

Supplementary Materials

Table S1. Seasonal and habitat information of soil samples.

Soil type	Winter	Spring	Summer	Autumn	Altitude(m)	Longitude and latitude
Landscape soil	1*	17	33	49	380	29°34'5"N, 103°45'11"E
	2	18	34	50	400	29°35'2"N, 103°44'25"E
	3	19	35	51	360	29°35'11"N, 103°44'15"E
	4	20	36	52	410	29°34'24"N, 103°44'55"E
returned farmland soil	5	21	37	53	390	29°35'4"N, 103°44'25"E
	6	22	38	54	380	29°34'38"N, 103°44'24"E
	7	23	39	55	410	29°35'25"N, 103°42'42"E
Forestland soil	8	24	40	56	370	29°34'3"N, 103°44'31"E
	9	25	41	57	390	29°34'23"N, 103°45'4"E
	10	26	42	58	400	29°35'40"N, 103°43'29"E
	11	27	43	59	400	29°34'22"N, 103°44'53"E
Wetland soil	12	28	44	60	380	29°34'9"N, 103°44'36"E
	13	29	45	61	370	29°35'51"N, 103°43'33"E
	14	30	46	62	380	29°34'45"N, 103°42'41"E
	15	31	47	63	370	29°34'8"N, 103°44'37"E
	16	32	48	64	380	29°34'8"N, 103°44'7"E

* indicates the sample number, there are 64 samples in total.

Table S2. Primers and PCR conditions.

Primer	Sequence(5'-3')	Amplicon size (bp)	Annealing temperature (°C)	Reference
<i>acd320f</i>	CGGTCCAGACTCCTACGGGA	112	55	[68]
<i>acd432r</i>	GACAGGGTTTTACAGTCCGAAGA			
<i>acm342f</i>	GCAATGGGGGAAACCCCTGAC	115	58	
<i>acm439r</i>	ACCGTCAATTTTCGTCCCTGC			
<i>hzsA_1597F</i>	WTYGGKTATCARTATGTAG	260	60	[69]
<i>hzsA_1857R</i>	AAABGGYGAATCATARTGGC			
<i>Geo494F</i>	AGGAAGCACCGGCTAACTCC	331	55	[70]
<i>Geo825R</i>	TACCCGCAC ACCTAGT			
16S-1F	CGAAGGCACCAATCCATCT	233	60	[71]
16S 2R	GTAGTCCACGCCGTAAACGA			

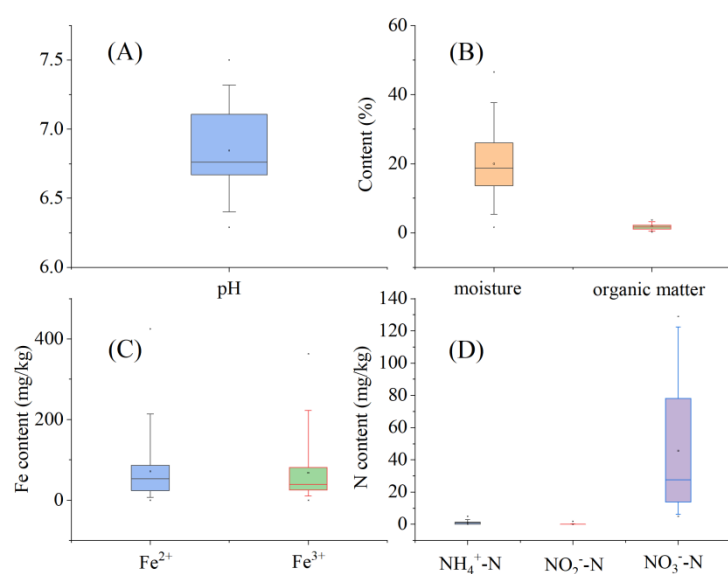


Figure S1. Box charts of soil pH (A), moisture content, OM content (B), Fe^{2+} , Fe^{3+} (C), and $\text{NH}_4^+\text{-N}$, $\text{NO}_2^-\text{-N}$, and $\text{NO}_3^-\text{-N}$ (D) of all 64 samples.

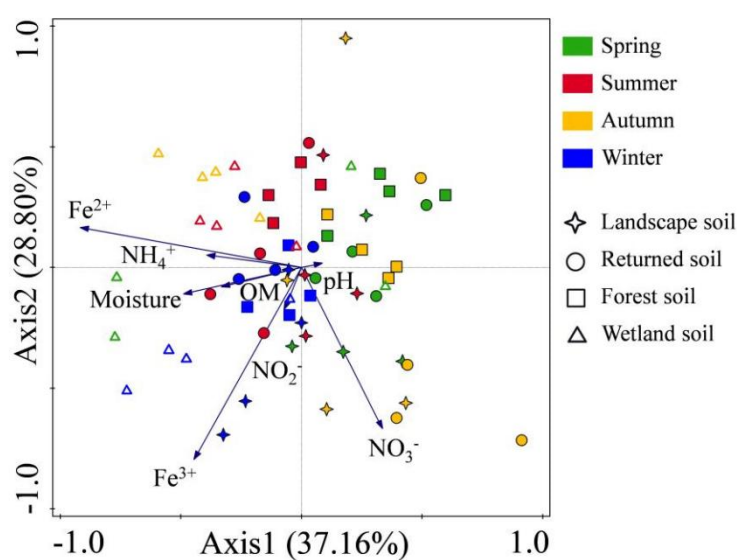


Figure S2. Principal component analysis (PCA) of soil physicochemical factors (blue hollow arrows). Note: season is distinguished by color while soil type is distinguished by shape.

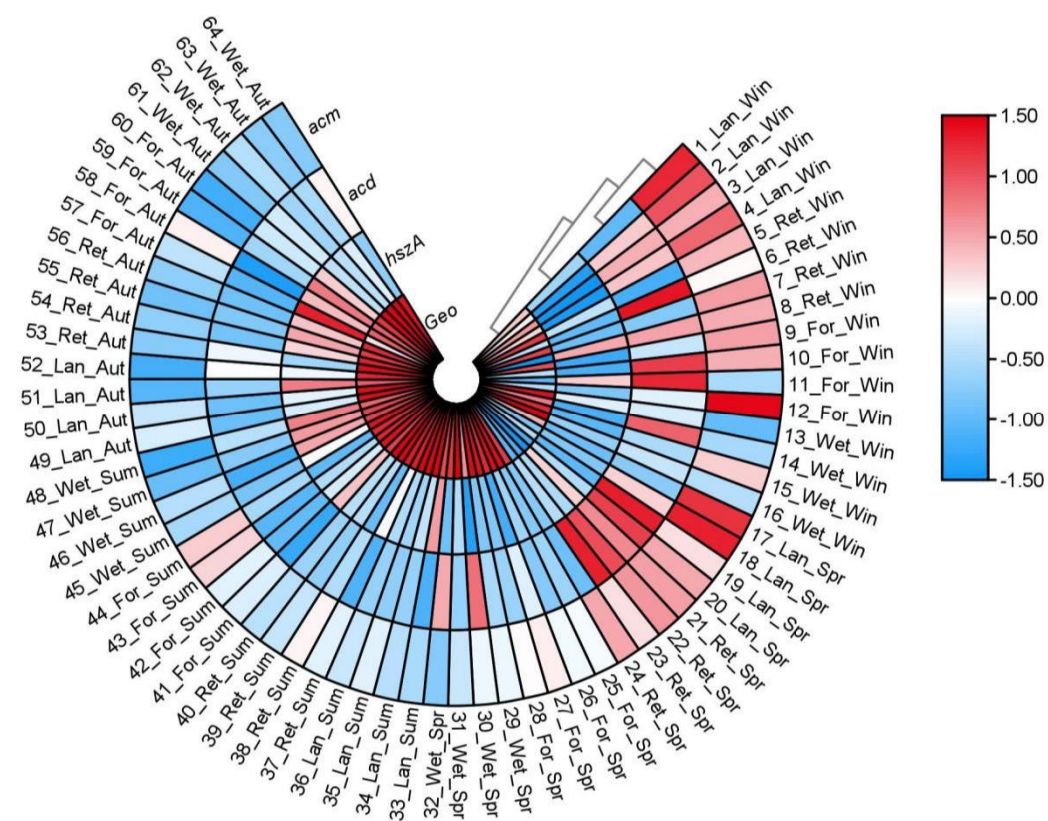


Figure S3. Heatmap of relative target gene abundance in soil samples. Note: data are presented in log10 format.

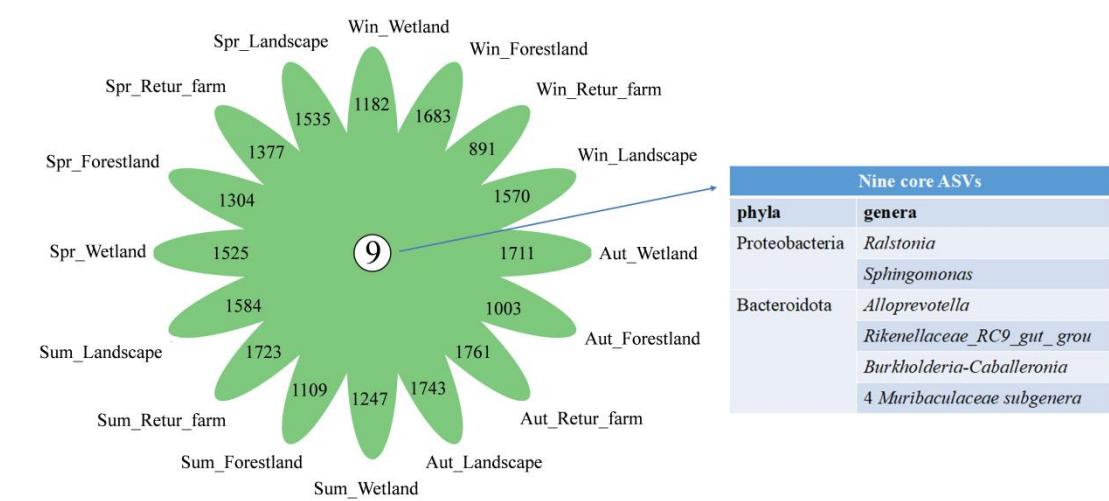


Figure S4. Flower plot of soil ASV and nine core ASVs.

Table S3. Effects of season and habitat on indices of microbial richness and biodiversity according to two-way ANOVA. Note: "+" indicates the significant influence of each factor on the indices or clear interaction between season and habitat; "-" indicates the non-significant influence of each factor on the indices or unclear interaction between season and habitat.

Factor	Chao1	Shannon	Simpson	ASV
Season	+	+	+	+
Habitat	+	+	+	+
Season–habitat interaction	+	+	+	+

Table S4. Coefficients of correlation among target genes, top 30 bacterial genera, and other putative Feammox, iron-reducing, and anammox bacteria.

Gene	Microbe	Microbe	R	p
<i>acd_re</i>	<i>Flavobacterium</i>	-	0.606	0.013
<i>acd_re</i>	<i>Thermomonas</i>	-	0.828	7.39E-05
<i>acm_re</i>	<i>RCP2-54</i>	-	-0.650	0.006
<i>Geo_re</i>	<i>Subgroup_2</i>	-	0.753	0.001
<i>Geo_re</i>	<i>Bryobacter</i>	-	0.633	0.008
<i>hszA_re</i>	<i>Candidatus_Solibacter</i>	-	0.902	1.83E-06
-	<i>Nitrospira</i>	<i>Sphingomonas</i>	-0.625	0.010
-	<i>Nitrospira</i>	<i>MND1</i>	0.638	0.008
-	<i>Dongia</i>	<i>MND1</i>	0.692	0.003
-	<i>Bryobacter</i>	<i>TRA3-20</i>	-0.643	0.007
-	<i>Subgroup_22</i>	<i>MND1</i>	0.625	0.010
-	<i>TRA3-20</i>	<i>MND1</i>	0.711	0.002
-	<i>TRA3-20</i>	<i>NB1-j</i>	0.776	4.07E-04
-	<i>Nitrospira</i>	<i>NB1-j</i>	0.650	0.006
-	<i>Subgroup_22</i>	<i>NB1-j</i>	0.954	9.87E-09
-	<i>MND1</i>	<i>Haliangium</i>	0.604	0.013
-	<i>Subgroup_22</i>	<i>Haliangium</i>	0.630	0.009
-	<i>Rhodanobacter</i>	<i>Pseudomonas</i>	0.696	0.003
-	<i>MND1</i>	<i>RCP2-54</i>	0.768	0.001
-	<i>TRA3-20</i>	<i>RCP2-54</i>	0.682	0.004
-	<i>Nitrospira</i>	<i>RCP2-54</i>	0.823	9.11E-05
-	<i>Dongia</i>	<i>RCP2-54</i>	0.678	0.004
-	<i>Subgroup_22</i>	<i>RCP2-54</i>	0.683	0.004
-	<i>NB1-j</i>	<i>RCP2-54</i>	0.770	0.000
-	<i>Sphingomonas</i>	<i>IMCC26256</i>	0.641	0.008
-	<i>Bryobacter</i>	<i>IMCC26256</i>	0.843	4.06E-05
-	<i>Arenimonas</i>	<i>Ramlibacter</i>	0.773	4.42E-04
-	<i>Massilia</i>	<i>Ramlibacter</i>	0.715	0.002

-	Subgroup_10	Ellin6055	0.690	0.003
-	Subgroup_2	Candidatus_Solibacter	0.671	0.004
-	Gemmatimonas	Candidatus_Solibacter	0.744	0.001
-	Gemmatimonas	Acidibacter	0.658	0.006
-	Candidatus_Solibacter	Acidibacter	0.712	0.002
-	Sphingomonas	OLB12	-0.651	0.006
-	Gemmatimonas	Acidimicrobiaceae family	0.681	0.004
-	Flavobacterium	Acidovorax	0.974	1.79E-10
-	OLB12	Acidovorax	0.591	0.016
-	Sphingomonas	Anaeromyxobacter	-0.660	0.005
-	OLB12	Anaeromyxobacter	0.617	0.011
-	Acidimicrobiaceae family	Bacillus	0.718	0.002
-	Bacillaceae family	Bacillus	0.777	3.98E-04
-	Gemmatimonas	Bradyrhizobium	0.663	0.005
-	Acidovorax	Clostridiaceae family	0.616	0.011
-	SC-I-84	Clostridium_sensu_stricto_1	-0.643	0.007
-	Clostridiaceae family	Clostridium_sensu_stricto_1	0.978	5.52E-11
-	Rhizobacter	Clostridium_sensu_stricto_10	0.642	0.007
-	Flavobacterium	Clostridium_sensu_stricto_12	0.839	4.95E-05
-	Acidovorax	Clostridium_sensu_stricto_12	0.778	3.84E-04
-	Flavobacterium	Crenothrix	0.810	1.41E-04
-	OLB12	Crenothrix	0.913	8.29E-07
-	Acidovorax	Crenothrix	0.834	6.04E-05
-	Anaeromyxobacter	Crenothrix	0.608	0.012
-	Clostridium_sensu_stricto_12	Crenothrix	0.710	0.002
-	Sphingomonas	Dechloromonas	-0.627	0.009
-	OLB12	Dechloromonas	0.969	6.37E-10
-	Anaeromyxobacter	Dechloromonas	0.649	0.007
-	Clostridium_sensu_stricto_12	Dechloromonas	0.503	0.047
-	Crenothrix	Dechloromonas	0.911	9.67E-07
-	Sphingomonas	Gallionellaceae family	-0.727	0.001
-	OLB12	Gallionellaceae family	0.607	0.013
-	Anaeromyxobacter	Gallionellaceae family	0.925	3.04E-07
-	Dechloromonas	Gallionellaceae family	0.652	0.006
-	Flavobacterium	Geobacter	0.771	4.71E-04
-	OLB12	Geobacter	0.926	2.67E-07
-	Acidovorax	Geobacter	0.795	2.29E-04
-	Anaeromyxobacter	Geobacter	0.645	0.007
-	Clostridium_sensu_stricto_12	Geobacter	0.671	0.004
-	Crenothrix	Geobacter	0.986	2.48E-12
-	Dechloromonas	Geobacter	0.947	2.58E-08
-	Gallionellaceae family	Geobacter	0.648	0.007

-	<i>Acinetobacter</i>	<i>Geobacteraceae</i> family	0.616	0.011
-	<i>Anaeromyxobacter</i>	<i>Geobacteraceae</i> family	0.979	4.38E-11
-	<i>Gallionellaceae</i> family	<i>Geobacteraceae</i> family	0.878	7.59E-06
-	<i>Geobacter</i>	<i>Geobacteraceae</i> family	0.525	0.037
-	<i>Dechloromonas</i>	<i>Ignavibacterium</i>	0.617	0.011
-	<i>Desulfovibrio</i>	<i>Ignavibacterium</i>	0.815	1.21E-04
-	<i>Sphingomonas</i>	<i>Methylocystis</i>	-0.663	0.005
-	<i>OLB12</i>	<i>Methylocystis</i>	0.959	4.80E-09
-	<i>Crenothrix</i>	<i>Methylocystis</i>	0.864	1.60E-05
-	<i>Dechloromonas</i>	<i>Methylocystis</i>	0.956	7.21E-09
-	<i>Gallionellaceae</i> family	<i>Methylocystis</i>	0.637	0.008
-	<i>Geobacter</i>	<i>Methylocystis</i>	0.907	1.23E-06
-	<i>Anaeromyxobacter</i>	<i>Rhodobacter</i>	0.744	0.001
-	<i>Geobacteraceae</i> family	<i>Rhodobacter</i>	0.791	2.60E-04
-	<i>Rhodanobacter</i>	<i>Rhodopseudomonas</i>	0.674	0.004
-	<i>Bradyrhizobium</i>	<i>Rhodopseudomonas</i>	0.608	0.012
-	<i>SC-I-84</i>	<i>SM1A02</i>	0.707	0.002
-	<i>Flavobacterium</i>	<i>Thermomonas</i>	0.925	2.85E-07
-	<i>Acidovorax</i>	<i>Thermomonas</i>	0.912	8.91E-07
-	<i>Clostridium_sensu_stricto_12</i>	<i>Thermomonas</i>	0.678	0.004
-	<i>Crenothrix</i>	<i>Thermomonas</i>	0.792	2.53E-04
-	<i>Geobacter</i>	<i>Thermomonas</i>	0.751	0.001
-	<i>Sphingomonas</i>	<i>Thiobacillus</i>	-0.632	0.009
-	<i>OLB12</i>	<i>Thiobacillus</i>	0.739	0.001
-	<i>Anaeromyxobacter</i>	<i>Thiobacillus</i>	0.760	0.001
-	<i>Crenothrix</i>	<i>Thiobacillus</i>	0.603	0.013
-	<i>Dechloromonas</i>	<i>Thiobacillus</i>	0.760	0.001
-	<i>Gallionellaceae</i> family	<i>Thiobacillus</i>	0.841	4.40E-05
-	<i>Geobacter</i>	<i>Thiobacillus</i>	0.686	0.003
-	<i>Geobacteraceae</i> family	<i>Thiobacillus</i>	0.699	0.003
-	<i>Ignavibacterium</i>	<i>Thiobacillus</i>	0.821	9.69E-05
-	<i>Methylocystis</i>	<i>Thiobacillus</i>	0.783	3.40E-04