Supplementary Materials

Measurement of soil properties

Soil properties, including soil pH, cation exchange capacity (CEC), and dissolved organic carbon (DOC), were measured in all soil samples. Soil pH was detected with a glass electrode in the soil with a water-to-soil ratio of 2.5:1 (Thermo Orion-868, MA, USA). CEC was measured using $BaCl_2$ extraction method (ISO11260 1994). DOC was measured in solutions obtained after extraction with borate buffer (pH = 7) using a soil sample to extractant ratio of 1:10 for 1 h and assayed with a total organic carbon (TOC) autoanalyzer (Analytik Jena, Germany). All soil geochemical data and paddy soil attributes in four climatic zones are available in the repository Figshare (https://doi.org/10.6084/m9.figshare.11493081.v2).

The N_2O emission potential and its temperature sensitivity

Microcosms were constructed by inoculating 20 g fresh soil in a 250 mL flask. Each soil group which in the sealed flasks were then acclimated under these five temperatures 1 day for pre-incubation. After incubation, 2 mL NH_4NO_3 solution (0.00714 mol/L) was applied uniformly to each sample over the soil surface, followed by in an equivalent addition of 10 mg NH_4^+-N and 10 mg NO_3^--N per kg soil. This resulted in a total amount of 0.2 mg NH_4^+-N and 0.2 mg NO_3^--N content in these microcosms. The final soil moisture contents were adjusted to 60% water holding capacity with deionized water. Then, all the flasks of soil samples were sealed and subsequently incubated at the respective temperature in the dark for an additional 9 days. During incubation, the samples were aerated for 5 min each day to maintain an aerobic condition inside the

flasks, and the soil moisture content was maintained by adding deionized water every 3 days to compensate for the water loss through evaporation. The emission rates of N_2O were measured 1, 2, 5, and 9 days after ammonium nitrate solution application. For each sampling time, a 20 mL gas sample was collected from each flask (after the flasks were sealed with a butyl rubber stopper for 0 and 4 hour) using a gas-tight syringe and transferred to a 50 mL evacuated gas-tight vial for N_2O analysis via gas chromatography. The concentration of N_2O was determined by using of a 3 m (2 mm inner diameter) stainless steel column. packed with Porapak Q (80/100 mesh), and an Agilent 7890 gas chromatograph fitted with an electron captured etector set at 300 °C. The column temperature was maintained at 40 °C and the carrier gas was argon–methane (5 %) at a flow rate of 30 mL min^{-1}.

The N_2O emission rate was calculated by the following equation:

$$F = \rho \times \Delta C \times V \times \frac{273}{(273 + T) \times W} \qquad (Eq.1)$$

Where F represents the flux of N_2O (μg N/(kg·day)); ρ is the density of N_2O-N under standard state (g/L); ΔC (ppbV/day or ppmV/day) represents the change of gas concentration after 4-hour incubation; V (mL) is the gas space volume of conical flasks used in present experiment; T (°C) is the incubation temperature, and W (kg) represents the dry weight of soil. For N_2O emission potential, we regarded the soil samples that incubated at 25 °C (the optimal condition of denitrification) during experiment and calculated the N_2O emission rate. For the temperature sensitivity of N_2O emission, the N_2O emission rates (F) were calculated under 5 temperatures (8, 15, 20, 25, and 35 °C) and then calculated the coefficient of variation (CV).

The CV was calculated by the following equation:

$$CV = \frac{\sigma}{\mu} \qquad (Eq.2)$$

Where σ represents the standard deviation and the μ represents the means of the N_2O emission rates.

Gene amplicon sequencing

Soil microbial communities were analyzed by amplicon sequencing of archaea (16S 1106F-1378R) (Dubey et al., 2014), bacteria (16S 515F-806R) (Caporaso et al., 2012), fungi (ITS2) (Ihrmark et al., 2012), algae and micro-fauna (18S C4) (Stoeck et al., 2010), respectively. Both forward and reverse primers were tagged with adapter, pad and linker sequences. The barcode sequence (12 mer) was added to reverse primer for pooling multiple samples in one run of MiSep sequencing. All primers were synthesized by Invitrogen (Carlsbad, CA, USA). PCR amplification was performed in triplicate using a Gene Amp PCR-System 9700 (Applied Biosystems, Foster City, CA, USA) in a total volume of 25 μL containing 2.5 μL 10 × PCR bufferIIand 0.5 unit of AccuPrime Taq DNA Polymerase High Fidelity (Invitrogen, Carlsbad, CA, USA), 0.4 μM of each primer, 10 ng template DNA. To target the bacterial 16S rRNA genes, the first step PCR was carried out by primers without the barcode by cycling conditions of initial denaturation at 94 °C for 1 min, and 10 cycles at 94 °C for 20 sec, 53 °C for 25 sec, and 68 °C for 45 sec, with a final extension at 68 °C for 10 min. To target the archaeal 16S rRNA genes, PCR was carried out in the same reaction as that for the 16S rRNA gene fragments, and the samples were subjected to 35 cycles of 95 °C for 45 s, 56 °C for 45 s, and 72 °C for 60 s, followed by a final extension at 72 °C for 7 min. For the ITS2 rRNA

gene, initial denaturation was at 98°C for 30 s, 32 cycles at 98°C for 10 s, 56°C for 20 s and 72°C for 30 s, with a final extension at 72°C for 8 min. For the 18S rRNA gene, initialization was at 95°C for 5 min, 30 cycles at 94°C for 30 s, 47°C for 45 s and 72°C for 1 min, with a final extension at 72°C for 5 min. The PCR products from three replicates were combined and purified using an Agencourt AMPure XP kit (Beckman Coulter, Brea, CA, USA) following the manufacturer's instructions and eluted in 50 μL deionized water. We used the purified PCR product (15 μL) as the template for the second step PCR amplification through barcoded primers in three technical replicates under the same cycling conditions as the first step except an extension of 10 cycles. PCR products were examined from the second step by electrophoresis with 1% agarose gel. Amplification products of three technical replicates were then combined and quantified by PicoGreen using a FLUOstar Optima (BMG Labtech, Jena, Germany). PCR products were pooled from different samples together with an equal amount and purified through QIAGEN Gel Extraction Kit (QIAGEN Sciences, Germantown, MD, USA) following the manufacturer’s instruction and re-quantified by PicoGreen. According to MiSeqTM Reagent Kit Preparation Guide (Illumina, San Diego, CA, USA), the purified mixture was diluted and denatured to obtain 8 pM sample DNA library, and mixed with an equal volume of 8 pM PhiX (Illumina, San Diego, CA, USA). Finally, 600 μL of mixture library was loaded with read 1, read 2 and index sequencing primers (Caporaso et al., 2012) on a 300-cycle (2 × 150 paired ends) kit, and run on a MiSeq at the Institute for Environmental Genomics of the University of Oklahoma.

After assigning the sequence to its sample in terms of the barcode, the sequences

were then trimmed using Btrim with threshold of quality scores higher than 20 over a 5 bp window size and a minimum length of 100 bp (Kong, 2011), and pair-end reads were merged into longer reads by FLASH (Magoč & Salzberg, 2011). Unqualified sequences were removed using the following criteria: (*i*) Phred quality score Q < 20, (*ii*) reads that shorter than 200 bp, and (*iii*) reads containing ambiguous residues.. Chimeric sequences were discarded based on the prediction by UPARSE (Edgar, 2013). OTUs were clustered at the 97% similarity level. Final OTUs were generated based on the clustering results, and taxonomic annotations were assigned to each OTU's representative sequence by RDP's Classifier (for 16S rRNA gene, http://rdp.cme.msu.edu/), Unite v6 (for ITS rRNA gene, http://unite.ut.ee/index.php) and PR2 (for 18S rRNA gene, https://pr2-database.org/) database. Each sample was rarefied at 20,000 sequences for the bacterial 16S rRNA gene, 36,984 sequences for archaeal 16S rRNA gene, 10,000 sequences for ITS rRNA gene, and 20,000 sequences for 18S rRNA gene.

Network construction

Network analyses were conducted to explore the co-occurrence patterns of microbiomes in paddy soils across four climatic zones based on OTU relative abundances at each field. The relative abundances were calculated as the number of individuals of the total number of archaeal, bacteria, fungal, algal, and micro-faunal sequences, respectively. Covariations were measured across 11 biological replicates of each network to structure a total of 39 networks. Those OTUs which detected more than 4 out of 11 replicate samples were employed for network construction. The Spearman's

correlation between two OTUs was estimated using R (version 3.6.0; http://www.r-project.org/). Robust correlations were defined as those with Spearman's correlation coefficients > 0.5 and FDR-corrected *P*-values < 0.01. All significant correlations identified here from a pairwise comparison of OTU abundance formed a correlation network.

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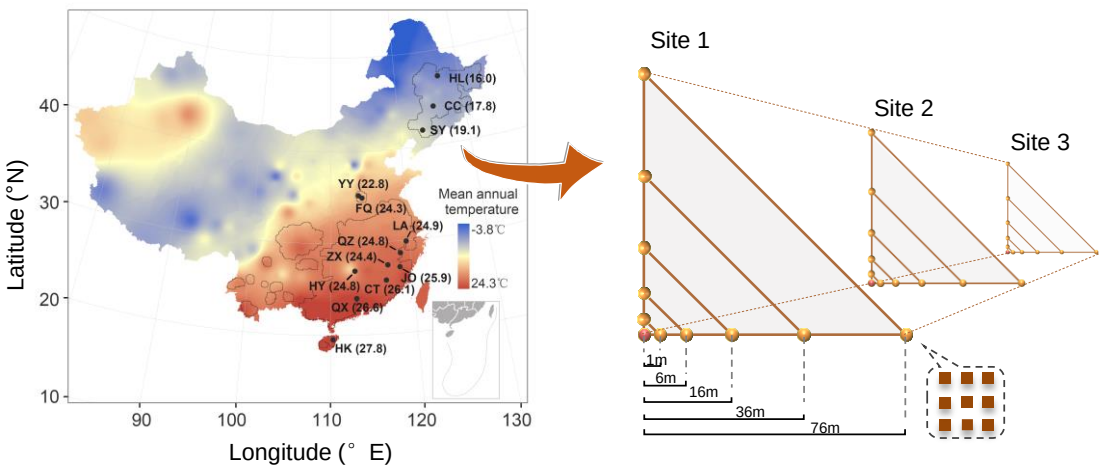


Fig. S1 Sampling locations and strategy. Paddy soil samples were taken from 39 paddy soil sites located in 13 regions of China. Number in parentheses represents mean temperature during the growing season of rice plants (℃) in sampling region. Mid-temperate zone includes 3 regions, that is Hailun (HL), Chuangchun (CC), and Shenyang (SY). Warm-temperate zone includes 2 regions, that is Yuanyang (YY) and Fengqiu (FQ). Subtropical zone includes 7 regions, that is Lin'an (LA), Quzhou (QZ), Zixi (ZX), Jian'ou (JO), Changting (CT), Hengyang (HY), and Qingxin (QX). Tropical zone includes 1 region, that is Haikou (HK). At each site, 11 nested samples were collected at distances of 1, 6, 16, 36 and 76 m.

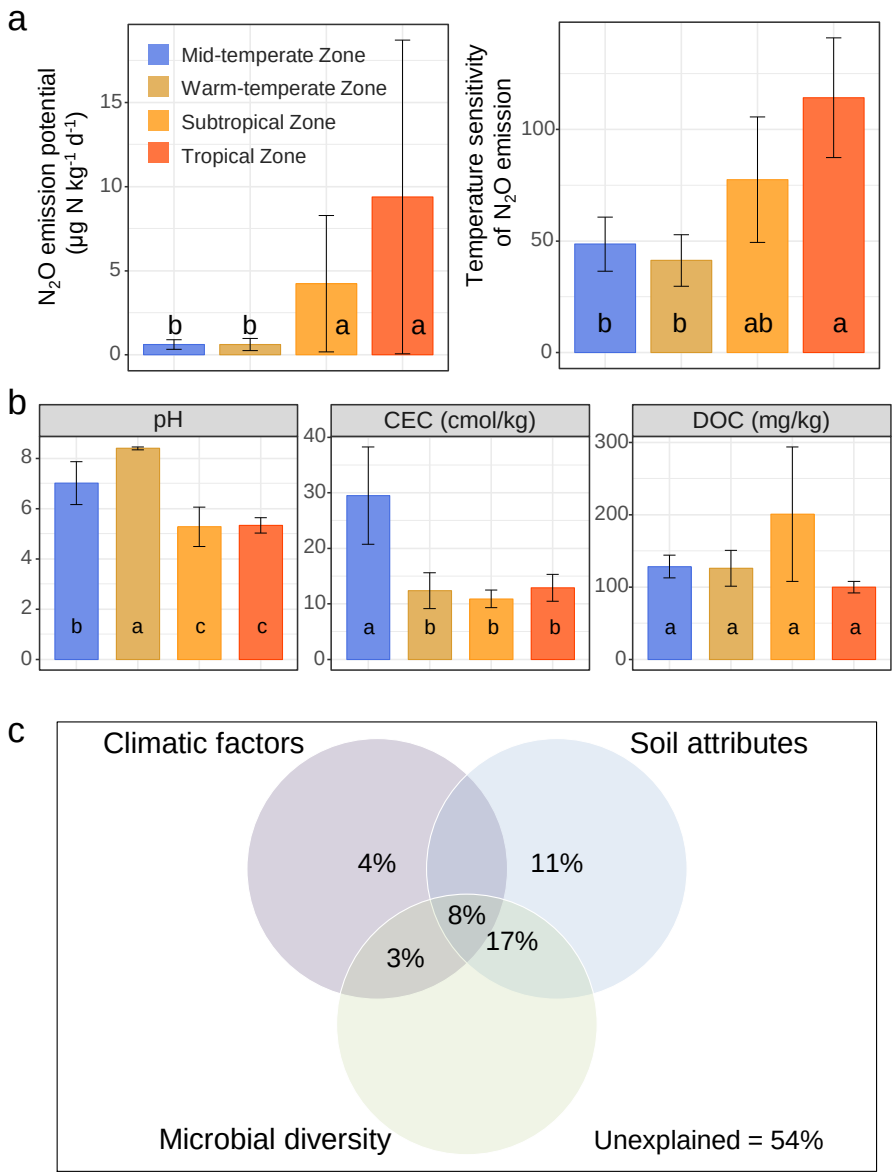


Fig. S2 (a) The N_2O emission potential and the temperature sensitivity, (b) soil attributes of the rice paddies in mid-temperate, warm-temperate, subtropical, and tropical zones; (c) Variation partitioning analysis of the N_2O emissions and its temperature sensitivity explained by climatic factors, soil attributes, and microbial diversity. Different letters in the panel (a) and (b) indicate significant differences among climatic zones ($p < 0.05$, ANOVA, Tukey HSD). CEC = cation exchange capacity; DOC = dissolved organic carbon. Climatic factors included mean annual temperature and precipitation. Soil attributes included soil pH, CEC, and dissolved organic carbon. The percentage numbers in panel (c) indicated the contributions of different variables to the variation of N_2O emission and its temperature sensitivity quantified by variance partitioning analysis.

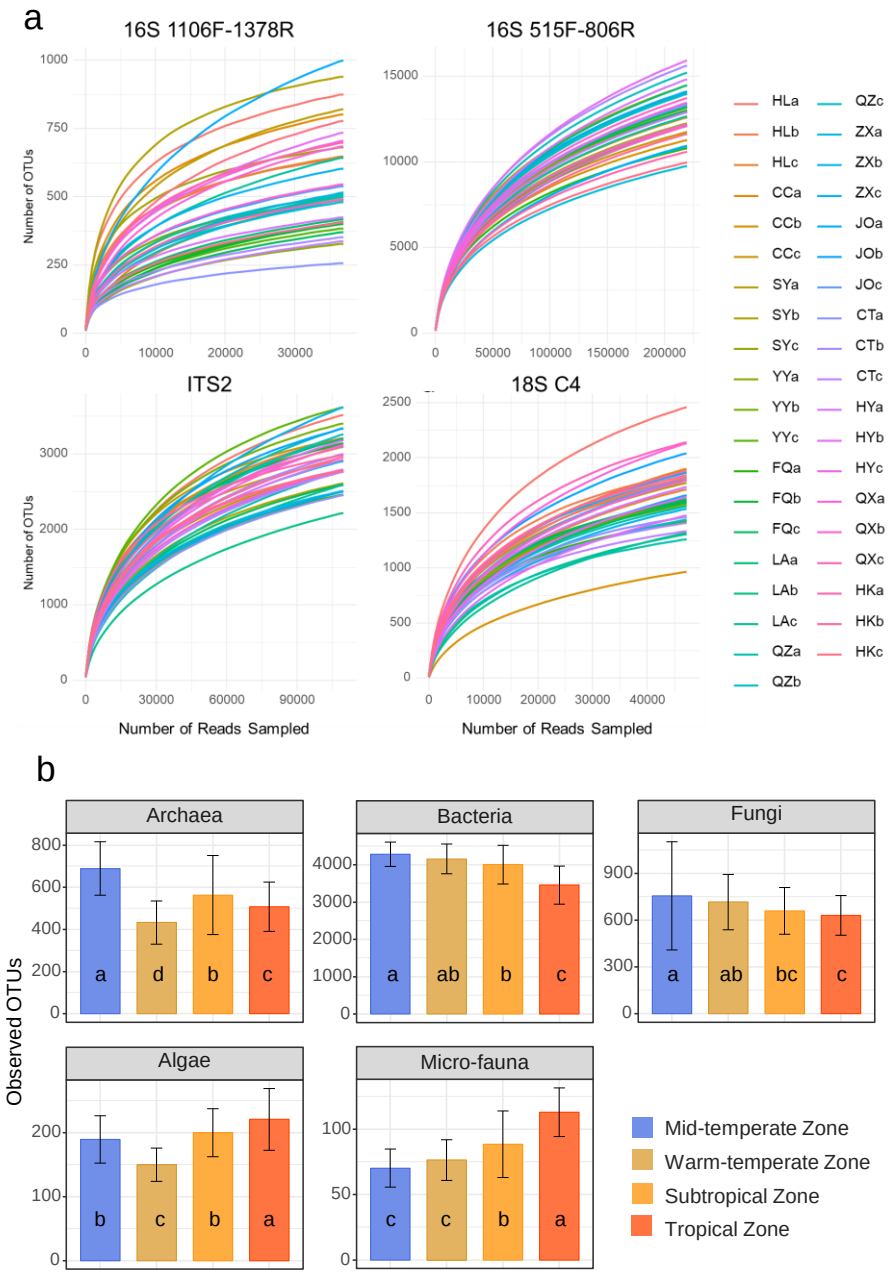
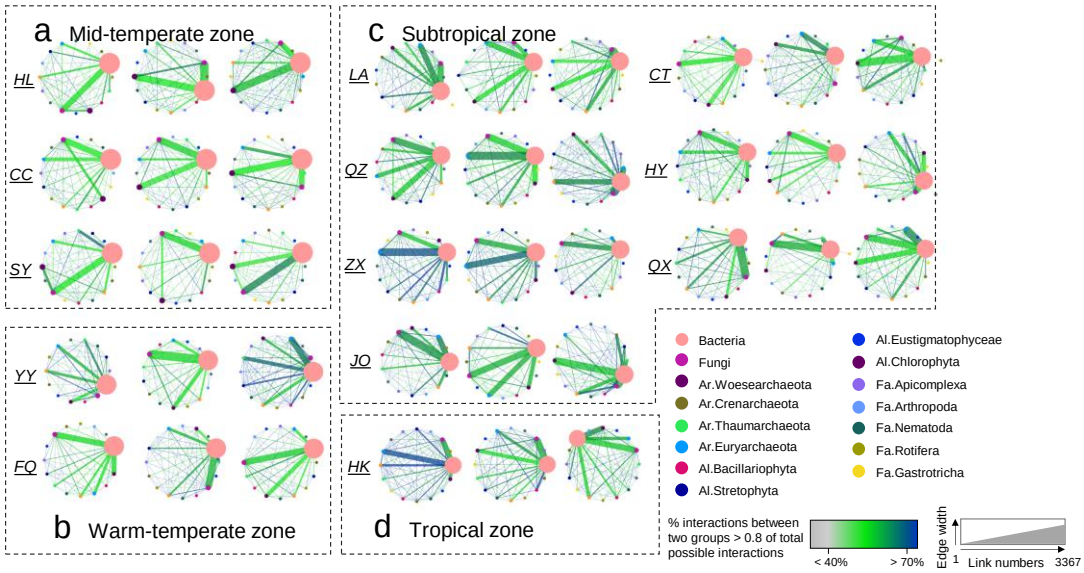


Fig. S3 Rarefaction curves for archaea (16S 1106F-1378R), bacteria (16S 515F-806R), fungi (ITS2), and algae and micro-fauna (18S C4); and the observed OTUs of soil microbiome (archaea, bacteria, fungi, algae, and micro-fauna) of the rice paddies in mid-temperate, warm-temperate, subtropical, and tropical zones. Different letters in the panel indicate significant differences among different climatic zones ($p < 0.05$, ANOVA, Tukey HSD).



e

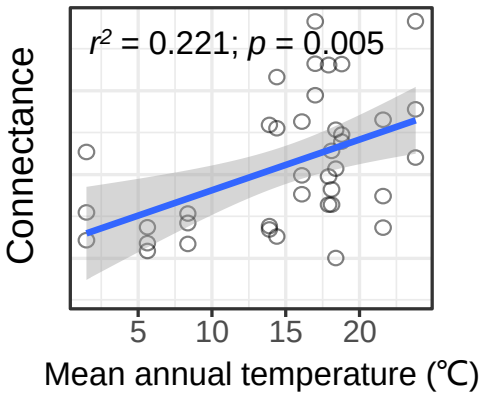
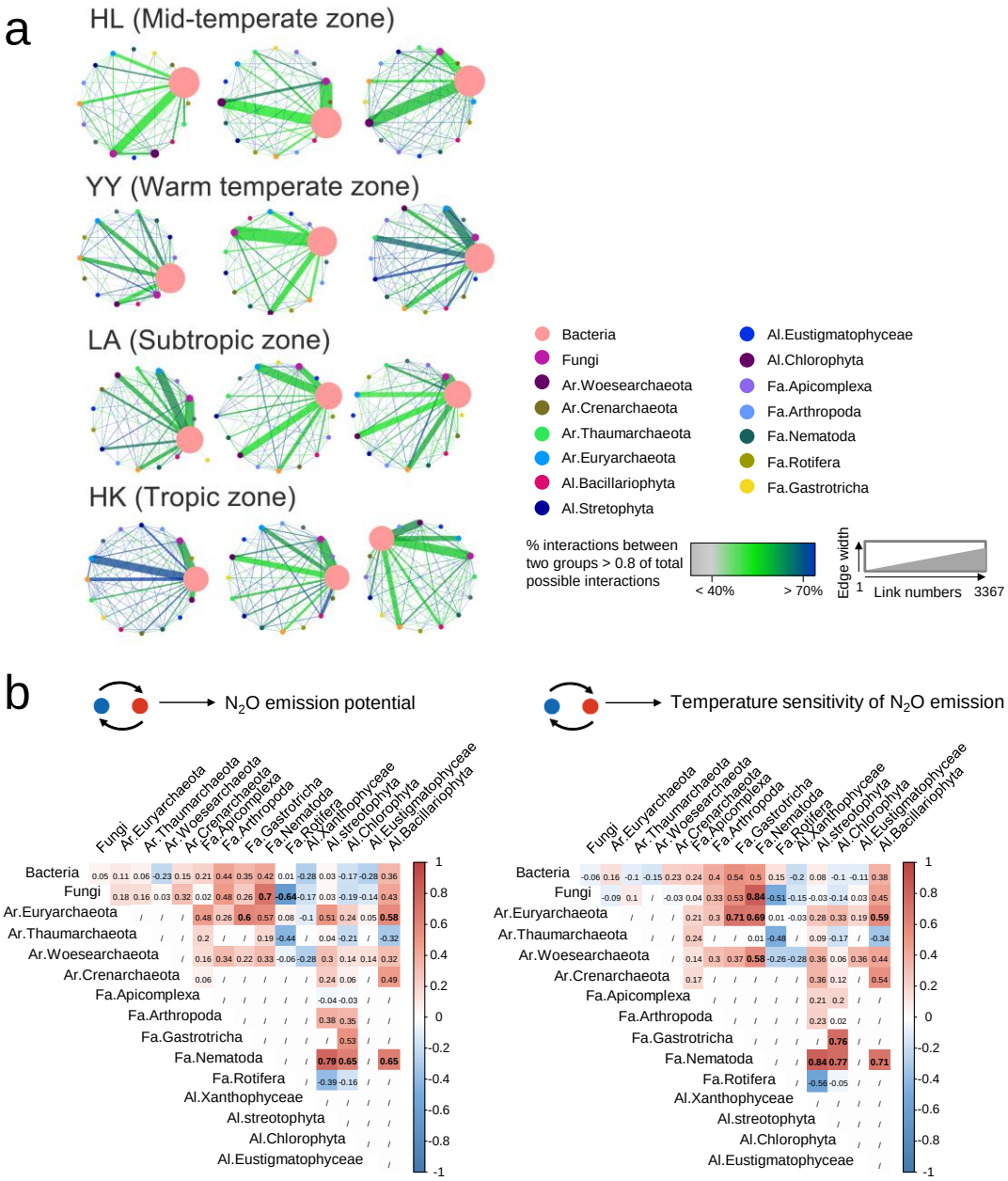


Fig. S4 Network visualization of the interaction strengths between the main microbial groups in 39 paddy soils located in four climatic zones (a-d); The percentage connectance of networks changes with mean annual temperature (e). Main microbial groups were aggregated by taxonomical classification at the kingdom (bacteria and fungi) or phylum level (archaea and eukaryota). Line width is proportional to the absolute number of correlations > 0.8, which was divided by the total number of possible interactions to obtain the interaction strength between two groups of species. Line color and transparency are proportional to the interaction strength, as indicated in the legend in the figure. The size of the circles is proportional to the number of species in that group. The connectance of networks in e was calculated by the proportion of correlations > 0.8 divided by the total number of possible interactions. Ar = archaea; Fa = micro-fauna; Al = algae.


a
HL (Mid-temperate zone)
YY (Warm temperate zone)
LA (Subtropic zone)
HK (Tropic zone)
Bacteria
Fungi
Ar.Woesearchaeota
Ar.Crenarchaeota
Ar.Thaumarchaeota
Ar.Euryarchaeota
Al.Bacillariophyta
Al.Stretophyta
Al.Eustigmatophyceae
Al.Chlorophyta
Fa.Apicomplexa
Fa.Arthropoda
Fa.Nematoda
Fa.Rotifera
Fa.Gastrotricha
% interactions between two groups > 0.8 of total possible interactions
< 40%
> 70%
Edge width
1
Link numbers
3367
b
N2O emission potential
Temperature sensitivity of N2O emission

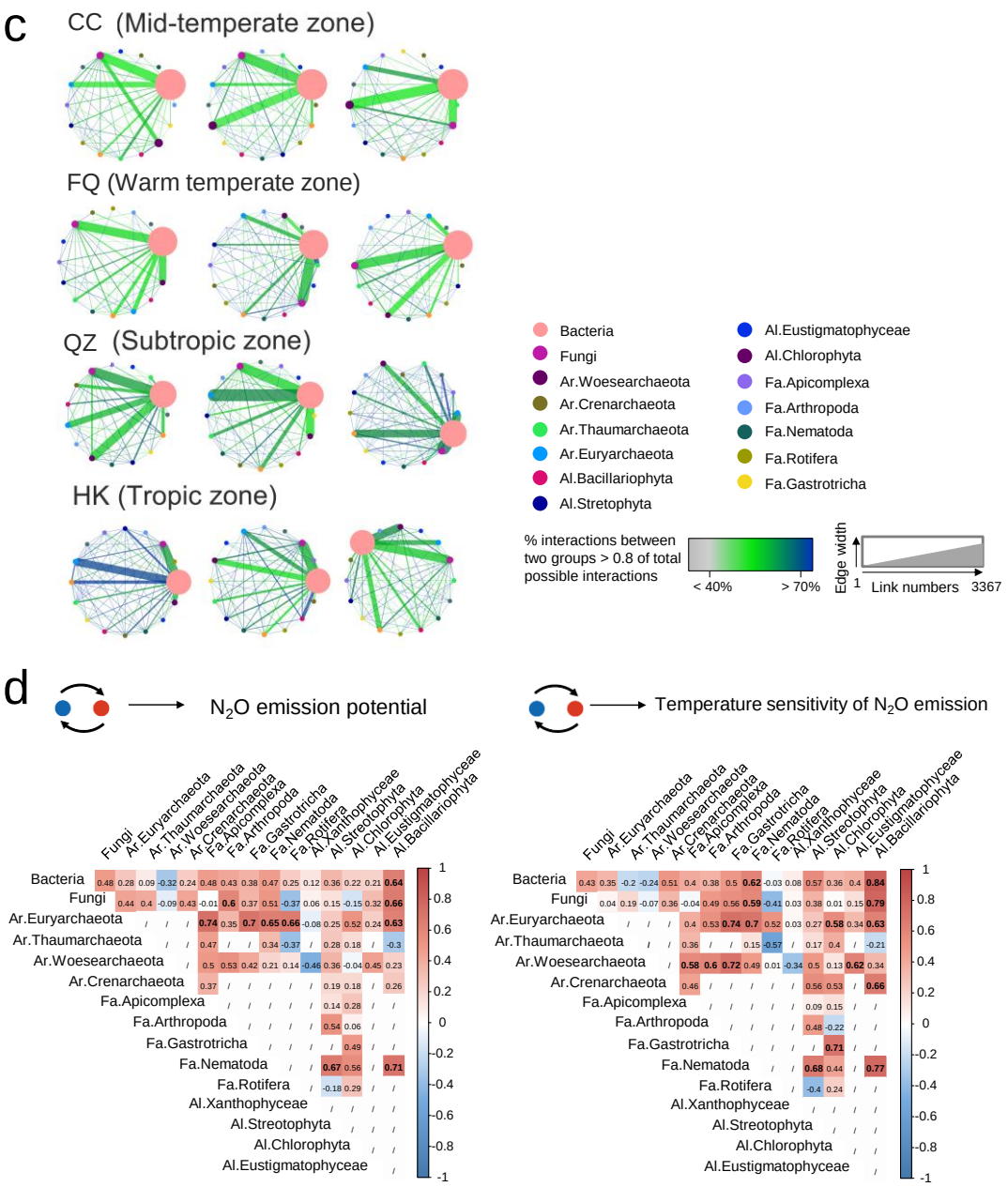


Fig. S5 Relating the main microbial group interaction strengths with N_2O emission in paddy soils using random choosing region from each climatic zone. We first selected the data sets from HL, YY, LA, and HK, respectively from mid-temperate, warm temperate, subtropic, and tropic zones (a, b); we then selected the data sets from CC, FQ, QZ, and HK (c, d). Network visualization of the interaction strengths among the main microbial groups in paddy soils from mid-temperate, warm-temperate, subtropical, and tropical zone (a, c); the correlations between the main group interaction

strengths and the N_2O emission potential and its temperature sensitivity (b, d). Main groups were aggregated by taxonomical classification at the kingdom (bacteria and fungi) or phylum level (archaea and Eukaryotaeukaryota). The proportion of correlations > 0.8 was divided by the total number of possible interactions to obtain the interaction strength between two groups of soil organisms (connectance). Edge width in panel a, c is proportional to the absolute number of correlations > 0.8. Edge color and transparency is proportional to the interaction strength, as indicated in the legend in the figure. The size of the circles is proportional to the number of OTUs in that group. '/' indicate the absence of interactions between these two groups. Significant correlations were indicated marked in bold. Ar = archaea; Fa = micro-fauna; Al = algae.

a **Spearman correlations (*r*) between the dissimilarity of core microbiome and the difference in functional gene abundances determined using Mantel tests.**

	N_2O emission potential		Temperature sensitivity of N_2O emission	
	r	*p*	*r*	*p*
nirK	0.121	< 0.001	0.126	< 0.001
nirS	0.075	< 0.001	0.056	0.003
nosZ	0.146	< 0.001	0.15	< 0.001
nirK/nirS/nosZ	0.129	< 0.001	0.132	< 0.001
Nitrogen cycling genes	0.144	< 0.001	0.157	< 0.001

r and *p* represent the Mantel test statistic and the *p* value.

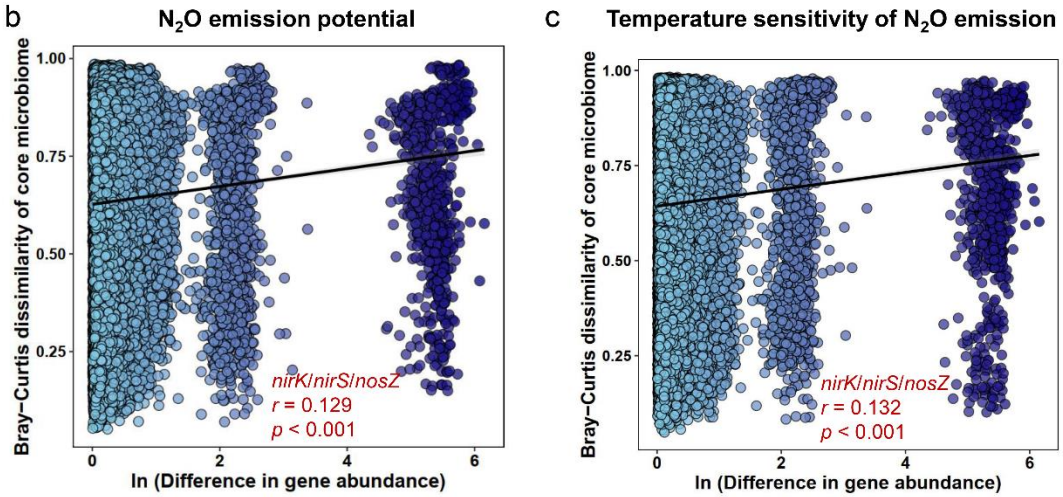


Fig. S6 Linking the core microbiome to nitrogen cycling genes directly involved in N_2O production and reduction. Spearman correlations between the dissimilarity of core microbiome and the log-transformed difference in nitrogen cycling gene abundances determined using Mantel tests (a). Linking the core microbiome related to N_2O emission potential (b) and its temperature sensitivity (c) to nitrogen cycling genes directly contribute to the N_2O pool (i.e., *nirK*, *nirS*, *nosZ*).

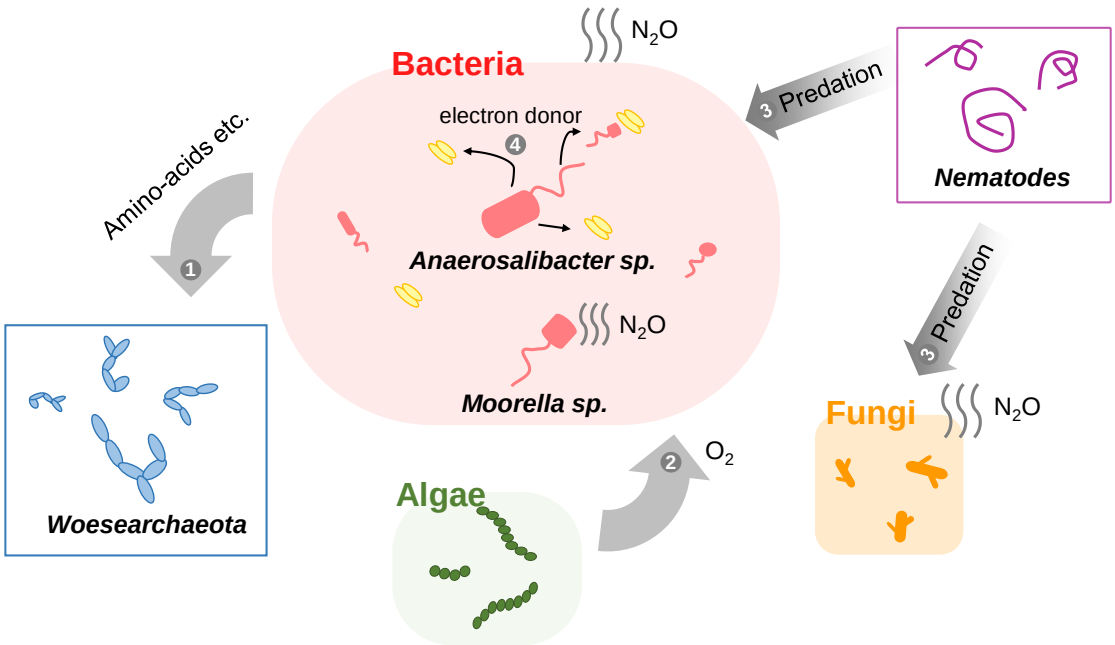


Fig. S7 A pathway diagram visualizing the identified core pair interspecies association in affecting N_2O emission in rice paddy soils according to the two-step method. (1) There might be a potential syntrophic relationship between Woesearchaeota and bacterial members, where bacteria may provide amino-acids and other compounds to compensate for the metabolic deficiencies of Woesearchaeota. (2) Bacteria can break down organic matter using the O_2 produced by photosynthesis of algae, thus providing more electron donor for the denitrification process. (3) Nematode grazing will lead to higher N_2O emissions in soils both indirectly through stimulating microbial activity and directly through excreting N compounds. (4) *Anaerosalibacter* sp. played a central role in enhancing the N_2O emission potential with other bacterial members, which might serve as the provider of electron donor for the denitrification process.

Table S1 Predicting the N_2O emission with environmental factors and microbial interaction strength

Table S1A Multiple linear regressions between environmental factors and the N_2O emission potential or its temperature sensitivity in paddy soils across main rice-cropping areas in China.

	N_2O emission potential		Temperature sensitivity of N_2O emission	
	Standardized coefficients	*p*	Standardized coefficients	*p*
MAT	0.587	0.040	0.785	0.002
pH	-0.249	0.176	-0.470	0.002
CEC	0.335	0.235	0.450	0.048
DOC	0.117	0.470	-0.221	0.090

MAT = mean annual temperature; CEC = cation exchange capacity; DOC = dissolved organic carbon.

Table S1B Summary of the significant regression between MAT and N_2O emission potential and the temperature sensitivity in rice paddies.

	N_2O emission potential			Temperature sensitivity of N_2O emission		
	r^2	*p*	AIC	r^2	*p*	AIC
Linear model	0.19	0.005	227.6	0.34	0.0001	369.6
Exponential model	**0.27**	**0.0006**	**117.0**	**0.30**	**0.0001**	**42.8**
Logarithmic model	0.11	0.04	233.7	0.20	0.005	377.08

The best fit models with lower Akaike information criterion (AIC) and higher r^2 were marked in bold. Both linear and non-linear regressions were fitted and only significant relationships were shown.

Table S1C The interaction strength (%) between main groups of soil organisms in mid-temperate, warm-temperate, subtropical, and tropical zones in paddy soils across main rice-cropping areas in China.

From	To	Mid-temperate zone	Warm-temperate zone	Subtropical zone	Tropical zone
Bacteria	Ar.Euryarchaeota	52.87	59.92	61.83	67.64
Bacteria	Ar.Thaumarchaeota	60.64	68.04	63.65	80.27
Bacteria	Ar.Woesearchaeota	54.66	55.01	56.72	60.48
Bacteria	Ar.Crenarchaeota	46.97	54.49	61.46	62.56
Bacteria	Fa.Apicomplexa	55.51	58.02	58.90	60.63
Bacteria	Fa.Arthropoda	50.00	59.27	59.48	59.22
Bacteria	Fa.Gastrotricha	55.67	72.82	65.15	66.92
Bacteria	Fa.Nematoda	59.38	58.27	58.28	63.88
Bacteria	Fa.Rotifera	58.71	59.43	52.09	62.81
Bacteria	Al.Xanthophyceae	55.11	49.18	64.31	22.94
Bacteria	Al.streotophyta	60.51	65.10	64.68	72.88
Bacteria	Al.Chlorophyta	50.93	57.01	60.11	62.17
Bacteria	Al.Eustigmatophyceae	52.99	59.55	55.56	57.54
Bacteria	Al.Bacillariophyta	58.20	69.11	61.92	66.15
Bacteria	Fungi	56.29	59.21	60.55	60.26
Fungi	Ar.Euryarchaeota	67.82	68.44	64.73	49.81
Fungi	Ar.Thaumarchaeota	64.90	69.58	70.42	70.62
Fungi	Ar.Woesearchaeota	60.44	60.94	60.77	69.35
Fungi	Ar.Crenarchaeota	56.82	63.11	64.28	37.50
Fungi	Fa.Apicomplexa	66.38	70.71	68.27	63.37
Fungi	Fa.Arthropoda	51.11	70.53	73.51	74.32
Fungi	Fa.Gastrotricha	66.25	85.00	76.02	74.58
Fungi	Fa.Nematoda	76.64	68.53	67.14	72.19
Fungi	Fa.Rotifera	68.24	67.39	62.86	64.29
Fungi	Al.Xanthophyceae	58.16	40.63	66.67	83.33
Fungi	Al.streotophyta	68.04	71.11	71.91	73.91
Fungi	Al.Chlorophyta	59.34	68.62	69.91	62.60
Fungi	Al.Eustigmatophyceae	57.14	63.64	67.67	69.57
Fungi	Al.Bacillariophyta	64.04	74.42	66.40	68.51
Ar.Euryarchaeota	Fa.Apicomplexa	69.86	55.88	66.92	81.40
Ar.Euryarchaeota	Fa.Arthropoda	62.16	45.45	69.39	73.33
Ar.Euryarchaeota	Fa.Gastrotricha	50.00	42.86	75.61	77.50
Ar.Euryarchaeota	Fa.Nematoda	59.46	64.29	62.70	72.07
Ar.Euryarchaeota	Fa.Rotifera	77.14	62.50	60.71	60.00
Ar.Euryarchaeota	Al.Xanthophyceae	60.42	50.00	39.58	86.96
Ar.Euryarchaeota	Al.streotophyta	54.17	70.00	67.23	81.94

From	To	Mid-temperate zone	Warm-temperate zone	Subtropical zone	Tropical zone
Ar.Euryarchaeota	Al.Chlorophyta	60.67	65.22	66.29	93.40
Ar.Euryarchaeota	Al.Eustigmatophyceae	54.55	55.56	57.38	32.89
Ar.Euryarchaeota	Al.Bacillariophyta	62.29	78.70	75.53	77.96
Ar.Thaumarchaeota	Fa.Apicomplexa	85.71	68.75	75.56	64.29
Ar.Thaumarchaeota	Fa.Arthropoda	57.14	77.78	75.76	88.89
Ar.Thaumarchaeota	Fa.Gastrotricha	100.00	/	83.33	60.00
Ar.Thaumarchaeota	Fa.Nematoda	71.43	74.36	72.16	53.33
Ar.Thaumarchaeota	Fa.Rotifera	81.08	77.27	54.55	100.00
Ar.Thaumarchaeota	Al.Xanthophyceae	11.11	0.00	72.22	71.43
Ar.Thaumarchaeota	Al.streotophyta	44.19	80.00	87.55	80.00
Ar.Thaumarchaeota	Al.Chlorophyta	65.44	70.06	101.59	69.89
Ar.Thaumarchaeota	Al.Eustigmatophyceae	0.00	77.78	58.97	/
Ar.Thaumarchaeota	Al.Bacillariophyta	76.92	83.04	74.07	66.67
Ar.Woesearchaeota	Fa.Apicomplexa	65.75	69.35	67.21	64.71
Ar.Woesearchaeota	Fa.Arthropoda	67.86	54.55	70.44	84.44
Ar.Woesearchaeota	Fa.Gastrotricha	64.10	66.67	38.14	48.72
Ar.Woesearchaeota	Fa.Nematoda	60.98	72.32	67.47	68.92
Ar.Woesearchaeota	Fa.Rotifera	71.83	40.00	57.14	28.57
Ar.Woesearchaeota	Al.Xanthophyceae	63.39	50.00	55.32	50.00
Ar.Woesearchaeota	Al.streotophyta	63.33	54.46	67.64	74.40
Ar.Woesearchaeota	Al.Chlorophyta	60.42	59.82	72.98	121.85
Ar.Woesearchaeota	Al.Eustigmatophyceae	58.14	36.36	15.82	60.00
Ar.Woesearchaeota	Al.Bacillariophyta	63.75	68.85	64.86	83.01
Ar.Crenarchaeota	Fa.Apicomplexa	75.00	77.78	80.77	57.14
Ar.Crenarchaeota	Fa.Arthropoda	100.00	50.00	74.19	16.67
Ar.Crenarchaeota	Fa.Gastrotricha	/	0.00	100.00	100.00
Ar.Crenarchaeota	Fa.Nematoda	0.00	33.33	67.57	75.00
Ar.Crenarchaeota	Fa.Rotifera	83.33	100.00	87.50	/
Ar.Crenarchaeota	Al.Xanthophyceae	0.00	/	79.49	100.00
Ar.Crenarchaeota	Al.streotophyta	33.33	50.00	58.22	80.56
Ar.Crenarchaeota	Al.Chlorophyta	43.75	63.64	73.25	71.76
Ar.Crenarchaeota	Al.Eustigmatophyceae	/	40.00	40.74	75.00
Ar.Crenarchaeota	Al.Bacillariophyta	50.00	40.00	76.40	56.25
Fa.Apicomplexa	Al.Xanthophyceae	71.43	100.00	83.33	45.45
Fa.Apicomplexa	Al.streotophyta	83.33	89.29	69.79	62.96
Fa.Apicomplexa	Al.Chlorophyta	74.55	100.00	85.45	83.33
Fa.Apicomplexa	Al.Eustigmatophyceae	100.00	100.00	20.00	100.00
Fa.Apicomplexa	Al.Bacillariophyta	77.78	71.43	47.54	69.57
Fa.Arthropoda	Al.Xanthophyceae	50.00	100.00	100.00	25.00
Fa.Arthropoda	Al.streotophyta	57.14	81.25	60.00	70.00
Fa.Arthropoda	Al.Chlorophyta	56.52	44.44	64.20	33.33

From	To	Mid-temperate zone	Warm-temperate zone	Subtropical zone	Tropical zone
Fa.Arthropoda	Al.Eustigmatophyceae	0.00	50.00	100.00	/
Fa.Arthropoda	Al.Bacillariophyta	40.00	80.00	63.64	100.00
Fa.Gastrotricha	Al.Xanthophyceae	50.00	/	42.86	100.00
Fa.Gastrotricha	Al.streotophyta	33.33	100.00	73.68	50.00
Fa.Gastrotricha	Al.Chlorophyta	54.55	80.00	75.93	72.73
Fa.Gastrotricha	Al.Eustigmatophyceae	/	0.00	62.50	0.00
Fa.Gastrotricha	Al.Bacillariophyta	71.43	/	60.00	51.35
Fa.Nematoda	Al.Xanthophyceae	100.00	100.00	55.56	100.00
Fa.Nematoda	Al.streotophyta	81.82	73.33	82.40	84.62
Fa.Nematoda	Al.Chlorophyta	62.07	70.73	61.36	62.67
Fa.Nematoda	Al.Eustigmatophyceae	60.00	0.00	27.50	40.00
Fa.Nematoda	Al.Bacillariophyta	58.06	80.00	69.23	78.33
Fa.Rotifera	Al.Xanthophyceae	/	/	80.00	0.00
Fa.Rotifera	Al.streotophyta	75.00	100.00	80.00	0.00
Fa.Rotifera	Al.Chlorophyta	65.52	73.33	122.73	75.00
Fa.Rotifera	Al.Eustigmatophyceae	0.00	0.00	100.00	/
Fa.Rotifera	Al.Bacillariophyta	60.00	100.00	62.50	41.67

Note: Darker colors in the cells indicate stronger interaction strength between microbial groups. Ar = archaea; Fa = micro-fauna; Al = algae.

Table S1D The relationships between within-group interaction strength and the N_2O emission potential and its temperature sensitivity based on Spearman's correlation in rice paddy soils.

		N_2O emission potential	Temperature sensitivity of N_2O emission
Archaea	R	-0.01	-0.06
	p	0.93	0.72
Bacteria	R	0.01	0.10
	p	0.94	0.54
Fungi	R	0.04	0.20
	p	0.79	0.23
Algae	R	0.23	0.40
	p	0.06	0.02
Micro-fauna	R	-0.24	-0.29
	p	0.14	0.05

Table S2 Pairs of core microorganisms and their independent and cooperative effects on maximizing the N_2O emission in paddy soils based on the two-step criterion.

Table S2A Pairs of core microorganisms and their independent effects on maximizing the N_2O emission potential in paddy soils based on the two-step criterion.

Interaction type	Node A	Node B	B' (A)[a]	B' (B)[b]	C_{ij} [c]	R_{ij}[d]
Between-group	*Methanosphaerula* sp. (Ar.OTU10)	*Halobacteriovorax* sp. (Ba.OTU37210)	0.924	0.916	6,441	5,451.299
	Methanosphaerula sp. (Ar.OTU10)	*Clostridium* sp. (Ba.OTU39051)	0.924	0.916	5,700	4,824.277
	Methanosphaerula sp. (Ar.OTU10)	*Chondromyces* sp. (Ba.OTU6099)	0.924	0.916	5,600	4,738.760
	Methanosphaerula sp. (Ar.OTU10)	*Oxobacter* sp. (Ba.OTU5558)	0.924	0.916	5,424	4,591.830
	Halobacteriovorax sp. (Ba.OTU37210)	*Methanobacterium* sp. (Ar.OTU1004)	0.916	0.917	4,536	3,807.707
	Halobacteriovorax sp. (Ba.OTU37210)	*Methermicoccus* sp. (Ar.OTU189)	0.916	0.911	4,368	3,644.259
	Methanosphaerula sp. (Ar.OTU10)	*Sporotomaculum* sp. (Ba.OTU23447)	0.924	0.916	4,180	3,537.063
	Methanosphaerula sp. (Ar.OTU10)	*Luteitalea* sp. (Ba.OTU6324)	0.924	0.915	4,181	3,536.236
	Chondromyces sp. (Ba.OTU6099)	*Methanobacterium* sp. (Ar.OTU1004)	0.916	0.917	4,182	3,509.979
	Halobacteriovorax sp. (Ba.OTU37210)	Unclassified *Woesearchaeota* (Ar.OTU23)	0.916	0.915	4,088	3,426.253
	Clostridium sp. (Ba.OTU39051)	*Methanobacterium* sp. (Ar.OTU1004)	0.916	0.917	4,018	3,372.959
	Halobacteriovorax sp. (Ba.OTU37210)	Unclassified *archaeon* (Ar.OTU82)	0.916	0.907	3,990	3,315.794
	Oxobacter sp. (Ba.OTU5558)	*Methanobacterium* sp. (Ar.OTU1004)	0.916	0.917	3,936	3,304.951
	Clostridium sp. (Ba.OTU39051)	*Methermicoccus* sp. (Ar.OTU189)	0.916	0.911	3,871	3,229.687
	Oxobacter sp. (Ba.OTU5558)	*Methermicoccus* sp. (Ar.OTU189)	0.916	0.911	3,792	3,164.567
Within-group (Archaea)	*Methanocella* sp. (Ar.OTU17)	*Methanocella* sp. (Ar.OTU340)	1	0.649	54	35.042
	Methanocella sp. (Ar.OTU17)	*Methanocella* sp. (Ar.OTU242)	1	0.444	63	27.978
	Nitrososphaera sp. (Ar.OTU394)	*Methanocella* sp. (Ar.OTU17)	0.161	1	84	13.519

	Methanocella sp. (Ar.OTU340)	*Methanomethylovorans* sp. (Ar.OTU321)	0.649	0.410	40	10.631
	Methanocella sp. (Ar.OTU109)	*Methanocella* sp. (Ar.OTU17)	0.084	1	108	9.078
	Methanosphaerula sp. (Ar.OTU10)	*Methanobacterium* sp. (Ar.OTU160)	0.171	0.072	713	8.764
	Methanocella sp. (Ar.OTU17)	*Methanocella* sp. (Ar.OTU322)	1	0.113	72	8.135
	Methanosarcina sp. (Ar.OTU50)	*Methanobacterium* sp. (Ar.OTU1004)	0.145	0.106	504	7.769
	Methanocella sp. (Ar.OTU17)	*Methanocella* sp. (Ar.OTU593)	1	0.238	32	7.619
	Methanocella sp. (Ar.OTU242)	*Methanocella* sp. (Ar.OTU367)	0.444	0.305	54	7.321
Within-group (Bacteria)	*Anaerosalibacter* sp. (Ba.OTU41112)	*Moorella* sp. (Ba.OTU52410)	0.475	0.420	8,000	1,598.890
	Anaerosalibacter sp. (Ba.OTU41112)	Unclassified *bacterium* (Ba.OTU52965)	0.475	0.270	8,256	1,059.414
	Moorella sp. (Ba.OTU52410)	*Ammoniphilus* sp. (Ba.OTU41498)	0.420	0.217	6,903	629.026
	Anaerosalibacter sp. (Ba.OTU41112)	*Pyrinomonas* sp. (Ba.OTU53333)	0.475	0.265	4,148	521.597
	Anaerosalibacter sp. (Ba.OTU41112)	*Sterolibacterium* sp. (Ba.OTU11112)	0.475	0.128	7,872	479.746
	Unclassified *bacterium* (Ba.OTU36668)	*Anaerosalibacter* sp. (Ba.OTU41112)	0.114	0.475	7,298	394.367
	Anaerosalibacter sp. (Ba.OTU41112)	*Conexibacter* sp. (Ba.OTU4903)	0.475	0.146	4,664	322.705
	Unclassified *bacterium* (Ba.OTU52965)	*Ammoniphilus* sp. (Ba.OTU41498)	0.270	0.217	5,429	317.627
	Haliangium sp. (Ba.OTU24054)	*Anaerosalibacter* sp. (Ba.OTU41112)	0.156	0.475	4,176	309.247
	Haliangium sp. (Ba.OTU24054)	*Moorella* sp. (Ba.OTU52410)	0.156	0.420	4,386	287.292
Within-group (Fungi)	Unclassified *fungus* (Fu.OTU1)	*Cyathus* sp. (Fu.OTU10084)	1	0.390	8	3.122
	Unclassified *fungus* (Fu.OTU1)	*Lobulomyces* sp. (Fu.OTU21789)	1	0.050	8	0.402
	Unclassified *fungus* (Fu.OTU1)	*Dominikia* sp. (Fu.OTU21962)	1	0.050	8	0.402
	Cyathus sp. (Fu.OTU10084)	Unclassified *Zygorhynchus* (Fu.OTU27233)	0.390	0.092	4	0.144
	Unclassified *Rhizophydium* (Fu.OTU4002)	Unclassified *Zygorhynchus* (Fu.OTU27233)	0.082	0.092	4	0.030
	Unclassified *Rhizophydium* (Fu.OTU4002)	Unclassified *fungus* (Fu.OTU10890)	0.082	0.054	4	0.018
	Lobulomyces sp. (Fu.OTU21789)	Unclassified *Tremellales* (Fu.OTU21826)	0.050	0.017	4	0.003
	Dominikia sp. (Fu.OTU21962)	Unclassified *Tremellales* (Fu.OTU21826)	0.050	0.017	4	0.003
	Unclassified *fungus* (Fu.OTU1)	Unclassified *fungus* (Fu.OTU10224)	1	0	4	0

	Goffeauzyma sp. (Fu.OTU780)	Unclassified *Mucorales* (Fu.OTU22000)	0.025	0	2	0
Within-group (Algae)	*Tetracystis* sp. (Al.OTU8)	*Chloroparvula* sp. (Al.OTU52)	1	0.947	25	23.674
	Tetracystis sp. (Al.OTU8)	*Pseudopleurococcus* sp. (Al.OTU89)	1	0.318	15	4.773
	Nannochloris sp. (Al.OTU43)	*Chloroparvula* sp. (Al.OTU52)	0.365	0.947	8	2.766
	Nautococcus sp. (Al.OTU32)	*Pterosperma* sp. (Al.OTU388)	0.536	0.279	15	2.245
	Chloroparvula sp. (Al.OTU52)	*Pterosperma* sp. (Al.OTU388)	0.947	0.279	8	2.114
	Tetracystis sp. (Al.OTU8)	*Crustomastix* sp. (Al.OTU100)	1	0.156	6	0.937
	Nephroselmis sp. (Al.OTU34)	*Nautococcus* sp. (Al.OTU32)	0.101	0.536	12	0.650
	Monomastix sp. (Al.OTU180)	*Nautococcus* sp. (Al.OTU32)	0.101	0.536	12	0.650
	Tetracystis sp. (Al.OTU8)	*Nephroselmis* sp. (Al.OTU34)	1	0.101	6	0.606
	Tetracystis sp. (Al.OTU8)	*Monomastix* sp. (Al.OTU180)	1	0.101	6	0.606
Within-group (Micro-fauna)	Unclassified *eukaryote* (Fa.OTU12)	*Mayamaea* sp. (Fa.OTU13)	1	1	1	1
	Unclassified *eukaryote* (Fa.OTU12)	*Phascolodon* sp. (Fa.OTU23)	1	1	1	1
	Mayamaea sp. (Fa.OTU13)	*Phascolodon* sp. (Fa.OTU23)	1	1	1	1
	Aplanochytrium sp. (Fa.OTU7)	Unclassified *eukaryote* (Fa.OTU12)	0	1	2	0
	Aplanochytrium sp. (Fa.OTU7)	*Mayamaea* sp. (Fa.OTU13)	0	1	2	0
	Aplanochytrium sp. (Fa.OTU7)	*Enchelyodon* sp. (Fa.OTU16)	0	1	4	0
	Aplanochytrium sp. (Fa.OTU7)	*Phascolodon* sp. (Fa.OTU23)	0	1	2	0
	Aplanochytrium sp. (Fa.OTU7)	*Prodorylaimus* sp. (Fa.OTU26)	0	0	1	0
	Unclassified *eukaryote* (Fa.OTU12)	*Prodorylaimus* sp. (Fa.OTU26)	1	0	2	0
	Mayamaea sp. (Fa.OTU13)	*Prodorylaimus* sp. (Fa.OTU26)	1	0	2	0

[a, b] denotes the species keystoneness after standardizing (Eq. 4)

[c] represents the number of checkboard units based on Eq. 7

[d] represents their independent effects on maximizing the function calculated by Eq. 11

Table S2B Pairs of core microorganisms and their cooperative effects on maximizing the N_2O emission potential in paddy soils based on the two-step criterion.

Interaction type	Node A	Node B	B' (A)[a]	B' (B)[b]	T_{ij} [c]	R_{ij}[d]
Between-group	*Chlamydomonadales* sp. (Al.OTU16)	*Methanobacterium* sp. (Ar.OTU13)	0.950	0.930	54,696	48,337.783
	Chlamydomonadales sp. (Al.OTU16)	*Methanocella* sp. (Ar.OTU32)	0.950	0.942	53,193	47,598.570
	Methanosphaerula sp. (Ar.OTU10)	*Nautococcus* sp. (Al.OTU32)	0.924	0.916	50,550	42,779.783
	Chlamydomonadales sp. (Al.OTU16)	*Nitrososphaera* sp. (Ar.OTU9)	0.950	0.928	46,530	41,019.957
	Nautococcus sp. (Al.OTU32)	Unclassified *archaeon* (Ar.OTU135)	0.916	0.912	47,790	39,914.262
	Nautococcus sp. (Al.OTU32)	*Methanocella* sp. (Ar.OTU143)	0.916	0.927	44,058	37,400.229
	Chlamydomonadales sp. (Al.OTU16)	*Nitrososphaera* sp. (Ar.OTU4)	0.950	0.924	42,517	37,318.420
	Chlamydomonadales sp. (Al.OTU16)	*Methanocella* sp. (Ar.OTU22)	0.950	0.942	40,677	36,390.424
	Nautococcus sp. (Al.OTU32)	*Methanosphaerula* sp. (Ar.OTU36)	0.916	0.920	37,908	31,932.379
	Chlamydomonadales sp. (Al.OTU16)	*Methanocella* sp. (Ar.OTU18)	0.950	0.929	33,216	29,325.348
	Nautococcus sp. (Al.OTU32)	*Methanococcoides* sp. (Ar.OTU74)	0.916	0.920	29,708	25,030.224
	Nautococcus sp. (Al.OTU32)	Unclassified *archaeon* (Ar.OTU531)	0.916	0.916	25,656	21,515.044
	Frontonia sp. (Fu.OTU23455)	Unclassified *archaeon* (Ar.OTU23)	0.917	0.915	25,416	21,318.021
	Frontonia sp. (Fu.OTU23455)	*Methanobacterium* sp. (Ar.OTU1004)	0.917	0.917	25,224	21,190.226
Within-group (Archaea)	*Nautococcus* sp. (Al.OTU32)	Unclassified *archaeon* (Ar.OTU57)	0.916	0.917	24,380	20,466.593
	Methanocella sp. (Ar.OTU17)	*Methanocella* sp. (Ar.OTU340)	1	0.649	932	604.802
	Methanocella sp. (Ar.OTU17)	*Methanocella* sp. (Ar.OTU242)	1	0.444	928	412.115
	Methanocella sp. (Ar.OTU17)	*Methanocella* sp. (Ar.OTU593)	1	0.238	1,175	279.763
	Methanocella sp. (Ar.OTU17)	*Methanocella* sp. (Ar.OTU162)	1	0.177	1,175	207.645
	Methanocella sp. (Ar.OTU242)	*Methanocella* sp. (Ar.OTU593)	0.444	0.238	1,428	150.991
	Methanocella sp. (Ar.OTU340)	*Nitrosopumilus* sp. (Ar.OTU321)	0.649	0.410	474	125.976
	Methanocella sp. (Ar.OTU162)	*Methanocella* sp. (Ar.OTU242)	0.177	0.444	1,428	112.068

	Methanocella sp. (Ar.OTU340)	*Methanocella* sp. (Ar.OTU593)	0.649	0.238	708	109.391
	Methermicoccus sp. (Ar.OTU189)	*Methanobacterium* sp. (Ar.OTU1004)	0.109	0.106	9,065	104.528
	Methanosphaerula sp. (Ar.OTU10)	*Methermicoccus* sp. (Ar.OTU189)	0.171	0.109	5,292	98.415
Within-group (Bacteria)	*Moorella* sp. (Ba.OTU52410)	Unclassified *bacterium* (Ba.OTU52965)	0.420	0.270	79,106	8,978.741
	Anaerosalibacter sp. (Ba.OTU41112)	*Moorella* sp. (Ba.OTU52410)	0.475	0.420	39,936	7,981.657
	Anaerosalibacter sp. (Ba.OTU41112)	*Pyrinomonas* sp. (Ba.OTU53333)	0.475	0.265	54,213	6,817.098
	Anaerosalibacter sp. (Ba.OTU41112)	*Ammoniphilus* sp. (Ba.OTU41498)	0.475	0.217	61,544	6,340.246
	Anaerosalibacter sp. (Ba.OTU41112)	*Denitratisoma* sp. (Ba.OTU51233)	0.475	0.157	70,528	5,259.578
	Anaerosalibacter sp. (Ba.OTU41112)	*Peredibacter* sp. (Ba.OTU54965)	0.475	0.127	81,770	4,955.475
	Moorella sp. (Ba.OTU52410)	*Anaerosalibacter* sp. (Ba.OTU11112)	0.420	0.128	85,162	4,590.732
	Moorella sp. (Ba.OTU52410)	*Gemmata* sp. (Ba.OTU8890)	0.420	0.123	83,006	4,307.300
	Anaerosalibacter sp. (Ba.OTU41112)	*Cephalothrix* sp. (Ba.OTU50224)	0.475	0.131	56,967	3,549.047
	Pyrinomonas sp. (Ba.OTU53333)	*Ammoniphilus* sp. (Ba.OTU41498)	0.265	0.217	58,459	3,351.579
Within-group (Fungi)	*Coemansia* sp. (Fu.OTU7779)	Unclassified *fungus* (Fu.OTU13335)	0	0	28	0
	Coemansia sp. (Fu.OTU7779)	Unclassified *Cryptomycota* (Fu.OTU21900)	0	0	28	0
	Unclassified *fungus* (Fu.OTU13335)	Unclassified *Cryptomycota* (Fu.OTU21900)	0	0	28	0
	Inocybe sp. (Fu.OTU23234)	*Acaulospora* sp. (Fu.OTU24067)	0	0	28	0
	Rozella sp. (Fu.OTU13113)	*Inocybe* sp. (Fu.OTU23234)	0.092	0	26	0
	Rozella sp. (Fu.OTU13113)	*Acaulospora* sp. (Fu.OTU24067)	0.092	0	26	0
	Unclassified *fungus* (Fu.OTU1)	*Cyathus* sp. (Fu.OTU10084)	1	0.390	0	0
	Unclassified *fungus* (Fu.OTU1)	*Lobulomyces* sp. (Fu.OTU21789)	1	0.050	0	0
	Unclassified *fungus* (Fu.OTU1)	*Dominikia* sp. (Fu.OTU21962)	1	0.050	0	0
	Cyathus sp. (Fu.OTU10084)	Unclassified *Zygorhynchus* (Fu.OTU27233)	0.390	0.092	0	0
Within-group (Algae)	*Nannochloris* sp. (Al.OTU43)	*Chloroparvula* sp. (Al.OTU52)	0.365	0.947	43	14.865
	Tetracystis sp. (Al.OTU8)	*Crustomastix* sp. (Al.OTU100)	1.000	0.156	86	13.431
	Chloroparvula sp. (Al.OTU52)	*Pterosperma* sp. (Al.OTU388)	0.947	0.279	43	11.363

	Tetracystis sp. (Al.OTU8)	*Nephroselmis* sp. (Al.OTU34)	1	0.101	86	8.682
	Tetracystis sp. (Al.OTU8)	*Monomastix* sp. (Al.OTU180)	1	0.101	86	8.682
	Nannochloris sp. (Al.OTU43)	*Pterosperma* sp. (Al.OTU388)	0.365	0.279	45	4.584
	Nephroselmis sp. (Al.OTU34)	*Nautococcus* sp. (Al.OTU32)	0.101	0.536	42	2.274
	Monomastix sp. (Al.OTU180)	*Nautococcus* sp. (Al.OTU32)	0.101	0.536	42	2.274
	Nephroselmis sp. (Al.OTU34)	*Crustomastix* sp. (Al.OTU100)	0.101	0.156	88	1.387
	Crustomastix sp. (Al.OTU100)	*Monomastix* sp. (Al.OTU180)	0.156	0.101	88	1.387
Within-group (Fauna)	Unclassified *eukaryote* (Fa.OTU12)	*Mayamaea* sp. (Fa.OTU13)	1	1	3	3
	Unclassified *eukaryote* (Fa.OTU12)	*Phascolodon* sp. (Fa.OTU23)	1	1	3	3
	Mayamaea sp. (Fa.OTU13)	*Phascolodon* sp. (Fa.OTU23)	1	1	3	3
	Aplanochytrium sp. (Fa.OTU7)	Unclassified *eukaryote* (Fa.OTU12)	0	1	0	0
	Aplanochytrium sp. (Fa.OTU7)	*Mayamaea* sp. (Fa.OTU13)	0	1	0	0
	Aplanochytrium sp. (Fa.OTU7)	*Enchelyodon* sp. (Fa.OTU16)	0	1	0	0
	Aplanochytrium sp. (Fa.OTU7)	*Phascolodon* sp. (Fa.OTU23)	0	1	0	0
	Aplanochytrium sp. (Fa.OTU7)	*Prodorylaimus* sp. (Fa.OTU26)	0	0	0	0
	Unclassified *eukaryote* (Fa.OTU12)	*Prodorylaimus* sp. (Fa.OTU26)	1	0	0	0
	Mayamaea sp. (Fa.OTU13)	*Prodorylaimus* sp. (Fa.OTU26)	1	0	0	0

[a, b] denotes the species keystoneness after standardizing (Eq. 4)

[c] represents the number of togetherness units based on Eq. 9

[d] represents their cooperative effects on maximizing the functions calculated by Eq. 12

Table S2C Pairs of core microorganisms and their independent effects on maximizing the temperature sensitivity of N_2O emission in paddy soils based on the two-step criterion.

Interaction type	Node A	Node B	B' (A)[a]	B' (B)[b]	C_{ij} [c]	R_{ij}[d]
Between-group	*Methanosphaerula* sp. (Ar.OTU10)	*Halobacteriovorax* sp. (Ba.OTU37210)	0.926	0.831	6,441	4,958.129
	Methanosphaerula sp. (Ar.OTU10)	*Clostridium* sp. (Ba.OTU39051)	0.926	0.834	5,700	4,399.813
	Methanosphaerula sp. (Ar.OTU10)	*Chondromyces* sp. (Ba.OTU6099)	0.926	0.831	5,600	4,308.221
	Methanosphaerula sp. (Ar.OTU10)	*Oxobacter* sp. (Ba.OTU5558)	0.926	0.831	5,424	4,175.017
	Methanosphaerula sp. (Ar.OTU10)	*Sporotomaculum* sp. (Ba.OTU23447)	0.926	0.832	4,180	3,221.426
	Methanosphaerula sp. (Ar.OTU10)	*Luteitalea* sp. (Ba.OTU6324)	0.926	0.830	4,181	3,213.887
	Halobacteriovorax sp. (Ba.OTU37210)	*Methanobacterium* sp. (Ar.OTU1004)	0.831	0.842	4,536	3,173.720
	Halobacteriovorax sp. (Ba.OTU37210)	*Methermicoccus* sp. (Ar.OTU189)	0.831	0.849	4,368	3,083.170
	Unclassified *Chondromyces* (Ba.OTU6099)	*Methanobacterium* sp. (Ar.OTU1004)	0.831	0.842	4,182	2,924.321
	Halobacteriovorax sp. (Ba.OTU37210)	Unclassified *Woesearchaeota* (Ar.OTU23)	0.831	0.837	4,088	2,842.783
	Clostridium sp. (Ba.OTU39051)	*Methanobacterium* sp. (Ar.OTU1004)	0.834	0.842	4,018	2,819.034
	Methanosphaerula sp. (Ar.OTU10)	*Desulfomicrobium* sp. (Ba.OTU13113)	0.926	0.832	3,616	2,784.748
	Methanosphaerula sp. (Ar.OTU10)	*Geobacter* sp. (Ba.OTU51222)	0.926	0.830	3,616	2,779.932
	Methanosphaerula sp. (Ar.OTU10)	*Lysobacter* sp. (Ba.OTU100)	0.926	0.836	3,584	2,774.933
	Oxobacter sp. (Ba.OTU5558)	*Methanobacterium* sp. (Ar.OTU1004)	0.831	0.842	3,936	2,753.751
Within-group (Archaea)	*Methanosphaerula* sp. (Ar.OTU10)	*Methanobacterium* sp. (Ar.OTU160)	0.818	0.359	713	209.188
	Methanocella sp. (Ar.OTU8)	*Methanosphaerula* sp. (Ar.OTU10)	0.648	0.818	374	198.269
	Methanosphaerula sp. (Ar.OTU10)	*Methanobacterium* sp. (Ar.OTU101)	0.818	0.308	616	155.206
	Methanosphaerula sp. (Ar.OTU10)	*Methanobacterium* sp. (Ar.OTU125)	0.818	0.336	544	149.320
	Methanosarcina sp. (Ar.OTU50)	*Methanobacterium* sp. (Ar.OTU1004)	0.568	0.491	504	140.657
	Methanosphaerula sp. (Ar.OTU10)	Unclassified *archaeon* (Ar.OTU151)	0.818	0.317	525	136.302
	Methanosphaerula sp. (Ar.OTU10)	Unclassified *archaeon* (Ar.OTU372)	0.818	0.302	551	136.067

	Methanosphaerula sp. (Ar.OTU10)	*Acidianus* sp. (Ar.OTU380)	0.818	0.271	612	135.587
	Methanosphaerula sp. (Ar.OTU10)	*Methanocella* sp. (Ar.OTU18)	0.818	0.707	231	133.545
	Methanocella sp. (Ar.OTU22)	*Methanobacterium* sp. (Ar.OTU93)	1	0.632	210	132.695
Within-group (Bacteria)	*Anaerosalibacter* sp. (Ba.OTU41112)	*Moorella* sp. (Ba.OTU52410)	0.659	1	8,000	5,271.483
	Anaerosalibacter sp. (Ba.OTU41112)	Unclassified *bacterium* (Ba.OTU52965)	0.659	0.478	8,256	2,598.729
	Moorella sp. (Ba.OTU52410)	*Ammoniphilus* sp. (Ba.OTU41498)	1	0.238	6,903	1,645.947
	Moorella sp. (Ba.OTU52410)	*Pirellula* sp. (Ba.OTU5736)	1	0.477	2,618	1,248.117
	Anaerosalibacter sp. (Ba.OTU41112)	*Pyrinomonas* sp. (Ba.OTU53333)	0.659	0.442	4,148	1,209.039
	Moorella sp. (Ba.OTU52410)	Unclassified *bacterium* (Ba.OTU31890)	1	0.198	6,018	1,188.684
	Moorella sp. (Ba.OTU52410)	*Thermanaerothrix* sp. (Ba.OTU5016)	1	0.130	8,667	1,128.093
	Moorella sp. (Ba.OTU52410)	*Calditerricola* sp. (Ba.OTU12669)	1	0.096	11,663	1,115.685
	Moorella sp. (Ba.OTU52410)	*Unclassified* bacterium (Ba.OTU52965)	1	0.478	2,275	1,086.750
	Frateuria sp. (Ba.OTU45500)	*Moorella* sp. (Ba.OTU52410)	0.099	1	10,062	995.917
Within-group (Fungi)	Unclassified *fungus* (Fu.OTU1)	*Lobulomyces* sp. (Fu.OTU21789)	1	0.301	8	2.407
	Unclassified *fungus* (Fu.OTU1)	*Dominikia* sp. (Fu.OTU21962)	1	0.301	8	2.407
	Unclassified *fungus* (Fu.OTU1)	*Cyathus* sp. (Fu.OTU10084)	1	0.050	8	0.399
	Unclassified *fungus* (Fu.OTU1)	Unclassified *fungus* (Fu.OTU10224)	1	0.067	4	0.270
	Lobulomyces sp. (Fu.OTU21789)	Unclassified *Tremellales* (Fu.OTU21826)	0.301	0.168	4	0.202
	Dominikia sp. (Fu.OTU21962)	Unclassified *Tremellales* (Fu.OTU21826)	0.301	0.168	4	0.202
	Rozella sp. (Fu.OTU13113)	Unclassified *fungus* (Fu.OTU21534)	0.124	0.067	4	0.034
	Rozella sp. (Fu.OTU13113)	Unclassified *fungus* (Fu.OTU22761)	0.124	0.067	4	0.034
	Rozella sp. (Fu.OTU13113)	*Inocybe* sp. (Fu.OTU23234)	0.124	0.067	3	0.025
	Rozella sp. (Fu.OTU13113)	*Acaulospora* sp. (Fu.OTU24067)	0.124	0.067	3	0.025
Within-group (Algae)	*Nannochloris* sp. (Al.OTU43)	*Chloroparvula* sp. (Al.OTU52)	0.287	0.907	8	2.080
	Tetracystis sp. (Al.OTU8)	*Crustomastix* sp. (Al.OTU100)	1	0.116	6	0.695
	Chloroparvula sp. (Al.OTU52)	*Pterosperma* sp. (Al.OTU388)	0.907	0.251	8	1.823

	Tetracystis sp. (Al.OTU8)	*Nephroselmis* sp. (Al.OTU34)	1	0.088	6	0.527
	Tetracystis sp. (Al.OTU8)	*Monomastix* sp. (Al.OTU180)	1	0.088	6	0.527
	Nannochloris sp. (Al.OTU43)	*Pterosperma* sp. (Al.OTU388)	0.287	0.251	4	0.288
	Nephroselmis sp. (Al.OTU34)	*Nautococcus* sp. (Al.OTU32)	0.088	0.448	12	0.472
	Monomastix sp. (Al.OTU180)	*Nautococcus* sp. (Al.OTU32)	0.088	0.448	12	0.472
	Nephroselmis sp. (Al.OTU34)	*Monomastix* sp. (Al.OTU180)	0.088	0.088	1	0.008
	Nephroselmis sp. (Al.OTU34)	*Crustomastix* sp. (Al.OTU100)	0.088	0.116	4	0.041
Within-group (Micro-fauna)	Unclassified *eukaryote* (Fa.OTU12)	*Mayamaea* sp. (Fa.OTU13)	1	1	1	1
	Unclassified *eukaryote* (Fa.OTU12)	*Phascolodon* sp. (Fa.OTU23)	1	1	1	1
	Mayamaea sp. (Fa.OTU13)	*Phascolodon* sp. (Fa.OTU23)	1	1	1	1
	Aplanochytrium sp. (Fa.OTU7)	Unclassified *eukaryote* (Fa.OTU12)	0	1	2	0
	Aplanochytrium sp. (Fa.OTU7)	*Mayamaea* sp. (Fa.OTU13)	0	1	2	0
	Aplanochytrium sp. (Fa.OTU7)	*Mayamaea* sp. (Fa.OTU16)	0	1	4	0
	Aplanochytrium sp. (Fa.OTU7)	*Phascolodon* sp. (Fa.OTU23)	0	1	2	0
	Aplanochytrium sp. (Fa.OTU7)	*Prodorylaimus* sp. (Fa.OTU26)	0	0	1	0
	Unclassified *eukaryote* (Fa.OTU12)	*Prodorylaimus* sp. (Fa.OTU26)	1	0	2	0
	Mayamaea sp. (Fa.OTU13)	*Prodorylaimus* sp. (Fa.OTU26)	1	0	2	0

[a, b] denotes the species keystoneness after standardizing (Eq. 4)

[c] represents the number of checkboard units based on Eq. 7

[d] represents their independent effects on maximizing the functions calculated by Eq. 11

Table S2D Pairs of core microorganisms and their cooperative effects on maximizing the temperature sensitivity of N_2O emission in paddy soils based on the two-step criterion.

Interaction type	Node A	Node B	B' (A)[a]	B' (B)[b]	T_{ij} [c]	$R_{ij}t$[d]
Between-group	*Chlamydomonadales* sp. (Al.OTU16)	*Methanobacterium* sp. (Ar.OTU13)	0.958	1	54,696	52,390.998
	Chlamydomonadales sp. (Al.OTU16)	*Methanocella* sp. (Ar.OTU32)	0.958	0.920	53,193	46,877.402
	Chlamydomonadales sp. (Al.OTU16)	*Nitrososphaera* sp. (Ar.OTU9)	0.958	0.924	46,530	41,185.715
	Methanosphaerula sp. (Ar.OTU10)	*Nautococcus* sp. (Al.OTU32)	0.926	0.865	50,550	40,507.698
	Chlamydomonadales sp. (Al.OTU16)	*Methanocella* sp. (Ar.OTU22)	0.958	0.962	40,677	37,487.655
	Chlamydomonadales sp. (Al.OTU16)	*Nitrososphaera* sp. (Ar.OTU4)	0.958	0.895	42,517	36,443.019
	Nautococcus sp. (Al.OTU32)	Unclassified *Archaeon* (Ar.OTU135)	0.865	0.847	47,790	35,034.359
	Nautococcus sp. (Al.OTU32)	*Methanocella* sp. (Ar.OTU143)	0.865	0.865	44,058	32,984.802
	Chlamydomonadales sp. (Al.OTU16)	*Methanocella* sp. (Ar.OTU18)	0.958	0.892	33,216	28,385.398
	Nautococcus sp. (Al.OTU32)	*Methanosphaerula* sp. (Ar.OTU36)	0.865	0.856	37,908	28,081.625
	Nautococcus sp. (Al.OTU32)	*Methanococcoides* sp. (Ar.OTU74)	0.865	0.838	29,708	21,536.073
	Nautococcus sp. (Al.OTU32)	Unclassified *Archaeon* (Ar.OTU531)	0.865	0.832	25,656	18,462.526
	Chlamydomonadales sp. (Al.OTU16)	*Methanosarcina* sp. (Ar.OTU98)	0.958	0.856	22,218	18,227.753
	Frontonia sp. (Fu.OTU23455)	Unclassified *Archaeon* (Ar.OTU23)	0.852	0.837	25,416	18,108.302
	Frontonia sp. (Fu.OTU23455)	*Methanobacterium* sp. (Ar.OTU1004)	0.852	0.842	25,224	18,082.032
Within-group (Archaea)	*Methermicoccus* sp. (Ar.OTU189)	*Methanobacterium* sp. (Ar.OTU1004)	0.478	0.491	9,065	2,129.871
	Methanosphaerula sp. (Ar.OTU10)	*Methanobacterium* sp. (Ar.OTU1004)	0.818	0.491	5,220	2,096.382
	Methanosphaerula sp. (Ar.OTU10)	*Methermicoccus* sp. (Ar.OTU189)	0.818	0.478	5,292	2,070.224
	Methanosphaerula sp. (Ar.OTU10)	*Methanobacterium* sp. (Ar.OTU170)	0.818	0.393	5,626	1,805.726
	Methanobacterium sp. (Ar.OTU170)	*Methanobacterium* sp. (Ar.OTU1004)	0.393	0.491	8,789	1,694.258
	Unclassified *Woesearchaeota* (Ar.OTU23)	*Methanobacterium* sp. (Ar.OTU1004)	0.366	0.491	9,000	1,619.703
	Methanobacterium sp. (Ar.OTU170)	*Methermicoccus* sp. (Ar.OTU189)	0.393	0.478	8,536	1,602.847

	Methanobacterium sp. (Ar.OTU125)	*Methanobacterium* sp. (Ar.OTU1004)	0.336	0.491	8,460	1,394.688
	Methanosphaerula sp. (Ar.OTU10)	Unclassified *Woesearchaeota* (Ar.OTU23)	0.818	0.366	4,500	1,348.396
	Unclassified *Woesearchaeota* (Ar.OTU23)	*Methermicoccus* sp. (Ar.OTU189)	0.366	0.478	7,644	1,340.020
Within-group (Bacteria)	*Moorella* sp. (Ba.OTU52410)	Unclassified *bacterium* (Ba.OTU52965)	1	0.478	79,106	37,788.342
	Anaerosalibacter sp. (Ba.OTU41112)	*Moorella* sp. (Ba.OTU52410)	0.659	1	39,936	26,315.246
	Moorella sp. (Ba.OTU52410)	*Gemmata* sp. (Ba.OTU8890)	1	0.251	83,006	20,862.333
	Moorella sp. (Ba.OTU52410)	*Calditerricola* sp. (Ba.OTU1225)	1	0.236	74,550	17,613.370
	Moorella sp. (Ba.OTU52410)	*Sterolibacterium* sp. (Ba.OTU11112)	1	0.192	85,162	16,349.244
	Anaerosalibacter sp. (Ba.OTU41112)	*Pyrinomonas* sp. (Ba.OTU53333)	0.659	0.442	54,213	15,801.748
	Moorella sp. (Ba.OTU52410)	*Chryseobacterium* sp. (Ba.OTU14780)	1	0.252	44,321	11,189.741
	Anaerosalibacter sp. (Ba.OTU41112)	*Denitratisoma* sp. (Ba.OTU51233)	0.659	0.240	70,528	11,171.385
	Anaerosalibacter sp. (Ba.OTU41112)	*Peredibacter* sp. (Ba.OTU54965)	0.659	0.193	81,770	10,393.831
	Moorella sp. (Ba.OTU52410)	*Pirellula* sp. (Ba.OTU5736)	1	0.477	21,640	10,316.748
Within-group (Fungi)	*Rozella* sp. (Fu.OTU13113)	*Inocybe* sp. (Fu.OTU23234)	0.124	0.067	26	0.218
	Rozella sp. (Fu.OTU13113)	*Acaulospora* sp. (Fu.OTU24067)	0.124	0.067	26	0.218
	Coemansia sp. (Fu.OTU7779)	Unclassified *fungus* (Fu.OTU13335)	0.067	0.067	28	0.127
	Coemansia sp. (Fu.OTU7779)	Unclassified *Cryptomycota* (Fu.OTU21900)	0.067	0.067	28	0.127
	Unclassified *fungus* (Fu.OTU13335)	Unclassified *Cryptomycota* (Fu.OTU21900)	0.067	0.067	28	0.127
	Inocybe sp. (Fu.OTU23234)	Unclassified *fungus* (Fu.OTU24067)	0.067	0.067	28	0.127
	Unclassified *Metazoa* (Fu.OTU1)	*Lobulomyces* sp. (Fu.OTU21789)	1	0.301	0	0
	Unclassified *Metazoa* (Fu.OTU1)	*Dominikia* sp. (Fu.OTU21962)	1	0.301	0	0
	Unclassified *Metazoa* (Fu.OTU1)	*Cyathus* sp. (Fu.OTU10084)	1	0.050	0	0
	Unclassified *Metazoa* (Fu.OTU1)	Unclassified *fungus* (Fu.OTU10224)	1	0.067	0	0
Within-group (Algae)	*Nannochloris* sp. (Al.OTU43)	*Chloroparvula* sp. (Al.OTU52)	0.287	0.907	43	11.178
	Tetracystis sp. (Al.OTU8)	*Crustomastix* sp. (Al.OTU100)	1	0.116	86	9.957
	Chloroparvula sp. (Al.OTU52)	*Pterosperma* sp. (Al.OTU388)	0.907	0.251	43	9.796

	Tetracystis sp. (Al.OTU8)	*Nephroselmis* sp. (Al.OTU34)	1	0.088	86	7.550
	Tetracystis sp. (Al.OTU8)	*Monomastix* sp. (Al.OTU180)	1	0.088	86	7.550
	Nannochloris sp. (Al.OTU43)	*Pterosperma* sp. (Al.OTU388)	0.287	0.251	45	3.240
	Nephroselmis sp. (Al.OTU34)	*Nautococcus* sp. (Al.OTU32)	0.088	0.448	42	1.650
	Monomastix sp. (Al.OTU180)	*Nautococcus* sp. (Al.OTU32)	0.088	0.448	42	1.650
	Nephroselmis sp. (Al.OTU34)	*Monomastix* sp. (Al.OTU180)	0.088	0.088	135	1.041
	Nephroselmis sp.Al.OTU34	*Crustomastix* sp.Al.OTU100	0.088	0.116	88	0.895
Within-group (Micro-fauna)	Unclassified *eukaryote* (Fa.OTU12)	*Mayamaea* sp. (Fa.OTU13)	1	1	3	3
	Unclassified *eukaryote* (Fa.OTU12)	*Phascolodon* sp. (Fa.OTU23)	1	1	3	3
	Mayamaea sp. (Fa.OTU13)	*Phascolodon* sp. (Fa.OTU23)	1	1	3	3
	Aplanochytrium sp. (Fa.OTU7)	Unclassified *eukaryote* (Fa.OTU12)	0	1	0	0
	Aplanochytrium sp. (Fa.OTU7)	*Mayamaea* sp. (Fa.OTU13)	0	1	0	0
	Aplanochytrium sp. (Fa.OTU7)	*Enchelyodon* sp. (Fa.OTU16)	0	1	0	0
	Aplanochytrium sp. (Fa.OTU7)	*Phascolodon* sp. (Fa.OTU23)	0	1	0	0
	Aplanochytrium sp. (Fa.OTU7)	*Prodorylaimus* sp. (Fa.OTU26)	0	0	0	0
	Unclassified *eukaryote* (Fa.OTU12)	*Prodorylaimus* sp. (Fa.OTU26)	1	0	0	0
	Mayamaea sp. (Fa.OTU13)	*Prodorylaimus* sp. (Fa.OTU26)	1	0	0	0

[a, b] denotes the species keystoneness after standardizing (Eq. 4)

[c] represents the number of togetherness units based on Eq. 9

[d] represents their cooperative effects on maximizing the functions calculated by Eq. 12