

**Table S1 Stand characteristics (mean±SD) in the *Pinus massoniana*—*Lithocarpus glaber* coniferous and evergreen broadleaved mixed forest (PLF) and *L. glaber*—*Quercus glauca* evergreen broadleaved forest (LGF). DBH represents tree diameter at breast height, H represents tree height.**

Forest type	Plot number	Stand density (tree ha <sup>-1</sup> )	Average DBH (cm)	Average H (m)	Basal area (cm <sup>2</sup> )	Dominant tree species
PLF	4	2550±772	13.35±4.35	10.45±2.20	4085.80±701.36	<i>Pinus massoniana</i> , <i>Lithocarpus glaber</i> , <i>Choerospondias axillaris</i> , <i>Loropetalum chinense</i>
LGF	4	1800±648	11.55±2.10	10.30±1.00	3500.22±1010.81	<i>Quercus glauca</i> , <i>Lithocarpus glaber</i> , <i>Pinus massoniana</i> , <i>Symplocos setchuensis</i> Brand

**Table S2 Details on the 27 functional genes related to P cycling studied in this study.**

<b>Pathway</b>	<b>Gene</b>	<b>Enzyme</b>	<b>KEGG ID</b>
Organic P mineralization	phoA	Alkaline phosphatase A	K01077
	phoD	Alkaline phosphatase D	K01113
	phoX	Alkaline phosphatase X	K07093
	phoN	Acid phosphatase class A	K09474
	aphA	Acid phosphatase class B	K03788
	olpA	Acid phosphatase class C	K01078
	appA	4-phytase	K01093
	3-phytase	3-phytase	K01083
	phnA	C-P lyase multienzyme complex	K19670
	phnW	C-P lyase multienzyme complex	K03430
	phnX	C-P lyase multienzyme complex	K05306
	phnG	C-P lyase multienzyme complex	K06166
	phnH	C-P lyase multienzyme complex	K06165
	phnI	C-P lyase multienzyme complex	K06164
	phnJ	C-P lyase multienzyme complex	K06163
	phnL	C-P lyase multienzyme complex	K05780
	phnM	C-P lyase multienzyme complex	K06162
	phnN	C-P lyase multienzyme complex	K05774
	phnP	C-P lyase multienzyme complex	K06167
Inorganic P solubilization	ppa	Inorganic pyrophosphatase	K01507
	ppx	Exopolyphosphatase	K01514
	ppk1	Polyphosphate kinase	K00937
	gcd	Quinoprotein glucose dehydrogenase	K00117
	pqqC	Pyrroloquinoline quinone synthase C	K06137
P-starvation response regulation	phoB	Phosphate regulon response regulator	K07657
	phoR	Phosphate regulon sensor histidine kinase	K07636
	phoU	PhoR/phoB inhibitor protein	K02039

**Table S3 The abundance (RPKM) of species (phyla taxa) for a specific functional (KEGG gene) in organic and mineral soils.**

Taxon	phoA	phoD	phoX	phoN	aphA	olpA	appA	3-phytase	phnA	phnW	phnX	phnG	phnH	phnI	phnJ	phnL	phnM	phnN	phnP	ppa	ppx	ppk1	gcd	pqqC	phoB	phoR	phoU
Average values of organic soils																											
Archaea																											
Thaumarchaeota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.66	2.73	0.00	0.00	1.20	0.00	0.83	2.43
Candidatus_Thermoplasmatota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.41	0.00	0.00	1.03	0.00	0.00	0.00
Euryarchaeota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.43
Candidatus_Bathyarchaeota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.75	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria																											
Proteobacteria	2.04	51.25	0.06	18.58	0.00	0.04	6.48	1.37	52.27	33.07	13.47	18.47	19.33	31.37	28.76	19.83	51.50	17.80	56.18	75.27	206.66	206.17	178.79	58.86	96.03	154.83	115.31
Acidobacteria	4.13	36.51	0.00	3.04	0.00	1.03	7.28	0.00	15.95	7.75	30.78	0.00	0.00	0.00	0.00	0.00	0.18	0.00	74.00	74.65	145.97	176.01	468.22	103.11	28.31	204.28	149.16
Actinobacteria	0.00	0.16	0.00	0.00	0.00	0.67	0.00	0.00	7.93	0.24	0.00	2.24	1.11	4.44	1.61	3.48	7.33	0.70	0.20	63.30	117.18	137.20	1.80	8.99	10.06	29.92	56.46
Verrucomicrobia	0.00	0.22	0.00	2.17	0.09	0.00	0.03	0.08	0.36	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.22	0.00	5.35	2.04	2.91	21.46	8.77	3.05	9.64	10.27	22.74
Chloroflexi	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.57	0.20	0.11	0.00	0.00	0.66	0.55	0.15	0.55	0.00	1.93	0.55	6.48	17.73	1.06	0.76	2.17	23.00	9.53
Bacteroidetes	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.12	0.00	0.00	0.00	1.15	0.91	0.45	0.60	1.17	0.15	0.80	1.62	0.57	1.53	3.49	0.00	0.76	2.92	1.79
Gemmatimonadetes	0.00	0.91	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.18	0.42	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.99	1.24	3.59	8.33	11.27	0.92	2.78	3.58	2.87
Planctomycetes	1.10	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.87	2.91	0.92	11.69	5.22	0.77	2.80	4.21	1.85
Candidatus_Eremiobacteraeota	0.00	0.00	0.00	0.15	0.00	0.00	0.82	0.00	0.00	0.00	0.12	0.00	0.09	0.57	0.00	0.29	0.21	0.00	0.00	1.34	2.54	2.83	0.00	1.10	0.08	1.24	1.51
fungi																											
Ascomycota	0.06	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Basidiomycota	0.00	0.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Average values of mineral soils																											
Archaea																											
Thaumarchaeota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.05	1.37	0.00	0.00	0.54	0.00	0.19	1.37
Candidatus_Thermoplasmatota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00
Euryarchaeota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.04
Candidatus_Bathyarchaeota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00	0.00	0.00

<b>Bacteria</b>																											
Proteobacteria	2.32	63.32	0.26	21.40	0.49	0.11	7.59	2.28	46.79	35.72	20.44	19.45	22.23	35.81	30.45	20.93	59.63	22.91	65.12	95.27	230.80	237.61	207.48	48.27	104.03	159.27	137.78
Acidobacteria	3.51	35.62	0.00	5.74	0.00	0.66	16.04	0.00	6.75	3.88	15.27	0.00	0.00	0.38	0.00	0.00	0.00	0.00	57.09	82.04	105.96	143.66	346.03	71.58	16.14	133.20	117.32
Actinobacteria	0.00	0.10	0.00	0.00	0.00	1.06	0.00	0.00	14.97	0.08	0.00	5.92	5.51	9.68	4.91	8.01	19.63	1.78	0.16	106.25	210.74	216.67	2.56	17.29	17.31	47.81	101.65
Verrucomicrobia	0.12	0.00	0.00	2.52	0.00	0.00	0.91	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.52	0.76	0.00	3.62	2.18	4.15	7.86	10.45	1.21	4.62	7.77	9.53
Chloroflexi	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.15	0.22	0.16	0.00	0.13	0.12	0.05	0.16	0.00	0.03	0.41	1.74	5.00	0.69	0.19	0.81	4.33	1.71
Bacteroidetes	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.69	0.00	0.09	0.00	1.76	2.36	2.03	1.62	5.92	1.11	2.09	4.10	4.55	4.46	11.28	0.00	1.47	9.81	3.25
Gemmatimonadetes	0.00	1.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.23	1.05	3.03	7.66	8.05	0.56	3.13	6.10	2.74
Planctomycetes	0.09	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.66	1.09	0.85	6.39	4.31	0.26	1.43	2.86	1.50
Candidatus_Eremiobacteraeota	0.00	0.00	0.00	0.79	0.00	0.00	1.65	0.00	0.00	0.00	0.07	0.00	0.23	0.63	0.00	0.36	0.12	0.00	0.00	2.62	5.82	6.81	0.00	2.06	0.00	3.22	3.85
<b>Fungi</b>																											
Ascomycota	0.00	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Basidiomycota	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

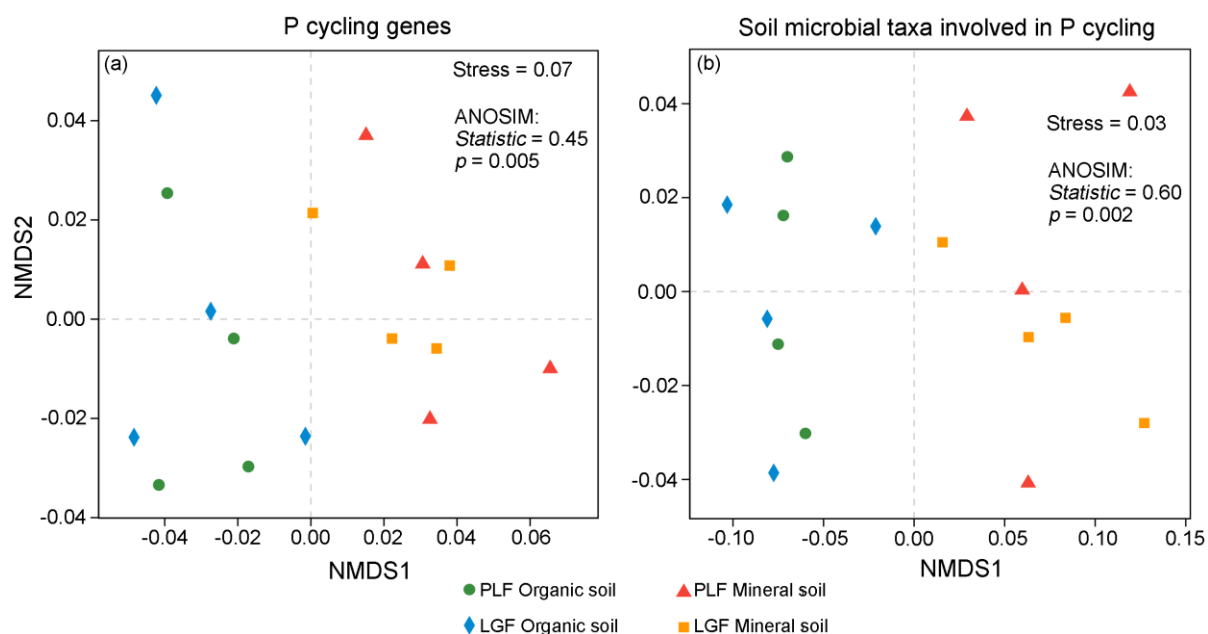
Average values of organic and mineral soils

<b>Archaea</b>																											
Thaumarchaeota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.35	2.05	0.00	0.00	0.87	0.00	0.51	1.90
Candidatus_Thermoplasmatota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.00	0.00	0.55	0.00	0.00	0.00
Euryarchaeota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.24
Candidatus_Bathyarchaeota	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.00
<b>Bacterial</b>																											
Proteobacteria	2.18	57.28	0.16	19.99	0.24	0.08	7.04	1.82	49.53	34.40	16.95	18.96	20.78	33.59	29.61	20.38	55.56	20.35	60.65	85.27	218.73	221.89	193.14	53.57	100.03	157.05	126.55
Acidobacteria	3.82	36.06	0.00	4.39	0.00	0.84	11.66	0.00	11.35	5.82	23.03	0.00	0.00	0.19	0.00	0.00	0.09	0.00	65.54	78.35	125.97	159.84	407.13	87.34	22.22	168.74	133.24
Actinobacteria	0.00	0.13	0.00	0.00	0.00	0.87	0.00	0.00	11.45	0.16	0.00	4.08	3.31	7.06	3.26	5.74	13.48	1.24	0.18	84.77	163.96	176.93	2.18	13.14	13.68	38.86	79.06
Verrucomicrobia	0.06	0.11	0.00	2.34	0.05	0.00	0.47	0.10	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.35	0.49	0.00	4.49	2.11	3.53	14.66	9.61	2.13	7.13	9.02	16.13
Chloroflexi	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.32	0.18	0.16	0.08	0.00	0.40	0.34	0.10	0.36	0.00	0.98	0.48	4.11	11.37	0.87	0.47	1.49	13.66	5.62
Bacteroidetes	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.41	0.00	0.05	0.00	1.45	1.64	1.24	1.11	3.54	0.63	1.45	2.86	2.56	3.00	7.39	0.00	1.11	6.36	2.52
Gemmatimonadetes	0.00	0.96	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.09	0.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.11	1.15	3.31	8.00	9.66	0.74	2.96	4.84	2.80
Planctomycetes	0.59	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.77	2.00	0.88	9.04	4.76	0.51	2.12	3.54	1.68

[illegible]

**Table S4 Pearson correlations between the available soil P concentration and the relative abundance of the P cycling genes selected by Random Forest analysis.**

<b>Gene</b>	<b><i>df</i></b>	<b><i>r</i></b>	<b><i>P</i> value</b>
pqqC	14	-0.681	0.004
phoR	14	-0.691	0.003
<b>appA</b>	<b>14</b>	<b>0.732</b>	<b>0.001</b>
phnP	14	-0.737	0.001
<b>3-phytase</b>	<b>14</b>	<b>0.672</b>	<b>0.004</b>
gcd	14	-0.582	0.018
<b>ppa</b>	<b>14</b>	<b>0.707</b>	<b>0.002</b>



**Figure S1 Nonmetric multidimensional scaling plots (NMDS) of P cycling genes (a) and soil microbial taxa involved in P cycling (b) in soils.** NMDS had a good explanation of variation as stress < 0.1. ANOSIM showed significant differences in variables between organic and mineral soil as  $p < 0.05$ .