Table S1. Physicochemical properties. Data are mean (SD).

Physicochemical properties	Control	NPK	NPK+WS	NPK+PM	NPK+CM
pH	7.46(0.16)a	5.69(0.2)c	5.58(0.2)c	7.14(0.12)b	7.22(0.15)b
SM (%)	15.26(6.13)c	16.71(6.4)bc	18.18(6.47)bc	19.55(5.88)b	25.09(8.34)a
TC (%)	0.79(0.06)d	1.07(0.14)c	1.56(0.1)b	1.64(0.15)b	2.61(0.18)a
TN (%)	0.09(0.01)d	0.12(0.01)c	0.16(0.01)b	0.18(0.01)b	0.26(0.01)a
TP (g/kg)	0.27(0.06)d	0.42(0.1)c	0.45(0.1)c	1.46(0.2)a	0.85(0.12)b
TK (g/kg)	12.85(0.44)c	12.96(0.37)bc	13.19(0.36)b	13.1(0.5)bc	13.99(0.49)a
DOC (mg/kg)	22.72(6.64)c	26.21(9.39)c	48.46(14.16)a	33.98(9.85)b	45.95(10.97)a
DON (mg/kg)	7.64(2.54)b	9.28(3.52)ab	10.94(2.14)a	9.89(3.86)ab	11.21(3.56)a
NH_4^+-N (mg/kg)	3.2(2.26)ab	9.7(15.48)a	8.21(10.5)a	2.52(1.8)b	2.59(2.4)b
NO_3^--N (mg/kg)	3.12(1.33)ab	5.24(5.37)ab	2.93(2.55)b	5.49(6.81)ab	7.43(7.98)a
AK (mg/kg)	161.29(5.86)c	164.54(10.11)c	240.25(22.98)b	211.57(20.25)b	429.54(51.62)a
AP (mg/kg)	2.24(0.5)d	19.36(5.12)c	23.84(4.64)c	148.03(27.82)a	67.7(10.56)b
ALP (U/d)	1.99(0.65)b	1.45(0.74)c	1.6(1.03)bc	1.97(0.95)b	2.62(0.83)a

Different lowercase letters indicate the values that differ significantly among treatments at $P < 0.05$ (Kruskal-Wallis tests). Control: non fertilization; NPK: nitrogen-phosphorus-potassium mineral fertilizer only; NPK+WS: mineral fertilizer plus wheat straw; NPK+PM: mineral fertilizer plus pig manure. NPK+CM: mineral fertilizer plus cow manure.

Table S2. Soil physicochemical properties at each time under each fertilization treatments. Data are mean (SD).

		2022.2.26	2022.3.04	2022.3.11	2022.3.18	2022.3.30	2022.4.11	2022.4.23
pH	Control	7.46 (0.20)	7.33 (0.16)	7.44 (0.10)	7.47 (0.30)	7.59 (0.03)	7.43 (0.13)	7.50 (0.10)
	NPK	5.39 (0.27)	5.66 (0.13)	5.64 (0.09)	5.74 (0.14)	5.77 (0.16)	5.79 (0.21)	5.81 (0.07)
	NPK+WS	5.36 (0.17)	5.46 (0.26)	5.53 (0.24)	5.62 (0.02)	5.69 (0.13)	5.75 (0.06)	5.69 (0.13)
	NPK+PM	7.06 (0.07)	7.14 (0.08)	7.21 (0.06)	7.26 (0.07)	6.94 (0.03)	7.17 (0.09)	7.17 (0.08)
	NPK+CM	7.22 (0.14)	7.29 (0.06)	7.30 (0.12)	7.37 (0.14)	7.08 (0.14)	7.10 (0.05)	7.17 (0.16)
SM(%)	Control	16.07 (0.00)	13.45 (1.35)	11.27 (0.62)	24.45 (2.24)	22.42 (5.74)	10.65 (1.42)	8.53 (0.61)
	NPK	19.84 (8.24)	13.02 (2.56)	10.83 (5.94)	25.54 (1.52)	21.61 (1.40)	14.04 (1.40)	12.08 (1.25)
	NPK+WS	16.60 (2.11)	12.32 (3.53)	15.09 (0.08)	30.80 (1.26)	23.08 (0.88)	16.66 (1.99)	12.70 (1.89)
	NPK+PM	17.64 (1.85)	16.98 (1.25)	16.25 (1.44)	31.14 (1.96)	24.29 (0.89)	16.95 (2.08)	13.57 (0.85)
	NPK+CM	25.23 (8.89)	21.27 (2.38)	19.80 (1.36)	39.81 (4.00)	31.81 (1.92)	20.21 (2.28)	17.49 (0.67)
TC(%)	Control	0.83 (0.01)	0.78 (0.04)	0.80 (0.05)	0.75 (0.02)	0.84 (0.06)	0.80 (0.05)	0.71 (0.02)
	NPK	1.01 (0.07)	1.04 (0.07)	1.11 (0.23)	1.00 (0.06)	1.11 (0.04)	1.00 (0.05)	1.18 (0.26)
	NPK+WS	1.55 (0.07)	1.50 (0.11)	1.57 (0.11)	1.52 (0.15)	1.56 (0.11)	1.60 (0.07)	1.60 (0.11)
	NPK+PM	1.61 (0.18)	1.66 (0.17)	1.66 (0.13)	1.70 (0.21)	1.74 (0.12)	1.54 (0.12)	1.56 (0.11)
	NPK+CM	2.51 (0.37)	2.70 (0.13)	2.63 (0.10)	2.66 (0.12)	2.77 (0.06)	2.56 (0.10)	2.49 (0.12)
TN(%)	Control	0.10 (0.00)	0.09 (0.00)	0.09 (0.00)	0.09 (0.00)	0.10 (0.01)	0.09 (0.00)	0.08 (0.00)
	NPK	0.12 (0.01)	0.12 (0.01)	0.12 (0.01)	0.11 (0.01)	0.13 (0.01)	0.11 (0.01)	0.13 (0.03)
	NPK+WS	0.17 (0.01)	0.16 (0.01)	0.16 (0.01)	0.16 (0.01)	0.17 (0.01)	0.17 (0.01)	0.16 (0.01)
	NPK+PM	0.18 (0.02)	0.18 (0.02)	0.18 (0.01)	0.18 (0.02)	0.19 (0.01)	0.17 (0.01)	0.17 (0.01)
	NPK+CM	0.26 (0.03)	0.27 (0.01)	0.26 (0.01)	0.27 (0.01)	0.28 (0.01)	0.26 (0.01)	0.25 (0.01)
TK	Control	12.55 (0.21)	12.29 (0.33)	13.31 (0.36)	12.75 (0.41)	12.67 (0.17)	13.25 (0.06)	13.13 (0.23)
(g/kg)	NPK	12.69 (0.20)	12.96 (0.34)	13.20 (0.23)	12.73 (0.44)	12.74 (0.30)	13.14 (0.36)	13.30 (0.33)
	NPK+WS	13.11 (0.48)	13.03 (0.24)	13.47 (0.12)	12.84 (0.37)	13.44 (0.11)	12.95 (0.13)	13.50 (0.33)
	NPK+PM	12.93 (0.25)	13.11 (0.35)	12.76 (0.58)	12.68 (0.64)	13.71 (0.20)	13.19 (0.16)	13.29 (0.55)
	NPK+CM	14.01 (0.16)	14.04 (0.55)	14.01 (0.20)	13.48 (0.48)	14.75 (0.25)	14.15 (0.09)	13.51 (0.12)
TP	Control	0.26 (0.04)	0.23 (0.04)	0.29 (0.03)	0.28 (0.02)	0.31 (0.05)	0.24 (0.11)	0.29 (0.08)
(g/kg)	NPK	0.38 (0.08)	0.43 (0.04)	0.40 (0.05)	0.39 (0.12)	0.38 (0.06)	0.38 (0.06)	0.62 (0.06)
	NPK+WS	0.46 (0.12)	0.39 (0.11)	0.39 (0.08)	0.41 (0.06)	0.51 (0.06)	0.44 (0.11)	0.52 (0.08)
	NPK+PM	1.45 (0.27)	1.53 (0.16)	1.45 (0.14)	1.38 (0.19)	1.35 (0.18)	1.35 (0.13)	1.68 (0.17)
	NPK+CM	0.76 (0.13)	0.81 (0.11)	0.87 (0.08)	0.95 (0.05)	0.86 (0.15)	0.86 (0.17)	0.82 (0.11)
DOC	Control	23.70 (2.45)	25.06 (5.11)	27.15 (2.30)	16.52 (1.69)	13.61 (4.18)	20.54 (0.70)	32.45 (3.05)
(mg/kg)	NPK	26.25 (2.03)	28.73 (2.04)	33.25 (6.19)	19.42 (4.21)	11.84 (1.60)	24.05 (5.10)	39.96 (5.54)
	NPK+WS	48.86 (6.05)	47.85 (5.96)	57.35 (6.88)	38.11 (7.78)	31.05 (2.24)	50.30 (9.88)	65.68 (21.67)
	NPK+PM	38.72 (4.41)	41.80 (6.41)	43.60 (2.49)	25.88 (7.35)	20.17 (2.85)	31.24 (8.22)	36.47 (9.09)
	NPK+CM	53.18 (9.05)	53.54 (3.12)	59.27 (7.22)	32.93 (6.83)	34.00 (5.02)	47.40 (5.56)	41.35 (2.23)
DON	Control	7.82 (1.29)	8.66 (0.83)	6.93 (1.24)	9.73 (1.14)	10.78 (3.07)	4.88 (0.86)	4.70 (0.39)
(mg/kg)	NPK	9.67 (0.53)	13.28 (1.79)	8.86 (2.24)	7.72 (1.17)	9.88 (5.04)	10.02 (3.17)	5.51 (4.61)
	NPK+WS	10.12 (0.85)	12.23 (1.30)	11.88 (1.47)	10.60 (2.32)	11.99 (2.62)	11.18 (3.23)	8.56 (0.73)
	NPK+PM	8.60 (1.68)	11.59 (3.05)	9.09 (0.36)	8.43 (1.15)	14.53 (3.03)	10.85 (7.24)	6.13 (0.30)

	NPK+CM	9.67 (1.13)	11.19 (1.72)	10.18 (2.01)	10.27 (1.42)	17.90 (3.75)	10.23 (2.69)	9.01 (3.02)
NH_4^+-N	Control	7.15 (4.02)	2.27 (0.80)	1.75 (0.40)	3.12 (0.62)	2.09 (0.59)	2.60 (0.71)	3.39 (0.83)
(mg/kg)	NPK	5.23 (1.29)	2.67 (0.74)	1.70 (0.58)	2.07 (0.11)	40.93 (22.93)	10.09 (6.63)	5.21 (1.50)
	NPK+WS	3.53 (0.86)	2.41 (0.11)	2.03 (0.24)	1.33 (0.62)	25.32 (12.67)	12.65 (6.17)	10.24 (13.52)
	NPK+PM	2.89 (0.60)	1.62 (0.86)	1.32 (0.28)	1.43 (0.23)	4.77 (2.08)	3.73 (3.11)	1.90 (0.34)
	NPK+CM	1.71 (0.33)	1.28 (0.95)	0.94 (0.28)	1.28 (0.34)	6.56 (3.72)	4.01 (1.45)	2.38 (1.33)
NO_3^--N	Control	6.09 (0.32)	2.82 (0.43)	2.71 (0.29)	1.86 (0.18)	3.27 (0.30)	2.45 (0.24)	2.61 (0.33)
(mg/kg)	NPK	5.83 (1.52)	4.60 (3.50)	2.22 (0.63)	0.81 (0.13)	15.66 (6.83)	3.90 (2.68)	3.69 (1.12)
	NPK+WS	2.45 (0.96)	1.71 (0.64)	0.88 (0.25)	0.81 (0.10)	7.50 (1.83)	4.61 (2.84)	2.52 (0.37)
	NPK+PM	4.59 (0.85)	2.52 (1.06)	2.29 (0.28)	0.91 (0.29)	20.51 (6.91)	4.61 (1.20)	2.99 (1.19)
	NPK+CM	5.07 (0.35)	3.72 (0.41)	2.70 (0.33)	1.01 (0.09)	24.80 (7.17)	7.90 (1.42)	6.79 (2.28)
AK	Control	160.75 (6.40)	162.75 (5.56)	158.00 (3.56)	164.75 (3.77)	154.75 (2.99)	168.50 (5.97)	159.50 (1.29)
(mg/kg)	NPK	165.75 (12.37)	169.25 (8.30)	167.50 (11.90)	161.00 (11.05)	162.00 (15.19)	161.75 (5.06)	164.50 (9.95)
	NPK+WS	226.50 (5.45)	237.75 (4.57)	236.75 (24.90)	240.00 (32.86)	230.75 (9.18)	266.00 (14.31)	244.00 (37.61)
	NPK+PM	210.00 (17.91)	204.00 (13.04)	204.25 (18.28)	212.00 (27.64)	241.25 (19.60)	207.75 (13.35)	201.75 (8.02)
	NPK+CM	426.25 (65.55)	407.25 (19.82)	391.50 (12.37)	392.25 (49.88)	496.00 (21.79)	473.25 (45.69)	420.25 (32.83)
AP	Control	2.20 (0.20)	2.18 (0.71)	2.02 (0.71)	2.15 (0.55)	2.77 (0.16)	2.24 (0.33)	2.15 (0.53)
(mg/kg)	NPK	17.34 (2.76)	16.49 (1.40)	14.76 (0.82)	27.60 (7.42)	21.98 (2.67)	18.47 (0.98)	18.84 (4.13)
	NPK+WS	21.30 (1.83)	20.26 (1.89)	20.58 (3.00)	30.06 (5.93)	23.05 (1.35)	26.47 (4.22)	25.13 (4.39)
	NPK+PM	123.70 (7.42)	121.95 (21.12)	140.33 (14.07)	180.66 (31.95)	158.55 (24.24)	145.29 (21.89)	165.73 (20.19)
	NPK+CM	67.98 (14.24)	65.75 (13.69)	70.90 (12.73)	72.21 (7.92)	73.94 (9.38)	64.57 (6.63)	58.59 (5.89)
ALP	Control	2.10 (0.06)	2.45 (0.64)	2.37 (0.34)	2.49 (0.44)	0.79 (0.36)	1.73 (0.18)	1.99 (0.27)
(U/d)	NPK	0.52 (0.06)	1.42 (0.77)	2.20 (0.69)	2.15 (0.31)	1.54 (0.05)	1.32 (0.83)	0.97 (0.46)
	NPK+WS	1.85 (1.46)	1.44 (0.61)	2.76 (0.49)	1.13 (0.43)	0.90 (0.31)	0.44 (0.42)	2.64 (0.52)
	NPK+PM	1.84 (0.16)	2.63 (0.59)	2.77 (0.17)	1.46 (0.14)	0.18 (0.15)	1.86 (0.11)	3.04 (0.32)
	NPK+CM	2.22 (0.24)	3.55 (0.37)	2.08 (0.77)	1.50 (0.10)	2.37 (0.07)	3.21 (0.63)	3.42 (0.42)

Table S3. ADONIS variation test between treatments based on the Bray-Curtis distance matrix.

	R^2	*P*
Control vs NPK	0.58	0.001
Control vs NPK+WS	0.57	0.001
Control vs NPK+PM	0.46	0.001
Control vs NPK+CM	0.61	0.001
NPK vs NPK+WS	0.18	0.001
NPK vs NPK+PM	0.57	0.001
NPK vs NPK+CM	0.66	0.001
NPK+WS vs NPK+PM	0.56	0.001
NPK+WS vs NPK+CM	0.64	0.001
NPK+PM vs NPK+CM	0.50	0.001

Table S4. ADONIS variation test between times under each fertilization treatment based on the Bray-Curtis distance matrix. Data are R^2 (*P*).

	Control	NPK	NPK+CM	NPK+PM	NPK+WS
2022.2.26 vs 2022.3.04	0.10 (0.84)	0.07 (1.00)	0.17 (0.29)	0.10 (0.86)	0.08 (0.97)
2022.2.26 vs 2022.3.11	0.15 (0.76)	0.12 (0.83)	0.23 (0.13)	0.11 (0.82)	0.08 (0.97)
2022.2.26 vs 2022.3.18	0.11 (0.83)	0.13 (0.77)	0.26 (0.11)	0.12 (0.75)	0.14 (0.86)
2022.2.26 vs 2022.3.30	0.11 (0.83)	0.17 (0.60)	0.29 (0.11)	0.21 (0.20)	0.16 (0.86)
2022.2.26 vs 2022.4.11	0.13 (0.79)	0.17 (0.60)	0.28 (0.11)	0.15 (0.64)	0.16 (0.86)
2022.2.26 vs 2022.4.23	0.20 (0.57)	0.10 (0.83)	0.13 (0.72)	0.11 (0.75)	0.13 (0.86)
2022.3.04 vs 2022.3.11	0.11 (0.83)	0.12 (0.80)	0.10 (0.83)	0.09 (0.98)	0.08 (1.00)
2022.3.04 vs 2022.3.18	0.12 (0.83)	0.12 (0.80)	0.14 (0.52)	0.17 (0.31)	0.14 (0.86)
2022.3.04 vs 2022.3.30	0.16 (0.76)	0.21 (0.47)	0.21 (0.17)	0.25 (0.11)	0.15 (0.86)
2022.3.04 vs 2022.4.11	0.15 (0.76)	0.22 (0.47)	0.22 (0.13)	0.25 (0.11)	0.14 (0.86)
2022.3.04 vs 2022.4.23	0.20 (0.57)	0.15 (0.77)	0.18 (0.29)	0.18 (0.31)	0.14 (0.86)
2022.3.11 vs 2022.3.18	0.17 (0.76)	0.07 (0.98)	0.14 (0.52)	0.14 (0.66)	0.12 (0.89)
2022.3.11 vs 2022.3.30	0.22 (0.57)	0.17 (0.60)	0.23 (0.17)	0.22 (0.16)	0.14 (0.86)
2022.3.11 vs 2022.4.11	0.14 (0.79)	0.21 (0.47)	0.32 (0.11)	0.26 (0.11)	0.15 (0.86)
2022.3.11 vs 2022.4.23	0.17 (0.76)	0.15 (0.69)	0.28 (0.11)	0.21 (0.24)	0.15 (0.86)
2022.3.18 vs 2022.3.30	0.09 (0.83)	0.21 (0.47)	0.16 (0.37)	0.21 (0.26)	0.15 (0.86)
2022.3.18 vs 2022.4.11	0.15 (0.76)	0.24 (0.47)	0.29 (0.11)	0.25 (0.11)	0.18 (0.86)
2022.3.18 vs 2022.4.23	0.21 (0.57)	0.17 (0.65)	0.30 (0.11)	0.24 (0.14)	0.18 (0.86)
2022.3.30 vs 2022.4.11	0.16 (0.76)	0.16 (0.60)	0.22 (0.24)	0.25 (0.11)	0.12 (0.91)
2022.3.30 vs 2022.4.23	0.28 (0.56)	0.15 (0.71)	0.27 (0.14)	0.28 (0.11)	0.14 (0.86)
2022.4.11 vs 2022.4.23	0.18 (0.57)	0.08 (0.98)	0.17 (0.37)	0.14 (0.66)	0.06 (1.00)

Table S5. The relative abundance of the phoD-harboring bacterial phyla under different fertilization treatments, respectively.

Relative abundance (%)	Control	NPK	NPK+WS	NPK+PM	NPK+CM
Proteobacteria	34.29(7.06)c	74.73(9.04)a	69.87(7.37)b	35.08(4.25)c	23.37(4.47)d
Cyanobacteria	27.05(6.68)b	3.25(3.85)d	2.27(1.31)d	20.76(5.99)c	46.34(7.8)a
Actinobacteria	11.51(2.66)b	4.40(2.35)d	4.74(1.7)d	16.81(4.25)a	10.06(3.15)c
Planctomycetes	2.11(0.77)c	3.09(1.8)b	5.45(2.08)a	5.38(2.23)a	2.38(1.23)bc
Firmicutes	1.33(0.74)a	0.21(0.51)c	0.03(0.03)c	0.39(0.17)b	0.37(0.24)b
Chloroflexi	0.71(0.47)a	0.39(0.31)b	0.72(0.52)a	0.12(0.07)c	0.04(0.04)d
Acidobacteria	1.00(0.48)a	0.82(0.84)b	0.28(0.17)c	0.26(0.29)c	0.25(0.18)c
Verrucomicrobia	2.66(1.25)b	2.43(3.95)c	1.97(1.39)c	3.72(1.47)a	2.65(1.18)b
Other	19.33(3.62)a	10.67(3.07)d	14.68(3.2)c	17.49(3.17)b	14.55(2.88)c

Data are mean (SD). Different lowercase letters indicate the values that differ significantly among treatments at $P < 0.05$ (Kruskal-Wallis tests).

Table S6. Spearman correlations between the relative abundance of the phoD-harboring bacterial phyla and physiochemical variables.

	DOC	DON	NH_4^+-N	NO_3^--N	pH	SM
Acidobacteria	-0.45***	-0.14	0.06	-0.14	0.2*	-0.17*
Actinobacteria	-0.1	-0.21*	-0.23**	0.15	0.63***	0.1
Chloroflexi	-0.21*	-0.08	0.3***	-0.21*	-0.19*	-0.36***
Cyanobacteria	-0.03	0.02	-0.29***	0.27**	0.74***	0.35***
Firmicutes	-0.28***	-0.26**	-0.19*	0.07	0.73***	-0.04
Planctomycetes	0.26**	0.08	0.02	-0.15	-0.39***	-0.04
Proteobacteria	-0.02	0	0.3***	-0.21*	-0.69***	-0.37***
Unclassified	-0.12	-0.19*	-0.18*	-0.22*	0.35***	-0.14
Verrucomicrobia	0.06	-0.13	-0.03	0.03	0.36***	-0.03
	TP	TK	AP	AK	TN	TC
Acidobacteria	-0.58***	-0.3***	-0.62***	-0.54***	-0.57***	-0.55***
Actinobacteria	0.38***	0.06	0.37***	0.04	0.13	0.11
Chloroflexi	-0.67***	-0.4***	-0.66***	-0.49***	-0.67***	-0.64***
Cyanobacteria	0.24**	0.33***	0.22**	0.33***	0.35***	0.34***
Firmicutes	-0.05	-0.02	-0.11	-0.16	-0.14	-0.14
Planctomycetes	0.33***	-0.03	0.36***	0.17*	0.21*	0.22**
Proteobacteria	-0.3***	-0.33***	-0.3***	-0.39***	-0.41***	-0.39***
Unclassified	-0.1	-0.25**	-0.09	-0.2*	-0.24**	-0.23**
Verrucomicrobia	0.33***	0.13	0.3***	0.1	0.19*	0.19*

Significance levels of each predictor are *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.

Table S7. Spearman correlations between the phoD-harboring bacterial diversity index and physiochemical variables.

	Richness		Shannon	
	R	*P*	R	*P*
pH	0.68	0.000	0.17	0.090
TP	0.45	0.000	0.11	0.301
AP	0.45	0.000	0.15	0.155
NO_3^--N	0.02	0.894	-0.18	0.090
TN	0.02	0.894	-0.38	0.000
TC	0.01	0.920	-0.39	0.000
AK	-0.06	0.602	-0.47	0.000
SM	-0.07	0.528	-0.22	0.032
TK	-0.07	0.528	-0.38	0.000
DOC	-0.08	0.504	-0.10	0.342
DON	-0.11	0.301	-0.17	0.090
NH_4^+-N	-0.16	0.118	0.03	0.849

Table S8. Topological features of the phoD-harboring bacterial co-occurrence subnetworks of under different fertilization treatments.

Treatment	Control	NPK	NPK+WS	NPK+PM	NPK+CM
Nodes	1077	960	948	1095	946
Edges	31268	35831	32232	25563	21824
Positive correlations	0.95	0.73	0.76	0.88	0.93
Negative correlations	0.05	0.27	0.24	0.12	0.07
Average_degree	58.06	74.65	68.00	46.69	46.14
Transitivity	0.61	0.65	0.66	0.58	0.58
Connectance	0.05	0.08	0.07	0.04	0.05
Modularity	0.42	0.21	0.19	0.52	0.50

Table S9. Key variables that affect the topological features of subnetwork.

	Variable	Importance	*P*
Modularity	pH	24.47	**
	AP	17.84	**
	TN	13.34	**
	TC	12.91	**
	TP	12.53	**
	AK	8.83	*
Connectance	pH	26.86	**
	AP	15.65	**
	TC	13.70	**
	TP	12.92	**
	TN	11.52	**
Transitivity	pH	24.37	**
	AP	17.31	**
	TP	14.41	**
	TN	13.61	**
	TC	12.26	**
	AK	9.32	**
Positive correlations	pH	13.39	**
	TN	12.87	**
	AP	12.14	**
	TC	11.61	**
	AK	10.93	**

The importance value is calculated by a random forest analysis. Significance levels of each predictor are *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.

Table S10. The phoD-harboring bacteria community compositions of the main ecological clusters in high pH sub-network.

Phylum Level (%)	**Module#H1**	**Module#H2**	**Module#H3**	**Module#H4**	**Module#H5**
Proteobacteria	45.80	17.12	27.59	18.42	10.26
Actinobacteria	18.68	10.54	8.27	9.57	15.62
Cyanobacteria	26.18	12.55	11.64	55.23	0.20
Verrucomicrobia	0.84	7.90	8.19	4.41	10.84
Planctomycetes	2.24	3.82	2.06	4.13	13.83
Candidatus-Rokubacteria	0.00	9.91	0.00	0.00	0.00
Firmicutes	0.08	1.67	1.82	0.28	0.68
Acidobacteria	0.03	0.19	3.23	0.27	0.00
Gemmatimonadetes	0.00	0.00	2.18	0.00	0.69
Deinococcus-Thermus	0.00	1.53	0.00	0.00	0.00
Candidatus-Tectomicrobia	1.04	0.00	0.00	0.00	0.00
Terrabacteriagroup	0.00	0.00	0.06	0.70	0.00
Armatimonadetes	0.00	0.00	0.71	0.00	0.00
Chloroflexi	0.22	0.00	0.00	0.00	0.00
Candidatus-Parcubacteria	0.00	0.00	0.02	0.00	0.00
Unclassified	4.87	34.77	34.22	6.98	47.88
Genus Level (%)	**Module#H1**	**Module#H2**	**Module#H3**	**Module#H4**	**Module#H5**
Natrinema	0.00	0.00	0.00	44.36	0.00
Nostoc	9.45	12.55	3.15	2.02	0.00
Chroogloeocystis	12.07	0.00	0.00	2.64	0.00
Lentzea	14.16	0.00	0.00	0.12	0.00
Bradyrhizobium	2.10	4.96	0.83	3.33	2.95
Caulobacter	7.40	0.70	0.00	5.08	0.00
Duganella	11.69	0.00	0.00	0.00	0.00
Chroococcidiopsis	2.61	0.00	7.60	0.52	0.00
Gemmata	0.00	0.22	0.08	0.36	8.23
Pseudomonas	4.47	0.14	0.02	1.71	0.82
Prosthecobacter	0.00	4.79	1.76	0.00	0.00
Planctomyces	1.80	0.36	0.16	1.20	1.96
Rubrobacter	0.12	0.15	2.95	1.09	0.83
Persicimonas	0.54	0.00	4.39	0.00	0.00
Rhodoplanes	3.97	0.00	0.00	0.00	0.51
Streptomyces	0.45	0.89	1.23	0.42	1.25
Massilia	2.15	0.05	0.18	0.76	0.97
Amycolatopsis	0.40	2.42	0.63	0.33	0.27
Sphingopyxis	3.78	0.06	0.00	0.00	0.00
Actinoplanes	0.16	0.36	0.77	0.23	1.91
Rhodoferax	0.00	0.00	1.33	0.00	2.00
Phenylobacterium	0.20	0.00	0.10	0.00	2.87

Xanthomonas	0.08	0.68	1.86	0.39	0.00
Actinomadura	0.30	1.65	0.28	0.34	0.44
Ramlibacter	0.05	0.12	2.59	0.00	0.14
Kineococcus	0.00	0.30	0.04	1.72	0.75
Kibdelosporangium	0.00	0.00	0.00	2.81	0.00
Luteolibacter	0.17	0.00	1.98	0.41	0.00
Luteipulveratus	0.12	0.00	0.00	0.04	2.38
Saccharopolyspora	0.00	0.52	0.34	0.00	1.48
Gemmatimonas	0.00	0.00	2.18	0.00	0.09
Nocardiopsis	0.00	0.00	0.04	0.03	2.05
Allokutzneria	0.69	0.00	0.00	0.03	1.21
Kribbella	0.33	1.20	0.00	0.29	0.00
Reyranella	0.00	0.00	0.00	1.66	0.00
Bacillus	0.00	1.54	0.12	0.00	0.00
Dactylosporangium	0.00	0.63	0.44	0.05	0.54
Thermobispora	0.00	0.37	0.02	0.99	0.26
Urbifossiella	0.00	1.11	0.00	0.00	0.49
Deinococcus	0.00	1.53	0.00	0.00	0.00
Roseimaritima	0.00	0.00	0.00	0.46	1.04
Cephaloticoccus	0.00	0.00	0.00	1.44	0.00
Scytonema	0.79	0.00	0.55	0.06	0.00
Variovorax	0.68	0.23	0.38	0.00	0.00
Gloeocapsa	0.73	0.00	0.00	0.47	0.00
Nocardioides	0.00	0.21	0.34	0.35	0.22
Neobacillus	0.00	0.00	0.85	0.28	0.00
Halochromatium	0.00	1.09	0.00	0.00	0.00
Others	4.52	4.13	6.89	3.15	5.11
Unclassified	14.03	57.03	55.94	20.86	59.22

Table S11. The OTUs highly associated with ALP activity detected using random forest regression.

OTU	Phylum	Genus	Module
OTU5518	Actinobacteria	Amycolatopsis	Module#H1
OTU5507	Actinobacteria	Streptomyces	Module#H1
OTU5414	Actinobacteria	Jiangella	Module#H1
OTU6194	Actinobacteria	Rubrobacter	Module#H1
OTU5916	Cyanobacteria	Nostoc	Module#H1
OTU5579	Cyanobacteria	Nostoc	Module#H1
OTU5667	Cyanobacteria	Scytonema	Module#H1
OTU5840	Planctomycetes	Alienimonas	Module#H1
OTU5490	Proteobacteria	unclassified	Module#H1
OTU1440	Proteobacteria	Nitrospirillum	Module#H1
OTU5929	Unclassified	unclassified	Module#H1
OTU5530	Unclassified	unclassified	Module#H1
OTU4837	Actinobacteria	Actinoplanes	Module#H2
OTU3879	Actinobacteria	Micromonospora	Module#H2
OTU3791	Actinobacteria	Frankia	Module#H2
OTU5717	Actinobacteria	Streptomyces	Module#H2
OTU4139	Actinobacteria	Actinomadura	Module#H2
OTU4168	Actinobacteria	Actinomadura	Module#H2
OTU5763	Actinobacteria	Amycolatopsis	Module#H2
OTU3922	Actinobacteria	Rhabdothermincola	Module#H2
OTU1147	Actinobacteria	Jiangella	Module#H2
OTU3963	Cyanobacteria	Chroococcidiopsis	Module#H2
OTU10192	Cyanobacteria	Nostoc	Module#H2
OTU11345	Cyanobacteria	Chroococcidiopsis	Module#H2
OTU4163	Cyanobacteria	Chroococcidiopsis	Module#H2
OTU7694	Planctomycetes	Thalassoroseus	Module#H2
OTU11296	Planctomycetes	Tuwongella	Module#H2
OTU17140	Planctomycetes	Gemmata	Module#H2
OTU10555	Planctomycetes	Gemmata	Module#H2
OTU4160	Planctomycetes	Aquisphaera	Module#H2
OTU11283	Planctomycetes	Humisphaera	Module#H2
OTU3945	Proteobacteria	Bradyrhizobium	Module#H2
OTU4166	Proteobacteria	Rhodoplanes	Module#H2
OTU4298	Proteobacteria	Pseudomonas	Module#H2
OTU3818	Proteobacteria	Undibacterium	Module#H2
OTU4169	Proteobacteria	Azospira	Module#H2
OTU11090	Proteobacteria	Rhodoplanes	Module#H2
OTU3896	Proteobacteria	Methylotetracoccus	Module#H2
OTU3800	Proteobacteria	Pseudomonas	Module#H2

OTU4217	Proteobacteria	Undibacterium	Module#H2
OTU3864	Proteobacteria	Variovorax	Module#H2
OTU4646	Actinobacteria	Kibdelosporangium	Module#H4
OTU3793	Actinobacteria	Nocardioides	Module#H4
OTU4256	Planctomycetes	Planctomyces	Module#H4
OTU3902	Planctomycetes	Gemmata	Module#H4
OTU4229	Proteobacteria	Pseudomonas	Module#H4
OTU7833	Unclassified	unclassified	Module#H4
OTU9791	Unclassified	unclassified	Module#H4
OTU4068	Unclassified	unclassified	Module#H4
OTU4012	Unclassified	unclassified	Module#H4
OTU10117	Unclassified	unclassified	Module#H4
OTU4151	Unclassified	unclassified	Module#H4
OTU10236	Unclassified	unclassified	Module#H4
OTU3895	Unclassified	unclassified	Module#H4
OTU10219	Planctomycetes	Roseimaritima	Module#H5
OTU7817	Acidobacteria	Paludibaculum	Others
OTU717	Actinobacteria	Actinomadura	Others
OTU10999	Actinobacteria	Saccharopolyspora	Others
OTU6230	Actinobacteria	Jiangella	Others
OTU1015	Actinobacteria	Dactylosporangium	Others
OTU11453	Actinobacteria	Saccharothrix	Others
OTU6002	Actinobacteria	Rubrobacter	Others
OTU4587	Actinobacteria	Allokutzneria	Others
OTU11241	Actinobacteria	Thermomonospora	Others
OTU9873	Actinobacteria	Streptomyces	Others
OTU10060	Actinobacteria	Kineococcus	Others
OTU10903	Planctomycetes	Gimesia	Others
OTU4628	Planctomycetes	Aquisphaera	Others
OTU5082	Planctomycetes	Tautonia	Others
OTU14412	Planctomycetes	Singulisphaera	Others
OTU1277	Planctomycetes	Tautonia	Others
OTU11335	Planctomycetes	Humisphaera	Others
OTU11433	Proteobacteria	Variovorax	Others
OTU5473	Proteobacteria	unclassified	Others
OTU5859	Proteobacteria	Hylemonella	Others
OTU7890	Proteobacteria	Phenylobacterium	Others
OTU6244	Proteobacteria	Usitatibacter	Others
OTU3850	Proteobacteria	Pseudomonas	Others
OTU10258	Proteobacteria	Massilia	Others
OTU11487	Proteobacteria	Xanthomonas	Others
OTU10409	Proteobacteria	Bradyrhizobium	Others
OTU1206	Proteobacteria	Rhizobium	Others
OTU3760	Proteobacteria	Variovorax	Others

OTU16331	Proteobacteria	Massilia	Others
OTU3993	Proteobacteria	Phenylobacterium	Others
OTU6618	Unclassified	unclassified	Others
OTU5787	Unclassified	unclassified	Others
OTU3074	Unclassified	unclassified	Others
OTU5558	Unclassified	unclassified	Others
OTU4588	Unclassified	unclassified	Others
OTU12568	Unclassified	unclassified	Others
OTU4226	Unclassified	unclassified	Others
OTU10130	Unclassified	unclassified	Others
OTU15250	Unclassified	unclassified	Others
OTU6177	Unclassified	unclassified	Others
OTU7745	Unclassified	unclassified	Others
OTU4968	Verrucomicrobia	Luteolibacter	Others
OTU12435	Verrucomicrobia	Luteolibacter	Others
OTU4284	Proteobacteria	unclassified	Others
OTU8068	Proteobacteria	unclassified	Others

Table S12. Spearman correlations between the shared *phoD*-harboring bacterial OTUs (of Module# H2 and ALP indicators) and ALP activity. Significance levels of each predictor are *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.

OTU	Genus	*P*
OTU4837	Actinoplanes	0.36**
OTU3945	Bradyrhizobium	0.43**
OTU3879	Micromonospora	0.52***
OTU3791	Frankia	0.4**
OTU4166	Rhodoplanes	0.16
OTU3963	Chroococcidiopsis	0.04
OTU5717	Streptomyces	0.42**
OTU4298	Pseudomonas	0.39**
OTU10192	Nostoc	-0.06
OTU3818	Undibacterium	0.26
OTU7694	Thalassoroseus	0.13
OTU4169	Azospira	0.32*
OTU4139	Actinomadura	0.24
OTU4168	Actinomadura	0.32*
OTU11345	Chroococcidiopsis	0.25
OTU11296	Tuwongella	0.31*
OTU11090	Rhodoplanes	0.19
OTU3896	Methylotetracoccus	0.37**
OTU5763	Amycolatopsis	0.29*
OTU17140	Gemmata	0.03
OTU3800	Pseudomonas	0.46***
OTU4163	Chroococcidiopsis	0.27*
OTU10555	Gemmata	0.33*
OTU4160	Aquisphaera	0.22
OTU4217	Undibacterium	0.19
OTU3864	Variovorax	0.32*
OTU11283	Humisphaera	0.23
OTU3922	Rhabdothermincola	0.42**
OTU1147	Jiangella	-0.14

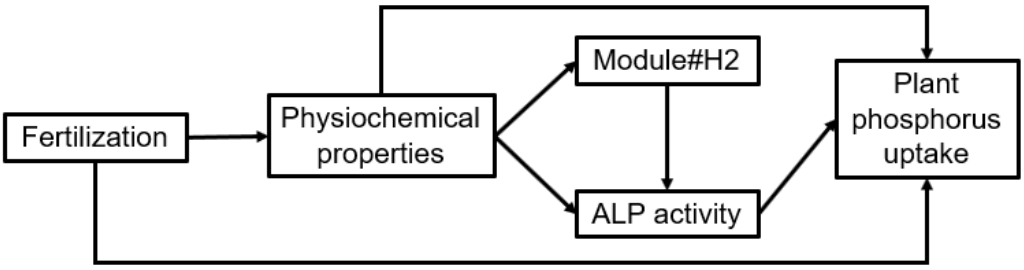

Figure S1. The priori conceptual model of hypothesized causal relationships from fertilization treatments, physiochemical properties, ALP activity and the relative abundance of the main ecological cluster (Module#H2) to plant phosphorus uptake.

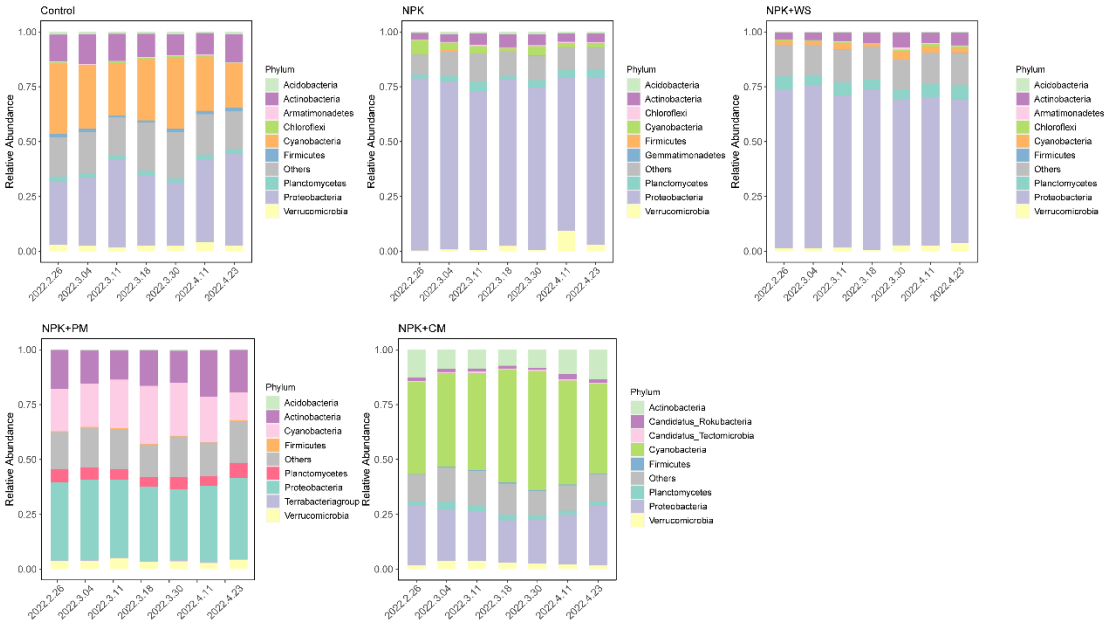

Figure S2. The phoD-harboring bacteria community compositions at each time under each fertilization treatment.

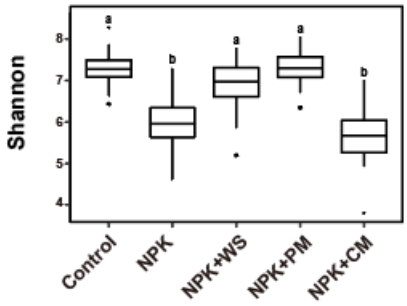

Figure S3. The phoD-harboring bacterial Shannon index under each fertilization treatment. Different lowercase letters indicate statistically significant ($P < 0.05$) differences as detected using Kruskal-Wallis tests.

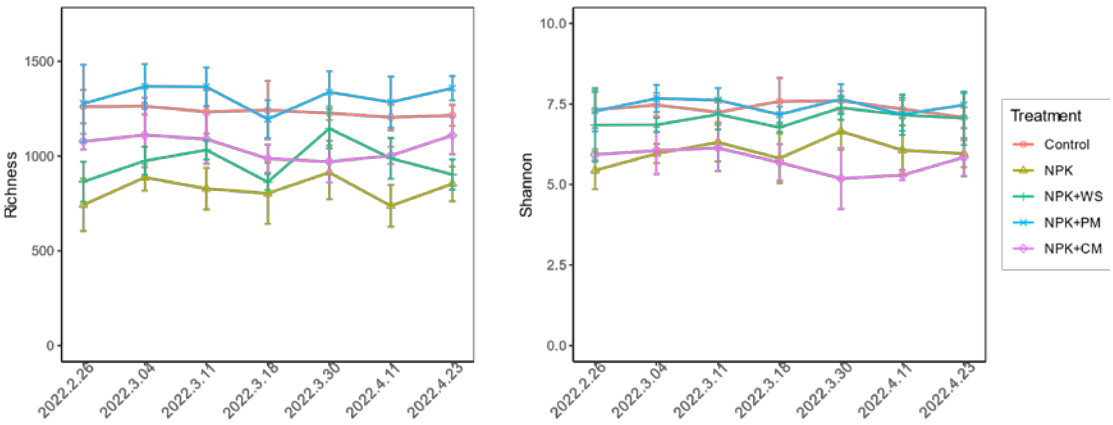

Figure S4. The phoD-harboring bacterial diversity at each time under each fertilization treatments represented by Richness and Shannon values. Control: non fertilization; NPK: nitrogen-phosphorus-potassium mineral fertilizer only; NPK+WS: mineral fertilizer plus wheat straw; NPK+PM: mineral fertilizer plus pig manure. NPK+CM: mineral fertilizer plus cow manure.

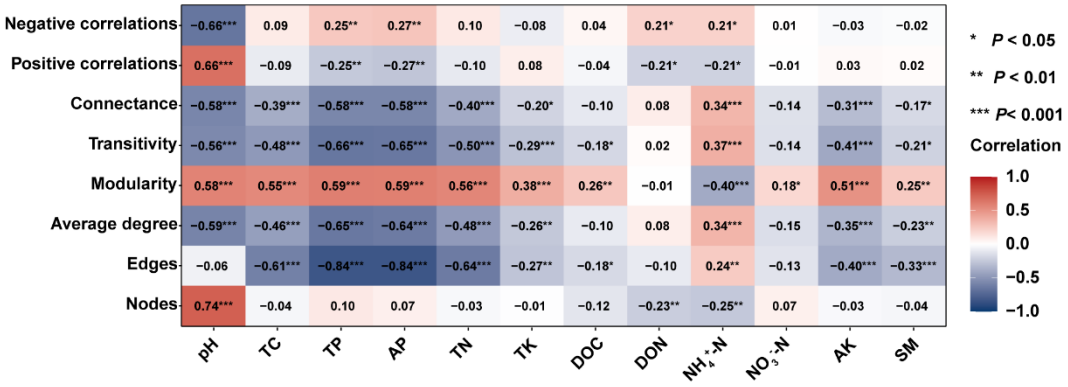

Figure S5. Spearman correlations between topological features of co-occurrence network and physiochemical variables. Different colors in the cells indicate different statistic correlations (r), shown in the legend. Significance levels of each predictor are *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.

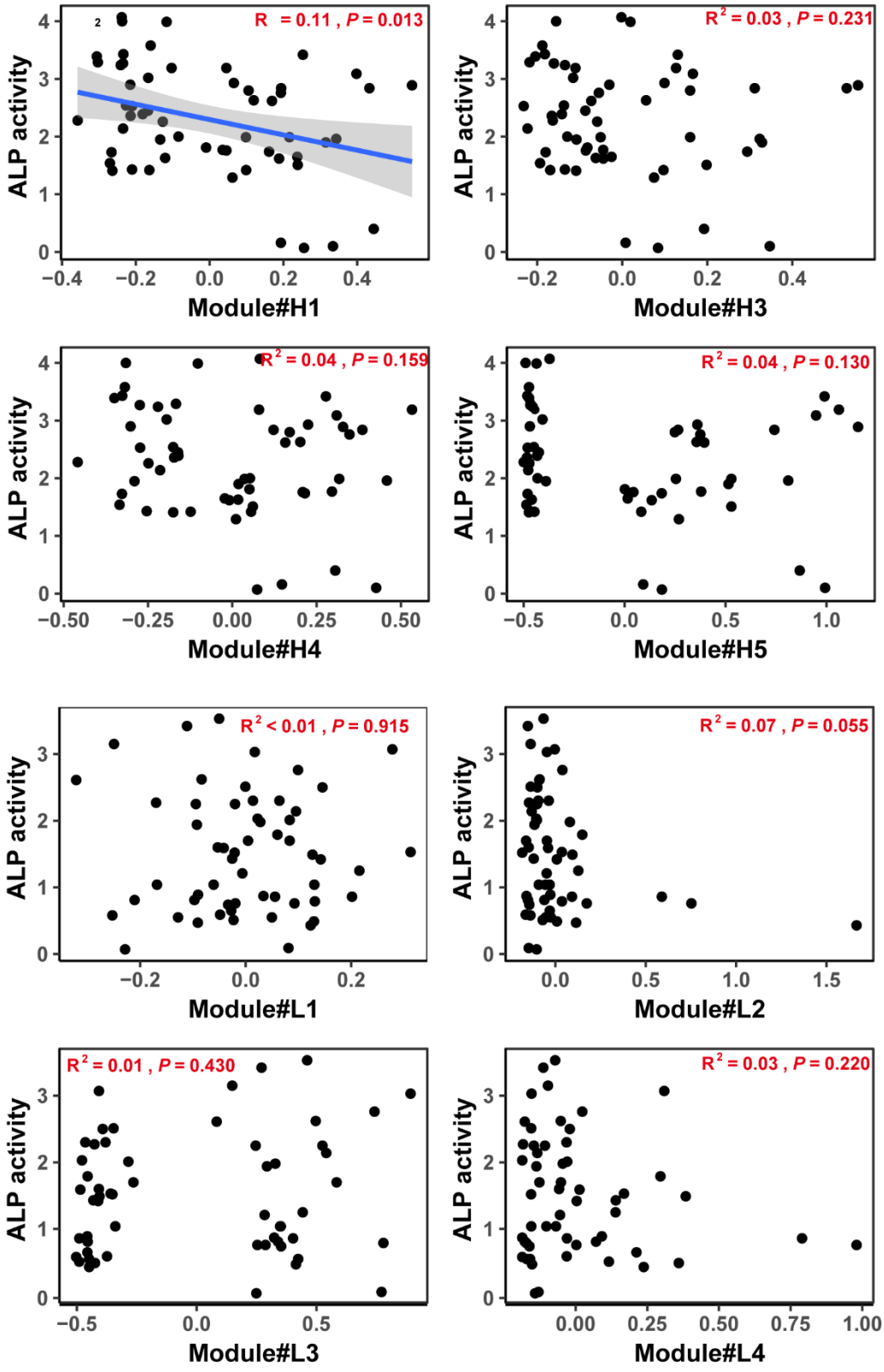

Figure S6. Linear regression between the relative abundance of the main ecological clusters (Z-score) and alkaline phosphatase (ALP) activity.

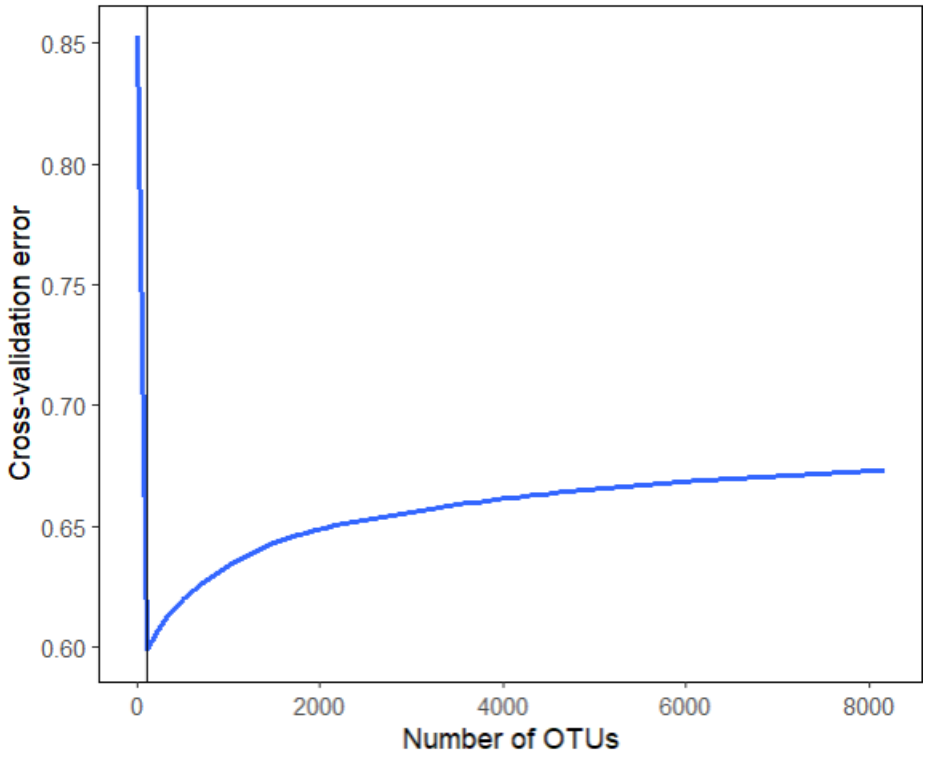

Figure S7. A random forest model was applied to regress the phoD-harboring bacterial OTU profiling in soil against the alkaline phosphatase activity. Five repeats of 10-fold cross-validation in the training set resulted in selection of 100 OTU markers for predicting alkaline phosphatase activity.

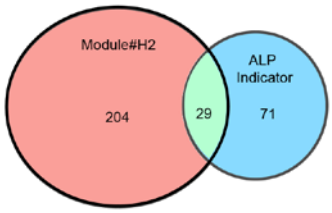

Figure S8. Venn diagram showing the shared and unique *phoD*-harboring bacterial OTUs of Module#H2 and ALP indicators.