Table S1 Spatial distribution of sediment bacterial richness and diversity estimates based on the 16S rRNA gene

Sampling sites	Clean data	faith_pd	observed_features	pielou_evenness	shannon_entropy	Goods_coverage
01F01	54294	96.75	1866	0.92	9.98	98.13%
02F01	54294	96.98	1866	0.92	9.96	98.15%
03F01	62415	109.86	2102	0.90	9.91	96.96%
04F01	62415	107.57	2081	0.90	9.88	96.87%
05F01	62415	107.46	2069	0.90	9.88	97.19%
06F01	76720	91.26	1671	0.89	9.55	98.49%
07F01	18056	44.57	671	0.90	8.44	99.91%
08F01	89521	114.47	2455	0.91	10.24	95.73%
09F01	89521	115.98	2473	0.91	10.22	95.55%
10F01	57376	72.66	1380	0.92	9.59	99.41%

Table S2 Spatial distribution of sediment archaeal richness and diversity estimates based on the 16S rRNA gene

Sampling sites	Clean data	faith_pd	observed_features	pielou_evenness	shannon_entropy	Goods_coverage
01F01	18678	23.15	536	0.88	7.98	99.95%
02F01	18678	23.15	537	0.88	7.99	99.96%
03F01	20524	20.26	451	0.84	7.38	99.92%
04F01	20524	20.43	454	0.84	7.39	99.96%
05F01	20524	20.33	453	0.84	7.38	99.92%
06F01	20539	12.43	314	0.84	6.99	99.98%
07F01	18418	7.06	157	0.79	5.79	100.00%
08F01	45548	31.25	619	0.72	6.64	99.41%
09F01	45548	31.41	623	0.72	6.65	99.40%
10F01	35267	13.31	345	0.82	6.89	99.97%

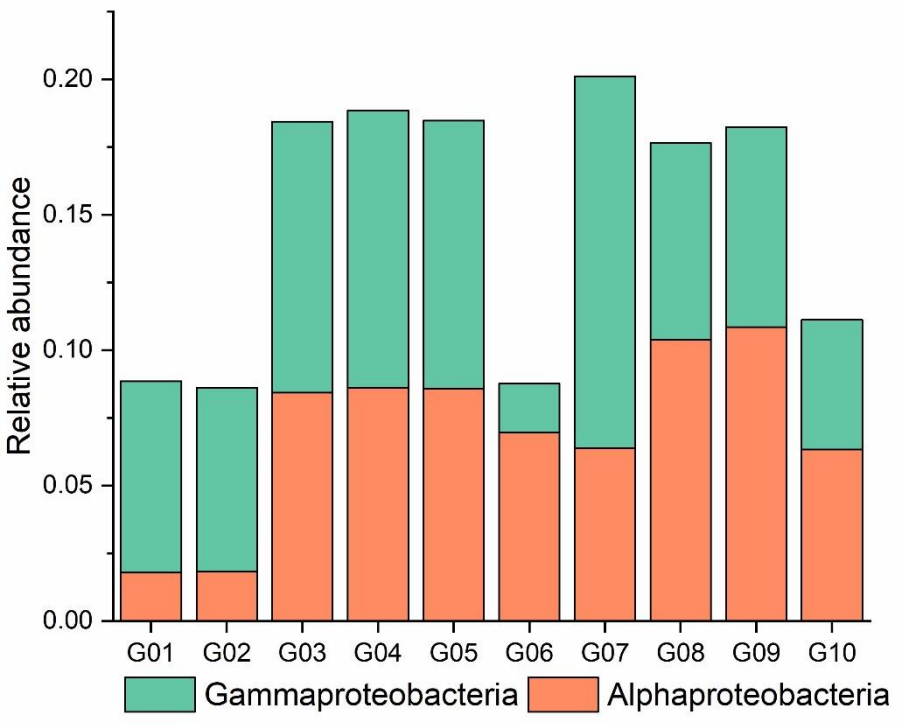


Figure S1 The composition of Proteobacteria