

Supplementary Material

Illuminating Anaerobic Microbial Community and Co-occurrence Patterns across a Quality Gradient in Chinese Liquor Fermentation Pit Muds

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Running title

Microbial community reflects pit-mud quality and stability

Supplementary method

Quantification of lactic acid in FPM

For the detection of lactate, the air-dried FPM was vortex mixed with ultrapure water on a 1:3 (w/v) ratio at room temperature and then centrifugated (5 min, 8000 rpm). The supernatant was filtered through 0.22 μm MCE syringe filter, and a 10 μL of this solution was injected onto a high-performance liquid chromatography apparatus (Agilent 1200 system) (Agilent Technologies, Palo Alto, CA, USA) with ultraviolet (UV) detector. The chromatographic separation was carried out on a Xselect™ HSS T3 column with particle size of 5 μm (4.6 \times 250 mm, Waters Corporation, Milford, MS, USA) at 30 °C. The mobile phase consisted of 10 mM of NaH_2PO_4 in ultrapure water (pH adjusted to 2.9). The flow rate and UV detector were set at 0.80 ml/min and a wavelength of 210 nm.

Construction of calibration curve for the quantification of *Clostridia*, *C. kluyveri* and LAB in FPM samples based on real-time quantitative PCR (qPCR)

The plasmid DNA used for the construction of calibration curve for quantifying the *Clostridia* and *C. kluyveri* was constructed based on the 16S rRNA gene from species of *C. kluyveri*, and the plasmid DNA used for the construction of calibration curve for quantifying the lactic acid bacteria (LAB, e.g., *Lactobacillus*, *Pediococcus*, *Leuconostoc* and *Weissella*, see reference 6) was constructed based on the 16S rRNA gene from species of *Lactobacillus homohiochii*. Firstly, the near full length 16S rRNA genes of *C. kluyveri* and *Lactobacillus homohiochii* amplified with primer set 27F/1492R (1), were ligated into pMD19-T vector (TaKaRa), cloned in *E.coli* JM109 and verified as described by Wang et al. (2). Secondly, the 16S rRNA gene copy numbers of above plasmids were calculated using the previous equation (3). Then, ten-fold serial dilutions of the above plasmids containing 16S rRNA genes of *C. kluyveri* or *L. homohiochii*, were amplified according to the PCR reaction system and conditions described in manuscript (section Real-Time quantitative PCR analysis) using corresponding specific primers SJ-F/SJ-R for *Clostridia* (generating an about 270-bp amplicon) (4), CloKly1F/CloKly1R for *C. kluyveri* (~ 185-bp amplicon) (5) and Lac1/ Lac2 for LAB (~ 345-bp amplicon) (6), and the standard curves for the quantification of *Clostridia*, *C. kluyveri* and LAB were respectively generated by plotting the threshold cycle (Ct) values against the Log₁₀ 16S rRNA gene copy numbers of above dilutions. Three replicates of each dilution were analyzed.

The amplification efficiency and R^2 value of calibration curve for *Clostridia* were 103% and 0.9998, for *C. kluyveri* were 105% and 0.9997, and for LAB were 106% and 0.992, indicating that the qPCR assay for quantifying above microbial taxa were suitable and accurate (7, 8).

Figures

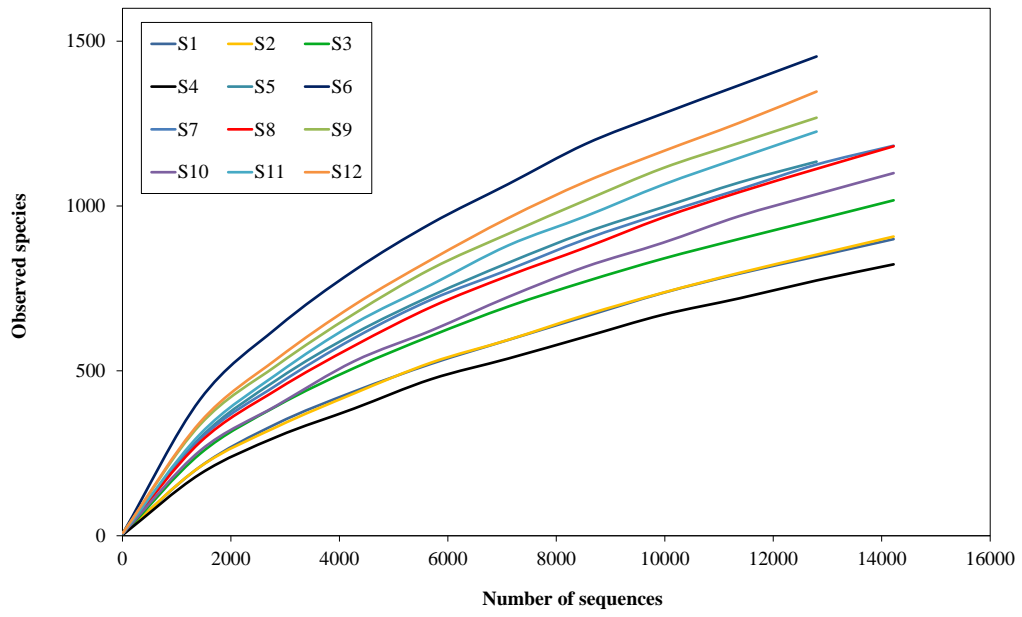


Fig. S1 Rarefaction curves based on the OTUs at the cutoff of 97% 16S rRNA sequence similarity.

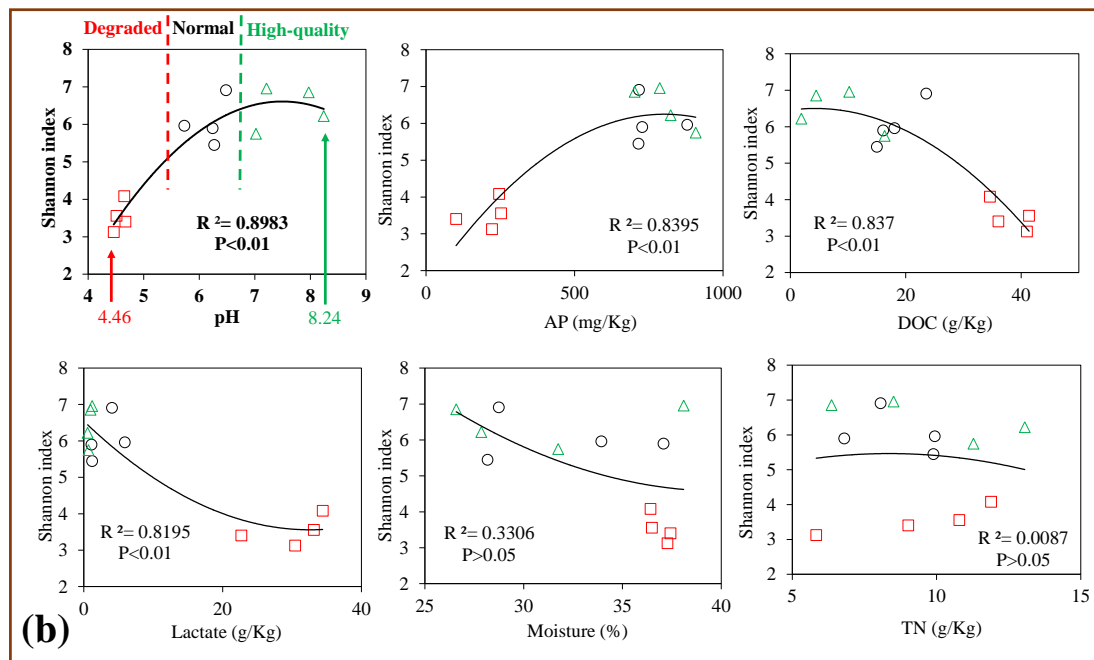
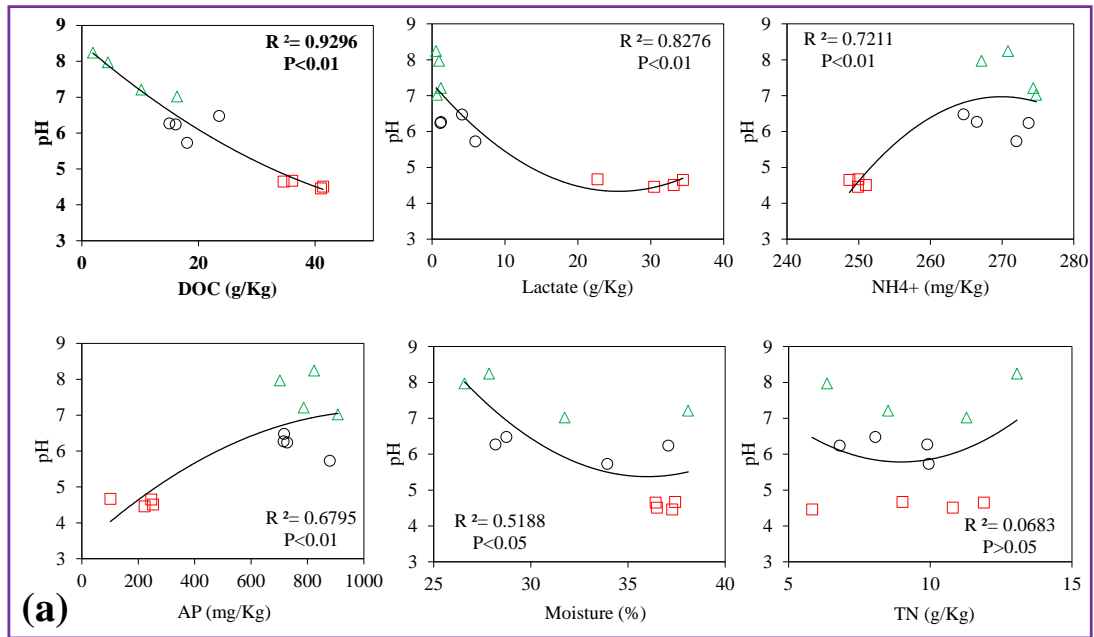


Fig. S2 Relationships between FPM pH and other biogeochemical attributes (a); Relationships between FPM biogeochemical attributes and FPM microbial community diversity (b). (Δ): High-quality FPMs, (\circ): Normal FPMs, (\square): Degraded FPMs.

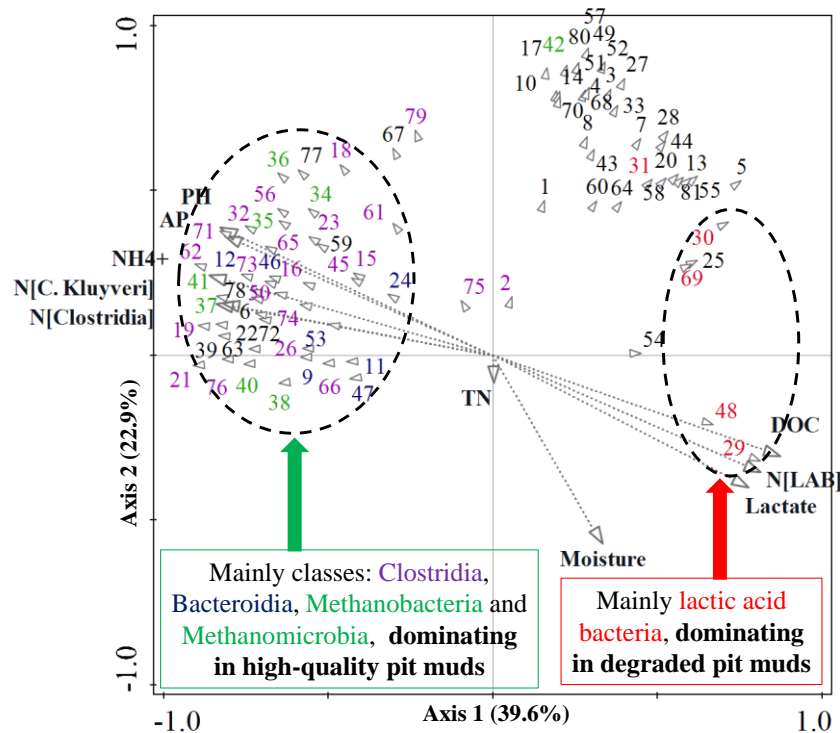


Fig. S3 Redundancy analysis of biogeochemical attributes and 81 targeted genera (abundance >0.1 % in at least one sample) in all samples. Arrows indicate the direction and magnitude of biogeochemical attributes associated with microbial community structures. 1:Acetobacter, 2:Acidaminococcus, 3:Acinetobacter, 4:Actinomyces, 5:Alicyclobacillus, 6:Aminobacterium, 7:Arthrobacter, 8:Bacillus, 9:*Bacteroides*, 10:Balneimonas, 11:*BF311*, 12:*Blvii28*, 13:Brochothrix, 14:Bulleidia, 15:*Caldicoprobacter*, 16:*Caloramator*, 17:Candidatus_Nitrososphaera, 18:*Clostridiaceae_Clostridium*, 19:*Coprococcus*, 20:*Corynebacterium*, 21:*Dehalobacterium*, 22:Desulfococcus, 23:*Desulfosporosinus*, 24:*Dysgonomonas*, 25:Enhydrobacter, 26:*Garciella*, 27:Hyphomicrobium, 28:Kaistobacter, 29:*Lactobacillus*, 30:*Lactococcus*, 31:*Leuconostoc*, 32:*Lutispora*, 33:Lysinibacillus, 34:*Methanobacterium*, 35:*Methanobrevibacter*, 36:*Methanocorpusculum*, 37:*Methanoculleus*, 38:*Methanofollis*, 39:Methanomassiliicoccus, 40:*Methanosaeta*, 41:*Methanosarcina*, 42:*Methanosphaera*, 43:Mycobacterium, 44:Myroides, 45:*Oscillospira*, 46:*Paludibacter*, 47:*Parabacteroides*, 48:*Pediococcus*, 49:Pedomicrobium, 50:*Pelotomaculum*, 51:Petrobacter, 52:Plesiocystis, 53:*Prevotella*, 54:Providencia, 55:Pseudomonas, 56:*Pseudoramibacter_Eubacterium*, 57:Pseudoxanthomonas, 58:Psychrobacter, 59:RFN20, 60:Rhodoplanes, 61:*Ruminococcus*, 62:*Sedimentibacter*, 63:SHD-231, 64:Sphingobacterium, 65:*Sporanaerobacter*, 66:*Sporotomaculum*, 67:Staphylococcus, 68:Steroidobacter, 69:*Streptococcus*, 70:Streptomyces, 71:*Syntrophomonas*, 72:T78, 73:*Tepidimicrobium*, 74:*Thermacetogenium*, 75:*Thermoanaerobacterium*, 76:*Tissierella_Soehngenia*, 77:Treponema, 78:vadinCA11, 79:*VadinHB04*, 80:Vogesella, 81:Yersinia. According to the distribution of genera of *Clostridia* (purple font), *Bacteroidia* (blue font), methanogens (i.e. *Methanobacteria*, *Methanomicrobia*, green font) and lactic acid bacteria (LAB, red font) observed in Fig. S3, two circles were manually drawn.

Tables

Table S1

The detailed sensory characteristics of degraded, normal and high-quality FPMs.




Sensory characteristics	Quality grades of fermentation pit muds		
	Degraded	Normal	High quality
Color	silvery-gray	earth-color	grey-black
Texture	white lumps or aciform crystals	moist, soft and uniform texture	moist, soft and uniform texture
Odor	no or little ester aroma	ester aroma	strong ester aroma, hydrogen sulfide and ammonia odor
Figures of pit muds	 Degraded FPM	 Normal FPM	 High quality FPM

Table S2

Relative abundances (% of total good quality sequences) of all phyla in each sample within different type of FPM. Twenty phyla with pink shading were shared by all samples, and total abundances of them in each sample were shown in the last line.

Phyla	Degraded				Normal				High quality			
	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12
<i>Firmicutes</i>	92.75	91.68	87.00	93.73	85.89	31.48	65.98	25.90	36.04	24.12	24.18	40.30
<i>Eurvarchaeota</i>	1.14	1.24	0.97	0.74	0.75	33.97	26.58	55.29	18.18	37.68	34.98	19.43
<i>Bacteroidetes</i>	1.16	1.04	1.41	0.95	0.88	2.94	1.58	9.15	26.78	28.79	28.70	25.78
<i>Proteobacteria</i>	1.72	2.14	5.95	1.63	4.19	11.13	1.47	0.79	1.46	0.91	1.11	1.43
<i>WWE1</i>	0.10	0.05	0.07	0.09	0.08	0.08	0.08	0.95	3.55	5.01	5.15	7.39
<i>Actinobacteria</i>	0.51	0.81	1.51	0.40	1.99	10.43	0.53	0.20	0.36	0.77	0.19	1.18
<i>Chloroflexi</i>	0.19	0.26	0.14	0.12	0.59	0.78	0.49	2.27	1.38	0.08	1.00	0.13
<i>Crenarchaeota</i>	0.08	0.17	0.15	0.06	0.96	3.81	0.08	0.08	0.13	0.09	0.13	0.09
<i>Synergistetes</i>	0.15	0.13	0.09	0.18	0.11	0.21	0.21	1.95	0.89	0.68	0.33	0.66
<i>Acidobacteria</i>	0.08	0.09	0.21	0.08	0.62	0.87	0.08	0.02	0.05	0.03	0.09	0.06
<i>Verrucomicrobia</i>	0.03	0.03	0.05	0.03	0.08	0.14	0.04	0.07	0.26	0.11	0.28	0.19
<i>Nitrospirae</i>	0.01	0.06	0.11	0.03	0.21	0.68	0.03	0.01	0.04	0.01	0.01	0.07
<i>Planctomycetes</i>	0.01	0.02	0.15	0.02	0.14	0.27	0.04	0.08	0.04	0.01	0.19	0.03
<i>WS1</i>	0.03	0.04	0.02	0.02	0.03	0.02	0.04	0.04	0.04	0.01	0.02	0.01
<i>Chlorobi</i>	0.01	0.01	0.01	0.02	0.02	0.01	0.01	0.01	0.03	0.02	0.01	0.02
<i>Tenericutes</i>	0.01	0.01	0.01	0.01	0.00	0.01	0.03	0.18	1.01	0.06	0.17	0.00
<i>Gemmatimonadetes</i>	0.03	0.03	0.01	0.01	0.21	0.75	0.02	0.00	0.02	0.01	0.01	0.01
<i>Lentisphaerae</i>	0.01	0.01	0.01	0.02	0.00	0.01	0.01	0.41	0.21	0.01	0.28	0.00
<i>Spirochaetes</i>	0.01	0.01	0.01	0.00	0.01	0.05	0.01	0.04	0.08	0.02	0.02	0.21
<i>OP9</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.04	0.00	0.33	0.00	0.02	0.01
<i>Armatimonadetes</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.08	0.00	0.00	0.07	0.00
<i>Cyanobacteria</i>	0.04	0.01	0.02	0.02	0.04	0.00	0.01	0.01	0.01	0.00	0.01	0.00
<i>Caldithrix</i>	0.01	0.01	0.01	0.02	0.01	0.00	0.03	0.00	0.03	0.00	0.00	0.01
<i>WS3</i>	0.00	0.00	0.01	0.01	0.02	0.02	0.00	0.00	0.01	0.00	0.00	0.00
<i>Thermi</i>	0.00	0.00	0.01	0.00	0.00	0.01	0.01	0.00	0.01	0.00	0.01	0.01
<i>GAL15</i>	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00
<i>TA06</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00
<i>TM7</i>	0.00	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Fusobacteria</i>	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01
<i>TM6</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Deferribacteres</i>	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
<i>Fibrobacteres</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
<i>OD1</i>	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Total shared phyla	97.95	97.77	97.82	98.09	96.54	96.83	97.24	96.82	89.21	98.34	96.36	96.79
Total identified phyla	98.07	97.85	97.91	98.18	96.84	97.77	97.41	97.53	90.96	98.44	96.95	97.05

Table S3

Relative abundances (% of total good quality sequences) of all classified classes in each sample within different type of FPM. Seven dominant classes with pink shading were shared by all samples, and total abundances of them in each sample were shown in the last line.

Class	Degraded				Normal				High quality				Average
	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	
<i>Bacilli</i>	85.56	85.46	81.54	89.10	7.84	8.73	4.84	2.67	4.26	2.69	3.74	4.48	31.74
<i>Clostridia</i>	6.59	5.67	4.91	4.13	76.47	22.09	58.56	22.25	30.32	20.26	19.62	34.11	25.42
<i>Methanobacteria</i>	0.83	0.90	0.77	0.53	0.50	33.16	24.51	44.22	11.37	29.80	4.66	15.27	13.88
<i>Bacteroidia</i>	1.08	0.96	0.84	0.83	0.84	2.78	1.55	9.08	26.66	28.74	28.63	25.71	10.64
<i>Methanomicrobia</i>	0.26	0.32	0.19	0.20	0.22	0.76	2.02	7.48	5.79	7.57	30.17	3.13	4.84
<i>Cloacamonae</i>	0.10	0.05	0.07	0.09	0.08	0.08	0.08	0.95	3.55	5.01	5.15	7.39	1.88
<i>Gammaproteobacteria</i>	0.72	0.66	4.09	0.67	1.30	3.90	0.60	0.28	0.57	0.31	0.32	0.49	1.16
<i>Alphaproteobacteria</i>	0.24	0.34	0.68	0.20	1.30	3.17	0.15	0.08	0.17	0.10	0.23	0.20	0.57
<i>Deltaproteobacteria</i>	0.37	0.59	0.48	0.42	0.70	1.12	0.45	0.22	0.52	0.29	0.38	0.48	0.50
<i>Anaerolineae</i>	0.14	0.18	0.08	0.08	0.14	0.15	0.45	2.24	1.33	0.07	0.98	0.12	0.50
<i>Actinobacteria</i>	0.27	0.43	1.13	0.25	0.88	2.23	0.11	0.12	0.18	0.06	0.09	0.21	0.50
<i>Thermoplasmata</i>	0.05	0.01	0.01	0.01	0.04	0.04	0.06	3.35	0.96	0.28	0.14	0.97	0.49
<i>Thaumarchaeota</i>	0.07	0.16	0.14	0.05	0.94	3.78	0.08	0.06	0.11	0.08	0.11	0.09	0.47
<i>Synergistia</i>	0.15	0.13	0.09	0.18	0.11	0.21	0.21	1.95	0.89	0.68	0.33	0.66	0.47
<i>Betaproteobacteria</i>	0.23	0.26	0.56	0.20	0.63	2.71	0.15	0.10	0.12	0.11	0.09	0.14	0.44
<i>Thermoleophilia</i>	0.08	0.22	0.19	0.03	0.57	2.55	0.04	0.05	0.04	0.01	0.03	0.06	0.32
<i>MB-A2-108</i>	0.01	0.08	0.02	0.05	0.13	1.26	0.03	0.01	0.01	0.01	0.02	0.02	0.14
<i>Nitrospira</i>	0.01	0.06	0.11	0.03	0.21	0.68	0.03	0.01	0.04	0.01	0.01	0.07	0.11
<i>Ignavibacteria</i>	0.01	0.01	0.01	0.02	0.02	0.01	0.01	0.01	0.03	0.02	0.01	0.02	0.02
<i>Planctomycetia</i>	0.01	0.01	0.10	0.01	0.08	0.17	0.01	0.06	0.04	0.01	0.18	0.02	0.06
<i>Epsilonproteobacteria</i>	0.04	0.07	0.03	0.04	0.05	0.02	0.06	0.03	0.01	0.04	0.06	0.04	0.04
<i>Coriobacteriia</i>	0.09	0.02	0.03	0.02	0.15	2.15	0.29	0.00	0.06	0.67	0.01	0.85	0.36
<i>Mollicutes</i>	0.00	0.01	0.01	0.01	0.00	0.01	0.01	0.08	0.88	0.06	0.13	0.00	0.10
<i>Acidimicrobiia</i>	0.04	0.03	0.05	0.03	0.20	0.74	0.01	0.00	0.02	0.01	0.01	0.02	0.10
<i>Gemm-1</i>	0.03	0.03	0.01	0.01	0.20	0.69	0.01	0.00	0.01	0.01	0.01	0.01	0.08
<i>Lentisphaeria</i>	0.01	0.01	0.01	0.02	0.00	0.01	0.01	0.41	0.21	0.01	0.28	0.00	0.08
<i>Acidobacteria-6</i>	0.01	0.03	0.05	0.01	0.28	0.37	0.04	0.02	0.00	0.01	0.02	0.03	0.07
<i>Verruco-5</i>	0.00	0.00	0.00	0.01	0.01	0.04	0.02	0.05	0.25	0.10	0.23	0.14	0.07
<i>Erysipelotrichi</i>	0.00	0.00	0.00	0.01	0.01	0.12	0.01	0.01	0.49	0.03	0.06	0.00	0.06
<i>Ellin6529</i>	0.01	0.03	0.01	0.00	0.25	0.29	0.02	0.00	0.01	0.01	0.00	0.00	0.05
<i>Chloracidobacteria</i>	0.02	0.01	0.10	0.01	0.25	0.14	0.01	0.00	0.01	0.01	0.01	0.00	0.05
<i>Gitt-GS-136</i>	0.01	0.03	0.04	0.02	0.14	0.27	0.00	0.01	0.00	0.00	0.00	0.00	0.04
<i>Flavobacteriia</i>	0.06	0.03	0.21	0.03	0.01	0.07	0.00	0.00	0.01	0.01	0.01	0.01	0.04
<i>Spirochaetes</i>	0.01	0.01	0.01	0.00	0.01	0.05	0.01	0.04	0.08	0.02	0.02	0.20	0.04
<i>Sphingobacteriia</i>	0.01	0.00	0.29	0.00	0.00	0.07	0.00	0.00	0.02	0.00	0.00	0.00	0.03
<i>Pedospaerae</i>	0.01	0.01	0.01	0.02	0.04	0.05	0.01	0.02	0.00	0.01	0.06	0.06	0.03
<i>RF3</i>	0.01	0.00	0.00	0.00	0.00	0.01	0.01	0.09	0.13	0.00	0.04	0.00	0.02
<i>JS1</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.24	0.00	0.00	0.00	0.02
<i>OPB54</i>	0.01	0.03	0.03	0.00	0.02	0.01	0.01	0.05	0.01	0.01	0.03	0.01	0.02
<i>Zetaproteobacteria</i>	0.01	0.01	0.01	0.02	0.02	0.01	0.00	0.01	0.04	0.01	0.01	0.01	0.01
<i>SJA-176</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.08	0.00	0.00	0.07	0.00	0.01
<i>iii1-8</i>	0.01	0.00	0.00	0.00	0.03	0.10	0.00	0.00	0.01	0.00	0.00	0.03	0.01
<i>Cytophagia</i>	0.01	0.01	0.02	0.05	0.00	0.01	0.01	0.02	0.01	0.01	0.00	0.01	0.01
<i>Chloroplast</i>	0.04	0.01	0.02	0.02	0.04	0.00	0.01	0.01	0.01	0.00	0.01	0.00	0.01
<i>OPB46</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.02	0.00	0.09	0.00	0.02	0.01	0.01
<i>Sva0725</i>	0.01	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.01	0.00	0.00	0.00	0.01
<i>Caldithrixae</i>	0.01	0.01	0.01	0.02	0.01	0.00	0.03	0.00	0.03	0.00	0.00	0.01	0.01
<i>Spartobacteria</i>	0.01	0.00	0.03	0.00	0.04	0.04	0.00	0.00	0.01	0.00	0.00	0.00	0.01
<i>Rubrobacteria</i>	0.01	0.01	0.01	0.01	0.01	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>MCG</i>	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00	0.01
<i>Saprosphirae</i>	0.00	0.01	0.00	0.03	0.01	0.02	0.00	0.01	0.00	0.01	0.01	0.01	0.01
<i>Acidobacteriia</i>	0.01	0.00	0.03	0.01	0.01	0.00	0.01	0.00	0.01	0.01	0.01	0.00	0.01
<i>DA052</i>	0.01	0.00	0.01	0.01	0.03	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.01
<i>OPB41</i>	0.00	0.00	0.01	0.01	0.01	0.04	0.00	0.01	0.00	0.00	0.00	0.00	0.01
<i>PRR-12</i>	0.00	0.00	0.01	0.01	0.02	0.02	0.00	0.00	0.01	0.00	0.00	0.00	0.01
<i>TMI</i>	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.00	0.02	0.00	0.00	0.00	0.01
<i>TK10</i>	0.00	0.00	0.00	0.00	0.03	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Pla3</i>	0.00	0.01	0.01	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.01	0.00	0.00
<i>S035</i>	0.00	0.01	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00

<i>Deinococci</i>	0.00	0.00	0.01	0.00	0.00	0.01	0.01	0.00	0.01	0.00	0.01	0.01	0.00
<i>OM190</i>	0.00	0.00	0.02	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>OS-K</i>	0.01	0.01	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00
<i>Acidobacteria-5</i>	0.00	0.00	0.01	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.01	0.01	0.00
<i>Solibacteres</i>	0.00	0.02	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00
<i>028H05-P-BN-P5</i>	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00
<i>Gemmatimonadetes</i>	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.01	0.00	0.00	0.00	0.00
<i>Fusobacteriia</i>	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	0.00
<i>SAR202</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00
<i>SJA-4</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Gemm-2</i>	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00
<i>BPC102</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00
<i>Opitutae</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00
<i>TM7-3</i>	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>MJK10</i>	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>MBGB</i>	0.00	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Leptospirae</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00
<i>MBGA</i>	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Deferribacteres</i>	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Thermomicrobia</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
<i>RB25</i>	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>MHVG</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
<i>Dehalococcoidetes</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00
<i>TG3</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00
<i>BME43</i>	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
<i>ZB2</i>	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
Total dominant classes	95.13	94.03	92.42	95.54	87.25	71.49	92.16	86.95	82.51	94.4	92.3	90.59	89.56

Table S4

Relative abundances (% of total classified sequences that can be identified into known genera) of classified genus in each sample within different type of FPM. Twenty seven genera with pink shading were shared by all samples. Total relative abundance of shared genera (% of total classified genera) in each sample and abundance of total classified genera (% of total good quality sequences) in each sample were shown in the last two lines.

Genus	Degraded				Normal				High quality			
	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12
<i>Lactobacillus</i>	92.01	92.62	86.58	94.64	8.05	10.30	6.98	2.87	9.38	4.30	4.46	7.67
<i>Leuconostoc</i>	0.08	0.10	0.06	0.04	0.08	0.15	0.01	0.02	0.08	0.04	0.04	0.06
<i>Methanocorpusculum</i>	0.02	0.02	0.01	0.01	0.03	0.14	0.06	0.07	0.04	0.05	0.10	0.11
<i>Acetobacter</i>	0.02	0.02	0.12	0.04	0.03	0.07	0.01	0.01	0.10	0.01	0.06	0.04
<i>Ruminococcus</i>	2.27	1.56	1.66	1.36	77.77	28.29	46.51	13.48	6.47	14.18	0.91	18.31
<i>Methanobrevibacter</i>	0.40	0.45	0.40	0.29	0.24	17.66	3.18	33.38	22.50	51.71	2.42	26.09
<i>Methanosarcina</i>	0.18	0.25	0.15	0.18	0.20	1.48	2.97	5.51	5.52	12.32	57.52	4.18
<i>Caloramator</i>	0.85	0.19	0.09	0.12	3.58	1.60	23.09	1.16	2.99	2.16	0.25	5.59
<i>Methanobacterium</i>	0.29	0.35	0.37	0.20	0.25	4.44	3.66	19.83	5.64	1.24	1.37	1.08
<i>Syntrophomonas</i>	0.17	0.19	0.18	0.12	0.30	1.55	0.37	1.93	7.99	3.00	6.11	9.82
<i>Sedimentibacter</i>	0.46	0.48	0.44	0.28	1.21	1.00	1.59	2.07	6.88	2.00	3.91	3.23
<i>Clostridiaceae Clostridium</i>	0.54	1.14	0.71	0.54	0.95	2.69	2.62	0.71	4.42	0.66	1.74	2.08
<i>Prevotella</i>	0.08	0.08	0.08	0.07	0.09	0.20	0.12	0.26	0.19	1.84	0.06	8.25
<i>Sporanaerobacter</i>	0.25	0.12	0.08	0.15	0.18	1.07	3.90	0.59	0.74	0.41	0.49	2.12
<i>Methanoculleus</i>	0.06	0.06	0.05	0.02	0.05	0.12	0.17	3.83	0.64	0.84	1.91	1.57
<i>T78</i>	0.02	0.01	0.02	0.03	0.03	0.05	0.53	2.82	3.14	0.01	1.84	0.07
<i>Blvi28</i>	0.02	0.02	0.01	0.04	0.06	0.14	0.06	0.89	0.87	0.10	4.82	0.12
<i>Aminobacterium</i>	0.13	0.12	0.03	0.11	0.08	0.31	0.17	2.14	1.55	1.10	0.32	0.69
<i>Bacillaceae Bacillus</i>	0.20	0.22	0.14	0.04	0.07	3.04	0.04	0.01	0.12	0.04	0.84	0.04
<i>Pseudomonas</i>	0.19	0.08	1.70	0.16	0.11	1.24	0.07	0.04	0.19	0.13	0.07	0.06
<i>Tissierella Soehngenia</i>	0.05	0.11	0.04	0.06	0.07	0.10	0.53	0.39	0.35	0.89	0.29	0.72
<i>Coprococcus</i>	0.08	0.08	0.08	0.06	0.18	0.10	0.52	0.26	0.54	0.19	0.27	1.01
<i>Lutispora</i>	0.04	0.02	0.03	0.02	0.37	0.19	0.29	0.08	0.19	0.22	0.43	0.26
<i>Staphylococcus</i>	0.05	0.13	0.13	0.13	0.17	0.26	0.12	0.11	0.35	0.14	0.17	0.17
<i>Tepidimicrobium</i>	0.09	0.02	0.05	0.03	0.09	0.12	0.54	0.12	0.10	0.05	0.23	0.25
<i>Caldicoprobacter</i>	0.05	0.06	0.07	0.08	0.05	0.12	0.25	0.20	0.43	0.01	0.25	0.07
<i>Acinetobacter</i>	0.04	0.04	0.39	0.03	0.07	0.75	0.04	0.04	0.06	0.03	0.09	0.06
<i>Methanosaeta</i>	0.01	0.02	0.01	0.01	0.01	0.00	0.20	1.18	9.05	0.06	1.01	0.06
<i>Candidatus Nitrososphaera vadinCA11</i>	0.05	0.05	0.13	0.00	1.20	8.43	0.07	0.01	0.17	0.01	0.09	0.07
<i>Lactococcus</i>	0.03	0.01	0.01	0.00	0.03	0.05	0.04	3.19	2.09	0.15	0.04	1.60
<i>Methanomassiliicoccus</i>	0.31	0.19	2.52	0.33	0.15	2.18	0.12	0.03	0.25	0.05	0.16	0.00
<i>Thermoanaerobacterium</i>	0.02	0.01	0.00	0.01	0.01	0.03	0.06	1.50	0.48	0.34	0.22	0.22
<i>Thermoanaerobacterium</i>	0.00	0.02	0.02	0.00	1.37	0.02	0.08	0.01	0.02	0.00	0.03	0.01
<i>Yersinia</i>	0.07	0.03	0.18	0.05	0.06	0.31	0.05	0.01	0.06	0.01	0.00	0.04
<i>Streptococcus</i>	0.02	0.03	0.09	0.05	0.51	0.10	0.02	0.01	0.02	0.00	0.00	0.00
<i>Treponema</i>	0.02	0.00	0.01	0.00	0.01	0.12	0.01	0.06	0.17	0.03	0.01	0.39
<i>Rhodoplanes</i>	0.05	0.02	0.06	0.04	0.17	0.20	0.04	0.00	0.04	0.03	0.00	0.11
<i>Corynebacterium</i>	0.04	0.09	0.16	0.01	0.14	0.19	0.00	0.02	0.06	0.00	0.01	0.01
<i>Desulfococcus</i>	0.02	0.03	0.02	0.00	0.07	0.02	0.06	0.02	0.14	0.08	0.09	0.12
<i>Enhydrobacter</i>	0.02	0.01	0.39	0.04	0.01	0.12	0.01	0.00	0.00	0.03	0.01	0.01
<i>Pediococcus</i>	0.08	0.12	0.09	0.10	0.04	0.03	0.05	0.00	0.00	0.00	0.06	0.01
<i>Thermoactinomyces</i>	0.04	0.04	0.03	0.07	0.02	0.05	0.06	0.00	0.02	0.00	0.01	0.03
<i>Gluconobacter</i>	0.01	0.02	0.02	0.01	0.02	0.00	0.06	0.02	0.10	0.04	0.00	0.06
<i>Arcobacter</i>	0.02	0.04	0.02	0.03	0.03	0.00	0.04	0.03	0.04	0.04	0.04	0.01
<i>Mycobacterium</i>	0.01	0.03	0.01	0.01	0.07	0.15	0.01	0.00	0.00	0.00	0.01	0.03
<i>Mariprofundus</i>	0.01	0.02	0.02	0.02	0.03	0.03	0.00	0.02	0.10	0.03	0.03	0.01
<i>Brevibacterium</i>	0.03	0.06	0.04	0.04	0.02	0.02	0.01	0.01	0.00	0.01	0.03	0.01
<i>Sulfurimonas</i>	0.02	0.01	0.01	0.01	0.03	0.03	0.02	0.01	0.00	0.04	0.03	0.03
<i>Ruminofilibacter</i>	0.00	0.02	0.01	0.00	0.01	0.02	0.02	0.01	0.02	0.00	0.06	0.03
<i>Brachybacterium</i>	0.02	0.02	0.02	0.01	0.02	0.05	0.00	0.01	0.02	0.00	0.00	0.01
<i>Pelotomaculum</i>	0.02	0.01	0.00	0.00	0.00	0.02	0.01	0.09	1.96	0.00	2.46	0.04
<i>Garciella</i>	0.01	0.01	0.01	0.00	0.01	0.00	0.01	0.00	0.10	0.00	2.16	0.06
<i>Kaistobacter</i>	0.02	0.04	0.05	0.01	0.39	1.26	0.00	0.00	0.00	0.00	0.00	0.01
<i>Steroidobacter</i>	0.02	0.00	0.02	0.00	0.27	1.28	0.01	0.00	0.02	0.00	0.00	0.00
<i>RFN20</i>	0.00	0.00	0.00	0.01	0.02	0.03	0.02	0.02	1.34	0.03	0.12	0.00
<i>Bacteroides</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.04	0.06	0.01	0.92

<i>Thermacetogenium</i>	0.00	0.00	0.02	0.00	0.00	0.02	0.01	0.07	0.02	0.03	0.80	0.01
<i>Methanosphaera</i>	0.00	0.00	0.00	0.00	0.00	0.78	0.00	0.01	0.00	0.00	0.00	0.00
<i>vadinHB04</i>	0.00	0.00	0.02	0.00	0.00	0.27	0.00	0.05	0.06	0.00	0.00	0.39
<i>Psychrobacter</i>	0.02	0.01	0.42	0.03	0.00	0.26	0.00	0.00	0.02	0.00	0.01	0.01
<i>Methanofollis</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.02	0.06	0.48	0.12	0.01
<i>Pedomicrobium</i>	0.00	0.00	0.02	0.00	0.03	0.53	0.00	0.00	0.02	0.00	0.00	0.00
<i>Lysinibacillus</i>	0.01	0.02	0.02	0.00	0.00	0.49	0.00	0.00	0.00	0.00	0.04	0.00
<i>SHD-231</i>	0.01	0.00	0.00	0.00	0.01	0.00	0.02	0.30	0.16	0.00	0.03	0.06
<i>Dehalobacterium</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.10	0.12	0.09	0.07	0.18
<i>Alicyclobacillus</i>	0.05	0.08	0.07	0.00	0.03	0.29	0.01	0.00	0.00	0.00	0.00	0.00
<i>Paludibacter</i>	0.00	0.01	0.00	0.00	0.04	0.02	0.00	0.01	0.04	0.05	0.06	0.28
<i>Pseudoramibacter_Eubacterium</i>	0.01	0.00	0.00	0.00	0.00	0.05	0.00	0.09	0.12	0.01	0.16	0.03
<i>Hyphomicrobium</i>	0.00	0.02	0.01	0.01	0.04	0.37	0.00	0.00	0.02	0.00	0.00	0.00
<i>Actinomyces</i>	0.00	0.00	0.00	0.01	0.03	0.41	0.00	0.00	0.00	0.01	0.00	0.00
<i>Sphingobacterium</i>	0.01	0.00	0.33	0.00	0.00	0.05	0.00	0.00	0.06	0.00	0.00	0.00
<i>Oscillospira</i>	0.01	0.00	0.00	0.00	0.00	0.03	0.04	0.02	0.00	0.01	0.00	0.32
<i>Dysgonomonas</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.00	0.00	0.00
<i>Pseudoxanthomonas</i>	0.00	0.00	0.00	0.00	0.00	0.43	0.00	0.00	0.00	0.00	0.00	0.00
<i>Sporotomaculum</i>	0.00	0.01	0.00	0.01	0.00	0.00	0.01	0.00	0.12	0.01	0.25	0.00
<i>Arthrobacter</i>	0.00	0.02	0.14	0.00	0.02	0.17	0.00	0.02	0.00	0.00	0.01	0.01
<i>Brochothrix</i>	0.05	0.01	0.13	0.01	0.00	0.14	0.00	0.00	0.04	0.00	0.00	0.00
<i>Desulfosporosinus</i>	0.00	0.01	0.00	0.00	0.01	0.02	0.00	0.01	0.14	0.00	0.16	0.01
<i>Bulleidia</i>	0.00	0.00	0.00	0.00	0.00	0.26	0.00	0.00	0.00	0.03	0.00	0.00
<i>Myroides</i>	0.00	0.01	0.12	0.00	0.01	0.12	0.00	0.00	0.00	0.00	0.01	0.00
<i>Plesiocystis</i>	0.00	0.00	0.01	0.00	0.00	0.26	0.00	0.00	0.00	0.00	0.00	0.00
<i>BF311</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.25
<i>Balneimonas</i>	0.00	0.00	0.00	0.01	0.06	0.17	0.00	0.00	0.02	0.00	0.00	0.00
<i>Anaerovorax</i>	0.01	0.01	0.02	0.00	0.00	0.02	0.00	0.00	0.06	0.06	0.03	0.04
<i>Streptomyces</i>	0.00	0.00	0.05	0.00	0.02	0.14	0.00	0.00	0.00	0.00	0.01	0.03
<i>Flavobacterium</i>	0.02	0.02	0.09	0.01	0.00	0.02	0.00	0.00	0.04	0.01	0.00	0.03
<i>Petrobacter</i>	0.00	0.00	0.00	0.00	0.00	0.24	0.00	0.00	0.00	0.00	0.00	0.00
<i>Parabacteroides</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.00	0.17
<i>Mogibacterium</i>	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.01	0.04	0.04	0.04	0.00
<i>Dehalobacter_Syntrophobotulus</i>	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.10	0.03	0.04	0.03
<i>Desulfosarcina</i>	0.00	0.02	0.00	0.01	0.01	0.02	0.04	0.00	0.06	0.00	0.00	0.04
<i>Sphingomonas</i>	0.01	0.00	0.03	0.01	0.08	0.03	0.00	0.00	0.00	0.01	0.00	0.00
<i>Nitrosopumilus</i>	0.01	0.01	0.00	0.00	0.01	0.00	0.01	0.01	0.00	0.04	0.06	0.03
<i>Acidaminococcus</i>	0.00	0.00	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.14	0.00	0.00
<i>Providencia</i>	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Stenotrophomonas</i>	0.00	0.01	0.02	0.00	0.01	0.05	0.00	0.00	0.02	0.01	0.03	0.00
<i>Anaerofustis</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.02	0.01	0.06	0.04
<i>Ochroactrum</i>	0.00	0.00	0.07	0.00	0.02	0.03	0.00	0.01	0.00	0.00	0.00	0.00
<i>Rummeliibacillus</i>	0.02	0.00	0.02	0.00	0.03	0.02	0.00	0.00	0.02	0.00	0.03	0.00
<i>Kocuria</i>	0.03	0.01	0.00	0.00	0.01	0.03	0.01	0.01	0.00	0.00	0.00	0.03
<i>Iamia</i>	0.00	0.00	0.01	0.00	0.04	0.09	0.00	0.00	0.00	0.00	0.00	0.00
<i>Rubrivivax</i>	0.01	0.00	0.02	0.00	0.00	0.07	0.02	0.00	0.00	0.00	0.00	0.00
<i>Agromyces</i>	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.02	0.00	0.00	0.01
<i>Planctomyces</i>	0.00	0.00	0.00	0.00	0.03	0.05	0.00	0.01	0.00	0.00	0.00	0.03
<i>Lysobacter</i>	0.00	0.01	0.01	0.00	0.03	0.05	0.01	0.01	0.00	0.00	0.00	0.00
<i>Nitrospira</i>	0.00	0.00	0.02	0.01	0.01	0.02	0.01	0.00	0.00	0.00	0.00	0.04
<i>Thermomonas</i>	0.02	0.01	0.01	0.00	0.01	0.07	0.00	0.00	0.00	0.00	0.00	0.00
<i>Gracilibacter</i>	0.00	0.00	0.00	0.00	0.04	0.00	0.01	0.02	0.02	0.00	0.00	0.01
<i>Vogesella</i>	0.00	0.00	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.00	0.00	0.00
<i>Paenibacillus</i>	0.01	0.01	0.02	0.00	0.01	0.03	0.00	0.00	0.00	0.00	0.01	0.00
<i>Nannocystis</i>	0.01	0.00	0.02	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.01	0.00
<i>Anaeromyxobacter</i>	0.00	0.03	0.00	0.00	0.01	0.05	0.00	0.00	0.00	0.00	0.00	0.00
<i>Sutterella</i>	0.00	0.01	0.02	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00
<i>JG37-AG-70</i>	0.01	0.01	0.01	0.00	0.03	0.00	0.00	0.00	0.04	0.00	0.00	0.00
<i>Desulfovibrio</i>	0.00	0.00	0.01	0.00	0.01	0.03	0.01	0.00	0.00	0.01	0.00	0.01
<i>Thalassomonas</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.04	0.00	0.01	0.00
<i>Candidatus Xiphinematobacter</i>	0.00	0.00	0.00	0.00	0.02	0.07	0.00	0.00	0.00	0.00	0.00	0.00
<i>Aneurinibacillus</i>	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.00
<i>Brevundimonas</i>	0.00	0.00	0.05	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.01
<i>Methanolobus</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.04	0.01	0.01	0.00
<i>Kribbella</i>	0.00	0.00	0.02	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00
<i>LCP-26</i>	0.01	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.00
<i>Aeromicrobium</i>	0.00	0.00	0.00	0.00	0.03	0.05	0.00	0.00	0.00	0.00	0.00	0.00

<i>Bradyrhizobium</i>	0.01	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.02	0.00	0.00	0.00
<i>Turicibacter</i>	0.00	0.01	0.02	0.01	0.00	0.03	0.01	0.00	0.00	0.00	0.00	0.00
<i>GOUTA19</i>	0.00	0.00	0.01	0.00	0.00	0.02	0.00	0.01	0.00	0.01	0.00	0.03
<i>Phenylobacterium</i>	0.00	0.02	0.00	0.00	0.00	0.03	0.00	0.01	0.00	0.00	0.01	0.00
<i>Paenochrobactrum</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00
<i>Gemmata</i>	0.00	0.00	0.02	0.00	0.02	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Phyllobacterium</i>	0.00	0.00	0.00	0.00	0.01	0.03	0.00	0.01	0.00	0.00	0.00	0.01
<i>Rubrobacter</i>	0.00	0.02	0.01	0.01	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Devosia</i>	0.00	0.00	0.01	0.00	0.01	0.03	0.01	0.00	0.00	0.00	0.00	0.00
<i>Christensenella</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.02	0.01	0.00	0.01
<i>Desulfotomaculum</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.04	0.00
<i>Sinorhizobium</i>	0.00	0.00	0.00	0.00	0.03	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Aquicella</i>	0.00	0.00	0.01	0.00	0.02	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Wolinella</i>	0.00	0.02	0.02	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00
<i>Acidiphilium</i>	0.01	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
<i>Agrobacterium</i>	0.00	0.00	0.01	0.00	0.00	0.02	0.01	0.00	0.02	0.00	0.00	0.00
<i>Mesorhizobium</i>	0.01	0.00	0.00	0.00	0.00	0.03	0.01	0.00	0.00	0.00	0.00	0.00
<i>B-42</i>	0.00	0.00	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.01	0.01
<i>Megasphaera</i>	0.00	0.01	0.01	0.00	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Planococcaceae Bacillus</i>	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00
<i>Desulfitobacter</i>	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00
<i>Paracoccus</i>	0.00	0.00	0.00	0.01	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Cellulosimicrobium</i>	0.00	0.00	0.02	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Amphritea</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.01
<i>Cohnella</i>	0.01	0.00	0.02	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Conexibacter</i>	0.02	0.02	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Cenarchaeum</i>	0.00	0.00	0.00	0.01	0.00	0.02	0.00	0.00	0.00	0.00	0.01	0.00
<i>Thermus</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.00	0.00	0.01
<i>Tepidibacter</i>	0.00	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Peptostreptococcaceae Clostridium</i>	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
<i>Ureibacillus</i>	0.00	0.00	0.01	0.00	0.02	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Saccharomonospora</i>	0.00	0.00	0.00	0.00	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Afifella</i>	0.00	0.00	0.01	0.00	0.01	0.00	0.01	0.00	0.00	0.01	0.00	0.00
<i>Saccharopolyspora</i>	0.01	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Geobacter</i>	0.01	0.00	0.00	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01
<i>Flaviumibacter</i>	0.00	0.00	0.00	0.01	0.00	0.02	0.00	0.00	0.00	0.00	0.01	0.00
<i>C1_B004</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00
<i>Pelobacteraceae_Pelobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00
<i>Desulfuromonadaceae_Pelobacter</i>	0.01	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.00
<i>Rubellimicrobium</i>	0.00	0.00	0.01	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Mycoplana</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.02	0.00	0.00	0.00
<i>Shimazuella</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.02	0.00	0.00	0.00
<i>Anaerofilum</i>	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03
<i>Desulfobacca</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01
<i>Brevibacillus</i>	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Cupriavidus</i>	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Haliangium</i>	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Leucobacter</i>	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>Veillonella</i>	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.00
<i>BD2-6</i>	0.00	0.00	0.00	0.01	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Dechloromonas</i>	0.00	0.02	0.01	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Propionibacterium</i>	0.00	0.00	0.02	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Rhodovibrio</i>	0.00	0.02	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Sphingopyxis</i>	0.01	0.00	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Dethiobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.00	0.00	0.00
<i>Hydrogenophilaceae_Thiobacillus</i>	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Halomonas</i>	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
<i>Photobacterium</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00
<i>Ruminococcaceae Clostridium</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03
<i>Desulfobacter</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.01	0.00	0.00	0.00	0.00
<i>Reinekea</i>	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00
<i>Actinomadura</i>	0.00	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Sorangium</i>	0.00	0.00	0.00	0.00	0.01	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Geosporobacter_Thermotalea</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.01
<i>Nocardia</i>	0.00	0.00	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Skermanella</i>	0.00	0.00	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00

<i>Luteimonas</i>	0.00	0.01	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Alcanivorax</i>	0.00	0.01	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Prauserella</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.01	0.00
<i>Geovibrio</i>	0.00	0.00	0.00	0.01	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00
<i>Ectothiorhodospiraceae Thiobacillus</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
<i>Cellvibrio</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Hyphomonas</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Wautersiella</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Laceyella</i>	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Microbulbifer</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00
<i>Fulvivirga</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00
<i>Leptospirillum</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Psychromonas</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Macrococcus</i>	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Syntrophobacter</i>	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00
<i>Myxococcus</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00
<i>Peptostreptococcus</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
<i>Lachnospiraceae Clostridium</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00
<i>Halothiobacillus</i>	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Nonomuraea</i>	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Peptoniphilus</i>	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Oceanospirillum</i>	0.00	0.00	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Achromobacter</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>DA101</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Pandoraea</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Pirellula</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Lutimonas</i>	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Symbiobacterium</i>	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Lutibacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00
<i>Flavisolibacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01
<i>Virgibacillus</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00
<i>Shewanella</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00
<i>Butyrivibrio</i>	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Chryseobacterium</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Opitutus</i>	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
<i>Gordonia</i>	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Abundance of total shared genera (% of all classified genera/sequences) in each sample	98.62	98.55	93.66	98.86	94.33	77.17	98.39	92.85	81.47	97.67	90.96	93.70
Abundance of total classified genera/sequences (% of total good quality sequences)	91.31	90.39	89.48	92.71	75.72	43.21	58.45	69.70	36.97	54.72	49.21	52.24

Table S5

Relative abundances (% of total good quality sequences) of dominant phyla and distinct classes in different type of FPMs.

Dominant phylum/Distinct class	Types of FPMs*		
	Degraded	Normal	High-quality
Firmicutes	91.29±2.98 ^a	52.31±28.55 ^b	31.16±8.28 ^b
Bacilli	85.42±3.09 ^a	6.02±2.78 ^b	3.79±0.8 ^b
Clostridia	5.33±1.05 ^a	44.84±27.18 ^b	26.08±7.26 ^{ab}
Cloacamonae	0.08±0.02 ^a	0.3±0.44 ^a	5.27±1.58 ^b
Bacteroidetes	1.14±0.2 ^a	3.64±3.77 ^a	27.51±1.48 ^b
Bacteroidia	0.93±0.12 ^a	3.56±3.77 ^a	27.44±1.49 ^b
Euryarchaeota	1.02±0.22 ^a	29.15±22.51 ^b	27.57±10.19 ^b
Methanobacteria	0.76±0.16 ^a	25.6±18.57 ^b	15.28±10.63 ^{ab}
Total abundance of dominant phyla	93.45	85.1	86.24
Total abundance of distinct classes	92.5	80.32	77.86

*Values with different letters in a row mean significant difference (p<0.05).

Table S6

Pearson's correlation coefficients between environmental measurable variables and dominant prokaryotic phyla (>10%) and distinct genera.

Phylum/Class	DOC	pH	Moisture	Lactate	TN	NH ₄ ⁺	AP	N[<i>Clostridia</i>] ^a	N[<i>C.kluyveri</i>]	N[LAB]
<i>Firmicutes</i>	.764**	-.805**	0.522	.763**	-0.149	-.803**	-.857**	-.649*	-.653*	.756**
<i>Bacilli</i>	.909**	-.857**	.589*	.971**	-0.002	-.962**	-.974**	-.911**	-.810**	.920**
<i>Clostridia</i>	-0.56	0.417	-0.336	-.671*	-0.189	.600*	0.551	.713**	0.531	-.592*
<i>Cloacamonae</i>	-.676*	.747**	-0.182	-0.536	0.207	.613*	0.566	0.553	.592*	-0.553
<i>Bacteroidetes</i>	-.751**	.833**	-0.408	-.592*	0.216	.634*	.628*	0.555	0.524	-.681*
<i>Bacteroidia</i>	-.753**	.835**	-0.408	-.596*	0.213	.639*	.631*	0.56	0.529	-.685*
<i>Euryarchaeota</i>	-0.576	0.546	-0.321	-.657*	0.148	.759**	.804**	.601*	.632*	-.598*
<i>Methanobacteria</i>	-0.339	0.295	-0.134	-0.548	-0.102	.654*	.684*	0.523	.580*	-0.423

** Correlation is significant at p<0.01. * Significant at p<0.05.

^a N[*Clostridia*], N[*C. kluyveri*] and N[LAB] respectively represent the absolute abundances (Log10 16S rRNA gene copies / g FPM) of *Clostridia*, *C. kluyveri* and LAB in FPM samples.

Table S7

Relative abundances (% of total classified sequences that can be identified into known genera) of core genera (in bold blue font) in different type of FPMs.

Domain	Class	Core genus	Types of FPMs		
			Degraded	Normal	High-quality
Bacteria	<i>Anaerolineae</i>	<i>T78</i>	0.02	0.86	1.26
	<i>Bacilli</i>	<i>Lactobacillus</i>	91.46	7.05	6.45
	<i>Bacteroidia</i>	<i>Blvii28</i>	0.02	0.28	1.48
	<i>Bacteroidia</i>	<i>Prevotella</i>	0.08	0.17	2.58
	<i>Clostridia</i>	<i>Caloramator</i>	0.31	7.35	2.74
	<i>Clostridia</i>	<i>Clostridium</i>	0.73	1.74	2.23
	<i>Clostridia</i>	<i>Pelotomaculum</i>	0.01	0.03	1.11
	<i>Clostridia</i>	<i>Ruminococcus</i>	1.71	41.51	9.97
	<i>Clostridia</i>	<i>Sedimentibacter</i>	0.41	1.47	4.00
	<i>Clostridia</i>	<i>Sporanaerobacter</i>	0.15	1.44	0.94
	<i>Clostridia</i>	<i>Syntrophomonas</i>	0.16	1.04	6.73
	Archaea	<i>Methanobacteria</i>	<i>Methanobacterium</i>	0.30	7.04
<i>Methanobacteria</i>		<i>Methanobrevibacter</i>	0.39	13.61	25.68
<i>Methanomicrobia</i>		<i>Methanoculleus</i>	0.05	1.04	1.24
<i>Methanomicrobia</i>		<i>Methanosaeta</i>	0.01	0.35	2.55
<i>Methanomicrobia</i>		<i>Methanosarcina</i>	0.19	2.54	19.89
<i>Thaumarchaeota</i>		<i>Nitrososphaera</i>	0.06	2.43	0.06
Total number of core genera			2	12	15
Total abundance of core genera			96.06	89.96	91.28

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