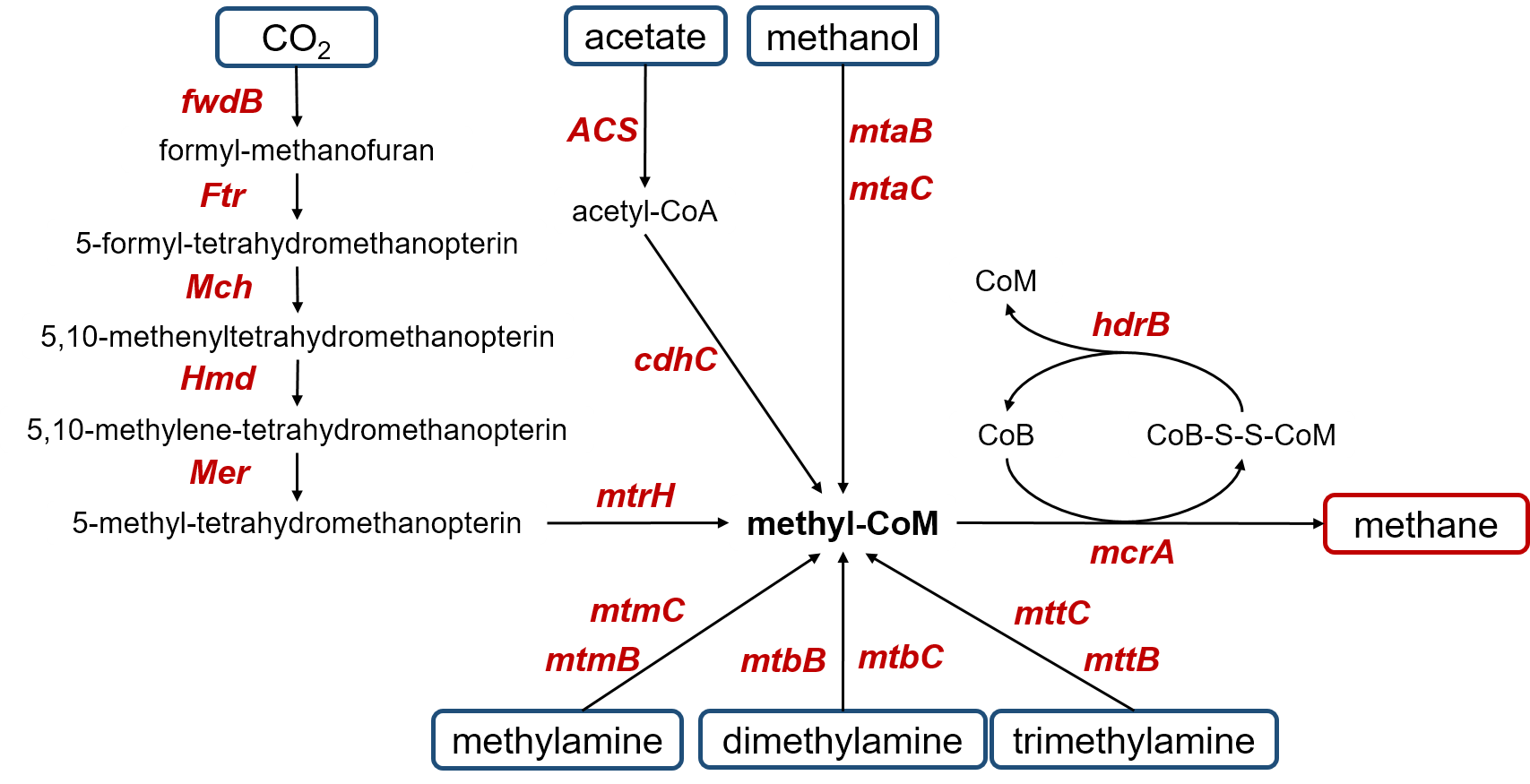
**Supplemental figures and tables**

**High variations of methanogenic microorganisms drive full-scale anaerobic digestion process**

Qiuting Zhang, Mengmeng Wang, Xingyu Ma, Qun Gao, Tengxu Wang, Xuchuan Shi, Jizhong Zhou, Jiane Zuo and Yunfeng Yang



**Fig. S1** Methanogenesis-related functional genes detected by GeoChip 5.0. The methanogenesis pathway and genes involved in each step are based on KEGG.

C:\Users\25438\Desktop\paper_3 wwtps\Tables and figures\Figure core and rare otu.tif

**Fig. S2** Numbers and relative abundance of core and rare OTUs in (a) microbial communities and (b) methanogenic taxa. The number inside each circle is the number of OTUs that exist only in that digester (rare), which is associated with the percentage of their relative abundance in the digester. The number in the overlapped section is the number of OTUs that exist in all digesters (core), with associated percentages of their relative abundance in each digester.

**C:\Users\25438\Desktop\paper_3 wwtps\Tables and figures\Figure S2.tif**

**Fig. S3** Temporal succession of community composition measured by weighted UniFrac distances between samples with time intervals. The dissimilarity values were fitted to linear regression models with turnover rate (*v*) presented as the slope coefficient ± standard error. The Adjusted *r2* values reflected variance explained by linear model and *P* values are based on permutation tests.

**a**

C:\Users\25438\Desktop\paper_3 wwtps\raw data of tables and figures\Figure S3 headmap\methanogenheatmap.tif

**b**

C:\Users\25438\Desktop\paper_3 wwtps\Tables and figures\Figure S3b.tif

**Fig. S4** Heatmaps for (a) methanogen genera and (b) methanogenic genes.

****

**Fig. S5** Relative abundance of microbial community at the phylum level.

**Table S1** Measurements of environmental parameters and biogas production

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Samples | Reactor type | Working volume (m3) | OLR (kg TS/(m3•d)) | HRT (d) | feed | TS | VS |
| BJ10 | CSTR | 12000 | 0.79 | 20 | N/Aa | 14.26 | 8.44 |
| BJ11 | CSTR | 12000 | 0.79 | 20 | N/A | 3.51 | 2.01 |
| BJ12 | CSTR | 12000 | 0.79 | 20 | N/A | 12.25 | 7.73 |
| BJ1 | CSTR | 12000 | 0.79 | 20 | N/A | 17.83 | 9.67 |
| BJ2 | CSTR | 12000 | 0.79 | 20 | N/A | 23.47 | 14.35 |
| BJ3 | CSTR | 12000 | 0.79 | 20 | N/A | 14.04 | 8.6 |
| BJ4 | CSTR | 12000 | 0.79 | 20 | N/A | 17.9 | 10.67 |
| BJ5 | CSTR | 12000 | 0.79 | 20 | N/A | 5.94 | 2.8 |
| BJ6 | CSTR | 12000 | 0.79 | 20 | N/A | 20.53 | 10.01 |
| BJ7 | CSTR | 12000 | 0.79 | 20 | N/A | 29.52 | 12.65 |
| BJ8 | CSTR | 12000 | 0.79 | 20 | N/A | 15.44 | 25.08 |
| BJ9 | CSTR | 12000 | 0.79 | 20 | N/A | 15.19 | 8.86 |
| QD10 | CSTR | 10000 | 1.01 | 15~20 | 614.39 | 12.51 | 4.84 |
| QD11 | CSTR | 10000 | 2.01 | 15~21 | 740.21 | 12.51 | 4.84 |
| QD12 | CSTR | 10000 | 3.01 | 15~22 | 721.62 | 14.47 | 5.38 |
| QD1 | CSTR | 10000 | 4.01 | 15~23 | 733.23 | 21.26 | 4.22 |
| QD2 | CSTR | 10000 | 5.01 | 15~24 | 521.83 | 21.5 | 7.39 |
| QD3 | CSTR | 10000 | 6.01 | 15~25 | 584.17 | 19.23 | 7.59 |
| QD4 | CSTR | 10000 | 7.01 | 15~26 | 697.6 | 13.02 | 4.34 |
| QD5 | CSTR | 10000 | 8.01 | 15~27 | 481 | 10.53 | 3.18 |
| QD6 | CSTR | 10000 | 9.01 | 15~28 | 549.47 | 17.18 | 5.27 |
| QD7 | CSTR | 10000 | 10.01 | 15~29 | 612.67 | 13.11 | 3.97 |
| QD8 | CSTR | 10000 | 11.01 | 15~30 | 617.58 | 14.04 | 5.63 |
| QD9 | CSTR | 10000 | 12.01 | 15~31 | 620.6 | 12.53 | 5.12 |
| NB10 | CSTR | 2700 | 2.56 | 30 | 101.57 | 84.15 | 34.79 |
| NB11 | CSTR | 2700 | 2.56 | 30 | 128.43 | 65.43 | 26.15 |
| NB12 | CSTR | 2700 | 2.56 | 30 | 113.85 | 60.15 | 24.12 |
| NB1 | CSTR | 2700 | 2.56 | 30 | 81 | 84.16 | 34.8 |
| NB2 | CSTR | 2700 | 2.56 | 30 | 81 | 68.38 | 27.57 |
| NB3 | CSTR | 2700 | 2.56 | 30 | 71.92 | 58.44 | 26.56 |
| NB4 | CSTR | 2700 | 2.56 | 30 | 64.25 | 79.72 | 32.57 |
| NB5 | CSTR | 2700 | 2.56 | 30 | 64.77 | 61.72 | 24.15 |
| NB6 | CSTR | 2700 | 2.56 | 30 | 62 | 98.96 | 36.71 |
| NB7 | CSTR | 2700 | 2.56 | 30 | 35.83 | 94.27 | 31.31 |
| NB8 | CSTR | 2700 | 2.56 | 30 | 41.44 | 122.09 | 42.87 |
| NB9 | CSTR | 2700 | 2.56 | 30 | 61.1 | 26.07 | 22.45 |

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Samples | COD | pH | VFA | alkalinity | ammonia | sulfate | Chloride |
| BJ10 | 24.26 | 8.35 | N/A | N/A | 746.3 | 6.07 | 142.88 |
| BJ11 | 30 | 7.17 | N/A | N/A | N/A | 1.07 | 130.62 |
| BJ12 | 36 | 7.23 | N/A | N/A | N/A | 1.52 | 151.59 |
| BJ1 | 62.18 | 7.52 | N/A | N/A | 876.77 | 10.56 | 174.38 |
| BJ2 | 199.12 | 7.13 | N/A | N/A | 784.25 | 5.42 | 164.84 |
| BJ3 | 28.41 | 7.32 | N/A | N/A | 843.23 | 4.88 | 96.81 |
| BJ4 | 247.31 | 7.32 | N/A | N/A | N/A | 1.7 | 141.25 |
| BJ5 | 52.63 | 7.75 | N/A | N/A | 311 | 1.06 | 84.28 |
| BJ6 | 115.79 | 7.44 | N/A | N/A | N/A | 3.05 | 149.51 |
| BJ7 | 9.43 | 7.22 | N/A | N/A | N/A | 2.09 | 91.3 |
| BJ8 | 56.34 | 7.5 | N/A | N/A | N/A | 1.77 | 111.12 |
| BJ9 | 18 | 7.43 | N/A | N/A | N/A | 2.18 | 108.39 |
| QD10 | 70.64 | 7.22 | 197.4 | 4737.7 | 572.82 | 36.42 | 1142.7 |
| QD11 | 82.13 | 7.49 | 241.5 | 3960 | 919.77 | 27.53 | 1182.2 |
| QD12 | 131.06 | 7.37 | 516 | 4356.7 | 572.82 | 23.39 | 1189.2 |
| QD1 | 101.42 | 7.65 | 222 | 5270 | 1200.58 | 61.4 | 1413.6 |
| QD2 | 116.3 | 7.6 | 462.6 | 6692.5 | 992.41 | 42.21 | 1762 |
| QD3 | 103.41 | 7.8 | 214.5 | 7270 | 1016.7 | 12.92 | 13.99 |
| QD4 | 298.92 | 7.65 | 327.4 | N/A | N/A | 8.68 | 1506.9 |
| QD5 | 84.21 | 8.01 | N/A | N/A | 442.06 | 29.6 | 1253.3 |
| QD6 | 31.58 | 7.8 | N/A | N/A | N/A | 12.98 | 1504 |
| QD7 | 42.45 | 7.26 | N/A | N/A | N/A | 1.07 | 1063.6 |
| QD8 | 107.04 | 7.38 | N/A | N/A | N/A | 28.45 | 1093.3 |
| QD9 | 66 | 7.14 | N/A | N/A | N/A | 7.01 | 945.45 |
| NB10 | 246.63 | 8.58 | 398 | 4037 | 1440.19 | 13.28 | 80.3 |
| NB11 | 99.15 | 8.52 | 563 | 3769 | 1440.19 | 17.67 | 108.2 |
| NB12 | 78.72 | 8.57 | 1041 | 4186 | 1613.67 | 11.55 | 92.86 |
| NB1 | 107.49 | 7.55 | 621 | 4506 | 1616.92 | 16.73 | 145.8 |
| NB2 | 197.36 | 8.03 | 894 | 5210 | 2172.04 | 17.09 | 92.73 |
| NB3 | 62.5 | 7.5 | 815 | 5540 | 1495.49 | 16.51 | 77.16 |
| NB4 | 395.7 | 7.37 | 1283 | 6478 | N/A | 7.06 | 138.74 |
| NB5 | 84.21 | 8.18 | 1201 | 8335 | 1825.49 | 5.22 | 83.36 |
| NB6 | 136.84 | 7.98 | 1618 | 8265 | N/A | 3.01 | 105.81 |
| NB7 | 89.62 | 7.7 | 2238 | 6603 | N/A | 1.07 | 78.7 |
| NB8 | 169.7 | 7.77 | 926 | 6677 | N/A | 2.12 | 97.27 |
| NB9 | 81 | 7.83 | 1795 | 7083 | N/A | 3.75 | 79.83 |

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Samples | Fe | Cu | Cr | airtemp | biogas/feed | biogas/biomass | biogas |
| BJ10 | 0.024 | 0.001 | 0.002 | 13 | N/A | N/A | N/A |
| BJ11 | 0.26 | 0.001 | 0.003 | 4 | N/A | N/A | N/A |
| BJ12 | 0.02 | 0.001 | 0.003 | -6 | N/A | N/A | N/A |
| BJ1 | 0.065 | 0.014 | 0.003 | -6 | N/A | N/A | N/A |
| BJ2 | 0.2 | 0.001 | 0.002 | -2 | N/A | N/A | N/A |
| BJ3 | 0.14 | 0.001 | 0.002 | 5 | N/A | N/A | N/A |
| BJ4 | 0.14 | 0.001 | 0.001 | 12 | N/A | N/A | N/A |
| BJ5 | 0.042 | 0.001 | 0.001 | 21 | N/A | N/A | N/A |
| BJ6 | 0.063 | 0.001 | 0.001 | 23 | N/A | N/A | N/A |
| BJ7 | 0.037 | 0.001 | 0.001 | 27 | N/A | N/A | N/A |
| BJ8 | 0.046 | 0.001 | 0.002 | 27 | N/A | N/A | N/A |
| BJ9 | 0.037 | 0.001 | 0.003 | 20 | N/A | N/A | N/A |
| QD10 | 0.062 | 0.003 | 0.006 | 16 | 14.51 | 226.2 | 8693 |
| QD11 | 0.087 | 0.001 | 0.01 | 7 | 13.95 | 225.9 | 10116 |
| QD12 | 0.072 | 0.001 | 0.01 | -1 | 20.24 | 256.12 | 13419 |
| QD1 | 0.05 | 0.001 | 0.016 | -2 | 18.14 | 166.02 | 12573 |
| QD2 | 0.49 | 0.001 | 0.016 | 0 | 33.85 | 315.97 | 15376 |
| QD3 | 0.34 | 0.011 | 0.018 | 6 | 29.98 | 241.76 | 13698 |
| QD4 | 0.17 | 0.001 | 0.011 | 11 | 18.59 | 243.78 | 10665 |
| QD5 | 0.096 | 0.001 | 0.011 | 18 | 18.43 | 259.54 | 7818.6 |
| QD6 | 0.045 | 0.001 | 0.011 | 22 | 14.96 | 163.55 | 7740.3 |
| QD7 | 0.053 | 0.002 | 0.01 | 27 | 11.99 | 159.3 | 7238.4 |
| QD8 | 0.1 | 0.001 | 0.011 | 28 | 12.49 | 180.85 | 7665 |
| QD9 | 0.034 | 0.002 | 0.005 | 23 | 12.77 | 196.39 | 7577.1 |
| NB10 | 0.18 | 0.005 | 0.044 | 19 | 9.92 | 24.1 | 995.75 |
| NB11 | 0.11 | 0.11 | 0.022 | 2 | 9.92 | 20.3 | 1257.6 |
| NB12 | 0.087 | 0.044 | 0.017 | 7 | 9.91 | 23.35 | 1048.2 |
| NB1 | 0.41 | 0.015 | 0.042 | 6 | 15.7 | 35.37 | 1265.6 |
| NB2 | 0.29 | 0.034 | 0.058 | 8 | 11.81 | 30.9 | 957.08 |
| NB3 | 0.2 | 0.014 | 0.039 | 12 | 14.85 | 35.29 | 1053.4 |
| NB4 | 0.61 | 0.019 | 0.12 | 18 | 17.08 | 33.66 | 1060.6 |
| NB5 | 0.4 | 0.003 | 0.087 | 22 | 13.01 | 25.23 | 796.07 |
| NB6 | 0.74 | 0.016 | 0.12 | 25 | 14.35 | 17.57 | 839.22 |
| NB7 | 0.53 | 0.05 | 0.059 | 32 | 17 | 18.21 | 398.5 |
| NB8 | 0.6 | 0.077 | 0.085 | 31 | 11.51 | 18.28 | 456.36 |
| NB9 | 0.63 | 0.082 | 0.05 | 25 | 9.81 | 14.21 | 573.33 |

aN/A means not available.

**Table S2** Spatial and temporal difference of archaeal and bacterial community and methanogenic genes by three dissimilarity tests

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Groups | Community | MRPP | | anosim | | adonis | |
| Delta | *P* | *r* | *P* | *r2* | *P* |
| BJ vs QD | archaea | 0.51 | 0.001 | 0.529 | 0.001 | 0.299 | 0.001 |
| bacteria | 0.43 | 0.001 | 0.476 | 0.001 | 0.274 | 0.001 |
| methanogenic genes | 0.139 | 0.001 | 0.481 | 0.001 | 0.337 | 0.001 |
| QD vs NB | archaea | 0.547 | 0.001 | 0.596 | 0.002 | 0.383 | 0.001 |
| bacteria | 0.644 | 0.001 | 0.684 | 0.001 | 0.322 | 0.001 |
| methanogenic genes | 0.153 | 0.001 | 0.61 | 0.001 | 0.359 | 0.001 |
| BJ vs NB | archaea | 0.533 | 0.001 | 0.697 | 0.001 | 0.409 | 0.001 |
| bacteria | 0.605 | 0.001 | 0.605 | 0.001 | 0.293 | 0.001 |
| methanogenic genes | 0.117 | 0.001 | 0.602 | 0.001 | 0.373 | 0.001 |

**Table S3** Core genera that exist in more than 75% samples

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| genus | phylum | Beijing | Qingdao | Ningbo | all samples |
| *Smithella* | *Proteobacteria* | 4.837a | 1.932 | 0.657 | 2.527 |
| *Syntrophomonas* | *Firmicutes* | 1.203 | 2.712 | 2.562 | 2.159 |
| *Methanolinea* | *Euryarchaeota* | 0.649 | 4.010 | 0.018 | 1.999 |
| *Saccharofermentans* | *Firmicutes* | 0.130 | 4.581 | 0.063 | 1.681 |
| *Thauera* | *Proteobacteria* | 4.181 | 0.023 | 0.104 | 1.476 |
| *Comamonas* | *Proteobacteria* | 2.872 | 0.028 | 0.481 | 1.159 |
| *Methanosaeta* | *Euryarchaeota* | 1.614 | 1.155 | 0.020 | 0.956 |
| *Bellilinea* | *Chloroflexi* | 0.521 | 1.118 | 1.219 | 0.953 |
| *Leptolinea* | *Chloroflexi* | 0.783 | 1.381 | 0.177 | 0.798 |
| *Paludibacter* | *Bacteroidetes* | 1.303 | 0.253 | 0.508 | 0.688 |
| *Petrimonas* | *Bacteroidetes* | 0.065 | 1.182 | 0.778 | 0.675 |
| *Lutispora* | *Firmicutes* | 0.015 | 0.018 | 1.170 | 0.511 |
| *Clostridium* | *Firmicutes* | 0.134 | 0.283 | 0.936 | 0.451 |
| *Desulfomicrobium* | *Proteobacteria* | 0.563 | 0.448 | 0.016 | 0.436 |
| *Syntrophorhabdus* | *Proteobacteria* | 0.740 | 0.270 | 0.192 | 0.401 |
| *Methanobacterium* | *Euryarchaeota* | 0.023 | 0.014 | 0.795 | 0.351 |
| *Syntrophus* | *Proteobacteria* | 0.352 | 0.576 | 0.032 | 0.328 |
| *Cloacibacillus* | *Synergistetes* | 0.494 | 0.289 | 0.110 | 0.303 |
| *Sedimentibacter* | *Firmicutes* | 0.059 | 0.297 | 0.527 | 0.301 |
| *Catellibacterium* | *Proteobacteria* | 0.075 | 0.012 | 0.643 | 0.287 |
| *Synergistes* | *Synergistetes* | 0.208 | 0.360 | 0.148 | 0.247 |
| *Anaerovorax* | *Firmicutes* | 0.128 | 0.490 | 0.101 | 0.240 |
| *OD1* | *OD1* | 0.273 | 0.270 | 0.024 | 0.236 |
| *Subdivision5* | *Verrucomicrobia* | 0.078 | 0.509 | 0.060 | 0.220 |
| *Dysgonomonas* | *Bacteroidetes* | 0.082 | 0.385 | 0.121 | 0.218 |
| *Longilinea* | *Chloroflexi* | 0.300 | 0.095 | 0.240 | 0.212 |
| *Methanospirillum* | *Euryarchaeota* | 0.511 | 0.055 | 0.021 | 0.212 |
| *Subdivision3* | *Verrucomicrobia* | 0.118 | 0.264 | 0.251 | 0.210 |
| *Treponema* | *Spirochaetes* | 0.040 | 0.478 | 0.014 | 0.182 |
| *Parabacteroides* | *Bacteroidetes* | 0.406 | 0.017 | 0.032 | 0.169 |
| *Caldilinea* | *Chloroflexi* | 0.343 | 0.031 | 0.068 | 0.154 |
| *Acetivibrio* | *Firmicutes* | 0.088 | 0.214 | 0.145 | 0.153 |
| *Desulfobulbus* | *Proteobacteria* | 0.286 | 0.060 | 0.012 | 0.141 |
| *Rhodobacter* | *Proteobacteria* | 0.225 | 0.011 | 0.154 | 0.141 |
| *Gelria* | *Firmicutes* | 0.282 | 0.030 | 0.052 | 0.135 |
| *Novosphingobium* | *Proteobacteria* | 0.133 | 0.010 | 0.165 | 0.129 |
| *Conexibacter* | *Actinobacteria* | 0.062 | 0.018 | 0.257 | 0.128 |
| *Paracoccus* | *Proteobacteria* | 0.268 | 0.015 | 0.047 | 0.122 |
| *Acinetobacter* | *Proteobacteria* | 0.108 | 0.176 | 0.029 | 0.111 |
| *Pasteuria* | *Firmicutes* | 0.128 | 0.114 | 0.076 | 0.106 |
| *Formivibrio* | *Proteobacteria* | 0.047 | 0.036 | 0.182 | 0.100 |
| *Gp2* | *Armatimonadetes* | 0.034 | 0.014 | 0.233 | 0.098 |
| *Blastopirellula* | *Planctomycetes* | 0.107 | 0.026 | 0.133 | 0.095 |
| *Geobacter* | *Proteobacteria* | 0.041 | 0.188 | 0.032 | 0.090 |
| *Bacteroides* | *Bacteroidetes* | 0.101 | 0.122 | 0.014 | 0.087 |
| *Levilinea* | *Chloroflexi* | 0.073 | 0.133 | 0.036 | 0.083 |
| *Syntrophobacter* | *Proteobacteria* | 0.158 | 0.057 | 0.027 | 0.081 |
| *Roseomonas* | *Proteobacteria* | 0.092 | 0.008 | 0.092 | 0.078 |
| *Papillibacter* | *Firmicutes* | 0.099 | 0.073 | 0.022 | 0.073 |
| *Sphingomonas* | *Proteobacteria* | 0.137 | 0.015 | 0.034 | 0.070 |
| *Devosia* | *Proteobacteria* | 0.076 | 0.015 | 0.092 | 0.068 |
| *Planctomyces* | *Planctomycetes* | 0.088 | 0.018 | 0.060 | 0.062 |
| *Leucobacter* | *Actinobacteria* | 0.059 | 0.013 | 0.102 | 0.060 |
| *Ferruginibacter* | *Bacteroidetes* | 0.070 | 0.010 | 0.057 | 0.056 |
| *Gracilibacter* | *Firmicutes* | 0.036 | 0.032 | 0.092 | 0.055 |
| *Sporobacter* | *Firmicutes* | 0.059 | 0.066 | 0.020 | 0.054 |
| *Vampirovibrio* | *Proteobacteria* | 0.054 | 0.023 | 0.069 | 0.053 |
| *Acetoanaerobium* | *Firmicutes* | 0.093 | 0.016 | 0.025 | 0.052 |
| *Tissierella* | *Firmicutes* | 0.013 | 0.077 | 0.061 | 0.050 |
| *Pseudomonas* | *Proteobacteria* | 0.047 | 0.047 | 0.030 | 0.043 |
| *Neochlamydia* | *Chlamydiae* | 0.060 | 0.011 | 0.039 | 0.043 |
| *Methanoculleus* | *Euryarchaeota* | 0.031 | 0.068 | 0.028 | 0.042 |
| *Alkaliflexus* | *Bacteroidetes* | 0.024 | 0.048 | 0.011 | 0.032 |
| *Desulfovibrio* | *Proteobacteria* | 0.040 | 0.037 | 0.011 | 0.030 |
| *Hydrogenophaga* | *Proteobacteria* | 0.035 | 0.020 | 0.032 | 0.030 |
| *Aminobacterium* | *Synergistetes* | 0.033 | 0.028 | 0.028 | 0.030 |
| aProportion of the average abundance (%) is presented. | | | |  |  |

**Table S4** Functional redundancy indices of fermentation and methanogenic groups

|  |  |  |
| --- | --- | --- |
| F/T | Fermentation | Methanogenesis |
| Beijing | 0.57(0.03)a | 0.43(0.04) |
| Qingdao | 0.54(0.05) | 0.28(0.06) |
| Ningbo | 0.45(0.10) | 0.37(0.07) |

aData are presented as mean (SD) calculated from 12 samples within each digester. The functional redundancy index is calculated as the ratio of functional structure to taxonomic composition using Shannon indices.

**Table S5** Results of MiSeq sequencing experiments

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Raw reads | Chimeras | Final reads | Coverage | Richness | Shannon index |
| BJ10 | 37691 | 0.646 | 29450 | 0.949 | 3451 | 6.93 |
| BJ11 | 45605 | 0.737 | 35836 | 0.959 | 3274 | 6.53 |
| BJ12 | 53463 | 0.711 | 41399 | 0.955 | 3395 | 6.76 |
| BJ1 | 39184 | 0.731 | 31499 | 0.972 | 2608 | 5.99 |
| BJ2 | 31650 | 0.743 | 25835 | 0.977 | 2344 | 5.87 |
| BJ3 | 43329 | 0.746 | 35722 | 0.979 | 2306 | 5.88 |
| BJ4 | 39177 | 0.709 | 31935 | 0.972 | 2548 | 6.13 |
| BJ5 | 36202 | 0.741 | 29697 | 0.976 | 2285 | 5.82 |
| BJ6 | 39823 | 0.706 | 31305 | 0.966 | 3055 | 6.42 |
| BJ7 | 53483 | 0.749 | 42126 | 0.965 | 3148 | 6.45 |
| BJ8 | 53790 | 0.728 | 41459 | 0.956 | 3463 | 6.75 |
| BJ9 | 54024 | 0.706 | 41007 | 0.947 | 3624 | 6.83 |
| QD10 | 40616 | 0.715 | 32580 | 0.958 | 2295 | 5.95 |
| QD11 | 54927 | 0.706 | 44754 | 0.956 | 2418 | 6.08 |
| QD12 | 43928 | 0.697 | 34801 | 0.947 | 2545 | 6.33 |
| QD1 | 52428 | 0.740 | 42770 | 0.959 | 2282 | 5.72 |
| QD2 | 43867 | 0.720 | 34952 | 0.957 | 2319 | 5.84 |
| QD3 | 18214 | 0.686 | 14247 | 0.950 | 2469 | 6.15 |
| QD4 | 22271 | 0.696 | 17537 | 0.955 | 2451 | 6.25 |
| QD5 | 17671 | 0.685 | 13782 | 0.950 | 2632 | 6.39 |
| QD6 | 26728 | 0.696 | 21398 | 0.957 | 2469 | 6.21 |
| QD7 | 17642 | 0.725 | 14641 | 0.967 | 2037 | 5.53 |
| QD8 | 21023 | 0.693 | 17088 | 0.961 | 2596 | 6.27 |
| QD9 | 24329 | 0.683 | 19657 | 0.961 | 2455 | 6.43 |
| NB10 | 56399 | 0.748 | 43149 | 0.954 | 3504 | 6.14 |
| NB11 | 65551 | 0.726 | 48928 | 0.947 | 3841 | 6.70 |
| NB12 | 53089 | 0.711 | 39625 | 0.943 | 4161 | 6.92 |
| NB1 | 60393 | 0.728 | 46922 | 0.957 | 3667 | 6.56 |
| NB2 | 58531 | 0.717 | 44806 | 0.950 | 3866 | 6.73 |
| NB3 | 46338 | 0.715 | 35628 | 0.954 | 3890 | 6.85 |
| NB4 | 47117 | 0.745 | 35357 | 0.957 | 3415 | 6.23 |
| NB5 | 44771 | 0.730 | 32826 | 0.950 | 3618 | 6.50 |
| NB6 | 60647 | 0.750 | 44995 | 0.955 | 3470 | 6.16 |
| NB7 | 53646 | 0.732 | 39884 | 0.953 | 3571 | 6.53 |
| NB8 | 48028 | 0.728 | 35836 | 0.950 | 3615 | 6.43 |
| NB9 | 46729 | 0.735 | 34896 | 0.951 | 3557 | 6.35 |