.7 5.3 3.9 6.3 5.5 1.3 2.5 3.2 1 1.2 2.4 3.3 2.2 3.3 2.2 3.3 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.9 4 2.7 4 1.9 2 3.6 4 1.4 2 3.6 4 1.1 | 6 10.6 8.3 3 2.1 5 6.8 5 3.5 3 3.5 5 3.8 9 2.2 7 1.8 9 1.6 5 4.4 1 0.2 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 2.7 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.9 1.9 1 0.5 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 2.4 1.6 1.4 0.5 | 17.6 10.1 4.6 5.6 6.1 2.5 1.9 2 2.3 0.8 1.9 | 13.6 5.7 9.4 8.5 5 2.5 2.5 2.1 2.4 1.8 0.6 2.8 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Propionicimonas - Actinobacteria; Tetrasphaera - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1.7 2.8 3 0.7 2 2.5 1 | 7.6 4 3.2 6.3 5.7 14 3.7 5.3 5.5 1.3 5.5 5.3 1 1.4 2.25 3.3 1 1.4 3.9 2.3 3.9 2.3 3.9 2.3 3.9 2.4 3.9 2.1 1.4 0.1 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 1.3 5 3.6 7 1.9 4 2.7 4 1.9 2 3.6 4 1.1 7 1.6 | 6 10.6 8.3 2.1 5 6.8 6 3.5 3 3.5 5 3.8 9 2.2 7 1.8 9 1.6 5 4.4 1 0.2 5 1.2 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 2.7 1.5 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.9 1.9 1 0.5 0.8 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 2.4 1.6 1.4 0.5 0.6 | 17.6 10.1 4.6 5.6 6.1 2.5 1.9 2 2.3 0.8 1.9 0.8 | 13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Propionicimonas - Actinobacteria; Tetrasphaera - Firmicutes; OTU_154 - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1.3 0.7 1 0.6 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1.7 2.8 3 0.7 2 2.5 1 0.9 0 | 7.6 4 3.2 6.5 5.7 14 3.7 5.5 3.9 6.3 5 1.3 5.5 5.2 3.1 1.2 2.2.5 3.3 1 1.2 2.4 3.3 2.2 3.3 2.2 3.4 3.9 2.2 2.8 3.4 0.1 0.7 | 10. 2 5 4 3.3 7 6.6 9 2.6 9 2.6 9 2.6 1.3 5 5 1.3 5 3.6 7 1.9 4 2.7 4 1.9 2 3.6 4 1.1 7 1.6 7 3 | 6 10.6 8.3 2.1 5 6.8 5 3.5 3 3.5 5 3.8 9 2.2 7 1.8 9 1.6 6 4.4 1 0.2 5 1.2 1.7 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 | 9 5.9 5.5 6.7 5.3 3 3.7 2 2 1.4 1.5 2.7 1.5 1.4 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.9 1.9 1.9 1 0.5 0.8 1.7 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 2.4 1.6 1.4 0.5 0.6 1.2 | 17.6 10.1 4.6 5.6 6.1 2.5 1.9 2 2.3 0.8 1.9 0.8 0.8 0.8 | 13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1.4 1 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 0.8 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 1.2 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Propionicimonas Actinobacteria; Propionicimonas Firmicutes; OTU_154 - Proteobacteria; Rhodobacter - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 1.4 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1 0.6 1.2 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1.7 2.8 3 0.7 2 2.5 1 0.9 0 1.2 1 | 7.6 4 3.2 6.3 5.7 14 3.7 5.3 5 1.3 5.5 5.3 1 1.2 2.4 3.4 3.9 6.3 1.1 1.2 2.4 3.4 3.9 2.2 3.9 2.1 1.4 0.1 0.7 0.1 1.1 1.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.9 4 2.7 4 1.2 4 1.5 3.6 1.1 7 1.6 7 3 3 0.7 | 6 10.6 8.3 2.1 5 6.8 5 3.5 3 2.1 5 3.5 3 3.5 5 3.8 9 2.2 7 1.8 9 1.6 5 4.4 1 0.2 5 1.2 1.7 7 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 2.7 1.5 1.4 1.4 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.9 1 0.5 0.8 1.7 0.8 1.7 1 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 2.4 1.6 1.4 0.5 0.6 1.2 1.2 | 17.6 10.1 4.6 5.6 6.1 2.5 1.9 2 2.3 0.8 1.9 0.8 0.8 0.8 0.6 0.8 | 13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1.4 1 1 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 0.8 0.7 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 1.2 1.3 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; GUL _37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Propionicimonas - Actinobacteria; Tetrasphaera - Firmicutes; CJ54 - Proteobacteria; Rhodobacter - Chloroflexi; Candidatus Amarilinum - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 1.3 0.8 1.4 0 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1 0.6 1.2 0.1 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1.7 2 2.8 3 0.7 2 2.5 1 0.9 0 1.2 1 0.3 1 | 7.6 4 3.2 6.3 5.7 14 3.7 5.3 5.5 1.3 5.5 5.3 1.1 1.2 2.4 3.3 2.4 3.4 3.9 2.2 3.9 2.1 1.4 0.1 0.7 0.1 1.1 1.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 9 2.6 5 1.3 5 3.6 7 1.9 4 1.7 4 1.1 7 1.6 7 3 3 0.7 7 2 | 6 10.6 8.3 3 2.1 5 6.8 5 3.5 5 3.8 9 2.2 7 1.8 9 1.6 5 4.4 1 0.2 5 1.2 1.7 7 1 4.5 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 2.7 1.5 1.4 1.4 3.2 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 0.5 0.8 1.7 1 0.5 0.8 1.7 1 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 2.4 1.6 1.4 0.5 0.6 1.2 1.2 0.6 | 17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 2.3 0.8 1.9 0.8 0.8 0.8 0.6 0.8 0.2 | 13.6 5.7 9.4 8.5 5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1.4 1 1 0.2 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 0.8 0.7 0.1 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 1.2 1.3 0.2 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; Gelria - Actinobacteria; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Propionicimonas - Actinobacteria; Tetrasphaera - Firmicutes; OTU_154 - Proteobacteria; Rhodobacter - Chloroflexi; Candidatus Amarilinum - Firmicutes; Clostridium sensu stricto 1 | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 1.4 0 1 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1 0.6 1.2 0.1 1.5 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1.7 2.8 3 0.7 2 2.5 1 0.9 0 1.2 1 0.3 1 | 7.6 4 3.2 6.3 5.7 14 3.7 5.3 5.5 1.3 5.5 5.3 1.1 1.2 2.4 3.3 2.4 3.4 3.9 2.2 3.9 2.1 1.4 0.1 0.7 0.1 1.1 1.2 1.2 0.1 1.3 1.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.9 2 3.6 4 1.9 2 3.6 4 1.1 7 1.6 7 3 3 0.7 7 2 1 1 | 6 10.6 8.3 3 2.1 5 6.8 5 3.5 5 3.8 9 2.2 7 1.8 9 1.6 5 4.4 1 0.2 5 1.2 7 1.7 7 1 4.5 1.1 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 1.5 1.4 1.4 3.2 1.4 1.4 3.2 1 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.9 1.9 1 0.5 0.8 1.7 1 0.9 1.9 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 1.6 1.4 0.5 0.6 1.2 1.2 1.2 1.3 | 17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 2.3 0.8 1.9 0.8 0.8 0.8 0.8 0.8 0.8 0.2 0.9 | 13.6 5.7 9.4 8.5 5 2.5 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 1 0.2 0.9 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 0.8 0.7 0.1 1 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 1.2 1.3 0.2 0.6 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Actinobacteria; Tetrasphaera - Firmicutes; OTU_154 - Proteobacteria; Tetrasphaera - Firmicutes; Clostridium sensu stricto 1 - Actinobacteria; Tessaracoccus - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 1.4 0 1 1.8 | 9.7 8.8 7 3.6 4.8 2.8 1.6 0.5 0.6 1.3 0.7 1 0.6 1.2 0.1 1.5 1.9 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1 1.7 2 2.8 3 0.7 2 2.5 1 0.9 0 1.2 1 0.3 1 0.5 0 1.6 1 | 7.6 4 3.2 6.3 5.7 14 3.7 5.3 5.5 1.2 5.5 3.1 2.5 3.2 1 1.2 2.4 3.3 3.9 2.2 3.8 3.2 1.4 0.1 1.4 0.1 1.4 0.1 1.2 0.1 1.3 1.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.5 3.6 7 4 1.5 3.6 7 7 3.6 7 3.6 7 3.6 7 3.6 7 3.6 7 2.1.3 1 1 2 1.3 | 6 10.6 8.3 2.1 6 8.3 3 2.1 6 8.3 3 2.1 6 3.5 3 3.5 6 3.8 9 2.2 7 1.8 9 1.6 6 4.4 1 0.2 6 1.2 1.7 1 4.5 1.1 3 1.4 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 2.7 1.5 1.4 1.4 3.2 1 1 1 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 4.5 2 3.9 1.9 1.9 1 0.5 0.8 1.7 1 0.9 1.9 1.7 1.9 0.7 1.9 | 6.9 9.3 6.3 6.3 3.7 5.3 5.3 4.2 4.1 2.4 1.6 1.4 0.5 0.6 1.2 1.2 0.6 1.2 1.2 0.6 1.3 0.6 1.3 0.6 | 17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 2 2.3 0.8 1.9 0.8 0.8 0.8 0.8 0.8 0.8 0.2 0.9 0.7 | 13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 1 0.2 0.9 0.5 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 0.8 0.7 0.1 1 0.4 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.21 1.2 1.3 0.2 0.6 0.8 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Propionicimonas - Actinobacteria; Tetrasphaera - Firmicutes; OTU_154 - Proteobacteria; Rhodobacter - Chloroflexi; Candidatus Amarilinum - Firmicutes; Clostridium sensu stricto 1 - Actinobacteria; Tessaracoccus - Firmicutes; Romboutsia - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 1.4 0 1 1.8 1.2 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1 0.6 1.2 0.1 1.5 1.9 1.2 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2.2 2 0.6 1 1.7 2 2.8 3 0.7 2 2.5 1 0.9 0 1.2 1 0.3 1 0.5 0 1.6 1 0.6 0 | 7.6 4 3.2 6.3 5.7 14 3.7 5.3 5.5 1.2 5.5 5.2 3.9 6.3 1 1.2 2.4 3.3 3.9 2.2 3.8 3.4 0.1 1.1 1.2 0.1 1.1 1.2 1.2 0.1 1.3 1.2 1.3 1.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.5 3 0.7 4 1.5 2 3.6 4 1.1 7 1.6 7 3.8 0.7 2 1 1 1 1 2 1.3 7 1.2 | 6 10.6 8.3 2.1 5 6.8 6 3.5 6 3.5 6 3.8 9 2.2 7 1.8 9 1.6 5 1.2 1 1.2 1.1 1.1 3 1.4 2 0.9 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 1.2 1 | 9 5.9 5.5 6.7 5.3 3 3.7 2 2 1.4 1.5 1.4 1.5 1.4 1.4 3.2 1 1 1.1 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 4.5 2 3.9 1.9 1 0.5 0.8 1.7 1 0.9 1.7 1 0.9 1.9 0.7 1.5 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 1.6 1.4 0.5 0.6 1.2 0.6 1.2 1.2 0.6 1.2 1.3 0.6 1.3 | 17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 2 2.3 0.8 1.9 0.8 0.8 0.8 0.8 0.8 0.8 0.2 0.9 0.7 0.8 | 13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 0.2 0.9 0.5 0.7 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 0.9 | 128 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 0.8 0.7 0.1 1 0.4 0.9 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.21 1.2 1.3 0.2 0.6 0.8 0.7 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Tetrasphaera - Firmicutes; OTU_154 - Proteobacteria; Rhodobacter - Chloroflexi; Candidatus Amarilinum - Firmicutes; Clostridium sensu stricto 1 - Actinobacteria; Tessaracoccus - Firmicutes; Romboutsia - Thermotogae; Defluviitoga - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 1.4 0 1 1.8 1.2 0.4 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1 0.6 1.2 0.1 1.5 1.9 1.2 0.5 | 9.8 7 5.4 8 9.4 5 12.3 3 6.4 3 2.1 2 2 2 2.0 0 1.7 2 2.8 3 0.7 2 2.5 1 0.7 2 2.5 1 0.7 2 1.2 1 0.3 1 0.5 0 1.6 1 0.6 0 | 7.6 4 3.2 6.3 5.7 14 3.7 5.3 5 1.3 2.5 5.3 2.1 1.2 2.2 3.3 2.4 3.4 3.9 2.2 3.3.9 2.1 1.4 0.1 1.7 0.1 1.8 1.1 1.2 0.1 1.3 1.2 1.3 1.2 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3.5 5 3.6 4 2.7 4 2.7 4 1.5 2 3.6 4 1.1 7 1.6 7 3.07 7 2 1 1 2 1.3 7 1.2 1.2 1.2 | 6 10.6 8.3 2.1 5 6.8 5 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.6 9 2.2 7 1.8 9 1.2 1.7 1 4.55 1.1 3 1.4 2 0.9 2 0.7 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 1.2 1 1.2 7 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 1.4 1.4 3.2 1.4 1.4 3.2 1 1.4 1.1 0.7 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 4.5 2 3.9 1.9 1 0.5 0.8 1.7 1 0.9 1.7 1 0.9 1.9 0.7 1.5 0.5 0.5 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 1.6 1.4 0.5 0.6 1.2 1.2 0.6 1.2 1.2 0.6 1.3 0.6 1.3 0.6 1.3 1 | 17.6 10.1 4.6 5.6 6.1 2.5 1.9 2 2.3 0.8 1.9 0.8 0.8 0.8 0.8 0.2 0.9 0.7 0.8 1.4 | 13.6 5.7 9.4 8.5 5 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 0.2 0.9 0.5 0.7 0.6 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 0.9 0.5 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 1.0.8 0.7 0.1 1 0.4 0.9 0.9 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 1.2 1.3 0.2 0.6 0.8 0.7 1.1 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Actinobacteria; Propionicimonas - Actinobacteria; Propionicimonas - Actinobacteria; Tetrasphaera - Firmicutes; OTU_154 - Proteobacteria; Rhodobacter - Chloroflexi; Candidatus Amarilinum - Firmicutes; Clostridium sensu stricto 1 - Actinobacteria; Tessaracoccus - Firmicutes; Romboutsia - Thermotogae; Defluviitoga - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 1.3 0.8 1.3 0.8 1.4 0 1 1.8 1.2 0.4 1.8 1.2 0.4 8 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.5 0.6 1.3 0.7 1 0.6 1.2 0.1 1.5 1.9 1.2 0.5 | 9.8 7 5.4 8 9.4 5 9.4 5 9.4 5 9.4 5 12.3 3 2 2 2.6 3 2.7 2 2.6 3 0.7 2 2.6 1 0.7 2 2.6 3 0.7 2 2.6 1 0.7 2 2.6 1 0.7 2 2.6 1 0.7 2 2.6 1 0.7 2 1.2 1 0.3 1 0.5 1 1.6 1 1.6 1 1.6 1 1.6 1 | K.6 4 3.2 6. 5.7 14 3.7 5. 3.8 6. 5.5 1.1. 5.5 3.2. 5.5 3.2. 5.6 3.2. 5.7 3.4. 1.1 1.4. 2.4 3.0. 3.8.9 2.2. 3.8.9 2.2. 3.8.9 2.2. 3.1 1.1. 1.2. 3.1. 1.3 1.1. 3.3 1 1.3.3 1.1. 1.3.4 1.1. | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.5 2 3.6 7 1.5 2 3.6 7 1.5 3 0.7 7 2 1 1 2 1.3 7 1.2 1.2 1.3 7 1.2 1.2 1.3 7 1.2 1.2 1.3 7 1.2 1.2 1.3 1.2 1.3 1.2 1.3 1.2 1.3 | 6 10.6 8.33 2.1 5 6.8 6 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 1.2 4.5 1.1 3 1.4 2 0.9 2 0.7 8 1.4 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 1.2 1 1.2 1 5 8 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 2.7 1.5 1.5 1.4 1.4 1.4 1.4 1.1 1.1 0.7 5 | 13.5 6.3 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 1 0.5 0.8 1.7 1 0.9 1.7 1.9 0.7 1.5 0.5 0.5 8 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 2.4 2.4 1.6 1.4 1.6 1.5 0.6 1.2 0.6 1.2 1.6 1.3 0.6 1.3 0.6 1.3 1 5 5 | 17.6 10.1 4.6 4. 5.6 6.1 2.5 1.9 2 2.3 0.8 1.9 0.8 0.8 0.2 0.8 0.2 0.9 0.7 0.8 1.4 5.6 1.9 0.8 0.2 0.9 0.7 0.8 1.4 5.6 0.8 0.2 0.9 0.7 0.8 1.4 5.6 0.8 0.2 0.8 0.4 0.8 0.4 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 | 13.6 5.7 9.4 8.5 5 2.5 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 1 0.2 0.9 0.5 0.7 0.6 8 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 0.9 0.5 8 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 0.8 0.7 0.1 1 0.4 0.9 0.9 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 1.2 1.3 0.2 0.6 0.8 0.7 1.1 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; GUL_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Propionicimonas - Actinobacteria; Tetrasphaera - Firmicutes; Clostridium sensu stricto 1 - Actinobacteria; Tessaracoccus - Firmicutes; Romboutsia - Thermotogae; Defluviitoga - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 1.3 0.8 1.4 0 1 1.8 1.2 0.4 1.2 0.4 1.2 0.5 1.8 0.6 1.3 0.8 1.2 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.5 1.3 0.8 0.8 1.4 0.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1 0.6 1.2 0.1 1.5 1.9 1.2 0.5 | 9.8 7 5.4 8 9.4 5 9.4 5 9.4 5 9.4 5 12.3 3 6.4 3 2 2 2 2 2.2 2 2.0.6 1 1.7 2 2.8 3 0.7 2 2.8 3 0.7 2 2.5 1 0.7 2 2.5 1 0.3 1 0.5 0 1.6 1 0.5 0 1.6 1 5 8 | 46.6 4 3.2 6. 5.7 14 3.7 5. 5.8 6. 5.7 1. 2.5 5. 2.5 3. 1 1. 2.5 3. 1.1 1. 2.4 3. 3.9 2. 2.8 3. 3.7 0. 1.1 1. 1.2 0. 0.8 1. 1.3 1. 1.3 1. 1.3 1. 1.5 5. 5. 5. | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 7 1.5 3 0.7 1 1.5 3 0.7 1 1 2 1.2 1 1 2 1.2 1 1 2 1.2 1 1.2 1 1.2 1.2 1.2 1.2 1.2 2 1.2 3 0.7 2 2.8 2 1.2 1.2 1.2 2 2.8 | 6 10.6 8.3 2.1 8 3.3 1 6.8 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 1.0 4 5 3 1.4 4 5 5 3.4 4 5 5 3.4 5 3.4 6 3.7 7 1 4 5 5 5 6 5 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 2.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 1.2 1 1.2 1 5 9 9 | 9 5.9 5.5 6.7 5.3 3.7 2 1.4 1.5 1.4 1.4 1.4 1.4 1.1 0.7 | 13.5 6.3 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 1 0.5 0.8 1.7 1 0.9 1.7 1.9 0.7 1.5 0.5 0.5 0.5 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 1.6 1.4 0.5 0.6 1.2 0.6 1.3 0.6 1.3 0.6 1.3 0.6 1.3 0.6 1.3 0.6 1.3 0.6 | 17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 2 2.3 0.8 1.9 0.8 0.8 0.8 0.8 0.8 0.2 0.9 0.7 0.8 1.4 0.8 0.2 0.9 0.7 0.8 1.4 0.8 0.8 0.2 0.9 0.7 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 | 13.6 5.7 9.4 8.5 5 2.5 2.5 2.5 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 0.2 0.9 0.5 0.7 0.6 8 9.0 8 9.0 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 0.9 0.5 8 8 8 8 | 128 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 1.3 1.1 1.3 0.7 0.1 1 0.4 0.9 0.9 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 1.2 1.3 0.2 0.6 0.8 0.7 1.1 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OLJ_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Ternasphaera - Firmicutes; OTU_154 Proteobacteria; Tetrasphaera - Firmicutes; Clostridium sensu stricto 1 - Actinobacteria; Tessaracoccus - Firmicutes; Romboutsia - Thermotogae; Defluviitoga - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 1.4 0 1 1.8 1.2 0.4 * * * * * * * * * * * * * * * * * * * | 9.7 8.8 7 3.6 4.8 2 2.8 0.5 0.6 1.3 0.7 1 0.6 1.3 0.7 1 0.6 1.2 0.1 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1 | 9.8 7 5.4 8 9.4 5 9.4 5 9.4 5 9.4 5 2.1 2 2 2 2.2 2 2.6 1 0.7 2 2.8 2 0.7 2 2.8 1 0.9 0 0.9 1 0.3 1 0.5 1 0.6 1 0.6 1 0.6 1 0.8 5 | (.6 4 3.2 6. 3.7 14. 3.7 14. 3.7 14. 5.7 14. 5.8 1 5.5 1 5.5 3 1.1 1 2.8 3 3.9 2 3.0.7 0 1.1 1.1 1.2 0 0.8 1 1.3 1.1 1.3 1.1 1.3 1.1 1.3 1.1 1.3 1.1 1.3 1.1 1.3 1.1 1.4 0. 1.3 1.1 1.3 1.1 1.4 0. 1.3 1.1 1.4 0. 1.5 5 2.5 5 3.5 5 3.6 5 3.7 | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 4 1.5 4 1.5 4 1.7 7 1.2 3 0.7 7 1.2 1.1 1 2 1.3 7 1.2 1.3 1.1 2 1.3 8 6 | 6 10.6 8.3 2.1 8 3.3 1 6.8 3 2.1 1 6.8 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 1.4 4.5 1.7 3 1.4 3 1.4 3 1.4 4 0.9 5 5 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 2.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 1.2 1 1.2 1 5 6 | 9 5.9 5.5 6.7 5.3 3.7 2 1.4 1.5 2.7 1.4 1.5 1.4 1.2 1 1.1 0.7 50 6.7 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 1 0.5 0.8 1.7 1 0.9 1.9 1.9 1.9 0.7 1.5 0.7 1.5 0.7 1.5 0.7 1.5 0.6 1.9 0.7 1.5 0.5 - 0.6 0.7 1.5 0.5 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 1.6 1.4 0.6 1.2 1.2 0.6 1.3 0.6 1.3 1 0.6 1.3 1 1 5 5 5 5 1.3 1 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 17.6 4.6 4 5.6 6.1 2.5 1.9 2.3 0.8 0.8 0.6 0.8 0.6 0.8 0.6 0.8 0.2 0.9 0.7 0.8 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 1.4 | 13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 1 0.2 0.9 0.5 0.7 0.6 8 9.9 5 5 5 5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 2.5 | 6.9 1.9 2.3 7.5 4.6 6.5 3.6 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 0.9 0.5 8 8 8 8 5 5 | 128 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 1.1 1.3 1.1 0.8 0.7 0.1 1 0.4 0.9 0.9 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.1 1.2 1.3 0.2 0.1 1.2 1.3 0.2 0.6 0.8 0.7 1.1 -1.2 2.5 0.6 0.8 0.7 1.1 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Tetrasphaera - Firmicutes; OTU_154 - Proteobacteria; Tetrasphaera - Firmicutes; Clostridium sensu stricto 1 - Actinobacteria; Tessaracoccus - Firmicutes; Romboutsia - Thermotogae; Defluviitoga - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 1.4 0 1 1.8 0.8 1.4 0 1.8 0.8 1.4 0 1.8 0.8 1.2 0.5 5 1.8 0.6 1.3 0.8 1.4 0 1.8 0.8 1.4 1.4 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1 0.6 1.2 0.1 1.5 1.9 0.5 0.5 0.6 1.2 0.1 1.2 0.5 0.5 | 9.8 7 5.4 8 9.4 5 9.4 5 9.4 5 6.4 5 2 2 2 2 2.1 2 2.2 2 0.6 1 1.7 2 2.8 2 0.7 2 2.8 1 0.9 0 1.2 1 0.9 0 1.2 1 0.3 1 0.5 0 1.6 1 5 5 | 4.6. 4.4. 3.2. 6. 3.7. 14. 3.7. 14. 3.7. 14. 3.7. 14. 5.5. 1 5.5. 1 2.5. 3 1.1. 1 2.4. 0 1.7. 0 1.8. 0 1.2. 0 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 1.3. 1 <td>10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 4 1.5 3 0.7 7 1.2 3 0.7 7 1.2 1.1 1 2 1.3 7 1.2 1.3 1.7 1.2 1.3 8 6 8 6</td> <td>6 10.6 8.3 2.1 3 2.1 5 6.83 3 2.1 5 6.83 3 2.1 5 3.55 3 3.55 3 3.55 3 3.55 3 3.55 3 3.55 3 3.55 3 3.57 7 1.2 1.1 3 3 1.4 2 0.9 2 0.7 8 1.4 9 0.9 2 0.7</td> <td>4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 1.2 1 0.7 0.7 5 0.7</td> <td>9 5.9 5.5 6.7 5.3 3 3.7 2 1.4 1.5 1.7 1.5 1.4 1.4 1.4 1.4 1.4 1.1 0.7 2.000 0.7</td> <td>13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 4.5 2 3.9 1.7 1.7 4.5 0.5 0.8 1.7 1 0.9 1.9 1.7 1.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5</td> <td>6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 1.6 1.4 0.6 1.2 1.2 1.2 0.6 1.3 0.6 1.3 1 1 3 1 3 1 1 3 1 3 1 3 1 3 3 1 3</td> <td>17 6 4.6 4.6 4.6 5.6 6.1 2.5 1.9 2.3 0.8 0.8 0.6 0.8 0.6 0.8 0.6 0.8 0.6 0.8 0.2 0.9 0.7 0.8 1.4 1.4 1.4 1.4 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5</td> <td>13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 1 0.2 0.9 0.5 0.7 0.6 899955</td> <td>6.9 1.9 2.3 7.5 4.6 6.5 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 0.9 0.5</td> <td>12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 0.7 0.1 1 0.4 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9</td> <td>14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 1.2 0.5 0.5 0.2 2.2 1.3 0.2 0.6 0.8 0.7 1.1 2.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0</td> | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 4 1.5 3 0.7 7 1.2 3 0.7 7 1.2 1.1 1 2 1.3 7 1.2 1.3 1.7 1.2 1.3 8 6 8 6 | 6 10.6 8.3 2.1 3 2.1 5 6.83 3 2.1 5 6.83 3 2.1 5 3.55 3 3.55 3 3.55 3 3.55 3 3.55 3 3.55 3 3.55 3 3.57 7 1.2 1.1 3 3 1.4 2 0.9 2 0.7 8 1.4 9 0.9 2 0.7 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 1.2 1 0.7 0.7 5 0.7 | 9 5.9 5.5 6.7 5.3 3 3.7 2 1.4 1.5 1.7 1.5 1.4 1.4 1.4 1.4 1.4 1.1 0.7 2.000 0.7 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 4.5 2 3.9 1.7 1.7 4.5 0.5 0.8 1.7 1 0.9 1.9 1.7 1.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 1.6 1.4 0.6 1.2 1.2 1.2 0.6 1.3 0.6 1.3 1 1 3 1 3 1 1 3 1 3 1 3 1 3 3 1 3 | 17 6 4.6 4.6 4.6 5.6 6.1 2.5 1.9 2.3 0.8 0.8 0.6 0.8 0.6 0.8 0.6 0.8 0.6 0.8 0.2 0.9 0.7 0.8 1.4 1.4 1.4 1.4 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 | 13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 1 0.2 0.9 0.5 0.7 0.6 899955 | 6.9 1.9 2.3 7.5 4.6 6.5 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 0.9 0.5 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 1.1 1.3 0.7 0.1 1 0.4 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 0.9 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 0.5 2.2 2.1 1.2 0.5 0.5 0.2 2.2 1.3 0.2 0.6 0.8 0.7 1.1 2.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0 |
| в | Firmicutes; Coprothermobacter - Firmicutes; A55_D21 - Bacteroidetes; G35_D8 - Actinobacteria; Candidatus Microthrix - Firmicutes; OTU_37 - Chloroflexi; RB349 - Synergistetes; Anaerobaculum - Firmicutes; Gelria - Firmicutes; Gelria - Firmicutes; B55_F - Thermotogae; Fervidobacterium - Chloroflexi; Candidatus Promineofilum - Actinobacteria; Propionicimonas - Actinobacteria; Tetrasphaera - Firmicutes; CIU_154 - Proteobacteria; Rhodobacter - Chloroflexi; Candidatus Amarilinum - Firmicutes; Clostridium sensu stricto 1 - Actinobacteria; Tessaracoccus - Firmicutes; Romboutsia - Thermotogae; Defluviitoga - | 14 9.3 4.6 7.1 3.7 4.7 3.6 1.2 0.5 1.8 0.6 3.6 1.3 0.8 1.4 0 1 1.8 1.2 0.4 0.5 1.3 0.8 1.4 0 1 1.8 0.8 1.4 0 5 5 5 7 8 5 6 5 7 1 8 5 7 8 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 | 9.7 8.8 7 3.6 4.8 2 2.8 1.6 0.5 0.6 1.3 0.7 1 0.6 1.2 0.1 1.5 1.9 1.2 0.5 | 9.8 7 5.4 8 9.4 5 9.4 5 9.4 5 9.4 5 12.3 3 6.4 3 2 2 2.2 2 0.6 1 2.2.5 1 0.9 0 1.2 1 0.9 0 1.2 1 0.3 1 0.5 0 1.6 1 0.5 0 1.6 1 0.5 0 1.6 1 0.5 0 0.5 0 0.5 0 0.5 0 0.6 1 0.5 0 0.5 0 0.5 0 0.5 0 0.5 0 0.5 0 0.5 | (.6 4 12 6. 5.7 14 1.7 5. 5.9 5. 2.5 5. 2.5 3. 1 1.2 2.5 3. 1.1 1.2 2.8 3. 1.4 0. 1.7 0. 1.1 1.1 2.2 1.2 0.8 1. 1.3 1.2 0.8 1. 1.3 1. 0.8 0. 1.3 1. 0.5 5. 0.5 5. | 10. 2 5 4 3.3 7 6.6 9 2.6 5 1.3 5 3.6 4 1.5 2 3.6 4 1.7 4 1.5 3 0.7 7 1.2 1.3 1.2 1.2 1.3 7 1.2 1.2 1.2 1.2 1.2 2 3.6 4 1.1 2 1.2 1.2 1.2 1.2 1.2 2 5.6 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 5.7 <td>6 10.6 8.3 2.1 3 2.1 5 8.3 3 2.1 5 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 1.2 4 1.1 3 1.4 2 0.7 0.8 5 5 5 5 5 5 5</td> <td>4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 1 0.7 9 5 0.7 1.5 1 1.2 1 0.7 9 0.7 9 1.8 1.5 0.7 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5</td> <td>9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 2.7 1.5 1.5 1.4 1.4 1.4 3.2 1.4 1.1 0.7 - 0.5 9 4 6 2 9 6 8 6 7 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9</td> <td>13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 1.7 1.9 1.9 1 0.5 0.8 1.7 1.9 0.9 1.7 1.9 0.9 1.7 1.5 0.5 0.5 0.5 0.5</td> <td>6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 1.6 1.4 0.5 1.2 1.2 0.6 1.3 0.6 1.3 1 1.3 1 1.3 1 1.3</td> <td>17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 2 2.3 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8</td> <td>13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 1 0.2 0.9 0.5 0.7 0.6 8 5 9.5 0.7</td> <td>6.9 1.9 2.3 7.5 4.6 6.5 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 0.9 0.5 -8 -8 -8 -8 -8 -8 -8 -8 -8 -8</td> <td>12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 3.6 2 1.1 1.3 1.1 1.3 1.1 1.3 0.1 1 0.4 0.9 0.9 0.9 0.9 0.9</td> <td>14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 2.2 2.1 1.2 1.3 0.2 0.6 0.8 0.7 1.1 2.6 0.8 0.7 1.1 2.5</td> | 6 10.6 8.3 2.1 3 2.1 5 8.3 3 2.1 5 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 3.5 3 1.2 4 1.1 3 1.4 2 0.7 0.8 5 5 5 5 5 5 5 | 4.6 7.3 10.5 2.8 4.1 8.4 4.5 2.5 3.7 0.9 1.8 1.1 0.5 0.7 1.5 1 1.2 1 1 0.7 9 5 0.7 1.5 1 1.2 1 0.7 9 0.7 9 1.8 1.5 0.7 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 | 9 5.9 5.5 6.7 5.3 3.7 2 2 1.4 1.5 2.7 1.5 1.5 1.4 1.4 1.4 3.2 1.4 1.1 0.7 - 0.5 9 4 6 2 9 6 8 6 7 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | 13.5 6.3 3.9 3.7 3.8 1.7 4.5 2 3.9 1.7 1.7 1.9 1.9 1 0.5 0.8 1.7 1.9 0.9 1.7 1.9 0.9 1.7 1.5 0.5 0.5 0.5 0.5 | 6.9 9.3 6.3 3.7 5.3 4.2 4.1 2.4 1.6 1.4 0.5 1.2 1.2 0.6 1.3 0.6 1.3 1 1.3 1 1.3 1 1.3 | 17.6 10.1 4.6 4 5.6 6.1 2.5 1.9 2 2.3 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 0.8 | 13.6 5.7 9.4 8.5 5.2 2.5 2.1 2.4 1.8 0.6 2.8 1.4 1 1 0.2 0.9 0.5 0.7 0.6 8 5 9.5 0.7 | 6.9 1.9 2.3 7.5 4.6 6.5 3.5 4.3 2.2 1.1 1.3 1.8 0.4 0.5 0.1 1 0.4 0.9 0.5 -8 -8 -8 -8 -8 -8 -8 -8 -8 -8 | 12.8 5.4 9.6 5.2 4.5 7 2.8 3.6 2 1.8 3.6 2 1.1 1.3 1.1 1.3 1.1 1.3 0.1 1 0.4 0.9 0.9 0.9 0.9 0.9 | 14.7 5.8 5.3 8.4 4.3 4.1 3.1 2.6 1.7 2.5 2.2 2.1 1.2 1.3 0.2 0.6 0.8 0.7 1.1 2.6 0.8 0.7 1.1 2.5 |

Figure S10| A) Heatmap of the 15 most abundant genera in the mesophilic reactor at Viborg during the survey period. B) Heatmap of the 15 most abundant genera in the thermophilic reactor at Aalborg West during the survey period.

| 0 | | | | | | | | | | | | | | | | | | | | |
|---------------------|------------|-------------|---------------|---------------|----------|------------|--------|-------------|----------|---------------|------------|-----------|----------|-------|---------------|--------------|--------------|----------|-------------|-----------|
| | Mesophilic | | | | | | | | | | | | | | The | THP | | | | |
| Gelria; OTU_66 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1.3 | 2.1 | 1.7 | 1.9 | 1.7 | 1.7 | 0.3 |
| Gelria; OTU_109 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1.3 | 1 | 0.6 | 0.9 | 0.5 | 0 | 0 |
| Gelria; OTU_323 - | 0.1 | 0.2 | 0.3 | 0.2 | 0.4 | 0.3 | 0.8 | 0.3 | 0.3 | 0.2 | 0.2 | 0.5 | 0.2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Gelria; OTU_375 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1.3 | 1.8 |
| Gelria; OTU_303 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.2 | 0 | 0 | 0 | 0 | 0 | 0 | 0.4 | 2.4 |
| Gelria; OTU_12881 - | 0.1 | 0.1 | 0.2 | 0.2 | 0.1 | 0.2 | 0.3 | 0.2 | 0.2 | 0.2 | 0.1 | 0.1 | 0.3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Gelria; OTU_232 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.7 | 0.8 |
| Gelria; OTU_222 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1.2 | 0.2 |
| Gelria; OTU_16322 - | 0.1 | 0.1 | 0.1 | 0.1 | 0 | 0.2 | 0.2 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Gelria; OTU_61609- | 0.1 | 0.1 | 0.1 | 0 | 0 | 0.2 | 0.2 | 0.1 | 0.1 | 0 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Gelria; OTU_8064 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.7 | 0.4 |
| Gelria; OTU_857 - | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.4 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Gelria; OTU_1109 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Gelria; OTU_13927 - | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.1 | 0.3 |
| Gelria; OTU_1757 - | 0 | 0.1 | 0 | 0 | 0 | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | AVEDOERE - | DAMHUSAAEN- | EJBY_MOELLE - | ESBJERG_WEST- | FORNAES- | HJOERRING- | HOBRO- | LUNDTOFTE - | RANDERS- | RINGKOEBING - | SLAGELSE - | SOEHOLT - | VIBORG - | AABY- | AALBORG_EAST- | ALBORG_WEST- | BJERGMARKEN- | HERNING- | FREDERICIA- | NAESTVED- |

Figure S11| Heatmap of the 15 most abundant OTUs belonging to the genus Gelria in mesophilic and thermophilic systems. The wastewater treatment plants had a total of 32 AD reactors (1-4 per plant) and they were analysed 3-30 times. The mean read abundance is shown for each plant. The taxa are sorted by mean read abundance across the plants.

TableS1

Table S1 | Sample site information.

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TableS2

Table S2 | Digester to influent ratios, and mean read abundance values at the OTU level for mesophilic, thermophilic and mesophilic with THP.

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