Supplementary material:

Detailed calculation formulas for the potential DRs, DNRARs and NFRs.

(1) The formula for calculating the potential DR is as follows:

$$DR = D_{29} + 2 \times P_{30} \quad (1)$$

$$D_{29} = P_{30} \times 2 \times (1 - F_n) \times F_n^{-1} \quad (2)$$

where DR (μmol N kg^{-1} h^{-1}) is the potential rate of denitrification; D_{29} (μmol N kg^{-1} h^{-1}) is the rate of $^{29}N_2$ generation during denitrification; P_{30} (μmol N kg^{-1} h^{-1}) is the total production rate of $^{30}N_2$ measured in the slurry cultivation experiment; and Fn (%) represents ^{15}N in NO_3^-, calculated by the concentration of $^{15}NO_3^-$ added at the beginning of the slurry experiment and the concentration of residual NO_3^- measured at the end of the experiment.

(2) The calculation formula of the potential DNRAR is as follows:

$$DNRAR = (M_f - M_i) \times V \times W^{-1} \times T^{-1} \quad (3)$$

where DNRAR (μmol N kg^{-1} h^{-1}) is the potential rate of DNRA; M_i and M_f (μmol NL^{-1}) are the initial and final concentrations of $^{15}NH_4^+$-N in the sample bottles, respectively; V (L) is the volume of the slurry; W (g) is the dry weight of the sediment in the sample bottle; and T (h) is the culture time.

(3) The formula for calculating the potential NFR is as follows:

$$NFR = (C_i - C_f) \times V \times W^{-1} \times T^{-1} \quad (3)$$

where NFR (μmol N kg^{-1} h^{-1}) is the nitrogen fixation rate; C_i and C_f are the initial and final concentrations, respectively, of ^{15}N-labeled substances in the sample bottles (μmol NL^{-1}); V (L) is the volume of cultivation slurry; W (g) is the dry weight of the sediment in the sample bottle; and T (h) is the culture time.

Table S1. Physical and chemical properties of water around roots.

Type of ditch	T-W (℃)	DO-W (mg/L)	pH-W	ORP-W (mV)	TN-W(mg/L)	NH_4^+-W(mg/L)	NO_3^--W(mg/L)
A-Phr	29.13±0.66ab	5.88±0.68b	7.57±0.51a	206.36±11.25a	1.58±0.06b	0.69±0.06c	0.66±0.13a
A-Typ	27.80±1.08b	7.50±0.51a	7.53±0.37a	207.95±9.24a	1.66±0.08b	0.76±0.07bc	0.47±0.05b
N-Phr	30.80±1.19a	2.58±0.25c	7.35±0.15a	107.45±9.63c	1.86±0.12a	0.93±0.08b	0.74±0.13a
N-Typ	27.49±1.54b	6.51±0.59ab	7.50±0.34a	152.97±18.04b	2.03±0.14a	1.11±0.16a	0.63±0.05ab

A-Phr, artificially cultivated ditch with *P. australis* rhizosphere sediment; A-Typ, artificially cultivated ditch with *T. orientalis* rhizosphere sediment; N-Phr, natural ditch with *P. australis* rhizosphere sediment; N-Typ, natural ditch with *T. orientalis* rhizosphere sediment.

T-W is the temperature in water; DO-W is the dissolved oxygen in water; pH-W is the pH value in water; ORP-W is the oxidation–reduction potential in water; TN-W is the total nitrogen in water; NH_4^+-W is the ammonium nitrogen in water; and NO_3-W is the nitrate nitrogen in water.

The different lowercase letters indicate significant differences among the different rhizosphere sediment samples (p<0.05) according to one-way ANOVA and LSD. The values are the means ± SDs (n=3).

Table S2. Physical and chemical properties of all sediment samples (n = 3).

Type of ditch	EC (μs/cm)	TOC (g/kg)	DOC (g/kg)	TN (g/kg)	NH_4^+-N (mg/kg)	NO_3^--N (mg/kg)	C/N	DOC/NO_3^--N	Sand (wt, %)	Clay (wt, %)
A-Phr	428±39b	7.77±0.58a	0.035±0.004a	0.76±0.09b	2.90±0.08a	0.54±0.16b	10.27±0.84a	0.067±0.016a	37±8ab	28±13ab
A-Typ	424±35b	8.20±0.88a	0.027±0.002b	1.01±0.12a	1.97±0.26b	0.93±0.12a	8.13±0.16b	0.029±0.004b	29±16b	32±12a
N-Phr	270±37c	3.84±0.26b	0.036±0.002a	0.43±0.06c	2.09±0.04b	0.70±0.03b	9.02±1.13ab	0.052±0.004a	58±14a	11±4b
N-Typ	518±19a	8.08±0.64a	0.033±0.002a	0.95±0.08a	1.35±0.18c	1.03±0.13a	8.57±1.34ab	0.033±0.006b	33±07b	31±5a

A-Phr, artificially cultivated ditch with *P. australis* rhizosphere sediment; A-Typ, artificially cultivated ditch with *T. orientalis* rhizosphere sediment; N-Phr, natural ditch with *P. australis* rhizosphere sediment; N-Typ, natural ditch with *T. orientalis* rhizosphere sediment.

EC is the electrical conductivity of the sediments, TOC is the total organic carbon in the sediments, DOC is the dissolved organic carbon in the sediments, TN is the total nitrogen in the sediments, NH_4^+-N is the ammonium nitrogen in the sediments, NO_3^--N is the nitrate nitrogen in the sediments, C/N is the ratio of organic carbon to total nitrogen in the sediments, DOC/NO_3^--N is the ratio of dissolved organic carbon to nitrate nitrogen in the sediments, Sand is the sand content (the sediment particle size fraction is 2~0.02 mm) in the sediments, and Clay is the clay content (the sediment particle size fraction is <0.002 mm) in the sediments.

Table S3. RDA single environmental factor difference significance (envfit test).

Environmental factor	**R^2**	***p*-value**	**Environmental factor**	**R^2**	***p*-value**
Alpha diversity index (Figure 5a)			The nitrogen cycling pathways (Figure 5d)		
ORP-W	0.734	0.007	NH_4^+-N	0.9199	0.001
NH_4^+-N	0.554	0.032	DOC/NO_3^--N	0.8692	0.001
TOC	0.544	0.033	NO_3^--N	0.7734	0.002
EC	0.487	0.051	DOC	0.744	0.003
The phylum level of bacteria (Figure 5b)			ORP-W	0.7308	0.008
DOC	0.6708	0.007	DO-W	0.5305	0.034
TN	0.6238	0.019	Nitrogen conversion rates (Figure 5e)		
TOC	0.6206	0.012	NO_3^--N	0.8683	0.002
Sand	0.6018	0.011	DOC/NO_3^--N	0.7775	0.001
DO-W	0.5629	0.033	nrfC	0.7635	0.005
EC	0.5305	0.035	nrfA	0.7007	0.007
Clay	0.5291	0.037	DOC	0.6924	0.005
The genus level of bacteria (Figure 5c)			NH_4^+-N	0.6567	0.009
NH_4^+-N	0.953	0.001	nosZ	0.5993	0.018
DOC	0.7771	0.001	norB	0.5796	0.027
DOC/NO_3^--N	0.7724	0.001	TN	0.572	0.021
NO_3^--N	0.759	0.003	nirK	0.5613	0.031
ORP-W	0.6915	0.01	TOC	0.5364	0.026
DO-W	0.5958	0.019			
TN	0.5779	0.022			

Table S4. Pearson's correlation coefficients between the relative abundances of major functional genes involved in nitrogen cycling pathways and environmental factors. * significant at p <0.05; ** significant at p <0.01.

Nitrogen cycling pathways	Gene name	DO-W	ORP-W	EC	TOC	DOC	TN	NH_4^+-N	NO_3^--N	DOC/NO_3^--N
Denitrification	napA	0.180	0.430	0.170	0.150	0.400	-0.050	0.490	-0.520	0.628*
	norB	-0.460	0.070	-0.688*	-0.480	0.250	-0.597*	0.832**	-0.823**	0.711**
	nirK	-0.760**	-0.956**	-0.400	-0.708**	0.588*	-0.626*	-0.410	0.070	0.040
	nosZ	-0.858**	-0.897**	-0.560	-0.831**	0.720**	-0.781**	-0.170	-0.180	0.240
	nirS	-0.867**	-0.784**	-0.814**	-0.919**	0.550	-0.847**	-0.080	-0.230	0.150
Dissimilatory nitrate reduction	nrfC	-0.440	0.080	-0.440	-0.320	0.380	-0.520	0.857**	-0.885**	0.876**
	nrfA	-0.550	-0.100	-0.360	-0.350	0.662*	-0.634*	0.782**	-0.831**	0.886**
Nitrogen fixation	nifD	0.638*	0.825**	0.140	0.510	-0.705*	0.520	0.350	-0.030	-0.150
	nifK	0.637*	0.824**	0.140	0.510	-0.713**	0.520	0.330	0.000	-0.180
	nifH	0.638*	0.816**	0.130	0.500	-0.714**	0.510	0.320	0.000	-0.180
Nitrification	hao	-0.050	0.380	-0.040	0.060	0.350	-0.210	0.867**	-0.790**	0.847**
Anammox	hzsA	0.080	0.490	0.050	0.240	-0.110	0.030	0.858**	-0.767**	0.753**
	hzsC	0.080	0.500	0.130	0.250	0.240	-0.050	0.836**	-0.729**	0.789**

Table S5. Pearson's correlation coefficient between critical nitrogen conversion rates, environmental factors and the relative abundance of genes involved in nitrogen cycling pathways. * significant at p <0.05; ** significant at p <0.01.

Factor	**Gene name**	**DR**	**DNRAR**	**NFR**
Denitrification pathways		0.718**	0.380	-0.705*
Denitrification	napA	0.540	0.691*	-0.140
	norB	0.743**	0.693*	-0.050
	nirK	0.320	-0.020	-0.725**
	nosZ	0.570	0.240	-0.725**
	nirS	0.560	0.240	-0.500
Dissimilatory nitrate reductionpathways		0.800**	0.751**	-0.150
Dissimilatory nitrate reduction	nrfC	0.840**	0.824**	-0.110
	nrfA	0.862**	0.755**	-0.200
Nitrogen fixationpathways		-0.380	-0.110	0.697*
Nitrogen fixation	nifD	-0.370	-0.090	0.701*
	nifK	-0.380	-0.110	0.701*
	nifH	-0.380	-0.120	0.683*
DO-W		-0.693*	-0.350	0.480
ORP-W		-0.280	0.080	0.690*
NO_3^--W		0.729**	0.410	-0.550
EC		-0.610*	-0.330	0.360
TOC		-0.640*	-0.340	0.631*
DOC		0.716**	0.510	-0.694*
TN		-0.792**	-0.460	0.530
NH_4^+-N		0.589*	0.658*	0.290
NO_3^--N		-0.813**	-0.888**	-0.020
DOC/NO_3^--N		0.809**	0.871**	-0.140
Sand		0.644*	0.520	-0.570
Clay		-0.646*	-0.500	0.460

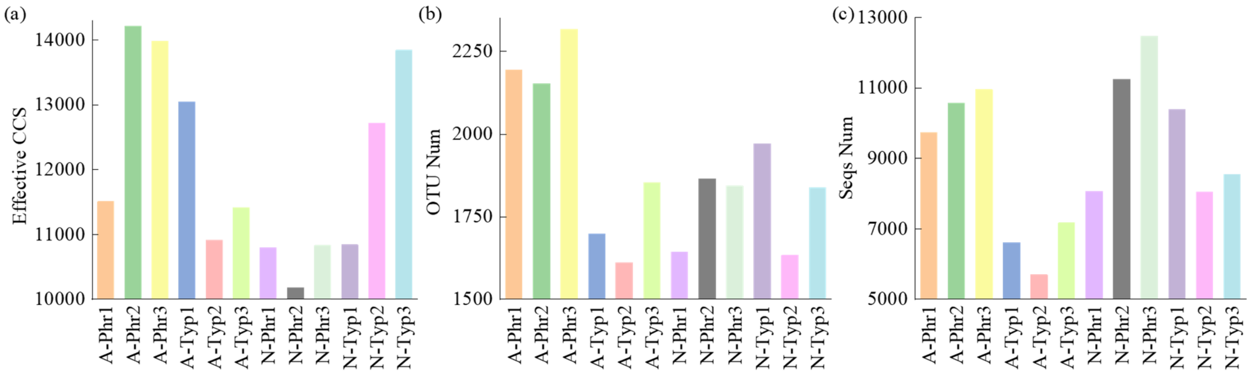

Figure S1. Number of high-quality sequences (Effective-CCS (**a**)), the number of features (OUT Num (**b**)) and the number of reads corresponding to the feature (Seq num (**c**)) obtained through 16S rRNA sequencing.