Supplementary files

Table S1. Diversity indices of pit-mud prokaryotic communities calculated based on the cutoff of 97% similarity of 16S rRNA gene sequence and 5652 reads per sample.

No.	**Phylogenetic distance whole tree**	**Chao1 estimator of richness**	**Observed species**	**Shannon's diversity index**
1yr-1	24.66±1.83	332±19	240±17	3.65±0.43
1yr-2	25.62±3.92	364±53	244±32	3.04±0.56
1yr-3	24.08±0.72	361±21	229±3	3.04±0.33
1yr-4	26.56±1.33	498±62	277±23	3.97±0.59
1yr-5	25.64±3.91	462±108	246±42	2.58±0.70
10yr-1	25.92±1.77	378±51	237±15	5.30±0.27
10yr-2	24.15±1.73	309±44	221±24	5.19±0.27
10yr-3	25.23±2.71	335±37	217±39	4.57±0.76
10yr-4	22.79±4.52	297±78	195±48	3.46±1.34
10yr-5	26.53±4.14	357±78	236±43	4.96±0.23
25yr-1	29.33±4.39	361±75	256±38	5.50±0.17
25yr-2	31.85±2.42	434±71	286±26	5.73±0.28
25yr-3	32.36±2.18	516±36	295±23	5.40±0.29
25yr-4	32.29±0.72	474±42	293±13	5.64±0.18
25yr-5	32.75±1.33	500±53	307±9	5.78±0.15
50yr-1	31.23±1.50	446±74	270±17	5.16±0.02
50yr-2	36.19±1.37	515±44	325±8	5.92±0.25
50yr-3	32.43±2.13	404±58	290±26	5.64±0.15
50yr-4	29.12±1.74	354±47	250±18	5.48±0.12
50yr-5	27.80±3.74	348±77	240±42	5.30±0.16

1yr-1 to 1yr-5 represent five replicates of pit-mud samples collected from 1-year-old cellars, 10yr-1 to 10yr-5 from 10-year-old cellars, 25yr-1 to 25yr-5 from 25-year-old cellars, 50yr-1 to 50yr-5 from 50-year-old cellars.

Table S2 The relative abundances of prokaryotic phyla in pit-mud samples with different cellar ages based on pyrosequencing data

No.	**Firmicutes**	**Bacteroidetes**	**Euryarchaeota**	**Spirochaetes**	**Actinobacteria**	**Chloroflexi**	**Synergistetes**	**Proteobacteria**	**WS1**	**Tenericutes**	**Chlorobi**	**Unclassified Bacteria**
1yr-1	93.65±2.40	2.15±1.26	0.84±0.46	0.08±0.03	0.97±0.16	0.09±0.06	0.01±0.00	0.68±0.39	0.02±0.01	0.10±0.01	0.01±0.01	2.29±0.02
1yr-2	93.92±2.04	1.95±1.17	0.93±0.41	0.19±0.10	0.87±0.46	0.03±0.02	0.02±0.01	0.48±0.34	0.06±0.03	0.12±0.03	0.00±0.00	3.65±0.16
1yr-3	94.86±0.96	1.40±0.95	0.58±0.16	0.15±0.15	0.85±0.28	0.03±0.01	0.04±0.01	0.46±0.11	0.02±0.02	0.11±0.01	0.00±0.00	2.00±0.55
1yr-4	95.90±0.37	0.40±0.29	0.14±0.05	0.06±0.04	0.62±0.14	0.02±0.00	0.01±0.00	0.18±0.04	0.00±0.00	0.06±0.04	0.00±0.00	1.64±0.39
1yr-5	96.07±0.93	1.06±0.39	0.40±0.12	0.14±0.03	0.34±0.11	0.02±0.01	0.01±0.00	0.20±0.09	0.03±0.01	0.04±0.02	0.01±0.01	2.30±0.83
10yr-1	53.28±8.40	33.46±9.85	7.44±1.62	0.01±0.01	0.97±0.47	0.18±0.11	0.35±0.28	1.32±1.07	0.01±0.01	0.95±0.63	0.00±0.00	2.28±0.85
10yr-2	54.10±1.92	23.33±8.90	18.41±6.30	0.01±0.01	1.50±1.07	0.06±0.06	0.17±0.09	0.41±0.33	0.02±0.01	0.11±0.07	0.00±0.00	2.35±1.21
10yr-3	68.98±15.98	16.12±9.88	6.19±3.06	4.48±4.08	2.12±1.12	0.20±0.13	0.42±0.20	0.19±0.09	0.04±0.01	0.28±0.14	0.00±0.00	4.65±1.24
10yr-4	76.73±10.82	6.06±3.05	9.17±5.66	3.05±2.12	2.16±1.44	0.44±0.43	0.08±0.07	0.62±0.36	0.14±0.14	0.09±0.04	0.02±0.02	5.61±1.59
10yr-5	57.90±5.34	25.41±9.45	10.63±3.74	0.39±0.38	0.50±0.24	0.26±0.13	0.31±0.01	2.28±1.86	0.06±0.05	0.75±0.31	0.01±0.01	2.73±0.58
25yr-1	63.06±3.14	15.36±3.22	10.61±1.45	2.18±0.80	1.61±0.68	1.98±0.66	0.89±0.19	0.26±0.14	0.30±0.15	0.92±0.21	0.18±0.07	1.95±1.70
25yr-2	48.43±2.92	28.09±6.12	10.20±0.65	2.79±1.39	1.04±0.22	1.33±0.63	1.00±0.69	0.27±0.12	2.26±2.19	0.99±0.49	0.91±0.61	1.78±0.19
25yr-3	46.26±3.11	22.51±3.98	14.79±5.13	6.70±2.12	0.93±0.24	0.89±0.58	0.71±0.33	0.11±0.04	0.83±0.80	0.75±0.18	0.36±0.22	0.94±0.37
25yr-4	47.40±5.42	26.64±5.53	9.99±1.63	5.34±2.74	1.01±0.22	1.55±0.42	0.45±0.22	0.27±0.11	0.36±0.23	1.02±0.16	0.20±0.20	1.32±0.93
25yr-5	51.75±4.30	24.04±3.45	11.71±1.73	2.52±0.25	1.37±0.63	1.45±0.51	1.09±0.13	0.20±0.15	2.00±1.69	0.77±0.15	0.22±0.08	1.43±0.53
50yr-1	66.62±1.53	11.52±1.94	7.42±0.71	0.32±0.00	7.58±0.78	0.92±0.21	0.96±0.17	0.07±0.03	1.49±1.01	0.42±0.07	0.14±0.06	1.40±0.28
50yr-2	40.19±6.84	20.13±3.83	15.56±2.51	4.16±1.61	4.71±1.83	4.88±2.39	2.16±0.80	1.02±0.21	0.78±0.41	0.90±0.42	0.73±0.32	1.43±0.53
50yr-3	44.82±4.20	26.50±5.62	12.71±1.19	5.55±3.27	1.09±0.62	4.20±1.03	0.59±0.23	1.04±0.79	0.25±0.13	0.64±0.08	0.00±0.00	1.47±0.19
50yr-4	50.11±4.31	23.15±5.17	10.82±1.01	5.43±2.80	3.30±2.45	1.74±0.30	0.77±0.47	0.69±0.42	1.60±1.03	0.41±0.07	0.05±0.05	2.58±0.88
50yr-5	62.11±2.76	11.92±1.98	16.64±5.08	1.38±0.39	2.74±0.39	0.84±0.53	0.93±0.48	0.12±0.04	0.06±0.03	0.76±0.05	0.04±0.04	1.66±0.63

Table S3. Pearson’s correlation coefficients between the relative abundances of prokaryotic phyla or genera and environmental variables.

	moisture	**pH**	**NH_4^+**	**Humic acid**	**TN**	**acetate**	**butyrate**	**caproate**	**lactate**
Firmicutes	-0.153	-.748**	-.580**	.402**	-0.194	0.172	.540**	-0.178	.883**
Lactobacillus	-0.25	-.658**	-.628**	.281*	-.269*	-0.035	.387**	-.355**	.892**
Clostridium IV	-0.04	-0.036	0.226	-0.098	-0.08	.406**	0.234	.380**	-0.216
Sedimentibacter	0.154	.596**	.258*	-0.164	0.138	-0.203	-.392**	0.059	-.622**
Syntrophomonas	0.198	.512**	.271*	-0.058	0.199	-0.185	-.329*	0.07	-.559**
unclassified Clostridiaceae 1	0.111	-0.215	.348**	0.034	0.061	.491**	0.145	.657**	-0.195
Unclassified anaerobrancaceae	0.252	.369**	.617**	-0.2	0.353*	0.185	-0.228	0.449**	-0.561**
Bacteroidetes	0.155	.752**	.409**	-.338**	0.132	-0.204	-.485**	0.016	-.788**
Petrimonas	0.178	.709**	.461**	-.348**	0.164	-0.098	-.411**	0.083	-.760**
unclassified Porphyromonadaceae	0.011	.599**	0.151	-.350**	-0.047	-0.203	-.423**	-0.041	-.601**
Euryarchaeota	0.19	.411**	.509**	-0.239	.297*	-0.05	-.297*	.305*	-.572**
Methanobacterium	0.078	0.084	.266*	-.262*	0.148	-0.074	-0.168	0.217	-0.157
Methanoculleus	0.096	0.204	0.097	0.002	0.179	-0.018	-0.087	0.094	-0.202
Methanosarcina	0.102	.376**	.466**	-0.214	0.13	-0.072	-.284*	0.157	-.516**

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

Figures

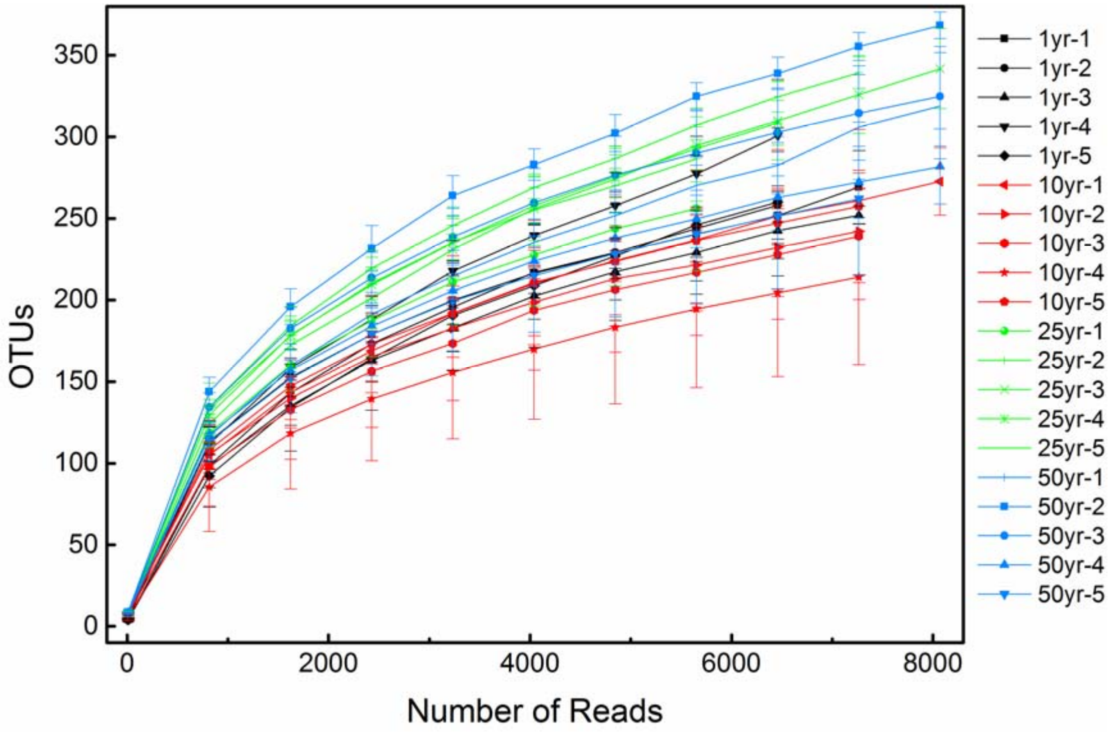


Figure S1 Rarefaction curves based on the OTUs at the cutoff of 97% 16S rRNA sequence similarity.

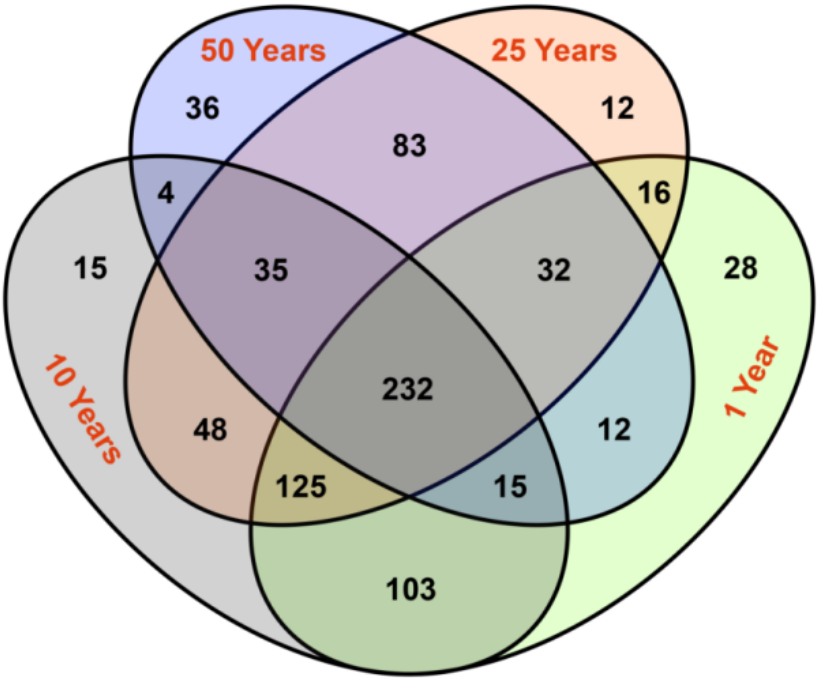
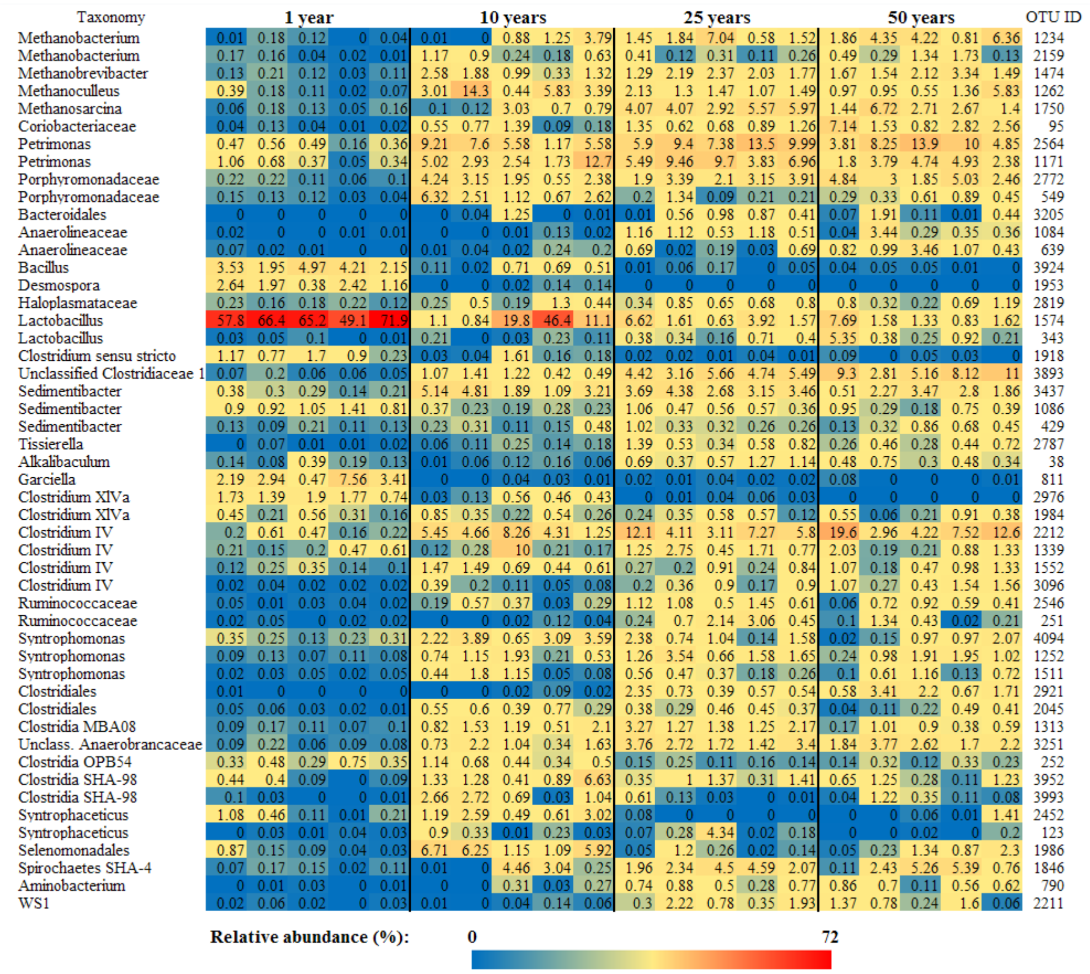


Figure S2 Unique and shared OTUs found in pit-mud samples. The parenthetical numbers indicate total OTUs in each treatment group; numbers in the Venn diagram indicate unique (non-overlapping panels) and shared (overlapping panels) OTUs. Only those OTUs containing ≥ 5 sequences were considered to be valid OTUs. A total of 796 OTUs were detected in this study.



Taxonomy	1 year					10 years					25 years					50 years					OTU ID
Methanobacterium	0.01	0.18	0.12	0	0.04	0.01	0	0.88	1.25	3.79	1.45	1.84	7.04	0.58	1.52	1.86	4.35	4.22	0.81	6.36	1234
Methanobacterium	0.17	0.16	0.04	0.02	0.01	1.17	0.9	0.24	0.18	0.63	0.41	0.12	0.31	0.11	0.26	0.49	0.29	1.34	1.73	0.13	2159
Methanobrevibacter	0.13	0.21	0.12	0.03	0.11	2.58	1.88	0.99	0.33	1.32	1.29	2.19	2.37	2.03	1.77	1.67	1.54	2.12	3.34	1.49	1474
Methanoculleus	0.39	0.18	0.11	0.02	0.07	3.01	14.3	0.44	5.83	3.39	2.13	1.3	1.47	1.07	1.49	0.97	0.95	0.55	1.36	5.83	1262
Methanosarcina	0.06	0.18	0.13	0.05	0.16	0.1	0.12	3.03	0.7	0.79	4.07	4.07	2.92	5.57	5.97	1.44	6.72	2.71	2.67	1.4	1750
Coriobacteriaceae	0.04	0.13	0.04	0.01	0.02	0.55	0.77	1.39	0.09	0.18	1.35	0.62	0.68	0.89	1.26	7.14	1.53	0.82	2.82	2.56	95
Petrimonas	0.47	0.56	0.49	0.16	0.36	9.21	7.6	5.58	1.17	5.58	5.9	9.4	7.38	13.5	9.99	3.81	8.25	13.9	10	4.85	2564
Petrimonas	1.06	0.68	0.37	0.05	0.34	5.02	2.93	2.54	1.73	12.7	5.49	9.46	9.7	3.83	6.96	1.8	3.79	4.74	4.93	2.38	1171
Porphyromonadaceae	0.22	0.22	0.11	0.06	0.1	4.24	3.15	1.95	0.55	2.38	1.9	3.39	2.1	3.15	3.91	4.84	3	1.85	5.03	2.46	2772
Porphyromonadaceae	0.15	0.13	0.12	0.03	0.04	6.32	2.51	1.12	0.67	2.62	0.2	1.34	0.09	0.21	0.21	0.29	0.33	0.61	0.89	0.45	549
Bacteroidales	0	0	0	0	0	0	0.04	1.25	0	0.01	0.01	0.56	0.98	0.87	0.41	0.07	1.91	0.11	0.01	0.44	3205
Anaerolineaceae	0.02	0	0	0.01	0.01	0	0	0.01	0.13	0.02	1.16	1.12	0.53	1.18	0.51	0.04	3.44	0.29	0.35	0.36	1084
Anaerolineaceae	0.07	0.02	0.01	0	0	0.01	0.04	0.02	0.24	0.2	0.69	0.02	0.19	0.03	0.69	0.82	0.99	3.46	1.07	0.43	639
Bacillus	3.53	1.95	4.97	4.21	2.15	0.11	0.02	0.71	0.69	0.51	0.01	0.06	0.17	0	0.05	0.04	0.05	0.05	0.01	0	3924
Desmospora	2.64	1.97	0.38	2.42	1.16	0	0	0.02	0.14	0.14	0	0	0	0	0	0	0	0	0	0	1953
Haloplasmataceae	0.23	0.16	0.18	0.22	0.12	0.25	0.5	0.19	1.3	0.44	0.34	0.85	0.65	0.68	0.8	0.8	0.32	0.22	0.69	1.19	2819
Lactobacillus	57.8	66.4	65.2	49.1	71.9	1.1	0.84	19.8	46.4	11.1	6.62	1.61	0.63	3.92	1.57	7.69	1.58	1.33	0.83	1.62	1574
Lactobacillus	0.03	0.05	0.1	0	0.01	0.21	0	0.03	0.23	0.11	0.38	0.34	0.16	0.71	0.4	5.35	0.38	0.25	0.92	0.21	343
Clostridium sensu stricto	1.17	0.77	1.7	0.9	0.23	0.03	0.04	1.61	0.16	0.18	0.02	0.02	0.01	0.04	0.01	0.09	0	0.05	0.03	0	1918
Unclassified Clostridiaceae 1	0.07	0.2	0.06	0.06	0.05	1.07	1.41	1.22	0.42	0.49	4.42	3.16	5.66	4.74	5.49	9.3	2.81	5.16	8.12	11	3893
Sedimentibacter	0.38	0.3	0.29	0.14	0.21	5.14	4.81	1.89	1.09	3.21	3.69	4.38	2.68	3.15	3.46	0.51	2.27	3.47	2.8	1.86	3437
Sedimentibacter	0.9	0.92	1.05	1.41	0.81	0.37	0.23	0.19	0.28	0.23	1.06	0.47	0.56	0.57	0.36	0.95	0.29	0.18	0.75	0.39	1086
Sedimentibacter	0.13	0.09	0.21	0.11	0.13	0.23	0.31	0.11	0.15	0.48	1.02	0.33	0.32	0.26	0.26	0.13	0.32	0.86	0.68	0.45	429
Tissierella	0	0.07	0.01	0.01	0.02	0.06	0.11	0.25	0.14	0.18	1.39	0.53	0.34	0.58	0.82	0.26	0.46	0.28	0.44	0.72	2787
Alkalibaculum	0.14	0.08	0.39	0.19	0.13	0.01	0.06	0.12	0.16	0.06	0.69	0.37	0.57	1.27	1.14	0.48	0.75	0.3	0.48	0.34	38
Garciella	2.19	2.94	0.47	7.56	3.41	0	0	0.04	0.03	0.01	0.02	0.01	0.04	0.02	0.02	0.08	0	0	0	0.01	811
Clostridium XIVa	1.73	1.39	1.9	1.77	0.74	0.03	0.13	0.56	0.46	0.43	0	0.01	0.04	0.06	0.03	0	0	0	0	0	2976
Clostridium XIVa	0.45	0.21	0.56	0.31	0.16	0.85	0.35	0.22	0.54	0.26	0.24	0.35	0.58	0.57	0.12	0.55	0.06	0.21	0.91	0.38	1984
Clostridium IV	0.2	0.61	0.47	0.16	0.22	5.45	4.66	8.26	4.31	1.25	12.1	4.11	3.11	7.27	5.8	19.6	2.96	4.22	7.52	12.6	2212
Clostridium IV	0.21	0.15	0.2	0.47	0.61	0.12	0.28	10	0.21	0.17	1.25	2.75	0.45	1.71	0.77	2.03	0.19	0.21	0.88	1.33	1339
Clostridium IV	0.12	0.25	0.35	0.14	0.1	1.47	1.49	0.69	0.44	0.61	0.27	0.2	0.91	0.24	0.84	1.07	0.18	0.47	0.98	1.33	1552
Clostridium IV	0.02	0.04	0.02	0.02	0.02	0.39	0.2	0.11	0.05	0.08	0.2	0.36	0.9	0.17	0.9	1.07	0.27	0.43	1.54	1.56	3096
Ruminococcaceae	0.05	0.01	0.03	0.04	0.02	0.19	0.57	0.37	0.03	0.29	1.12	1.08	0.5	1.45	0.61	0.06	0.72	0.92	0.59	0.41	2546
Ruminococcaceae	0.02	0.05	0	0.02	0.02	0	0	0.02	0.12	0.04	0.24	0.7	2.14	3.06	0.45	0.1	1.34	0.43	0.02	0.21	251
Syntrophomonas	0.35	0.25	0.13	0.23	0.31	2.22	3.89	0.65	3.09	3.59	2.38	0.74	1.04	0.14	1.58	0.02	0.15	0.97	0.97	2.07	4094
Syntrophomonas	0.09	0.13	0.07	0.11	0.08	0.74	1.15	1.93	0.21	0.53	1.26	3.54	0.66	1.58	1.65	0.24	0.98	1.91	1.95	1.02	1252
Syntrophomonas	0.02	0.03	0.05	0.02	0.05	0.44	1.8	1.15	0.05	0.08	0.56	0.47	0.37	0.18	0.26	0.1	0.61	1.16	0.13	0.72	1511
Clostridiales	0.01	0	0	0	0	0	0	0.02	0.09	0.02	2.35	0.73	0.39	0.57	0.54	0.58	3.41	2.2	0.67	1.71	2921
Clostridiales	0.05	0.06	0.03	0.02	0.01	0.55	0.6	0.39	0.77	0.29	0.38	0.29	0.46	0.45	0.37	0.04	0.11	0.22	0.49	0.41	2045
Clostridia MBA08	0.09	0.17	0.11	0.07	0.1	0.82	1.53	1.19	0.51	2.1	3.27	1.27	1.38	1.25	2.17	0.17	1.01	0.9	0.38	0.59	1313
Unclass. Anaerobrancaceae	0.09	0.22	0.06	0.09	0.08	0.73	2.2	1.04	0.34	1.63	3.76	2.72	1.72	1.42	3.4	1.84	3.77	2.62	1.7	2.2	3251
Clostridia OPB54	0.33	0.48	0.29	0.75	0.35	1.14	0.68	0.44	0.34	0.5	0.15	0.25	0.11	0.16	0.14	0.14	0.32	0.12	0.33	0.23	252
Clostridia SHA-98	0.44	0.4	0.09	0	0.09	1.33	1.28	0.41	0.89	6.63	0.35	1	1.37	0.31	1.41	0.65	1.25	0.28	0.11	1.23	3952
Clostridia SHA-98	0.1	0.03	0	0	0.01	2.66	2.72	0.69	0.03	1.04	0.61	0.13	0.03	0	0.01	0.04	1.22	0.35	0.11	0.08	3993
Syntrophaceticus	1.08	0.46	0.11	0.01	0.21	1.19	2.59	0.49	0.61	3.02	0.08	0	0	0	0	0	0	0.06	0.01	1.41	2452
Syntrophaceticus	0	0.03	0.01	0.04	0.03	0.9	0.33	0.01	0.23	0.03	0.07	0.28	4.34	0.02	0.18	0	0	0.02	0	0.2	123
Selenomonadales	0.87	0.15	0.09	0.04	0.03	6.71	6.25	1.15	1.09	5.92	0.05	1.2	0.26	0.02	0.14	0.05	0.23	1.34	0.87	2.3	1986
Spirochaetes SHA-4	0.07	0.17	0.15	0.02	0.11	0.01	0	4.46	3.04	0.25	1.96	2.34	4.5	4.59	2.07	0.11	2.43	5.26	5.39	0.76	1846
Aminobacterium	0	0.01	0.03	0	0.01	0	0	0.31	0.03	0.27	0.74	0.88	0.5	0.28	0.77	0.86	0.7	0.11	0.56	0.62	790
WS1	0.02	0.06	0.02	0	0.03	0.01	0	0.04	0.14	0.06	0.3	2.22	0.78	0.35	1.93	1.37	0.78	0.24	1.6	0.06	2211

Figure S3 Heat map of the relative abundances of most abundant 50 genera in pit-mud samples. The color intensity (log scale) in each panel shows the percentage of a genus in a sample, referring to color key at the right bottom.

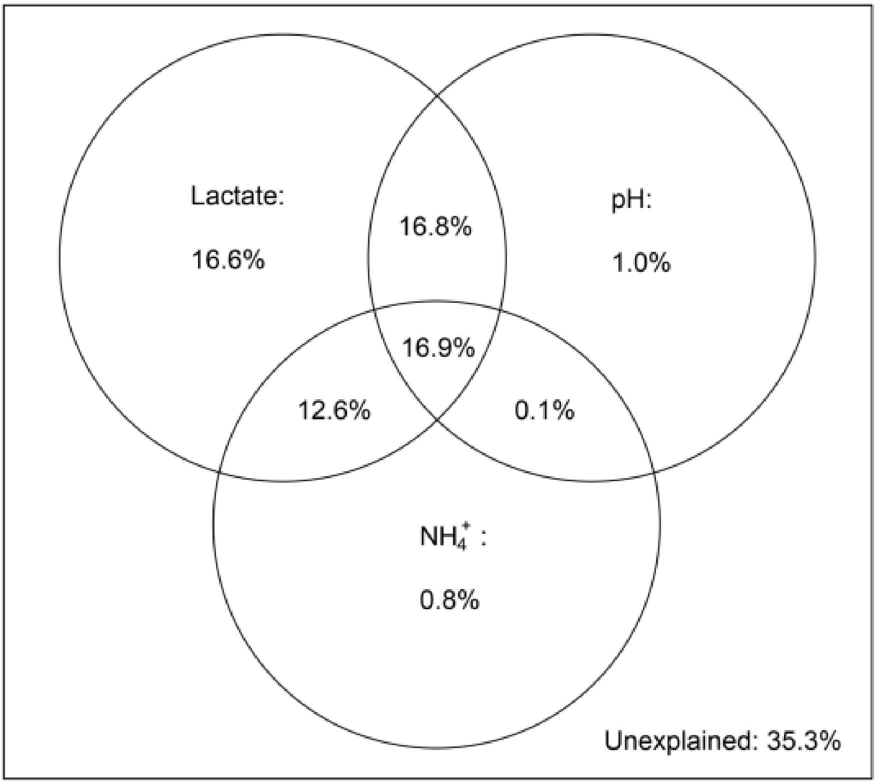


Figure S4 Contributions of different environmental factors to the variation of prokaryotic community structure in pit-mud samples by VPA analysis. Each diagram represents the biological variation partitioned into the relative contribution of each factor or a combination of multiple factors. The edge represents the variation explained by each factor alone. The overlaps represent interactions of any two factors, and the middle of overlap represents the interaction of all three factors.