

Table S1. Main characteristics of the sampling sites along the subtropical-temperate forest biomes in China

Group	Parameters	Temperate forest biomes				Subtropical forest biomes				<i>p</i>
		ME	DL	FX	HDT	MX	GG	AL	ML	
Geographical condition	Latitude (N)	45°41′	39°97′	36°11′	33°43′	31°79′	29°65′	23°87′	25°13′	/
	Longitude (E)	127°71′	115°43′	109°63′	108°45′	104°71′	102°11′	103°51′	108°05′	/
	Elevation (m)	600	1300	1035	1526	1625	1726	2300	652	/
Climate	Mean Annual Temperature (°C)	3.10	5.00	7.40	9.00	11.00	13.00	18.30	19.38	/
	Mean Annual Precipitation (mm)	629	650	580	1023	486	1000	1086	1529	/
Soil environment	pH	5.02±0.0	6.85±0.0	8.12±0.0	5.90±0.0	5.60±0.22	6.20±0.01	5.94±0.08	6.71±0.60	<0.001
		7e	3b	1a	1cd	d	c	cd	b	
	BD (g·cm ⁻³)	0.94±0.0	1.02±0.1	0.90±0.0	1.20±0.0	1.10±0.01	0.81±0.01	1.12±0.07	0.83±0.07	<0.001
		1de	1cd	1ef	1a	bc	f	ab	f	
	Sand (%)	63.77±5.	89.35±0.	14.79±3.	49.60±0.	26.33±0.9	33.07±2.5	24.02±1.5	14.45±0.5	<0.001
		51b	01a	28f	01c	3e	0d	3e	7f	
	Silt (%)	23.93±3.	9.65±0.0	60.93±3.	49.87±0.	64.14±3.7	4.97±0.21	62.58±1.4	64.56±0.5	<0.001
		62c	1d	13a	01b	0a	e	4a	9a	
Soil substrates	Clay (%)	12.30±2.	1.00±0.0	24.28±1.	0.53±0.0	9.52±3.45	61.97±2.3	13.40±2.5	21.00±0.3	<0.001
		10cd	1e	86b	1e	d	a	6c	7b	
	SOC (g·kg ⁻¹)	99.33±1	46.21±9.	39.37±9.	40.95±7.	28.60±4.9	38.92±10.	36.37±4.9	52.88±10.	<0.001
		0.46a	60b	94bc	88bc	1c	54bc	8bc	35b	
	TN (g·kg ⁻¹)	3.17±0.2	1.40±0.2	1.52±0.3	1.90±0.1	1.61±0.12	2.28±0.18	2.56±0.35	4.72±0.83	<0.001
		5b	3e	0e	9cde	de	cd	bc	a	
	TP (g·kg ⁻¹)	1.07±0.0	0.82±0.0	0.64±0.0	0.39±0.0	0.39±0.13	0.51±0.06	0.50±0.11	2.33±0.50	<0.001
		1b	6bc	04cd	3d	d	cd	cd	a	
	AP (mg·kg ⁻¹)	15.37±1.	2.73±0.3	1.87±0.9	4.43±1.8	4.83±14.6	14.63±1.8	5.6±1.56c	11.1±1.45	<0.001
		47a	2de	9e	0cd	3cd	0a		b	
	C:N	31.34±0.	33.40±8.	27.45±1	21.53±3.	17.67±2.0	17.06±4.5	14.23±0.0	11.20±0.8	0.002
		96ab	49a	2.63ab	46bcd	2cd	2cd	2d	8d	
	C:P	92.55±1	56.87±1	61.30±1	103.65±	82.24±40.	76.90±24.	76.19±22.	23.74±8.7	0.012
		0.35ab	6.23bc	5.84bc	16.91a	63ab	94ab	20ab	1c	
	N:P	2.95±0.2	1.70±0.2	2.36±0.4	4.81±0.1	4.55±1.87	4.45±0.31	5.35±1.56	2.09±0.60	0.001
		5bc	2c	5c	1a	ab	ab	a	c	

Microbial community	Fungal abundance	5.12±0.0 8a	4.18±0.4 3bc	4.50±0.2 0b	4.39±0.3 2b	4.06±0.10 bc	3.62±0.34 c	4.34±0.42 b	4.06±0.59 bc	0.00 5
	Bacterial abundance	7.90±0.1 1ab	6.96±0.3 4ab	8.06±0.2 1a	7.27±1.0 5ab	7.19±0.21 ab	6.62±0.85 b	7.43±0.51 ab	7.07±1.21 ab	0.25
	F:B	0.65±0.0 2a	0.60±0.0 3ab	0.56±0.0 2b	0.61±0.0 5ab	0.56±0.02 b	0.55±0.05 b	0.58±0.02 b	0.58±0.02 b	0.02 5
	α-diversity	1.79±0.0 9ab	1.60±0.0 5bc	1.86±0.1 0a	1.55±0.2 2c	1.25±0.06 d	1.65±0.06 abc	1.29±0.21 d	1.68±0.02 abc	<0.001
	β-diversity	0c	0.24±0.0 9ab	0.26±0.0 5ab	0.24±0.0 8ab	0.26±0.05 ab	0.18±0.08 b	0.37±0.05 a	0.25±0.12 ab	0.00 1

ME, Maoer Mountain; DL, Dongling Mountain; FX, Fuxian; HDT, Huoditang; MX, Maoxian; GG, Gongga Mountain; AL, Ailao Mountain; ML, Karst Mulun station. MAT, mean annual temperature; MAP, mean annual precipitation; BD, bulk density; SOC, soil organic carbon; TN, soil total nitrogen; TP, soil total phosphorus; AP, available phosphorus; C:N, the ratio of soil organic carbon to total nitrogen; C:P, the ratio of soil organic carbon to total phosphorus; N:P, the ratio of soil total nitrogen to total phosphorus; F:B, the ratio of fungal abundance-to-bacterial abundance. Values presented are means±SD (n=3), letters after means±SD indicate significant differences at $p<0.05$ using LSD (L) and Duncan(D) tests. Values in bold are statistically significant at $p<0.05$.

Table S2. Summary of the metagenome sequencing of 24 composite samples across forest biomes.

Fore st site	Raw reads	HQ Rea ds (%)	GC (%)	Q 20(%)	Q3 0 (%)	Contigs				Scaffolds			
						Total (bp)	Max(b p)	Min(b p)	N5 0 (b p)	Total (bp)	Max(b p)	Mi n (b p)	N5 0 (b p)
ME1	800544	99.9	63.	98.0	94.	15815	50299	200	43	15669	50299	20	43
	32	2	45	9	51	40			4	69		0	6
ME2	812155	99.9	63.	97.8	93.	15337	11858	200	44	15177	13304	20	44
	34	0	26	2	95	20			2	74		0	5
ME3	842551	99.9	63.	98.3	95.	20661	19298	200	42	20594	19298	20	42
	80	4	87	6	26	67			5	76		0	6
DL1	805422	99.8	63.	97.8	94.	15662	9623	200	42	15543	9816	20	42
	94	8	94	6	08	92			6	50		0	8
DL2	822465	99.8	63.	97.9	94.	17725	30057	200	44	17501	52621	20	45
	66	9	85	1	18	77	8		9	73	1	0	3
DL3	815351	99.9	64.	97.8	94.	14984	10853	200	43	14836	12556	20	43
	10	0	36	6	07	86			5	99		0	7
FX1	912668	99.8	64.	97.8	94.	24653	61327	200	47	24233	61834	20	48
	42	8	54	6	08	49			8	58		0	4
FX2	853437	99.8	64.	97.9	94.	22907	37221	200	49	22512	64337	20	50
	40	9	18	4	27	86	5		3	25	0	0	0
FX3	855071	99.8	64.	98.0	94.	23421	14238	200	49	23024	19039	20	50
	22	8	34	6	61	18	5		5	63	6	0	2
HD	723043	99.8	63.	97.8	93.	11296	42100	200	42	11175	42100	20	42
T1	92	8	24	4	96	31			3	48		0	6
HD	780069	99.9	62.	97.7	93.	14214	20797	200	43	14042	35023	20	43
T2	54	0	44	0	63	78			6	96		0	9
HD	796206	99.8	60.	97.9	94.	19710	69135	200	53	19334	71137	20	54
T3	46	9	97	2	14	89			6	60		0	6
MX	835531	99.9	62.	98.0	94.	23275	34488	200	60	22573	38663	20	62
1	10	1	65	4	38	17	6		5	02	7	0	7
MX	744530	99.8	61.	97.7	93.	19102	20866	200	55	18554	32346	20	56
2	44	9	60	7	80	11	9		0	34	5	0	6
MX	826831	99.9	62.	98.2	94.	26291	11218	200	49	26015	11218	20	49
3	92	4	37	6	96	69	7		5	37	7	0	9
GG1	850953	99.8	64.	97.8	93.	15964	21731	200	42	15847	21731	20	42
	26	6	85	0	98	32			1	10		0	3
GG2	812757	99.8	63.	97.8	94.	13003	37744	200	41	12897	37744	20	42
	62	8	47	8	09	87			9	52		0	1
GG3	785315	99.8	63.	97.8	93.	14611	46859	200	43	14440	65355	20	44
	36	8	54	0	93	72			7	90		0	0

AL1	886388	99.8	63.	97.8	94.	22996	12956	200	61	22322	15144	20	63
	76	7	67	8	14	59	9		2	28	0	0	3
AL2	915376	99.8	63.	97.8	94.	24214	56896	200	52	23638	56896	20	53
	20	7	79	7	09	94			3	24		0	3
AL3	903682	99.8	63.	98.0	94.	20478	16266	200	54	20008	16266	20	55
	40	8	22	2	48	37	3		5	68	3	0	6
ML1	872183	99.9	63.	98.1	94.	18360	37857	200	45	18070	39589	20	45
	92	4	98	5	63	42			3	02		0	8
ML2	103656	99.9	63.	97.9	94.	26424	71490	200	45	26094	71490	20	46
	100	1	70	9	40	34			9	84		0	2
ML3	886419	99.9	64.	98.1	94.	23930	61600	200	47	23582	61600	20	48
	44	5	16	9	72	64			4	29		0	0

Table S3. Abundance of 40 phosphorus functional genes along the subtropical-temperate forest biomes in China.

Gene name		ME	DL	FX	HDT	MX	GG	AL	ML
P-starvation response	phoU	219.17±	212.37±	199.93±	208.57±	190.46±	225.83±	178.61±	173.84±
		25.80	6.66	30.04	16.07	17.41	10.75	13.44	15.05
regulation	phoR	239.87±	223.44±	301.06±	245.52±	210.43±	248.54±	211.74±	246.45±
		5.42	18.22	18.48	13.48	27.02	29.20	70.93	25.04
	phoB	128.79±	133.80±	145.00±	130.33±	101.91±	139.81±	118.28±	114.53±
		12.23	11.87	17.44	41.73	21.60	14.11	21.24	13.98
P-uptake and transport	ugpB	110.40±	94.82±6.	71.08±1	100.12±	49.22±1	139.58±	103.24±	95.39±2
		23.9	98	2.05	52.02	7.85	9.40	28.82	1.98
	ugpA	56.86±1	41.87±1	38.11±5.	57.88±3	24.64±8.	74.43±8.	51.53±8.	48.26±1
		3.82	6.59	61	0.59	94	78	70	3.56
	ugpE	63.55±6.	47.93±1	42.37±9.	57.15±3	23.53±9.	74.49±1	50.03±1	51.99±9.
		81	3.67	67	4.29	15	4.62	6.01	83
	ugpC	58.51±1	43.94±1	31.93±3.	51.18±1	25.34±7.	66.01±1	49.40±1	39.67±1
		1.56	7.59	86	8.26	99	5.32	9.54	1.46
	phnC	45.61±9.	45.81±6.	64.99±1	64.16±2	34.20±1	44.67±7.	60.45±1	56.05±9.
		86	67	9.04	9.88	1.27	46	8.49	54
	phnE	63.30±4.	68.15±1	96.04±2	87.69±3	39.55±1	66.93±1	96.63±3	76.47±1
		58	0.39	2.61	7.57	2.53	3.54	2.43	3.14
	phnD	74.49±1	72.68±1	116.75±	100.62±	45.77±9.	73.05±1	94.92±2	117.95±
		1.27	7.99	22.08	60.98	01	3.20	6.24	8.88
	pstB	241.73±	279.78±	237.77±	215.60±	183.93±	289.93±	200.26±	196.94±
		28.93	18.05	10.61	51.54	13.19	47.89	29.57	14.08
	pstC	227.47±	248.25±	234.57±	203.05±	165.62±	233.89±	201.08±	190.39±
		30.94	5.11	10.94	62.6	5.88	23.70	18.68	12.80
	pstA	184.34±	196.12±	220.88±	173.51±	135.79±	206.23±	164.00±	171.11±
		11.21	7.21	12.11	37.25	4.24	38.84	16.00	10.77

P-solubilization and P-mineralization	pstS	263.63±16.38	299.75±40.4	329.32±21.13	278.24±16.81	264.77±14.58	286.78±54.14	307.26±9.46	228.75±8.78
	pit	229.02±11.27	206.81±25.83	76.10±5.46	183.95±36.21	166.99±30.71	275.55±57.89	189.66±18.23	167.22±13.57
	gcd	652.73±124.97	431.85±73.18	556.68±105.35	567.09±255.31	435.24±63.12	623.38±157.65	416.37±166.02	819.86±124.43
	phnN	3.91±2.12	7.72±7.08	5.75±2.53	7.78±7.39	6.59±3.31	4.49±3.36	15.68±7.35	5.06±2.13
	phnL	5.95±2.88	12.8±2.64	8.15±1.38	16.07±9.89	9.60±3.20	5.72±1.29	19.95±1.04	6.93±3.66
	phnK	10.04±3.80	16.24±5.34	12.68±0.94	18.51±4.15	12.87±6.02	9.74±3.74	25.17±1.15	10.33±3.20
	phnO	0.00±0.00	0.00±0.00	1.54±0.58	0.00±0.00	0.33±0.00	0.00±0.00	0.27±0.00	0.13±0.00
	phnM	18.41±9.74	24.37±8.3	18.75±2.88	34.39±1.764	30.00±1.802	15.36±3.56	54.94±3.156	16.89±0.69
	phnJ	11.38±3.45	23.47±3.33	14.82±3.21	21.29±2.72	19.12±3.36	16.23±8.02	28.46±1.503	11.46±2.64
	phnI	10.81±4.77	23.84±7.14	16.11±2.63	24.47±1.044	16.75±8.73	15.22±2.59	35.17±1.746	10.70±3.60
	phnH	4.13±0.87	9.93±3.4	6.81±1.77	8.54±3.56	6.85±4.92	5.54±3.71	18.37±1.175	4.26±1.76
	phnG	5.34±3.96	7.93±1.49	6.70±0.55	8.62±5.66	6.77±3.41	4.49±2.14	20.36±1.399	3.19±1.77
	phnP	53.22±8.12	59.01±7.91	69.32±2.006	74.18±2.325	76.71±1.549	66.46±1.676	69.76±9.52	46.28±5.22
	phnF	3.05±2.17	9.37±5.94	4.48±1.37	10.12±7.45	13.35±7.53	6.70±3.80	28.52±1.663	3.04±0.70
	ppx	304.22±39.43	349.64±36.98	338.89±9.91	302.51±55.71	254.59±5.32	374.97±16.74	287.50±22.05	309.23±11.45
	ppa	101.61±18.61	149.39±20	130.04±18.95	96.63±9.92	155.98±6.78	149.58±47.13	170.29±5.45	101.90±15.07
	phnA	2.31±1.86	4.14±5.06	2.77±3.80	1.51±0.47	1.80±1.46	1.31±0.84	6.46±5.69	1.68±0.00
	phnX	1.35±1.28	5.07±2.66	3.93±2.31	5.71±4.34	11.32±0.66	1.51±2.08	6.22±5.20	2.63±1.25
	phnW	35.42±1.76	26.74±5.01	31.61±3.05	38.86±1.944	17.50±1.068	41.94±1.32	26.80±1.096	43.86±6.72
	appA	3.36±4.05	2.42±0.63	1.49±2.23	5.01±1.48	5.85±2.17	5.29±1.50	5.74±5.72	5.67±1.22
	opd	86.43±3.298	63.70±1.425	95.53±1.383	80.31±2.868	51.45±1.158	93.50±1.604	62.25±1.901	100.01±2.96

ugpQ	205.47± 10.56	255.45± 5.47	318.06± 11.37	195.96± 38.37	157.81± 20.82	236.70± 38.38	237.31± 30.94	210.89± 10.51
phoA	70.38±7. 63	54.78±1 5.15	51.37±1 8.54	58.23±2 8.65	14.67±9. 99	41.56±2 0.56	63.84±3 5.42	79.10±1 1.81
phoD	237.86± 61.26	313.73± 59.95	274.27± 17.15	209.16± 122.65	92.21±2 5.38	293.71± 44.64	247.14± 89.36	259.47± 28.67
phoN	9.09±3.2 6	7.76±6.2 7	2.90±1.7 0	9.54±2.0 9	14.39±2. 76	73.4±1.0 1	13.88±3. 00	6.35±0.3 4
aphA	0.00±0.0 0	0.00±0.0 0	0.25±0.0 0	0.51±0.3 9	0.00±0.0 0	0.95±0.0 0	0.70±0.3 7	0.21±0.1 6
olpA	11.70±6. 33	8.97±2.9 5	4.77±1.2 2	20.36±1 5.69	35.60±1. 84	14.67±1 1.00	13.51±1 1.08	7.84±2.8 5

Table S4. Changes in the abundance of three major classes of phosphorus functional genes along the subtropical-temperate forest biomes of China.

Gene name	ME	DL	FX	HDT	MX	GG	AL	ML	<i>p</i>
P-starvati									
on	587±13.7	569.61±2	645.99±3	584.43±4	502.82±4	613.87±2	508.63±6	534.82±2	0.0
respons	6abc	2.49bcd	8.28a	4.72abc	5.11d	1.55ab	4.21d	8.00cd	03
e									
regulati									
on									
P-									
uptake	1618.91±	1645.90±	1559.90±	1573.14±	1159.35±	1831.47±	1568.55±	1440.18±	0.0
and	14.77ab	69.27ab	47.45b	276.11b	67.47c	178.45a	71.66b	77.63b	01
transpor									
t									
P-									
solubiliz									
ation	1848.29±	1868.10±	1977.19±	1814.85±	1447.13±	2035.71±	1874.46±	2065.68±	0.0
and	186.17a	81.39a	117.76a	309.70a	97.89b	169.00a	153.76a	103.74a	11
minerali									
zation									

Values presented are means±SD (n=3), letters after means±SD indicate significant differences at $p<0.05$ using LSD (L) and Duncan(D) tests.

Table S5. The average abundance of three major classes of phosphorus functional genes among temperate and subtropical forest biomes.

Gene name	Temperate forest biomes	Subtropical forest biomes	<i>P</i>
P-starvation response regulation	596.96±17.67	540.03±22.49	0.026
P-uptake and transport	1599.47±73.05	1499.89±58.86	0.14
P-solubilization and mineralization	1877.18±105.32	1855.75±69.47	0.78
Total	4073.61±185.92	3895.67±127.67	0.24

Values in bold are statistically significant at $P<0.05$.

Table S6. Abundance of phosphorus functional genes corresponding to phyla along the subtropical-temperate forest biomes of China.

[illegible]

P-uptake and transport	Raymondbacteria								0.33 a
	Candidatus	86 ±	35.67 ±	128 ±	96 ±	15.67 ±	75.67 ±	33.33 ±	194.33 ±
	Rokubacteria	19.97 bc	5.55 de	22.81 b	20.88 bc	0.88 e	3.93 cd	3.71 de	22.58 a
	Candidatus	1 ± 0.58							0.33 ±
	Tectomicrobia	a	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0.33 ab
	Chloroflexi	19 ±	22.33 ±	85 ±	10 ± 4 b	5.67 ±	21 ± 7.51	32 ±	11.33 ±
		2.52 b	4.91 b	20.07 a		1.86 b	b	27.06 b	3.84 b
	Cyanobacteria	0.67 ±							
		0.67 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
	Deinococcus-Thermus	0.67 ±	0.33 ±						
		0.67 a	0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
	Euryarchaeota	0.33 ±		0.33 ±					
		0.33 a	0 ± 0 a	0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
	Firmicutes	5.67 ±	1.33 ±	0.67 ±	0.33 ±	4.67 ±	0.67 ±		1 ± 0.58
		2.4 a	1.33 ab	0.67 b	0.33 b	3.28 ab	0.67 b	0 ± 0 b	ab
	Gemmatimonadetes	28 ±	70 ±	263 ±	40.33 ±	27 ± 5.03	75.33 ±	61.67 ±	35.67 ±
	Ignavibacteriae	11.14 b	12.17 b	98.81 a	12.88 b	b	24.13 b	5.55 b	3.84 b
		1.67 ±	0.67 ±	2.67 ±	1.33 ±		0.67 ±		13.33 ±
		0.88 b	0.67 b	1.2 b	0.67 b	0 ± 0 b	0.67 b	1 ± 1 b	1.67 a
	Nitrospinae	2.33 ±	1.67 ±			1.67 ±		0.67 ±	3.67 ±
		1.2 ab	1.2 ab	0 ± 0 b	0 ± 0 b	1.2 ab	0 ± 0 b	0.67 ab	2.19 a
	Nitrospirae	21.33 ±	1.67 ±	6.67 ±	30 ±		21.33 ±		54.67 ±
		6.33 bc	0.88 c	2.91 c	18.33 b	1 ± 1 c	2.91 bc	0 ± 0 c	7.36 a
	Planctomycetes	25 ±	8.33 ±	26 ±	11 ± 3.21	51.67 ±	12 ± 1.15	21.33 ±	32.33 ±
		7.51 bc	1.76 c	3.51 bc	c	10.53 a	c	5.78 bc	9.94 b
	Proteobacteria	594 ±	617.33 ±	627.67 ±	521.33 ±	694.33 ±	547 ±	1192.33	642.33 ±
		63.61 b	33.17 b	93.9 b	48.59 b	55.38 b	32.87 b	± 248.39 a	66.41 b
	Verrucomicrobia	354 ±	104 ±	49.67 ±	161.33 ±	124 ±	19.67 ±	186.67 ±	118.33 ±
	76.71 a	18.56 bcd	30.69 cd	70.05 bc	30.66 bcd	2.4 d	28.35 b	11.02 bcd	
P-uptake and transport	Acidobacteria	724.33 ±	579 ±	1148 ±	1475.33 ± 921.49 ab	1942 ±	733.33 ±	1324 ±	1045 ±
		90.39 b	79.48 b	78.08 ab		68.15 a	95.49 b	297.06 ab	131.93 ab
	Actinobacteria	893 ±	1456.67 ± 160.21 a	1268 ±	201.33 ±	621 ±	754.67 ±	1413.67 ± 135.69 a	317.67 ±
		57.81 bc		246.87 ab	43.05 e	161.6 cd	56.78 c		73.94 de
	Aquificae	1 ± 0.58 a	2 ± 1.15 a	0 ± 0 a	2.33 ±	2 ± 2 a	0.33 ±	1.67 ±	0 ± 0 a
					1.45 a		0.33 a	0.88 a	
	Armatimonadetes	9 ± 2.31 ab	11.33 ±	11.67 ±	4.33 ±	0.33 ±	7.67 ±	4.67 ±	1.67 ±
			5.17 a	3.93 a	4.33 ab	0.33 b	4.06 ab	3.71 ab	0.88 ab

<i>Bacteroidetes</i>	25 ± 2.89 a	24 ± 13.23 a	17.67 ± 1.86 ab	12 ± 6.81 ab	8.33 ± 3.28 ab	6.67 ± 2.19 b	13.33 ± 2.91 ab	8 ± 1.53 ab
<i>Balneolaeota</i>	0 ± 0 a	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Calditrichaeot a</i>	6.67 ± 2.6 bc	8.33 ± 1.67 bc	30 ± 1.53 a	5.33 ± 2.67 bc	1.67 ± 1.67 c	5.67 ± 4.26 bc	4 ± 3.06 bc	12.33 ± 4.48 b
<i>Candidate division AD3</i>	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Candidate division NC10</i>	28.33 ± 7.88 bc	13 ± 3.46 cd	48 ± 10.58 a	16.67 ± 2.85 cd	2.33 ± 1.86 d	13.67 ± 4.1 cd	6.67 ± 1.33 d	33.33 ± 2.73 ab
<i>Candidate division WOR-3</i>	1.33 ± 1.33 ab	0.33 ± 0.33 ab	0 ± 0 b	0 ± 0 b	2.33 ± 1.45 a	0 ± 0 b	0 ± 0 b	0 ± 0 b
<i>Candidate division WPS-2</i>	1 ± 0.58 a	0.67 ± 0.67 a	0.67 ± 0.67 a	1 ± 0.58 a	1.33 ± 0.67 a	0.67 ± 0.67 a	0.67 ± 0.67 a	0 ± 0 a
<i>Candidate division Zixibacteria</i>	5.33 ± 2.4 a	3.33 ± 1.86 a	5.33 ± 2.33 a	2 ± 1 a	1.67 ± 0.88 a	1.33 ± 0.33 a	2 ± 1 a	4.67 ± 2.33 a
<i>Candidatus Abyssobacteri a</i>	0.67 ± 0.33 a	0 ± 0 a	0 ± 0 a	0.67 ± 0.67 a	0 ± 0 a	0 ± 0 a	0.67 ± 0.67 a	1.33 ± 0.88 a
<i>Candidatus Aminicenante s</i>	2 ± 0.58 ab	3 ± 0.58 a	0.67 ± 0.67 c	0 ± 0 c	0 ± 0 c	0 ± 0 c	0.33 ± 0.33 c	1 ± 0.58 bc
<i>Candidatus Aureabacteria</i>	1 ± 1 ab	0 ± 0 b	0 ± 0 b	0 ± 0 b	2.33 ± 1.2 a	0.33 ± 0.33 b	0 ± 0 b	0.33 ± 0.33 b
<i>Candidatus Bathyarchaeot a</i>	0.67 ± 0.67 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Candidatus Cloacimonete s</i>	0.33 ± 0.33 a	0 ± 0 a	0.67 ± 0.67 a	0 ± 0 a	0 ± 0 a	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a
<i>Candidatus Coatesbacteri a</i>	0 ± 0 a	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Candidatus Dadabacteria</i>	5 ± 1.53 bc	1.33 ± 0.88 c	10.67 ± 2.6 a	1 ± 0.58 c	1 ± 1 c	2.33 ± 0.33 bc	0.67 ± 0.67 c	7.33 ± 3.84 ab
<i>Candidatus Edwardsbacte ria</i>	0 ± 0 a	0.67 ± 0.67 a	0.67 ± 0.67 a	0 ± 0 a	1 ± 1 a	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a

<i>Candidatus</i>	9.67 ±		10 ±	5.67 ±	0.33 ±	16 ± 2.52		32 ±
<i>Eisenbacteria</i>	1.33 bc	0 ± 0 d	0.58 bc	2.96 cd	0.33 d	b	3 ± 3 cd	6.81 a
<i>Candidatus</i>	0.33 ±							
<i>Fraserbacteria</i>	0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Candidatus</i>	0.67 ±	0.67 ±		0.67 ±	1.33 ±		0.33 ±	1 ± 0.58
<i>Glassbacteria</i>	0.67 a	0.67 a	0 ± 0 a	0.33 a	1.33 a	0 ± 0 a	0.33 a	a
<i>Candidatus</i>	1 ± 0.58							
<i>Goldbacteria</i>	a	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b
<i>Candidatus</i>	0.33 ±							
<i>Heimdallarchaeota</i>	0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Candidatus</i>	3.33 ±	0.33 ±			0.67 ±	0.67 ±	0.67 ±	2 ± 1.15
<i>Kaiserbacteria</i>	0.67 a	0.33 bc	0 ± 0 c	0 ± 0 c	0.67 bc	0.67 bc	0.67 bc	ab
<i>Candidatus</i>								
<i>Latescibacteria</i>	0 ± 0 a	0.33 ±	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>a</i>		0.33 a						
<i>Candidatus</i>	0.67 ±	1.67 ±						
<i>Marinimicrobia</i>	0.33 b	0.88 a	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b
<i>Candidatus</i>	0.33 ±	0.67 ±				0.67 ±		
<i>Melainabacteria</i>	0.33 a	0.67 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0.67 a	0 ± 0 a	0 ± 0 a
<i>Candidatus</i>	0.33 ±	0.67 ±			14.33 ±		10 ± 5.29	
<i>Microgenomates</i>	0.33 b	0.67 b	0 ± 0 b	0 ± 0 b	5.36 a	0 ± 0 b	a	0 ± 0 b
<i>Candidatus</i>								
<i>Nomurabacteria</i>	0 ± 0 b	2 ± 1.15	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0.67 ±	1 ± 0.58
<i>a</i>		a					0.67 ab	ab
<i>Candidatus</i>	17.67 ±	8.67 ±	25.67 ±	3.33 ±	1.67 ±	3.33 ±	4.33 ±	13 ±
<i>Omnitrophica</i>	4.63 ab	1.2 bc	8.84 a	2.03 c	0.33 c	1.2 c	3.38 c	1.53 bc
<i>Candidatus</i>	2.33 ±	0.67 ±	1.67 ±	0.33 ±	1.67 ±		0.33 ±	4 ± 1.15
<i>Poribacteria</i>	0.88 ab	0.67 bc	0.88 bc	0.33 bc	0.33 bc	0 ± 0 c	0.33 bc	a
<i>Candidatus</i>	0.67 ±	0.67 ±	2.33 ±		0.33 ±		0.67 ±	3.67 ±
<i>Raymondbacteria</i>	0.67 a	0.33 a	2.33 a	1 ± 1 a	0.33 a	0 ± 0 a	0.67 a	2.33 a
<i>Candidatus</i>								
<i>Roizmanbacteria</i>	0 ± 0 b	0.67 ±	1 ± 0.58					
<i>a</i>		0.67 ab	a	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b
<i>Candidatus</i>	864 ±	274.33 ±	1088.67	1016.33	39.33 ±	658.67 ±	236.33 ±	1842 ±
<i>Rokubacteria</i>	212.15 b	81.53	± 91 b	± 215.05	4.33 d	39.39 bc	133.32	232.17 a
		cd		b			cd	

<i>Candidatus</i>	0.67 ±	0.33 ±	1 ± 0.58	1.67 ±		1.33 ±	2.33 ±	0.67 ±
<i>Schekmanbact</i>	0.67 a	0.33 a	a	1.2 a	0 ± 0 a	0.33 a	1.45 a	0.67 a
<i>eria</i>								
<i>Candidatus</i>	0.33 ±					0.67 ±		1.33 ±
<i>Sumerlaeota</i>	0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0.67 a	0 ± 0 a	1.33 a
<i>Candidatus</i>	9 ± 5.51	7.33 ±	21 ±	9.33 ±	1.33 ±	3.33 ±	1.67 ±	12.67 ±
<i>Tectomicrobia</i>	bc	4.84 bc	6.11 a	3.76 bc	0.67 c	1.33 bc	1.67 bc	1.76 ab
<i>Candidatus</i>	1 ± 0.58							
<i>Woesebacteria</i>	a	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b
<i>Chlamydiae</i>	0.33 ±					1.33 ±		0.33 ±
	0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	1.33 a	0 ± 0 a	0.33 a
<i>Chlorobi</i>	2 ± 0.58	2 ± 1.53	3.33 ±	0.67 ±		1 ± 0.58	0.67 ±	6.33 ±
	b	b	1.76 ab	0.67 b	0 ± 0 b	b	0.67 b	2.19 a
<i>Chloroflexi</i>	133 ±	163 ±	586.33 ±	28.33 ±	41.67 ±	150.67 ±	252.33 ±	81 ±
	14.73 b	40.51 b	130.49 a	7.69 b	10.4 b	8.29 b	199.9 b	23.86 b
<i>Chrysiogenete</i>	1 ± 0.58	0.67 ±	3.67 ±	1.33 ±	0.33 ±	0.67 ±		5 ± 0.58
<i>s</i>	bc	0.33 c	1.86 ab	1.33 bc	0.33 c	0.67 c	0 ± 0 c	a
<i>Crenarchaeot</i>	0.33 ±	1.33 ±	3.33 ±				0.33 ±	
<i>a</i>	0.33 b	0.67 b	1.33 a	0 ± 0 b	0 ± 0 b	0 ± 0 b	0.33 b	0 ± 0 b
<i>Cyanobacteri</i>	65.33 ±	41.33 ±	72.33 ±	30 ± 5.29	35.67 ±	32.67 ±	44 ± 6.24	95.67 ±
<i>a</i>	8.97 b	1.86 c	9.28 b	c	2.19 c	3.76 c	c	8.88 a
<i>Deferribactere</i>	1.67 ±	2.67 ±	5.33 ±			1 ± 0.58		3 ± 1.73
<i>s</i>	1.2 ab	1.76 ab	2.33 a	0 ± 0 b	0 ± 0 b	b	0 ± 0 b	ab
<i>Deinococcus-</i>	3.67 ±	5.33 ±	3.67 ±	0.67 ±	2.33 ±	2.67 ±		
<i>Thermus</i>	1.33 a	2.73 a	2.73 a	0.67 a	0.67 a	1.33 a	4 ± 2 a	2 ± 1 a
<i>Elusimicrobia</i>	9.67 ±	5 ± 0.58	8.33 ±	4.33 ±		6.33 ±	8.67 ±	18.33 ±
	3.71 ab	b	2.91 b	0.67 b	6 ± 2 b	1.2 b	4.37 b	4.63 a
<i>Euryarchaeot</i>	14.33 ±	23.67 ±	18.33 ±	5 ± 1.53	5 ± 0.58	2 ± 0.58	9.67 ±	6.33 ±
<i>a</i>	0.88 abc	9.28 a	3.33 ab	bc	bc	c	8.17 bc	0.88 bc
<i>Firmicutes</i>	72.33 ±	60.67 ±	47 ±	20 ± 1.15	14.33 ±	19.67 ±	30 ± 3.06	23 ±
	14.68 a	11.67 ab	5.03 bc	d	1.2 d	6.64 d	cd	6.81 d
<i>Gemmatimon</i>	104.33 ±	180 ±	608 ±	94 ±	75.67 ±	199.33 ±	148.33 ±	84 ± 19
<i>adetes</i>	15.25 b	41.88 b	196.3 a	30.35 b	20.3 b	46.94 b	45.17 b	b
<i>Ignavibacteri</i>	9.67 ±	7 ± 4.04	24.33 ±	12.67 ±	16.67 ±	15.33 ±	5 ± 2.31	16.67 ±
<i>ae</i>	0.33 bcd	cd	1.33 a	4.81 bcd	4.1 ab	1.45 bc	d	1.86 ab
<i>Lentisphaerae</i>	5.33 ±	1.33 ±	9.33 ±		0.67 ±		1.33 ±	7.33 ±
	0.33 bc	0.88 d	1.33 a	1 ± 1 d	0.67 d	2 ± 2 cd	0.67 d	2.33 ab
<i>Nitrospinae</i>	8 ± 1.15	5.33 ±	16.33 ±	3.67 ±		2 ± 1.15	3.33 ±	9.67 ±
	bc	2.6 bcd	3.76 a	2.03 bcd	0 ± 0 d	cd	2.4 cd	1.2 b
<i>Nitrospirae</i>	122.33 ±	27.67 ±	75 ±	190 ±	10.67 ±	89.33 ±	13.33 ±	321.67 ±
	7.36 bc	4.67 c	17.95 bc	122.98 ab	3.53 c	12.68 bc	2.91 c	74.92 a

P- solubi lizatio n and miner alizati on	<i>Planctomycetes</i>	85.33 ± 26.36 bcd	67 ± 8.14 cd	148.33 ± 19.32 ab	76.67 ± 16.5 cd	122.33 ± 25.78 abc	49.67 ± 3.18 d	110.33 ± 19.46 abcd	167.67 ± 38.92 a
	<i>Proteobacteria</i>	3789.33 ± 338.96 b	3673.67 ± 428.22 b	3601.67 ± 401.76 b	3281.67 ± 623.33 b	3807.67 ± 405.83 b	3146.33 ± 136.67 b	8392.67 ± 2162.9 a	4078.67 ± 272.13 b
	<i>Spirochaetes</i>	4.33 ± 1.86 a	5.67 ± 3.67 a	2.67 ± 1.67 a	2 ± 1 a	1.33 ± 0.33 a	2 ± 1.53 a	5.67 ± 0.88 a	2.67 ± 1.76 a
	<i>Synergistetes</i>	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0.67 ± 0.67 a	0.33 ± 0.33 a	0 ± 0 a
	<i>Thaumarchaeota</i>	24.33 ± 15.06 ab	10 ± 1.53 ab	22.33 ± 10.74 ab	0 ± 0 b	1.33 ± 0.67 ab	26.67 ± 14.11 a	2 ± 1.15 ab	27.67 ± 9.24 a
	<i>Thermodesulfobacteria</i>	1.33 ± 0.88 a	0.67 ± 0.67 a	0 ± 0 a	0.33 ± 0.33 a	0.33 ± 0.33 a	3 ± 3 a	1 ± 1 a	1.33 ± 1.33 a
	<i>Thermotogae</i>	0 ± 0 a	0.67 ± 0.67 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	1 ± 1 a	0.67 ± 0.67 a
	<i>Verrucomicrobia</i>	1428.67 ± 226.52 a	449 ± 55.33 bcd	278.33 ± 97.89 cd	620.33 ± 228.47 bc	322.67 ± 81.61 cd	102.33 ± 9.39 d	757.33 ± 153.95 b	518 ± 53.27 bc
	<i>Abditibacteriota</i>	1.33 ± 1.33 a	2.33 ± 1.2 a	0.67 ± 0.67 a	0 ± 0 a	1.67 ± 0.88 a	0.67 ± 0.67 a	0 ± 0 a	0.33 ± 0.33 a
	<i>Acidobacteria</i>	2923 ± 331.69 bcde	1451 ± 238.68 e	3998.33 ± 406.8 abc	2554 ± 615.56 cde	4300.67 ± 410.28 ab	2224.67 ± 360.97 de	3056 ± 639.66 bcd	5494 ± 915.44 a
	<i>Actinobacteria</i>	197.67 ± 25.05 c	401.33 ± 13.72 ab	326.33 ± 61.26 b	66.33 ± 21.71 d	158.33 ± 42.91 cd	194.67 ± 33.51 c	471.67 ± 65.08 a	87.33 ± 26.43 cd
	<i>Armatimonadetes</i>	0.67 ± 0.67 ab	0.67 ± 0.33 ab	1.67 ± 0.88 ab	4.33 ± 2.33 a	0 ± 0 b	0 ± 0 b	3 ± 2.52 ab	0 ± 0 b
	<i>Ascomycota</i>	0.33 ± 0.33 ab	1.67 ± 1.2 a	0 ± 0 b	1 ± 0.58 ab	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b
	<i>Bacteroidetes</i>	101.33 ± 24.11 a	42 ± 9.29 bc	109.33 ± 14.52 a	40 ± 4.36 c	60 ± 4.16 bc	39.33 ± 7.84 c	80 ± 10.44 ab	75 ± 15.72 abc
	<i>Balneolaeota</i>	0.67 ± 0.67 b	0 ± 0 b	3.33 ± 1.33 a	0 ± 0 b	0 ± 0 b	0 ± 0 b	0.67 ± 0.67 b	0 ± 0 b
	<i>Calditrichaeota</i>	1.33 ± 0.67 ab	0 ± 0 b	0 ± 0 b	3.33 ± 1.76 a	0 ± 0 b	0 ± 0 b	0.33 ± 0.33 b	0 ± 0 b
	<i>Candidate division NC10</i>	0.33 ± 0.33 b	0 ± 0 b	4.33 ± 1.67 a	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b

<i>Candidate</i>								
<i>division</i>	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0.33 ± 0.33 a	0 ± 0 a
<i>Zixibacteria</i>								
<i>Candidatus</i>		0.67 ±	3.33 ±	0.67 ±	0.67 ±		2.33 ±	0.67 ±
<i>Glassbacteria</i>	0 ± 0 b	0.67 ab	1.2 a	0.67 ab	0.67 ab	0 ± 0 b	1.86 ab	0.33 ab
<i>Candidatus</i>								
<i>Hydrogeneden- tes</i>	2 ± 1.15 ab	5 ± 1 ab	4.33 ± 1.45 ab	2 ± 1.15 ab	0.67 ± 0.67 b	5 ± 2 ab	3.67 ± 0.67 ab	7.33 ± 4.37 a
<i>Candidatus</i>								
<i>Kerfeldbacteri- a</i>	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Candidatus</i>								
<i>Marinimicrob- ia</i>	24 ± 8.33 bc	7.33 ± 1.76 d	58 ± 7.77 a	8.33 ± 4.48 cd	5 ± 1.53 d	17 ± 4.73 cd	14 ± 6.35 cd	39 ± 4.16 b
<i>Candidatus</i>	2.67 ±			2.67 ±				5.67 ±
<i>Parcubacteria</i>	2.67 ab	0 ± 0 b	0 ± 0 b	1.45 ab	0 ± 0 b	0 ± 0 b	0 ± 0 b	2.85 a
<i>Candidatus</i>	152.67 ±	37.33 ±	173.67 ±	166.33 ±	9.33 ±	99.33 ±	40 ±	639.33 ±
<i>Rokubacteria</i>	60.15 bc	11.7 cd	7.42 b	41.16 bc	3.53 d	10.74 bcd	24.44 cd	95.73 a
<i>Chloroflexi</i>	29.33 ± 5.04 b	40 ± 4.04 b	127.67 ± 28.87 a	7 ± 2.08 b	10.33 ± 3.18 b	24.33 ± 3.38 b	46.67 ± 34.7 b	18 ± 7.55 b
<i>Cyanobacteri- a</i>	5.67 ± 2.73 b	12.67 ± 5.61 ab	18.33 ± 3.76 a	4 ± 1.15 b	1.67 ± 1.67 b	5 ± 1 b	8.33 ± 4.33 ab	9.33 ± 6.89 ab
<i>Deinococcus- Thermus</i>	0.67 ± 0.67 b	2.67 ± 0.67 a	0.67 ± 0.67 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b	0 ± 0 b
<i>Elusimicrobia</i>	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Euryarchaeot- a</i>	0 ± 0 a	1 ± 1 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Firmicutes</i>	7 ± 3.21 a	5 ± 2.52 ab	5 ± 1.53 ab	0.33 ± 0.33 b	0.67 ± 0.67 b	1.33 ± 0.88 b	4 ± 2.31 ab	2.67 ± 1.33 ab
<i>Gemmatimon- adetes</i>	131.67 ± 34.91 b	151 ± 13.65 b	697 ± 130.12 a	91 ± 32.05 b	54.33 ± 19.97 b	184 ± 44.07 b	155 ± 79.62 b	208.67 ± 14.84 b
<i>Nanoarchaeot- a</i>	0.33 ± 0.33 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Nitrospirae</i>	51 ± 12.66 b	2.67 ± 1.76 c	5 ± 1 c	50.33 ± 25.69 b	2.33 ± 1.86 c	29.67 ± 5.78 bc	1.67 ± 1.2 c	123.33 ± 20.95 a
<i>Planctomycet- es</i>	13.67 ± 4.26 c	21 ± 4 bc	26 ± 9.54 abc	11 ± 5.13 c	41.67 ± 9.96 ab	17.33 ± 9.94 c	45 ± 10.02 a	28.33 ± 7.22 abc
<i>Proteobacteri- a</i>	1305.33 ± 161.72 b	1658.33 ± 295.85 b	1309 ± 159.8 b	1342.67 ± 355.94 b	1558.33 ± 247.92 b	1012.33 ± 144.1 b	4466 ± 1404.28 a	1547.33 ± 129.35 b

<i>Rhodophyta</i>	0 ± 0 a	0.33 ± 0.33 a	1 ± 1 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Rhodotherma eota</i>	0.67 ± 0.67 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Spirochaetes</i>	0 ± 0 a	0.67 ± 0.67 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a	0 ± 0 a
<i>Thaumarchae ota</i>	2.33 ± 2.33 b	0 ± 0 b	7 ± 3.61 ab	0 ± 0 b	0 ± 0 b	12 ± 6.03 a	0 ± 0 b	1.67 ± 1.2 b
<i>Thermotogae</i>	0.67 ± 0.67 bc	5 ± 1.53 a	3.67 ± 0.33 ab	0 ± 0 c	0 ± 0 c	2.67 ± 1.33 abc	2.67 ± 2.67 abc	0 ± 0 c
<i>Verrucomicro bia</i>	406 ± 70.55 a	85.33 ± 19.22 bc	88.33 ± 31.83 bc	174.33 ± 68.44 b	110.33 ± 32.27 bc	12 ± 3.46 c	200.33 ± 53.31 b	162.67 ± 11.89 b