Supplementary information for

Soil microbial genomic responses to aridity-driven elemental imbalance across global biomes

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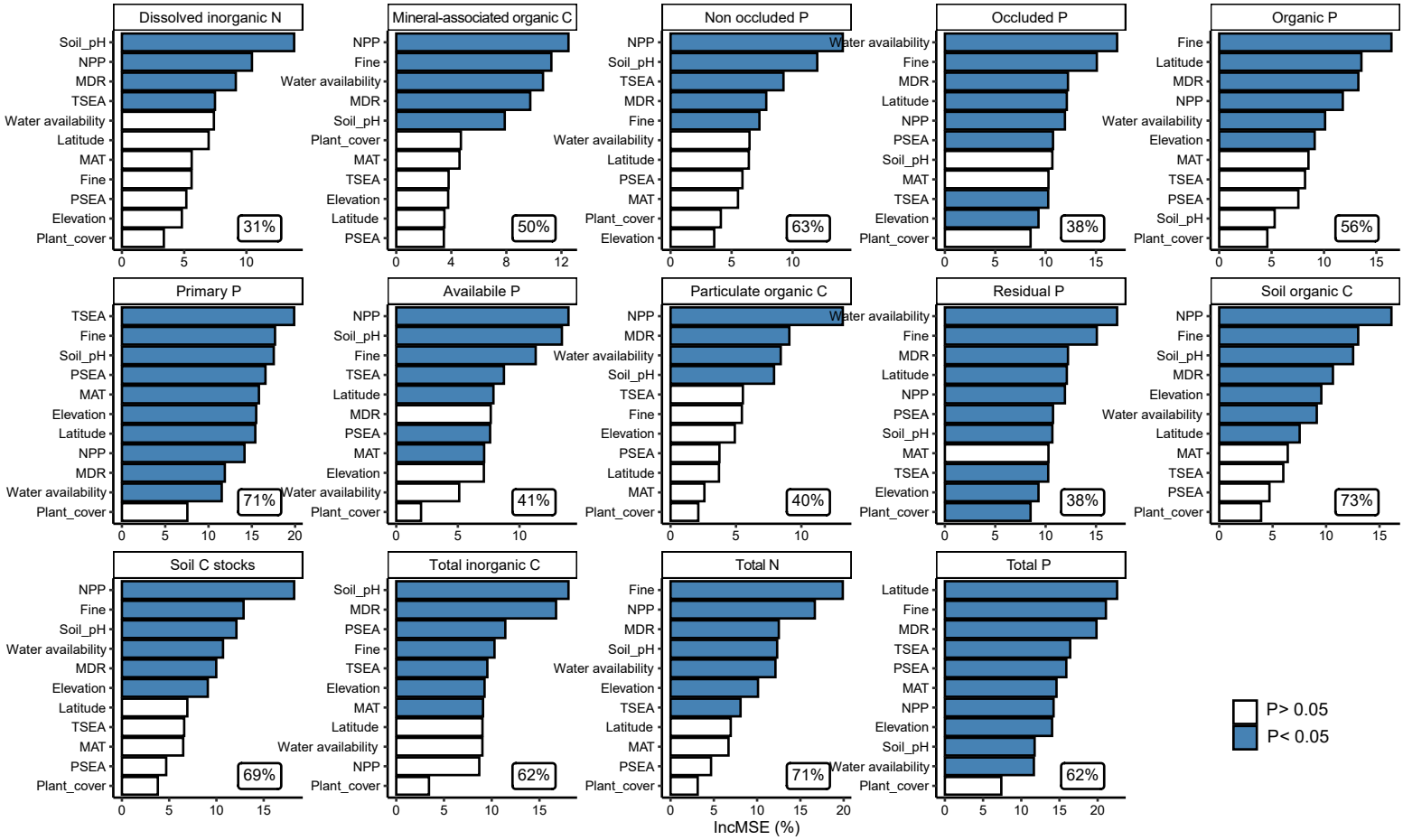
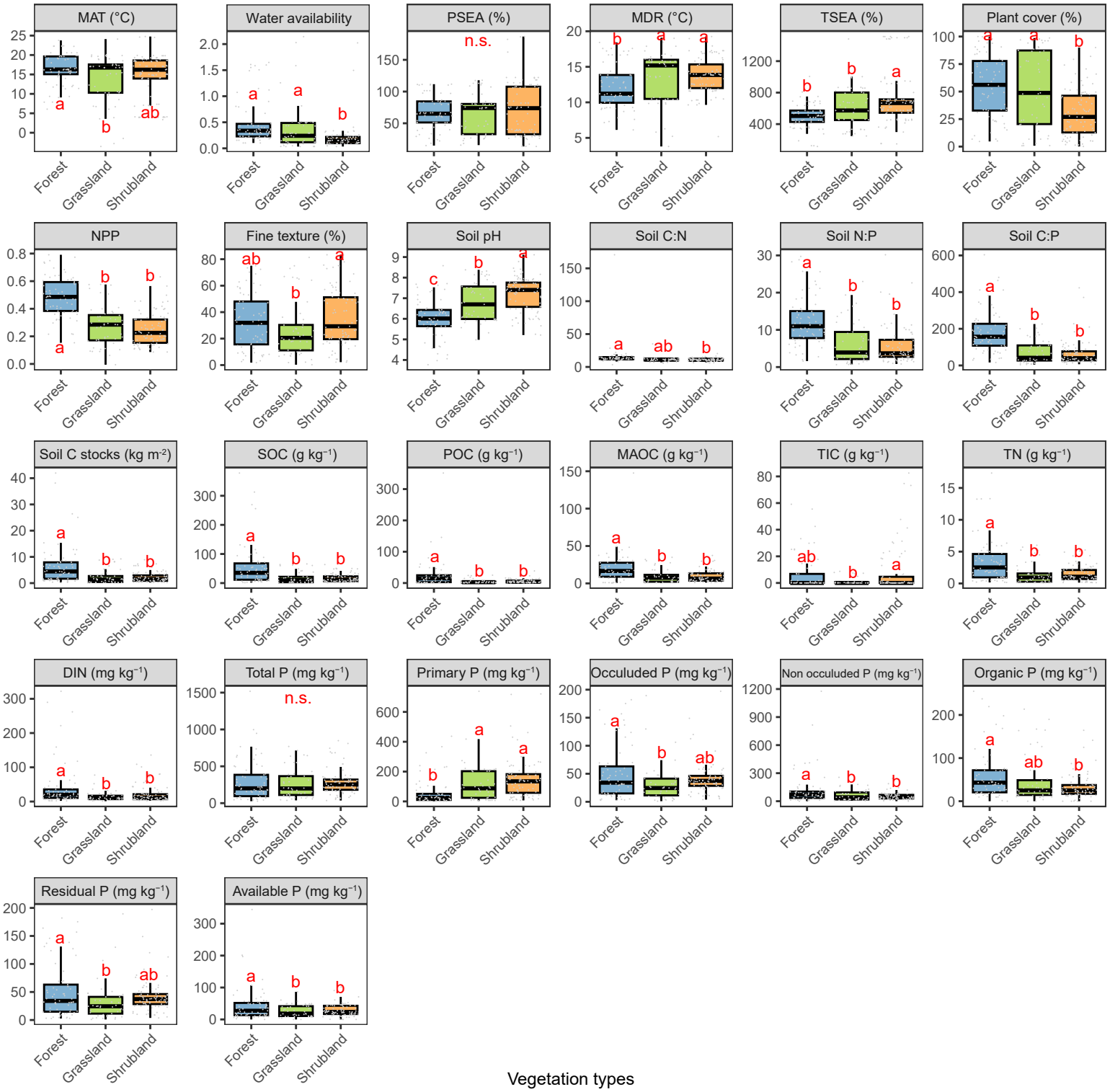
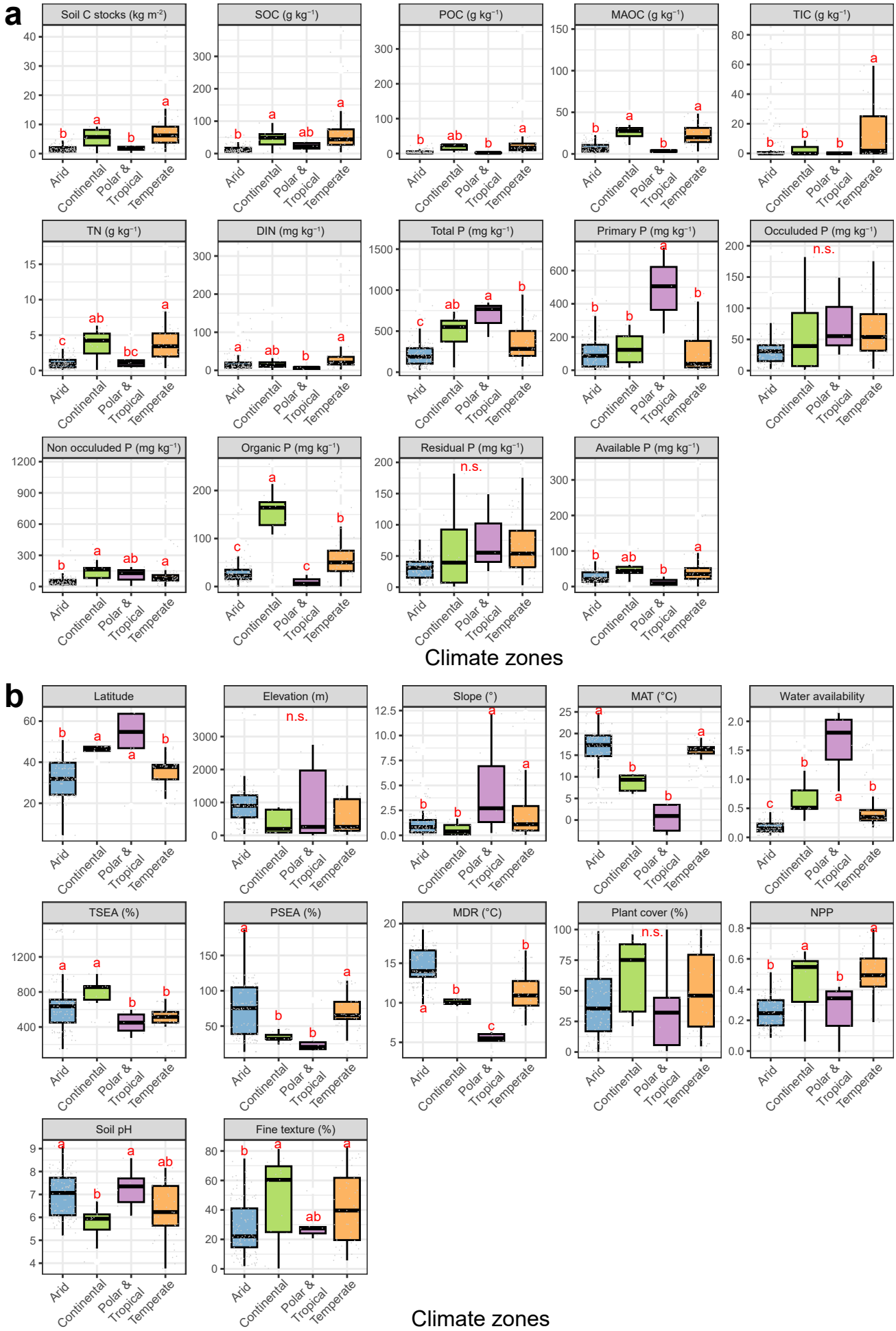


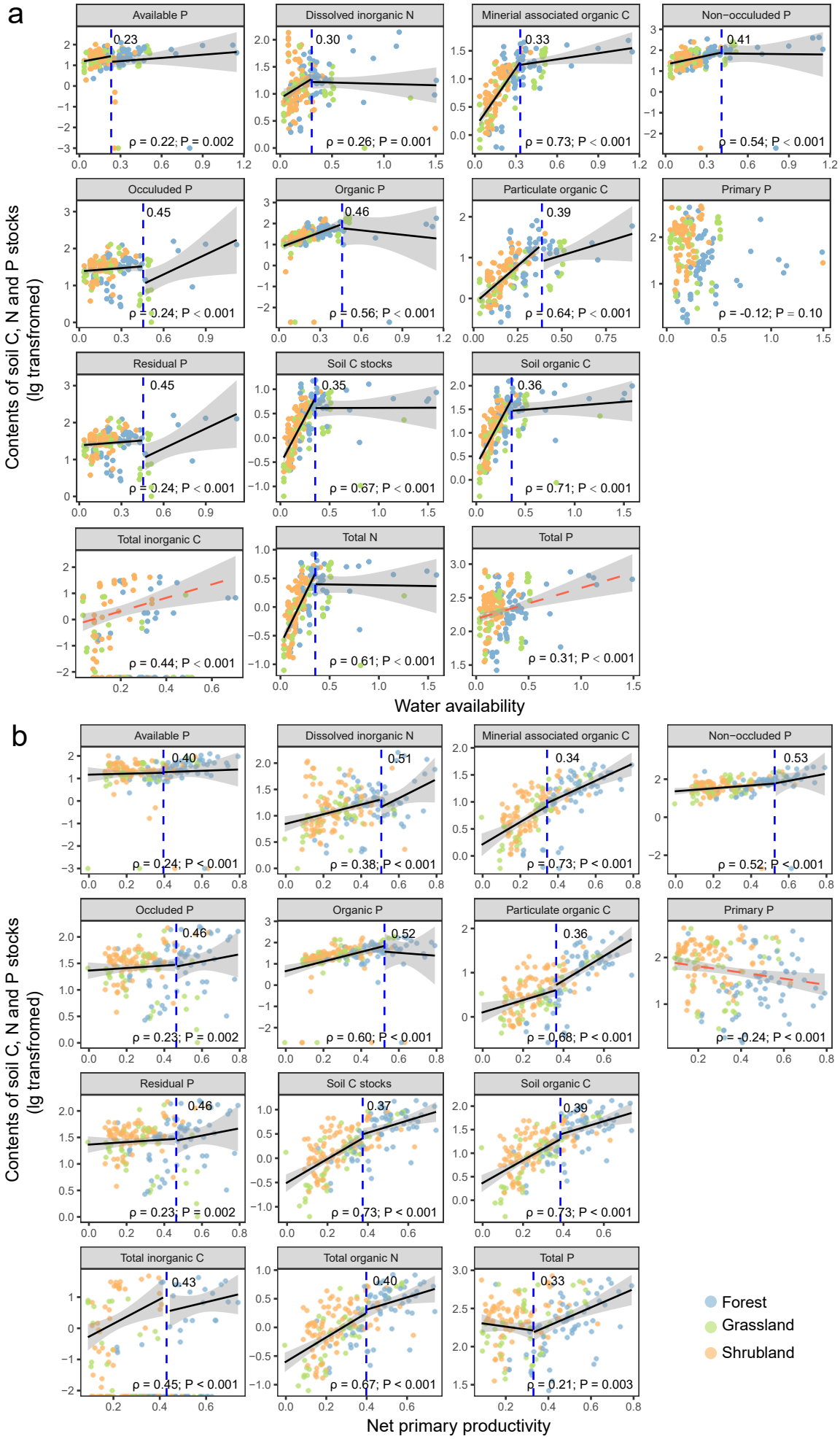
Supplementary Figure 1 | Random-forest identifying the main environmental factors predicting each stock and pool of C, N and P on global scales. The environmental factors include the latitude, elevation, mean annual temperature (MAT), mean annual precipitation (MAP), temperature seasonality (TSEA), precipitation seasonality (PSEA), mean diurnal range (MDR), net primary productivity (NPP), plant cover, soil pH and textural composition (Fine proportion). Soil C stocks and pools were represented by soil total C content, organic C, inorganic C, particulate organic C and mineral-associated organic C; soil N stocks and pools were represented by total (organic) N, and dissolved inorganic N; soil P stocks and pools were represented by total P, primary P, occluded, non-occluded P, organic P, residual P, and available P. The percentage inserted in each panel represents the total explanation of selected variables on the variations of soil elemental stocks and pools.



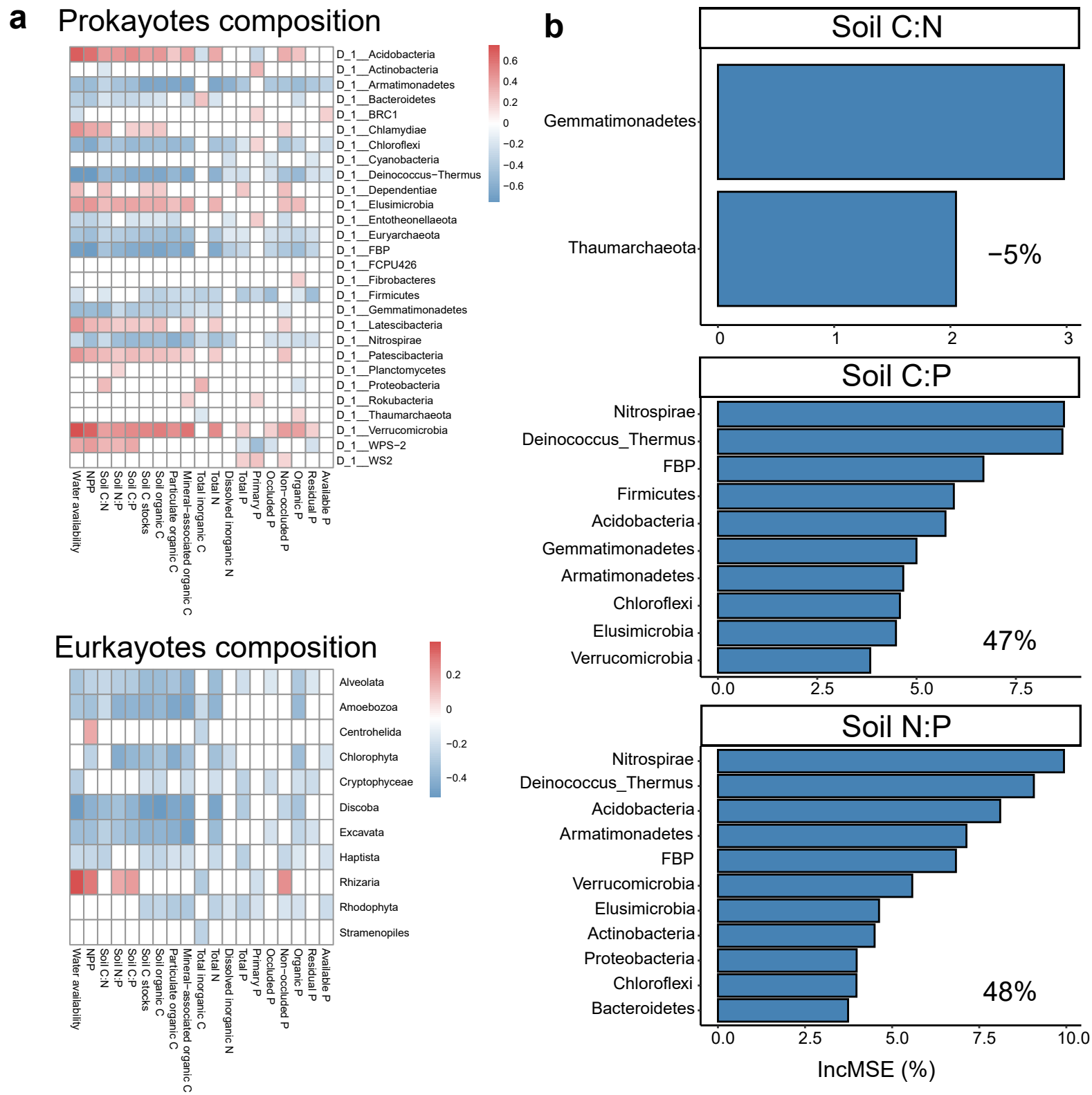
Supplementary Figure 2 | The changes of climate variables, vegetation characteristics, soil physico-chemical properties and stocks and pools for C, N and P along ecosystem types on global scale, they are forests, grasslands, and shrublands. Ecosystem types not sharing a letter (in each panel) differ significantly (Tukey's HSD test: $P < 0.05$).



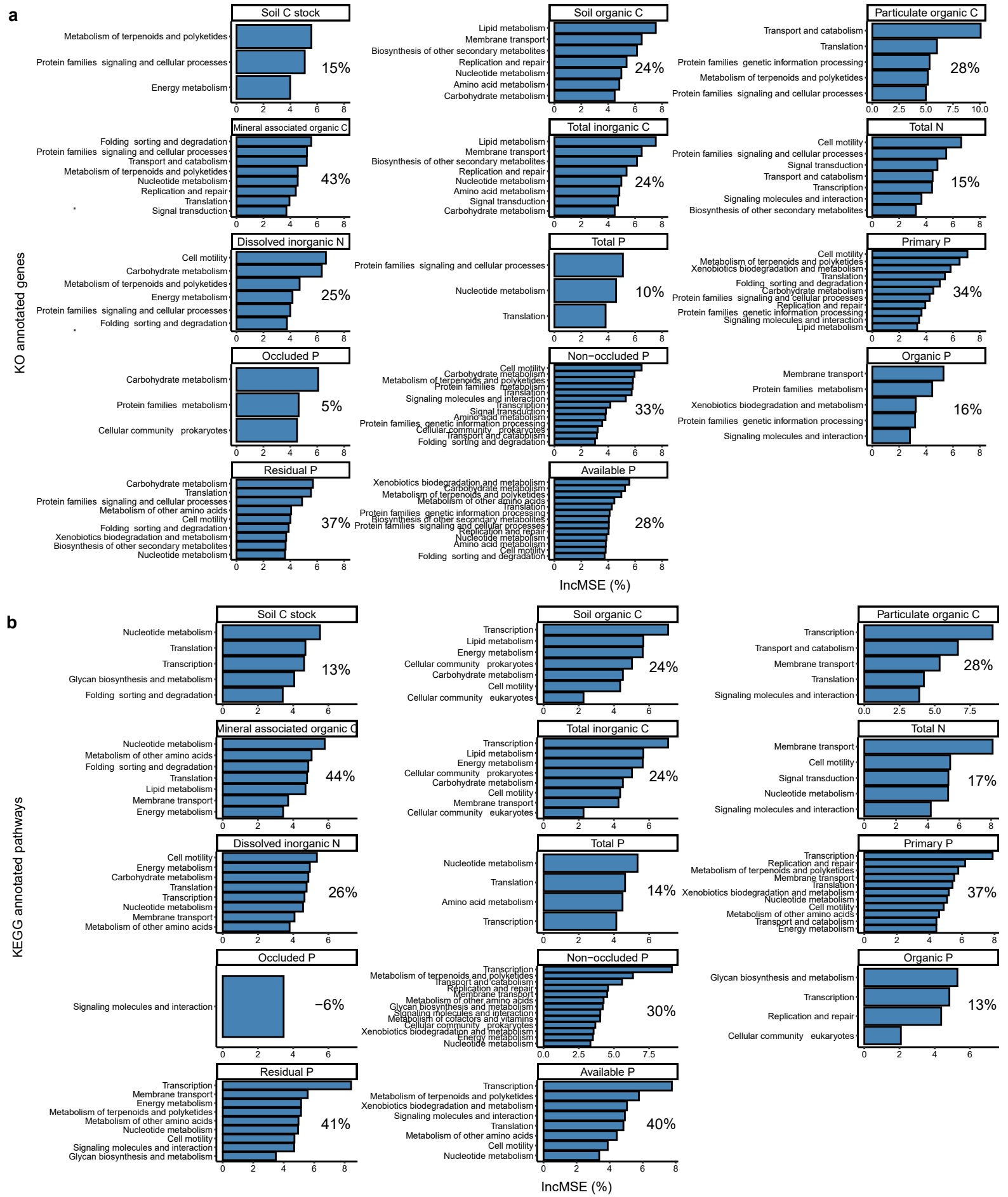
Supplementary Figure 3 | The changes of soil stocks and pools for C, N and P (a), as well as the main environmental factors (b) along the climate zones on global scale, they are arid, continental, temperate and others (i.e., polar and tropical) zones. Climate zones not sharing a letter (in each panel) differ significantly (Tukey's HSD test: $P < 0.05$).



Supplementary Figure 4 | The changes of soil properties, i.e., C, N and P stocks and pools along the water availability (a) and net primary productivity (b) on a global scale. The threshold of each nonlinear regression and the Spearman correlation result (ρ and P values) appears in each panel.

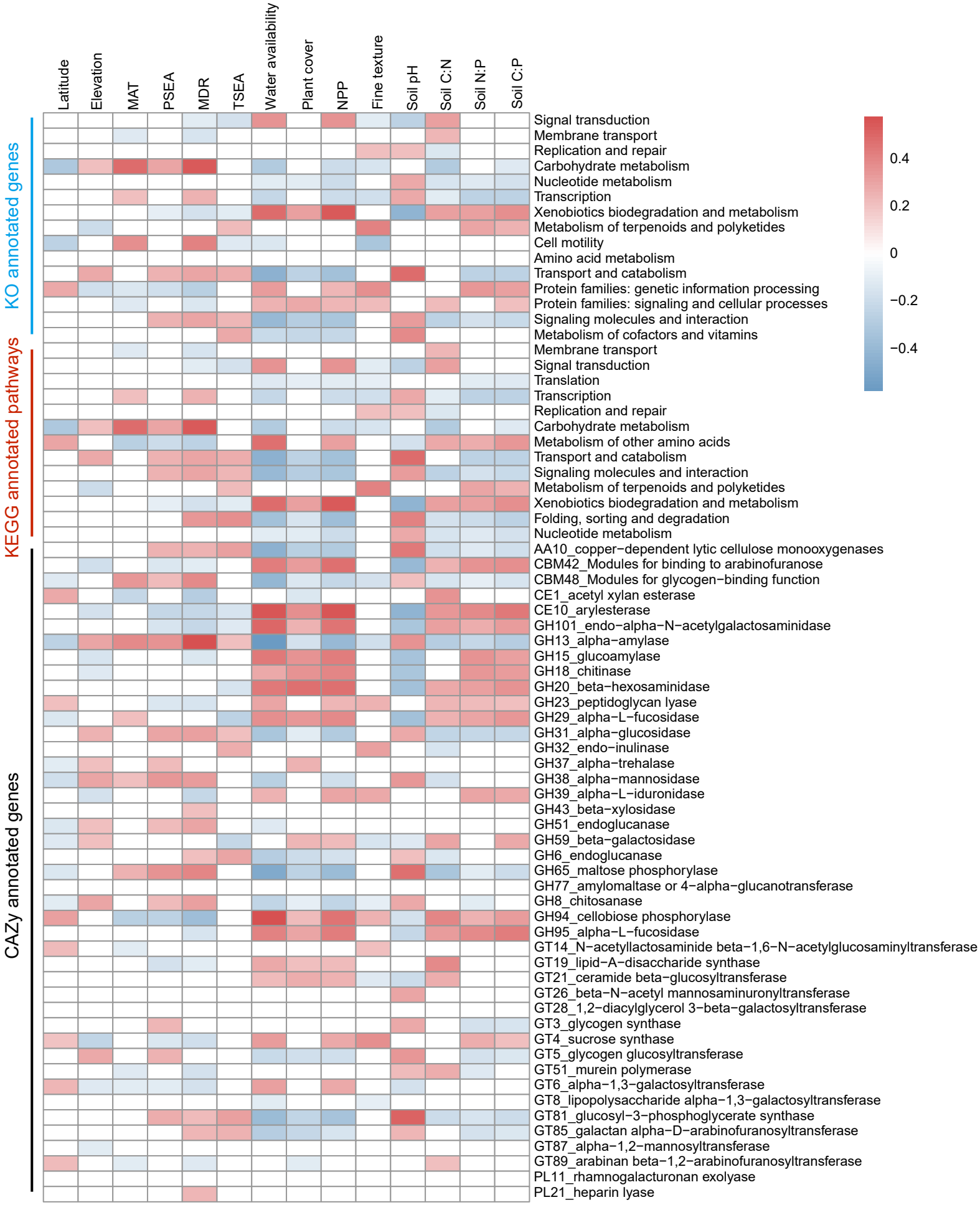


Supplementary Figure 5 | Spearman correlations between the key environmental variables as well as stocks and pools of C, N and P with the abundance of the key taxa of soil microbiome (a). Red boxes represent significantly positive relationships ($\rho > 0$, $P < 0.05$), blue boxes represent significantly negative relationships ($\rho < 0$, $P < 0.05$); The blank boxes represent non-significant relationships. Random-forest identifying the key variables in response to the variation in soil C:N, N:P and C:P ratios on global scales, the percentage inserted in each panel represents the total explanation of selected variables (b).



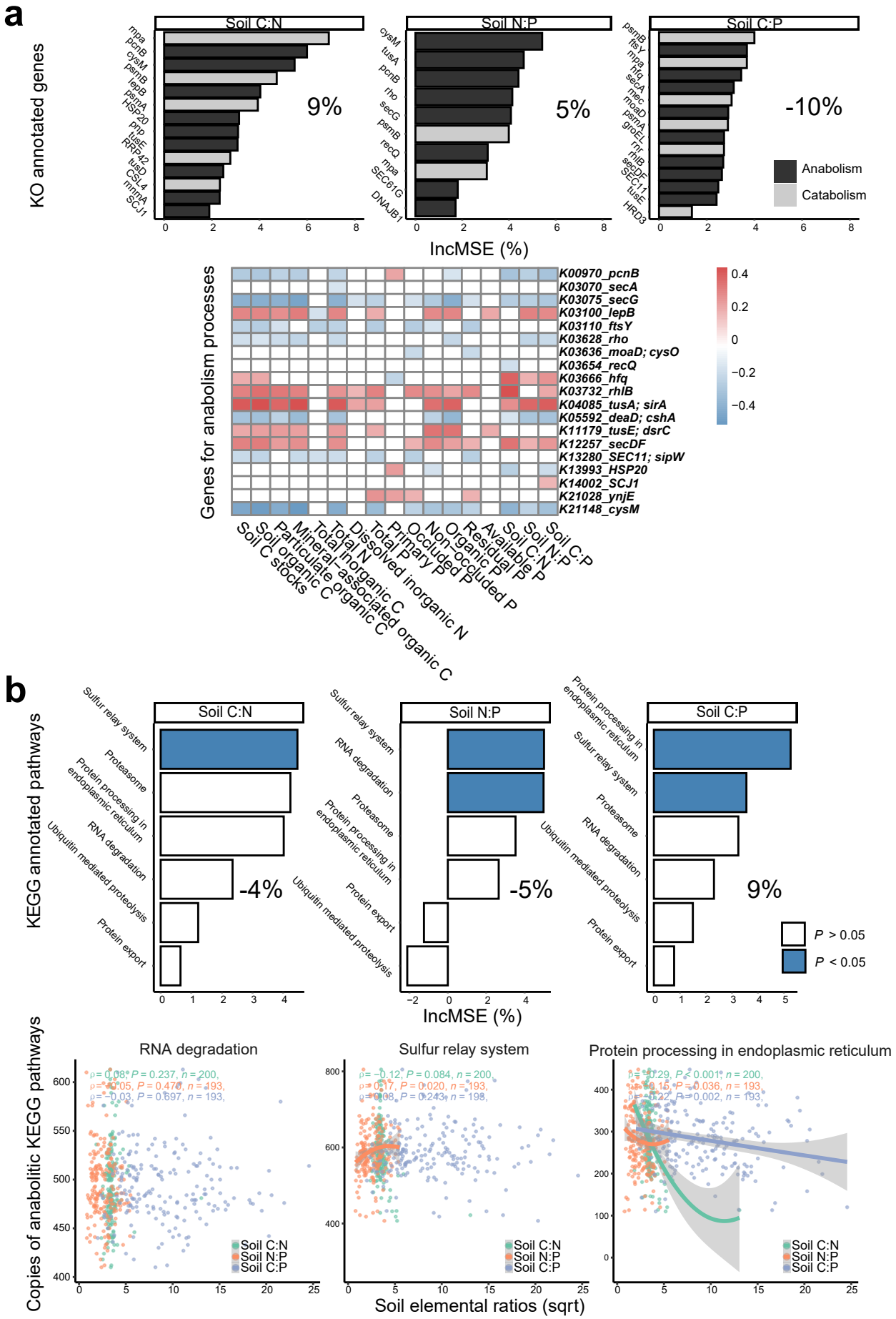
Supplementary Figure 6 | Random forest analyses identifying the key KO-annotated genes (a) and KEGG-annotated pathways (b) predicting the changes of soil C, N, and P stocks and pools, i.e., soil total C, organic and inorganic C, particulate organic C, mineral associated organic C, total (organic) N, dissolved inorganic N, total P, primary P, occluded and non-occluded P, residual P, organic P as well as available P.

Supplementary Figure 7 | Random forest analyses identifying the key CAZy-annotated genes modules predicting the changes of soil C, N, and P stocks and pools, i.e., soil total C, organic and inorganic C, particulate organic C, mineral associated organic C, total (organic) N, dissolved inorganic N, total P, primary P, occluded and non-occluded P, residual P, organic P as well as available P.

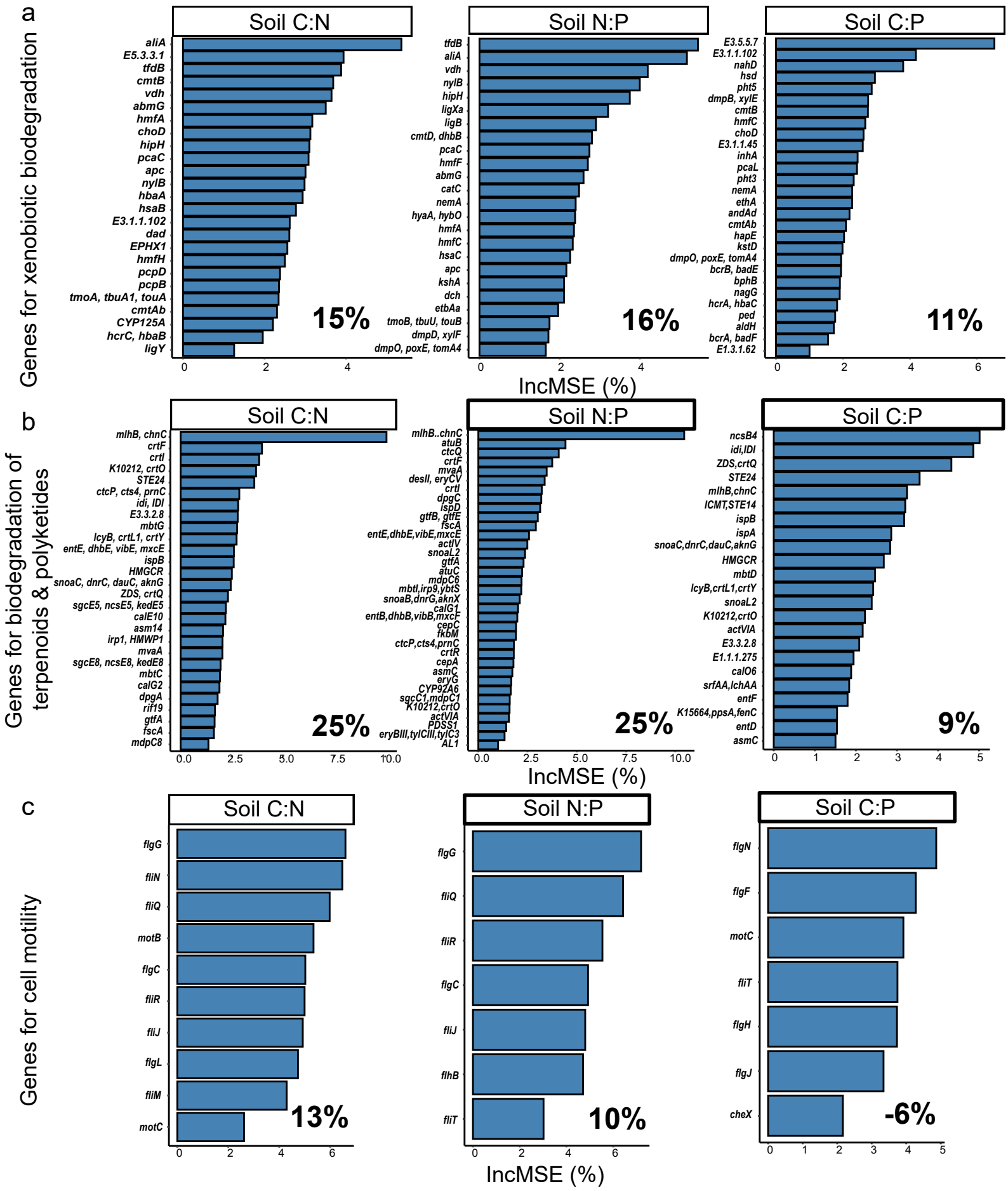


Supplementary Figure 8 | Spearman correlations between the key KO-annotated genes, KEGG-annotated metabolic pathways and CAZy-annotated gene modules and the ratios of soil C:N, N:P and C:P with the main environmental factors. Red boxes represent significantly positive relationships ($\rho > 0$, $P < 0.05$), blue boxes represent significantly negative relationships ($\rho < 0$, $P < 0.05$); The blank boxes represent non-significant relationships.

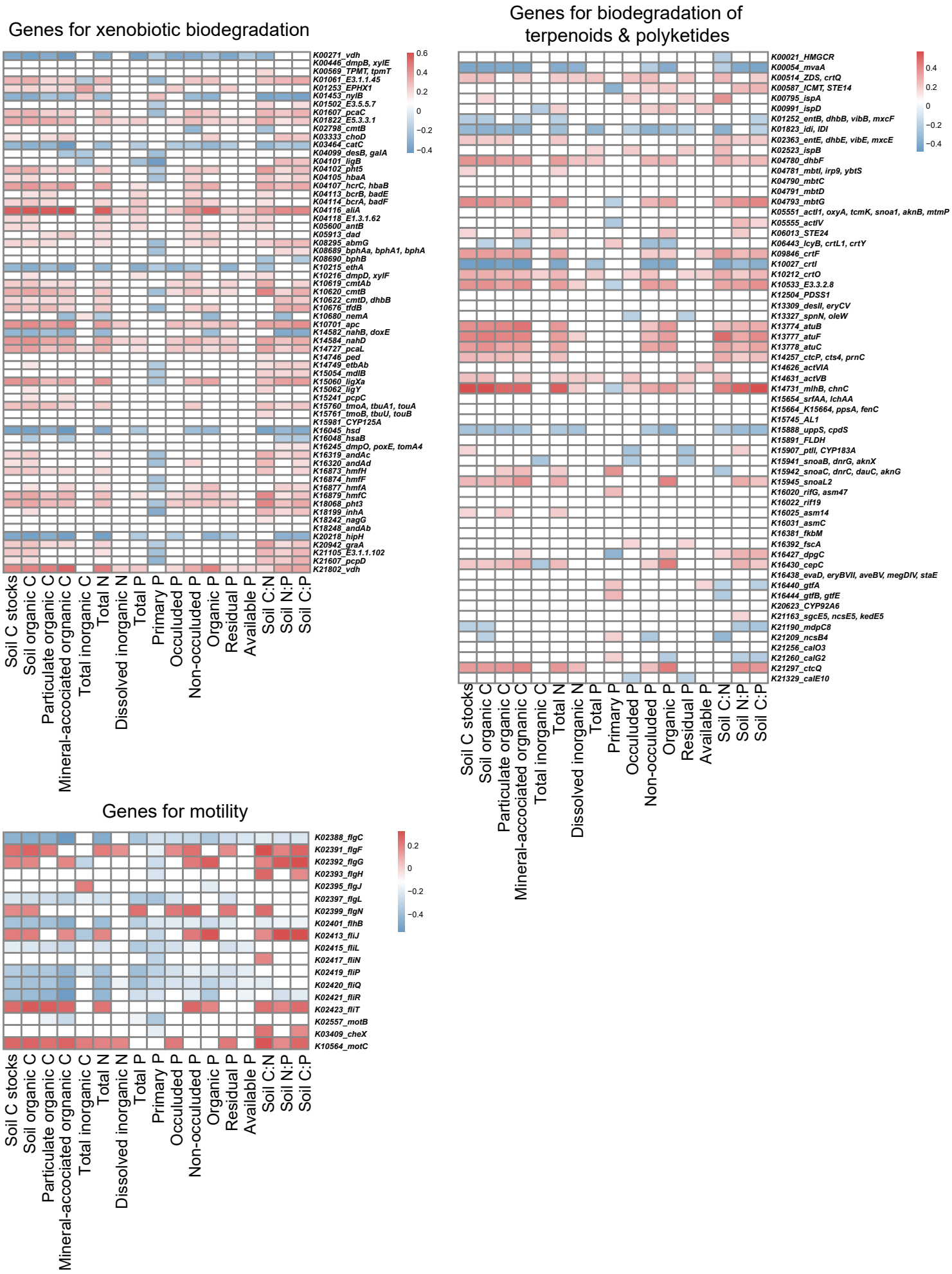
Supplementary Figure 9 | Spearman correlations between the key KO genes, KEGG pathways and CAZy genes and soil C, N, and P stocks and pools, i.e., soil total C, organic and inorganic C, particulate organic C, mineral associated organic C, total (organic) N, dissolved inorganic N, total P, primary P, occluded and non-occluded P, residual P, organic P as well as available P. Red boxes represent significantly positive r elationships ($\rho > 0$, $P < 0.05$), blue boxes represent significantly negative relationships ($\rho < 0$, $P < 0.05$); The blank boxes represent non-significant relationships.



Supplementary Figure 10 | Random forest identifying the protein synthesis and degradation related KO-annotated genes (only significant predictors with P<0.05 were shown) (a) and KEGG-annotated metabolic pathways in predicting the variations of the ratios of soil C:N, N:P and C:P (b). The spearman correlations of soil elemental ratios and environmental variables with the abundance of these significantly genes or pathways were inserted in each panel. In the heatmap, red boxes represent significantly positive relationships (ρ > 0, P < 0.05), blue boxes represent significantly negative relationships (ρ < 0, P < 0.05); The blank boxes represent non-significant relationships.



Supplementary Figure 11 | Random forest identifying the KO-annotated genes related to biodegradation of xenobiotics (a), terpenoids and polyketides (b) as well as cell motility (c) in predicting the variations of the ratios of soil C:N, N:P and C:P (only significant predictors with P<0.05 were shown).



Supplementary Figure 12 | Spearman correlations between the abundance of significant changed KO-annotated genes involved in degradation of xenobiotics, terpenoids and polyketides as well as cell motility with the ratios of soil C:N, N:P and C:P and the main environmental factors. Red boxes represent significantly positive relationships ($\rho > 0$, $P < 0.05$), blue boxes represent significantly negative relationships ($\rho < 0$, $P < 0.05$); The blank boxes represent non-significant relationships.

Supplementary Table 1 | Classification of KEGG database in the three levels.

LEVEL1	LEVEL2	LEVEL3
Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis [PATH:ko00010]
Metabolism	Lipid metabolism	Steroid biosynthesis [PATH:ko00100]
Metabolism	Lipid metabolism	Biosynthesis of unsaturated fatty acids [PATH:ko01040]
Metabolism	Metabolism of terpenoids and polyketides	Biosynthesis of ansamycins [PATH:ko01051]
Metabolism	Metabolism of terpenoids and polyketides	Type I polyketide structures [PATH:ko01052]
Metabolism	Metabolism of terpenoids and polyketides	Biosynthesis of siderophore group nonribosomal peptides [PATH:ko01053]
Metabolism	Metabolism of terpenoids and polyketides	Nonribosomal peptide structures [PATH:ko01054]
Metabolism	Metabolism of terpenoids and polyketides	Biosynthesis of vancomycin group antibiotics [PATH:ko01055]
Metabolism	Metabolism of terpenoids and polyketides	Biosynthesis of type II polyketide backbone [PATH:ko01056]
Metabolism	Metabolism of terpenoids and polyketides	Biosynthesis of type II polyketide products [PATH:ko01057]
Metabolism	Metabolism of terpenoids and polyketides	Biosynthesis of enediyne antibiotics [PATH:ko01059]
Metabolism	Lipid metabolism	Primary bile acid biosynthesis [PATH:ko00120]
Metabolism	Lipid metabolism	Secondary bile acid biosynthesis [PATH:ko00121]
Metabolism	Metabolism of cofactors and vitamins	Ubiquinone and other terpenoid-quinone biosynthesis [PATH:ko00130]
Metabolism	Lipid metabolism	Steroid hormone biosynthesis [PATH:ko00140]
Metabolism	Energy metabolism	Oxidative phosphorylation [PATH:ko00190]
Metabolism	Energy metabolism	Photosynthesis [PATH:ko00195]
Metabolism	Energy metabolism	Photosynthesis - antenna proteins [PATH:ko00196]
Metabolism	Carbohydrate metabolism	Citrate cycle (TCA cycle) [PATH:ko00020]
Environmental Information Processing	Membrane transport	ABC transporters [PATH:ko02010]
Environmental Information Processing	Signal transduction	Two-component system [PATH:ko02020]

Cellular Processes	Cellular community - prokaryotes	Quorum sensing [PATH:ko02024]
Cellular Processes	Cellular community - prokaryotes	Biofilm formation - Pseudomonas aeruginosa [PATH:ko02025]
Cellular Processes	Cellular community - prokaryotes	Biofilm formation - Escherichia coli [PATH:ko02026]
Cellular Processes	Cell motility	Bacterial chemotaxis [PATH:ko02030]
Cellular Processes	Cell motility	Flagellar assembly [PATH:ko02040]
Environmental Information Processing	Membrane transport	Phosphotransferase system (PTS) [PATH:ko02060]
Metabolism	Amino acid metabolism	Arginine biosynthesis [PATH:ko00220]
Metabolism	Nucleotide metabolism	Purine metabolism [PATH:ko00230]
Metabolism	Biosynthesis of other secondary metabolites	Caffeine metabolism [PATH:ko00232]
Metabolism	Nucleotide metabolism	Pyrimidine metabolism [PATH:ko00240]
Metabolism	Amino acid metabolism	Alanine, aspartate and glutamate metabolism [PATH:ko00250]
Metabolism	Metabolism of terpenoids and polyketides	Tetracycline biosynthesis [PATH:ko00253]
Metabolism	Amino acid metabolism	Glycine, serine and threonine metabolism [PATH:ko00260]
Metabolism	Biosynthesis of other secondary metabolites	Monobactam biosynthesis [PATH:ko00261]
Metabolism	Amino acid metabolism	Cysteine and methionine metabolism [PATH:ko00270]
Metabolism	Amino acid metabolism	Valine, leucine and isoleucine degradation [PATH:ko00280]
Metabolism	Metabolism of terpenoids and polyketides	Geraniol degradation [PATH:ko00281]
Metabolism	Amino acid metabolism	Valine, leucine and isoleucine biosynthesis [PATH:ko00290]
Metabolism	Carbohydrate metabolism	Pentose phosphate pathway [PATH:ko00030]
Metabolism	Amino acid metabolism	Lysine biosynthesis [PATH:ko00300]
Genetic Information Processing	Translation	Ribosome biogenesis in eukaryotes [PATH:ko03008]
Genetic Information Processing	Translation	Ribosome [PATH:ko03010]
Genetic Information Processing	Translation	RNA transport [PATH:ko03013]
Genetic Information	Translation	mRNA surveillance pathway

Processing		[PATH:ko03015]
Genetic Information Processing	Folding, sorting and degradation	RNA degradation [PATH:ko03018]
Genetic Information Processing	Transcription	Basal transcription factors [PATH:ko03022]
Genetic Information Processing	Replication and repair	DNA replication [PATH:ko03030]
Genetic Information Processing	Transcription	Spliceosome [PATH:ko03040]
Genetic Information Processing	Folding, sorting and degradation	Proteasome [PATH:ko03050]
Genetic Information Processing	Folding, sorting and degradation	Protein export [PATH:ko03060]
Environmental Information Processing	Membrane transport	Bacterial secretion system [PATH:ko03070]
Metabolism	Amino acid metabolism	Lysine degradation [PATH:ko00310]
Metabolism	Biosynthesis of other secondary metabolites	Penicillin and cephalosporin biosynthesis [PATH:ko00311]
Metabolism	Amino acid metabolism	Arginine and proline metabolism [PATH:ko00330]
Metabolism	Biosynthesis of other secondary metabolites	Clavulanic acid biosynthesis [PATH:ko00331]
Metabolism	Biosynthesis of other secondary metabolites	Carbapenem biosynthesis [PATH:ko00332]
Metabolism	Biosynthesis of other secondary metabolites	Prodigiosin biosynthesis [PATH:ko00333]
Metabolism	Amino acid metabolism	Histidine metabolism [PATH:ko00340]
Genetic Information Processing	Replication and repair	Base excision repair [PATH:ko03410]
Genetic Information Processing	Replication and repair	Nucleotide excision repair [PATH:ko03420]
Genetic Information Processing	Replication and repair	Mismatch repair [PATH:ko03430]
Genetic Information Processing	Replication and repair	Homologous recombination [PATH:ko03440]
Genetic Information Processing	Replication and repair	Non-homologous end-joining [PATH:ko03450]
Genetic Information Processing	Replication and repair	Fanconi anemia pathway [PATH:ko03460]
Metabolism	Amino acid metabolism	Tyrosine metabolism [PATH:ko00350]
Metabolism	Amino acid metabolism	Phenylalanine metabolism [PATH:ko00360]

Metabolism	Xenobiotics biodegradation and metabolism	Chlorocyclohexane and chlorobenzene degradation [PATH:ko00361]
Metabolism	Xenobiotics biodegradation and metabolism	Benzoate degradation [PATH:ko00362]
Metabolism	Xenobiotics biodegradation and metabolism	Bisphenol degradation [PATH:ko00363]
Metabolism	Xenobiotics biodegradation and metabolism	Fluorobenzoate degradation [PATH:ko00364]
Metabolism	Xenobiotics biodegradation and metabolism	Furfural degradation [PATH:ko00365]
Metabolism	Amino acid metabolism	Tryptophan metabolism [PATH:ko00380]
Metabolism	Carbohydrate metabolism	Pentose and glucuronate interconversions [PATH:ko00040]
Metabolism	Amino acid metabolism	Phenylalanine, tyrosine and tryptophan biosynthesis [PATH:ko00400]
Environmental Information Processing	Signal transduction	MAPK signaling pathway [PATH:ko04010]
Environmental Information Processing	Signal transduction	MAPK signaling pathway - yeast [PATH:ko04011]
Environmental Information Processing	Signal transduction	ErbB signaling pathway [PATH:ko04012]
Environmental Information Processing	Signal transduction	MAPK signaling pathway - fly [PATH:ko04013]
Environmental Information Processing	Signal transduction	Ras signaling pathway [PATH:ko04014]
Environmental Information Processing	Signal transduction	Rap1 signaling pathway [PATH:ko04015]
Environmental Information Processing	Signal transduction	MAPK signaling pathway - plant [PATH:ko04016]
Environmental Information Processing	Signal transduction	Calcium signaling pathway [PATH:ko04020]
Environmental Information Processing	Signal transduction	cGMP-PKG signaling pathway [PATH:ko04022]
Environmental Information Processing	Signal transduction	cAMP signaling pathway [PATH:ko04024]
Metabolism	Biosynthesis of other secondary metabolites	Staurosporine biosynthesis [PATH:ko00404]
Metabolism	Biosynthesis of other secondary metabolites	Phenazine biosynthesis [PATH:ko00405]
Environmental Information Processing	Signal transduction	NF-kappa B signaling pathway [PATH:ko04064]

Environmental Information Processing	Signal transduction	HIF-1 signaling pathway [PATH:ko04066]
Environmental Information Processing	Signal transduction	FoxO signaling pathway [PATH:ko04068]
Environmental Information Processing	Signal transduction	Phospholipase D signaling pathway [PATH:ko04072]
Environmental Information Processing	Signal transduction	Plant hormone signal transduction [PATH:ko04075]
Environmental Information Processing	Signaling molecules and interaction	Neuroactive ligand-receptor interaction [PATH:ko04080]
Metabolism	Metabolism of other amino acids	beta-Alanine metabolism [PATH:ko00410]
Cellular Processes	Cell growth and death	Cell cycle [PATH:ko04110]
Cellular Processes	Cell growth and death	Cell cycle - yeast [PATH:ko04111]
Cellular Processes	Cell growth and death	Cell cycle - Caulobacter [PATH:ko04112]
Cellular Processes	Cell growth and death	Meiosis - yeast [PATH:ko04113]
Cellular Processes	Cell growth and death	p53 signaling pathway [PATH:ko04115]
Genetic Information Processing	Folding, sorting and degradation	Ubiquitin mediated proteolysis [PATH:ko04120]
Genetic Information Processing	Folding, sorting and degradation	Sulfur relay system [PATH:ko04122]
Cellular Processes	Transport and catabolism	Autophagy - other [PATH:ko04136]
Cellular Processes	Transport and catabolism	Mitophagy - animal [PATH:ko04137]
Cellular Processes	Transport and catabolism	Autophagy - yeast [PATH:ko04138]
Cellular Processes	Transport and catabolism	Mitophagy - yeast [PATH:ko04139]
Cellular Processes	Transport and catabolism	Autophagy - animal [PATH:ko04140]
Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum [PATH:ko04141]
Cellular Processes	Transport and catabolism	Lysosome [PATH:ko04142]
Cellular Processes	Transport and catabolism	Endocytosis [PATH:ko04144]
Cellular Processes	Transport and catabolism	Phagosome [PATH:ko04145]
Cellular Processes	Transport and catabolism	Peroxisome [PATH:ko04146]
Environmental Information Processing	Signal transduction	mTOR signaling pathway [PATH:ko04150]
Environmental Information Processing	Signal transduction	PI3K-Akt signaling pathway [PATH:ko04151]
Environmental Information Processing	Signal transduction	AMPK signaling pathway [PATH:ko04152]
Cellular Processes	Cell growth and death	Apoptosis [PATH:ko04210]
Cellular Processes	Cell growth and death	Apoptosis - fly [PATH:ko04214]
Cellular Processes	Cell growth and death	Ferroptosis [PATH:ko04216]
Cellular Processes	Cell growth and death	Necroptosis [PATH:ko04217]

Metabolism	Metabolism of other amino acids	Taurine and hypotaurine metabolism [PATH:ko00430]
Environmental Information Processing	Signal transduction	Wnt signaling pathway [PATH:ko04310]
Environmental Information Processing	Signal transduction	Notch signaling pathway [PATH:ko04330]
Environmental Information Processing	Signal transduction	Hedgehog signaling pathway [PATH:ko04340]
Environmental Information Processing	Signal transduction	Hippo signaling pathway [PATH:ko04390]
Environmental Information Processing	Signal transduction	Hippo signaling pathway - fly [PATH:ko04391]
Metabolism	Metabolism of other amino acids	Phosphonate and phosphinate metabolism [PATH:ko00440]
Metabolism	Metabolism of other amino acids	Selenocompound metabolism [PATH:ko00450]
Cellular Processes	Cellular community - eukaryotes	Focal adhesion [PATH:ko04510]
Environmental Information Processing	Signaling molecules and interaction	ECM-receptor interaction [PATH:ko04512]
Environmental Information Processing	Signaling molecules and interaction	Cell adhesion molecules (CAMs) [PATH:ko04514]
Cellular Processes	Cellular community - eukaryotes	Tight junction [PATH:ko04530]
Cellular Processes	Cellular community - eukaryotes	Signaling pathways regulating pluripotency of stem cells [PATH:ko04550]
Metabolism	Metabolism of other amino acids	Cyanoamino acid metabolism [PATH:ko00460]
Environmental Information Processing	Signal transduction	TNF signaling pathway [PATH:ko04668]
Metabolism	Metabolism of other amino acids	D-Glutamine and D-glutamate metabolism [PATH:ko00471]
Metabolism	Metabolism of other amino acids	D-Arginine and D-ornithine metabolism [PATH:ko00472]
Metabolism	Metabolism of other amino acids	D-Alanine metabolism [PATH:ko00473]
Metabolism	Metabolism of other amino acids	Glutathione metabolism [PATH:ko00480]
Metabolism	Carbohydrate metabolism	Starch and sucrose metabolism [PATH:ko00500]
Metabolism	Carbohydrate metabolism	Fructose and mannose metabolism [PATH:ko00051]
Metabolism	Glycan biosynthesis and	N-Glycan biosynthesis

	metabolism	[PATH:ko00510]
Metabolism	Glycan biosynthesis and metabolism	Other glycan degradation [PATH:ko00511]
Cellular Processes	Cellular community - prokaryotes	Biofilm formation - Vibrio cholerae [PATH:ko05111]
Metabolism	Glycan biosynthesis and metabolism	Mucin type O-glycan biosynthesis [PATH:ko00512]
Metabolism	Glycan biosynthesis and metabolism	Various types of N-glycan biosynthesis [PATH:ko00513]
Metabolism	Glycan biosynthesis and metabolism	Other types of O-glycan biosynthesis [PATH:ko00514]
Metabolism	Glycan biosynthesis and metabolism	Mannose type O-glycan biosynthesis [PATH:ko00515]
Metabolism	Carbohydrate metabolism	Galactose metabolism [PATH:ko00052]
Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism [PATH:ko00520]
Metabolism	Biosynthesis of other secondary metabolites	Streptomycin biosynthesis [PATH:ko00521]
Metabolism	Metabolism of terpenoids and polyketides	Biosynthesis of 12-, 14- and 16-membered macrolides [PATH:ko00522]
Metabolism	Metabolism of terpenoids and polyketides	Polyketide sugar unit biosynthesis [PATH:ko00523]
Metabolism	Biosynthesis of other secondary metabolites	Acarbose and validamycin biosynthesis [PATH:ko00525]
Metabolism	Carbohydrate metabolism	Ascorbate and aldarate metabolism [PATH:ko00053]
Metabolism	Glycan biosynthesis and metabolism	Glycosaminoglycan degradation [PATH:ko00531]
Metabolism	Glycan biosynthesis and metabolism	Glycosaminoglycan biosynthesis - chondroitin sulfate / dermatan sulfate [PATH:ko00532]
Metabolism	Glycan biosynthesis and metabolism	Glycosaminoglycan biosynthesis - keratan sulfate [PATH:ko00533]
Metabolism	Glycan biosynthesis and metabolism	Glycosaminoglycan biosynthesis - heparan sulfate / heparin [PATH:ko00534]
Metabolism	Glycan biosynthesis and metabolism	Lipopolysaccharide biosynthesis [PATH:ko00540]
Metabolism	Glycan biosynthesis and metabolism	Peptidoglycan biosynthesis [PATH:ko00550]
Metabolism	Lipid metabolism	Glycerolipid metabolism [PATH:ko00561]

Metabolism	Carbohydrate metabolism	Inositol phosphate metabolism [PATH:ko00562]
Metabolism	Glycan biosynthesis and metabolism	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis [PATH:ko00563]
Metabolism	Lipid metabolism	Glycerophospholipid metabolism [PATH:ko00564]
Metabolism	Lipid metabolism	Ether lipid metabolism [PATH:ko00565]
Metabolism	Lipid metabolism	Arachidonic acid metabolism [PATH:ko00590]
Metabolism	Lipid metabolism	Linoleic acid metabolism [PATH:ko00591]
Metabolism	Lipid metabolism	alpha-Linolenic acid metabolism [PATH:ko00592]
Metabolism	Lipid metabolism	Sphingolipid metabolism [PATH:ko00600]
Metabolism	Glycan biosynthesis and metabolism	Glycosphingolipid biosynthesis - lacto and neolacto series [PATH:ko00601]
Metabolism	Lipid metabolism	Fatty acid biosynthesis [PATH:ko00061]
Metabolism	Lipid metabolism	Fatty acid elongation [PATH:ko00062]
Metabolism	Carbohydrate metabolism	Pyruvate metabolism [PATH:ko00620]
Metabolism	Xenobiotics biodegradation and metabolism	Dioxin degradation [PATH:ko00621]
Metabolism	Xenobiotics biodegradation and metabolism	Xylene degradation [PATH:ko00622]
Metabolism	Xenobiotics biodegradation and metabolism	Toluene degradation [PATH:ko00623]
Metabolism	Xenobiotics biodegradation and metabolism	Polycyclic aromatic hydrocarbon degradation [PATH:ko00624]
Metabolism	Xenobiotics biodegradation and metabolism	Chloroalkane and chloroalkene degradation [PATH:ko00625]
Metabolism	Xenobiotics biodegradation and metabolism	Naphthalene degradation [PATH:ko00626]
Metabolism	Xenobiotics biodegradation and metabolism	Aminobenzoate degradation [PATH:ko00627]
Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism [PATH:ko00630]
Metabolism	Xenobiotics biodegradation and metabolism	Nitrotoluene degradation [PATH:ko00633]
Metabolism	Carbohydrate metabolism	Propanoate metabolism

		[PATH:ko00640]
Metabolism	Xenobiotics biodegradation and metabolism	Ethylbenzene degradation [PATH:ko00642]
Metabolism	Xenobiotics biodegradation and metabolism	Styrene degradation [PATH:ko00643]
Metabolism	Carbohydrate metabolism	Butanoate metabolism [PATH:ko00650]
Metabolism	Carbohydrate metabolism	C5-Branched dibasic acid metabolism [PATH:ko00660]
Metabolism	Metabolism of cofactors and vitamins	One carbon pool by folate [PATH:ko00670]
Metabolism	Energy metabolism	Methane metabolism [PATH:ko00680]
Metabolism	Lipid metabolism	Fatty acid degradation [PATH:ko00071]
Metabolism	Energy metabolism	Carbon fixation in photosynthetic organisms [PATH:ko00710]
Metabolism	Lipid metabolism	Synthesis and degradation of ketone bodies [PATH:ko00072]
Metabolism	Energy metabolism	Carbon fixation pathways in prokaryotes [PATH:ko00720]
Metabolism	Lipid metabolism	Cutin, suberine and wax biosynthesis [PATH:ko00073]
Metabolism	Metabolism of cofactors and vitamins	Thiamine metabolism [PATH:ko00730]
Metabolism	Metabolism of cofactors and vitamins	Riboflavin metabolism [PATH:ko00740]
Metabolism	Metabolism of cofactors and vitamins	Vitamin B6 metabolism [PATH:ko00750]
Metabolism	Metabolism of cofactors and vitamins	Nicotinate and nicotinamide metabolism [PATH:ko00760]
Metabolism	Metabolism of cofactors and vitamins	Pantothenate and CoA biosynthesis [PATH:ko00770]
Metabolism	Metabolism of cofactors and vitamins	Biotin metabolism [PATH:ko00780]
Metabolism	Metabolism of cofactors and vitamins	Lipoic acid metabolism [PATH:ko00785]
Metabolism	Metabolism of cofactors and vitamins	Folate biosynthesis [PATH:ko00790]
Metabolism	Xenobiotics biodegradation and metabolism	Atrazine degradation [PATH:ko00791]
Metabolism	Metabolism of cofactors and vitamins	Retinol metabolism [PATH:ko00830]
Metabolism	Metabolism of cofactors	Porphyrin and chlorophyll

	and vitamins	metabolism [PATH:ko00860]
Metabolism	Metabolism of terpenoids and polyketides	Terpenoid backbone biosynthesis [PATH:ko00900]
Metabolism	Biosynthesis of other secondary metabolites	Indole alkaloid biosynthesis [PATH:ko00901]
Metabolism	Metabolism of terpenoids and polyketides	Monoterpenoid biosynthesis [PATH:ko00902]
Metabolism	Metabolism of terpenoids and polyketides	Limonene and pinene degradation [PATH:ko00903]
Metabolism	Metabolism of terpenoids and polyketides	Diterpenoid biosynthesis [PATH:ko00904]
Metabolism	Metabolism of terpenoids and polyketides	Brassinosteroid biosynthesis [PATH:ko00905]
Metabolism	Metabolism of terpenoids and polyketides	Carotenoid biosynthesis [PATH:ko00906]
Metabolism	Metabolism of terpenoids and polyketides	Zeatin biosynthesis [PATH:ko00908]
Metabolism	Metabolism of terpenoids and polyketides	Sesquiterpenoid and triterpenoid biosynthesis [PATH:ko00909]
Metabolism	Energy metabolism	Nitrogen metabolism [PATH:ko00910]
Metabolism	Energy metabolism	Sulfur metabolism [PATH:ko00920]
Metabolism	Xenobiotics biodegradation and metabolism	Caprolactam degradation [PATH:ko00930]
Metabolism	Biosynthesis of other secondary metabolites	Phenylpropanoid biosynthesis [PATH:ko00940]
Metabolism	Biosynthesis of other secondary metabolites	Flavonoid biosynthesis [PATH:ko00941]
Metabolism	Biosynthesis of other secondary metabolites	Isoflavonoid biosynthesis [PATH:ko00943]
Metabolism	Biosynthesis of other secondary metabolites	Tropane, piperidine and pyridine alkaloid biosynthesis [PATH:ko00960]
Metabolism	Biosynthesis of other secondary metabolites	Betalain biosynthesis [PATH:ko00965]
Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis [PATH:ko00970]
Metabolism	Xenobiotics biodegradation and metabolism	Metabolism of xenobiotics by cytochrome P450 [PATH:ko00980]
Metabolism	Xenobiotics biodegradation and metabolism	Drug metabolism - cytochrome P450 [PATH:ko00982]
Metabolism	Xenobiotics biodegradation and metabolism	Drug metabolism - other enzymes [PATH:ko00983]
Metabolism	Xenobiotics biodegradation	Steroid degradation [PATH:ko00984]

Supplementary Table 2 | Categories of KO-annotated genes involved in soil C degradation, N and P cycling.

Ecosystems Functions	Microbial processes	Gene Names	Gene ID in KEGG
Carbon fixation	Reductive pentose phosphate cycle (Calvin cycle)	rbcL	K01601
	Reductive pentose phosphate cycle (Calvin cycle)	rbcS	K01602
	Reductive pentose phosphate cycle (Calvin cycle)	GAPA	K05298
	Reductive pentose phosphate cycle (Calvin cycle)	gap2	K00150
	Reductive pentose phosphate cycle (Calvin cycle)	GAPDH	K00134
	Reductive pentose phosphate cycle (Calvin cycle)	ALDO	K01623
	Reductive pentose phosphate cycle (Calvin cycle)	FBA	K01624
	Reductive pentose phosphate cycle (Calvin cycle)	FBP	K03841
	Reductive pentose phosphate cycle (Calvin cycle)	glpX	K02446
	Reductive pentose phosphate cycle (Calvin cycle)	glpX-SEBP	K11532
	Reductive pentose phosphate cycle (Calvin cycle)	fbp-SEBP	K01086
	Reductive pentose phosphate cycle (Calvin cycle)	E2.2.1.1	K00615
	Reductive pentose phosphate cycle (Calvin cycle)	rpiA	K01807
	Reductive pentose phosphate cycle (Calvin cycle)	rpiB	K01808
	Reductive citrate cycle (Arnon-Buchanan cycle)	porA	K00169
	Reductive citrate cycle (Arnon-Buchanan cycle)	porB	K00170
	Reductive citrate cycle (Arnon-Buchanan cycle)	porD	K00171
	Reductive citrate cycle (Arnon-Buchanan cycle)	porC	K00172
	Reductive citrate cycle (Arnon-Buchanan cycle)	por	K03737
	Reductive citrate cycle (Arnon-Buchanan cycle)	pps	K01007
	Reductive citrate cycle (Arnon-Buchanan cycle)	ppdK	K01006
	Reductive citrate cycle (Arnon-Buchanan cycle)	ppc	K01595
	Reductive citrate cycle (Arnon-Buchanan cycle)	pycA	K01959
	Reductive citrate cycle (Arnon-Buchanan cycle)	pycB	K01960
	Reductive citrate cycle (Arnon-Buchanan cycle)	PC	K01958
	Reductive citrate cycle (Arnon-Buchanan cycle)	mdh	K00024
	Reductive citrate cycle (Arnon-Buchanan cycle)	E4.2.1.2A	K01676
	Reductive citrate cycle (Arnon-Buchanan cycle)	E4.2.1.2B	K01679
	Reductive citrate cycle (Arnon-Buchanan cycle)	E4.2.1.2AA	K01677
	Reductive citrate cycle (Arnon-Buchanan cycle)	E4.2.1.2AB	K01678
	Reductive citrate cycle (Arnon-Buchanan cycle)	sdhA	K00239
	Reductive citrate cycle (Arnon-Buchanan cycle)	sdhB	K00240
	Reductive citrate cycle (Arnon-Buchanan cycle)	sdhC	K00241
	Reductive citrate cycle (Arnon-Buchanan cycle)	sdhD	K00242
	Reductive citrate cycle (Arnon-Buchanan cycle)	frdA	K00244
	Reductive citrate cycle (Arnon-Buchanan cycle)	frdB	K00245
	Reductive citrate cycle (Arnon-Buchanan cycle)	frdC	K00246
	Reductive citrate cycle (Arnon-Buchanan cycle)	frdD	K00247
	Reductive citrate cycle (Arnon-Buchanan cycle)	frdA	K00244
	Reductive citrate cycle (Arnon-Buchanan cycle)	frdB	K00245

Reductive citrate cycle (Arnon-Buchanan cycle)	frdC	K00246
Reductive citrate cycle (Arnon-Buchanan cycle)	frdD	K00247
Reductive citrate cycle (Arnon-Buchanan cycle)	sucD	K01902
Reductive citrate cycle (Arnon-Buchanan cycle)	sucC	K01903
Reductive citrate cycle (Arnon-Buchanan cycle)	korA	K00174
Reductive citrate cycle (Arnon-Buchanan cycle)	korB	K00175
Reductive citrate cycle (Arnon-Buchanan cycle)	korC	K00177
Reductive citrate cycle (Arnon-Buchanan cycle)	korD	K00176
Reductive citrate cycle (Arnon-Buchanan cycle)	IDH1	K00031
Reductive citrate cycle (Arnon-Buchanan cycle)	ACO	K01681
Reductive citrate cycle (Arnon-Buchanan cycle)	acnB	K01682
Reductive citrate cycle (Arnon-Buchanan cycle)	aclA	K15230
Reductive citrate cycle (Arnon-Buchanan cycle)	aclB	K15231
Reductive citrate cycle (Arnon-Buchanan cycle)	ccsA	K15232
Reductive citrate cycle (Arnon-Buchanan cycle)	ccl	K15234
3-Hydroxypropionate bi-cycle	accB	K02160
3-Hydroxypropionate bi-cycle	accC	K01961
3-Hydroxypropionate bi-cycle	accA	K01962
3-Hydroxypropionate bi-cycle	accD	K01963
3-Hydroxypropionate bi-cycle	K14469	K14469
3-Hydroxypropionate bi-cycle	K15052	K15052
3-Hydroxypropionate bi-cycle	MCEE	K05606
3-Hydroxypropionate bi-cycle	MUT	K01847
3-Hydroxypropionate bi-cycle	E5.4.99.2A	K01848
3-Hydroxypropionate bi-cycle	E5.4.99.2B	K01849
3-Hydroxypropionate bi-cycle	smtA1	K14471
3-Hydroxypropionate bi-cycle	smtB	K14472
3-Hydroxypropionate bi-cycle	sdhA	K00239
3-Hydroxypropionate bi-cycle	sdhB	K00240
3-Hydroxypropionate bi-cycle	sdhC	K00241
3-Hydroxypropionate bi-cycle	E4.2.1.2B	K01679
3-Hydroxypropionate bi-cycle	mcl	K08691
3-Hydroxypropionate bi-cycle	mch	K14449
3-Hydroxypropionate bi-cycle	mct	K14470
3-Hydroxypropionate bi-cycle	meh	K09709
Hydroxypropionate-hydroxybutylate cycle	K01964	K01964
Hydroxypropionate-hydroxybutylate cycle	K15036	K15036
Hydroxypropionate-hydroxybutylate cycle	K15019	K15019
Hydroxypropionate-hydroxybutylate cycle	K15020	K15020
Hydroxypropionate-hydroxybutylate cycle	MCEE	K05606
Hydroxypropionate-hydroxybutylate cycle	E5.4.99.2A	K01848
Hydroxypropionate-hydroxybutylate cycle	E5.4.99.2B	K01849
Hydroxypropionate-hydroxybutylate cycle	K15038	K15038
Hydroxypropionate-hydroxybutylate cycle	K14465	K14465

Hydroxypropionate-hydroxybutylate cycle	K18861	K18861
Hydroxypropionate-hydroxybutylate cycle	abfD	K14534
Hydroxypropionate-hydroxybutylate cycle	K15016	K15016
Hydroxypropionate-hydroxybutylate cycle	ACAT	K00626
Dicarboxylate-hydroxybutyrate cycle	porA	K00169
Dicarboxylate-hydroxybutyrate cycle	porB	K00170
Dicarboxylate-hydroxybutyrate cycle	porD	K00171
Dicarboxylate-hydroxybutyrate cycle	porC	K00172
Dicarboxylate-hydroxybutyrate cycle	pps	K01007
Dicarboxylate-hydroxybutyrate cycle	ppc	K01595
Dicarboxylate-hydroxybutyrate cycle	mdh	K00024
Dicarboxylate-hydroxybutyrate cycle	E4.2.1.2AA	K01677
Dicarboxylate-hydroxybutyrate cycle	E4.2.1.2AB	K01678
Dicarboxylate-hydroxybutyrate cycle	sdhA	K00239
Dicarboxylate-hydroxybutyrate cycle	sdhB	K00240
Dicarboxylate-hydroxybutyrate cycle	sdhC	K00241
Dicarboxylate-hydroxybutyrate cycle	sucD	K01902
Dicarboxylate-hydroxybutyrate cycle	sucC	K01903
Dicarboxylate-hydroxybutyrate cycle	K15038	K15038
Dicarboxylate-hydroxybutyrate cycle	K14465	K14465
Dicarboxylate-hydroxybutyrate cycle	K18861	K18861
Dicarboxylate-hydroxybutyrate cycle	abfD	K14534
Dicarboxylate-hydroxybutyrate cycle	K15016	K15016
Dicarboxylate-hydroxybutyrate cycle	ACAT	K00626
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	cooS	K00198
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	fdhA	K05299
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	fdhB	K15022
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	fhs	K01938
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	folD	K01491
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	fchA	K01500
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	metF	K00297
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	acsE	K15023
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	acsB	K14138
Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	cdhE	K00197

	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	cdhD	K00194
	Incomplete reductive citrate cycle	porA	K00169
	Incomplete reductive citrate cycle	porB	K00170
	Incomplete reductive citrate cycle	porD	K00171
	Incomplete reductive citrate cycle	porC	K00172
	Incomplete reductive citrate cycle	pycA	K01959
	Incomplete reductive citrate cycle	pycB	K01960
	Incomplete reductive citrate cycle	mdh	K00024
	Incomplete reductive citrate cycle	E4.2.1.2AA	K01677
	Incomplete reductive citrate cycle	E4.2.1.2AB	K01678
	Incomplete reductive citrate cycle	tfrA	K18209
	Incomplete reductive citrate cycle	tfrB	K18210
	Incomplete reductive citrate cycle	sucD	K01902
	Incomplete reductive citrate cycle	sucC	K01903
	Incomplete reductive citrate cycle	korA	K00174
	Incomplete reductive citrate cycle	korB	K00175
	Incomplete reductive citrate cycle	korD	K00176
	Incomplete reductive citrate cycle	korC	K00177
Carbon degradation	Cellulose	celF	K01179
	Cellulose	cbhA	K19668
	Chitin	chi	K01183
	Hemicellulose	rfbB	K01710
	Hemicellulose	xylA	K01805
	Hemicellulose	xylF	K10543
	Hemicellulose	xylH	K10544
	Pectin	pel	K01728
	Pectin	pgl	K01184
	Starch	iam	K01214
	Starch	malZ	K01187
	Starch	malQ	K00705
Carbon methane	Methane oxidation	pmoA-amoA	K10944
	Methane oxidation	pmoB-amoB	K10945
	Methane oxidation	pmoC-amoC	K10946
	Methane oxidation	mdh1, mxaF	K14028
	Methane oxidation	mmoX	K16157
	Methane oxidation	xoxF	K23995
	Methanogenesis	cdhE, acsC	K00197
	Methanogenesis	fwdA, fmdA	K00200
	Methanogenesis	fwdB, fmdB	K00201
	Methanogenesis	fwdC, fmdC	K00202
	Methanogenesis	fwdD, fmdD	K00203
	Methanogenesis	mer	K00320
	Methanogenesis	mtrA	K00577

	Methanogenesis	E2.3.1.8, pta	K00625
	Methanogenesis	ftr	K00672
	Methanogenesis	ackA	K00925
	Methanogenesis	mch	K01499
	Methanogenesis	ACSS1_2, acs	K01895
	Methanogenesis	hdrA2	K03388
	Methanogenesis	hdrB2	K03389
	Methanogenesis	hdrC2	K03390
	Methanogenesis	hdrD	K08264
	Methanogenesis	fwdE, fmdE	K11261
	Methanogenesis	mtaA	K14080
	Methanogenesis	mtbA	K14082
	Methanogenesis	mttB	K14083
	Methanogenesis	mttC	K14084
	Methanogenesis	mvhA, vhuA, vhcA	K14126
	Methanogenesis	mvhD, vhuD, vhcD	K14127
	Methanogenesis	mvhG, vhuG, vhcG	K14128
	Methanogenesis	mtmB	K16176
	Methanogenesis	fdhA	K22516
N-cycling	Nitrogen fixation	nifD	K02586
	Nitrogen fixation	nifH	K02588
	Nitrogen fixation	nifK	K02591
	Nitrification	pmoA-amoA	K10944
	Nitrification	pmoB-amoB	K10945
	Nitrification	pmoC-amoC	K10946
	Nitrification	hao	K10535
	Denitrification	nirS	K15864
	Denitrification	nirK	K00368
	Denitrification	norB	K04561
	Denitrification	norC	K02305
	Denitrification	nosZ	K00376
	Denitrification	narG/nxrA	K00370
	Denitrification	narH/nxrB	K00371
	Denitrification	narI	K00374
	Denitrification	napA	K02567
	Denitrification	napB	K02568
	Denitrification	napC	K02569
	Ammonia assimilation	gdhA	K00261
	Ammonia assimilation	gltB	K00265
	Ammonia assimilation	gltD	K00266
	Ammonia assimilation	gdhB	K00262

	Ammonia assimilation	glnA	K01915
	Ammonification	ureB	K01429
	Ammonification	ureC	K01428
	Ammonification	ureA	K01430
P-cycling	Organic P mineralization	phnX	K05306
	Organic P mineralization	phnW	K03430
	Organic P mineralization	phoA	K01077
	Organic P mineralization	phoD	K01113
	Organic P mineralization	appA	K01093
	Organic P mineralization	phnG	K06166
	Organic P mineralization	phnH	K06165
	Organic P mineralization	phnI	K06164
	Organic P mineralization	phnJ	K06163
	Organic P mineralization	phnL	K05780
	Organic P mineralization	phnM	K06162
	Organic P mineralization	phnN	K05774
	Organic P mineralization	phnP	K06167
	Organic P mineralization	phoN	K09474
	Organic P mineralization	phnA	K19670
	Inorganic P solubilization	gcd	K00117
	Inorganic P solubilization	ppa	K01507
	Inorganic P solubilization	ppx-gppA	K01524
	P-starvation response regulation	phoB	K07657
	P-starvation response regulation	phoR	K07636
	P-starvation response regulation	phoP	K07660
	P-starvation response regulation	phoU	K02039
	P-uptake and transport system	phnC	K02041
	P-uptake and transport system	phnD	K02044
	P-uptake and transport system	phnE	K02042
	P-uptake and transport system	pstA	K02038
	P-uptake and transport system	pstB	K02036
	P-uptake and transport system	pstC	K02037
	P-uptake and transport system	pstS	K02040
	P-uptake and transport system	phnK	K05781
	P-uptake and transport system	phnF	K02043
	P-uptake and transport system	TC.PIT	K03306
	P-uptake and transport system	ugpA	K05814
	P-uptake and transport system	ugpB	K05813
	P-uptake and transport system	ugpC	K05816
	P-uptake and transport system	ugpE	K05815
	P-uptake and transport system	glpQ	K01126