Figures

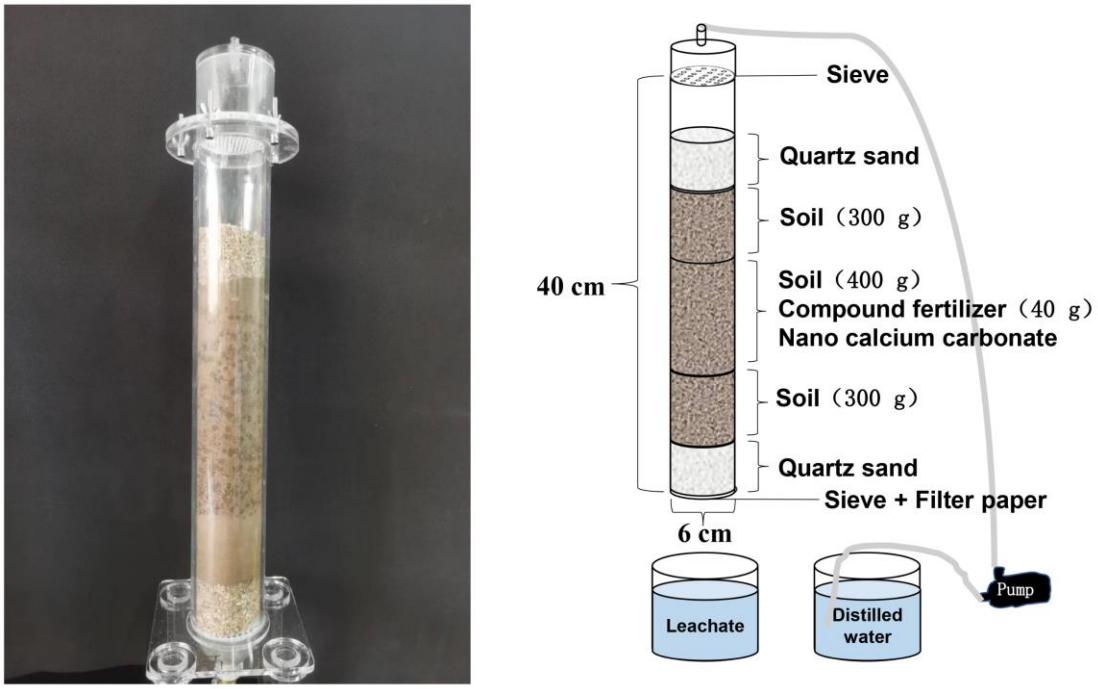

Fig. S1 Schematic diagram of soil column leaching experiment.

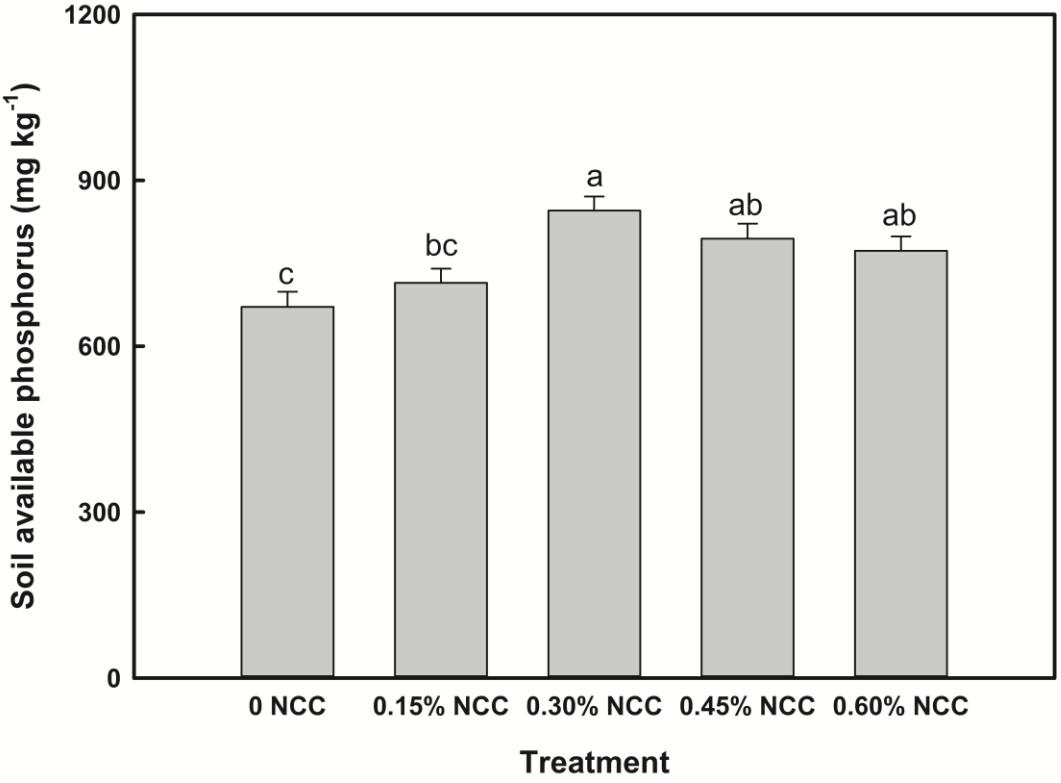

Fig. s2 Effect of NCC on soil available phosphorus content in soil column

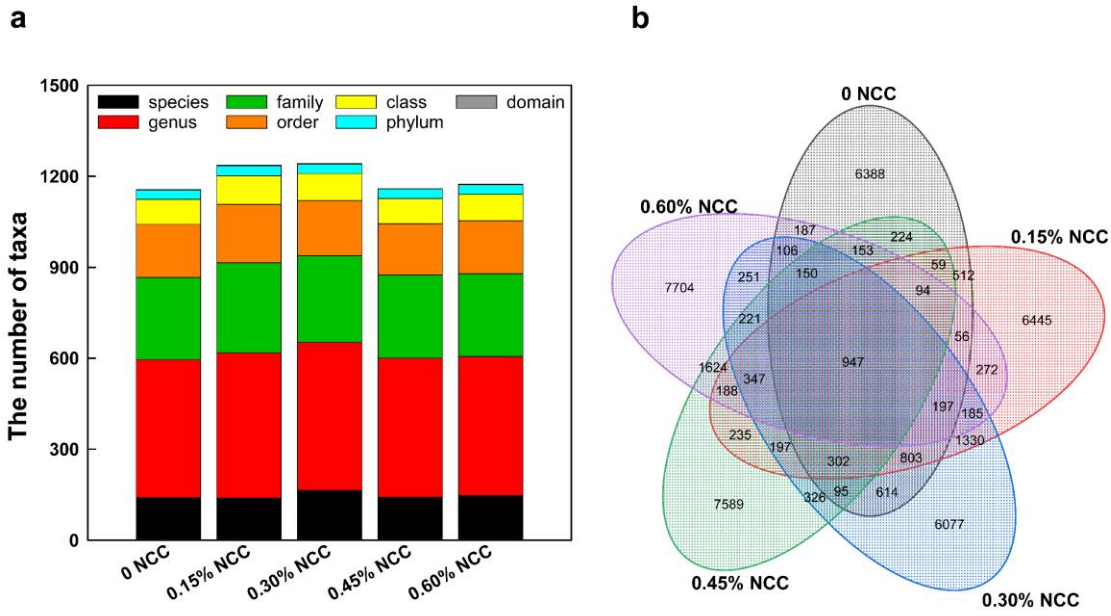

Fig. s3 Effect of NCC on the number of taxa at different classification levels (a) and OTUs (b) of soil microorganisms

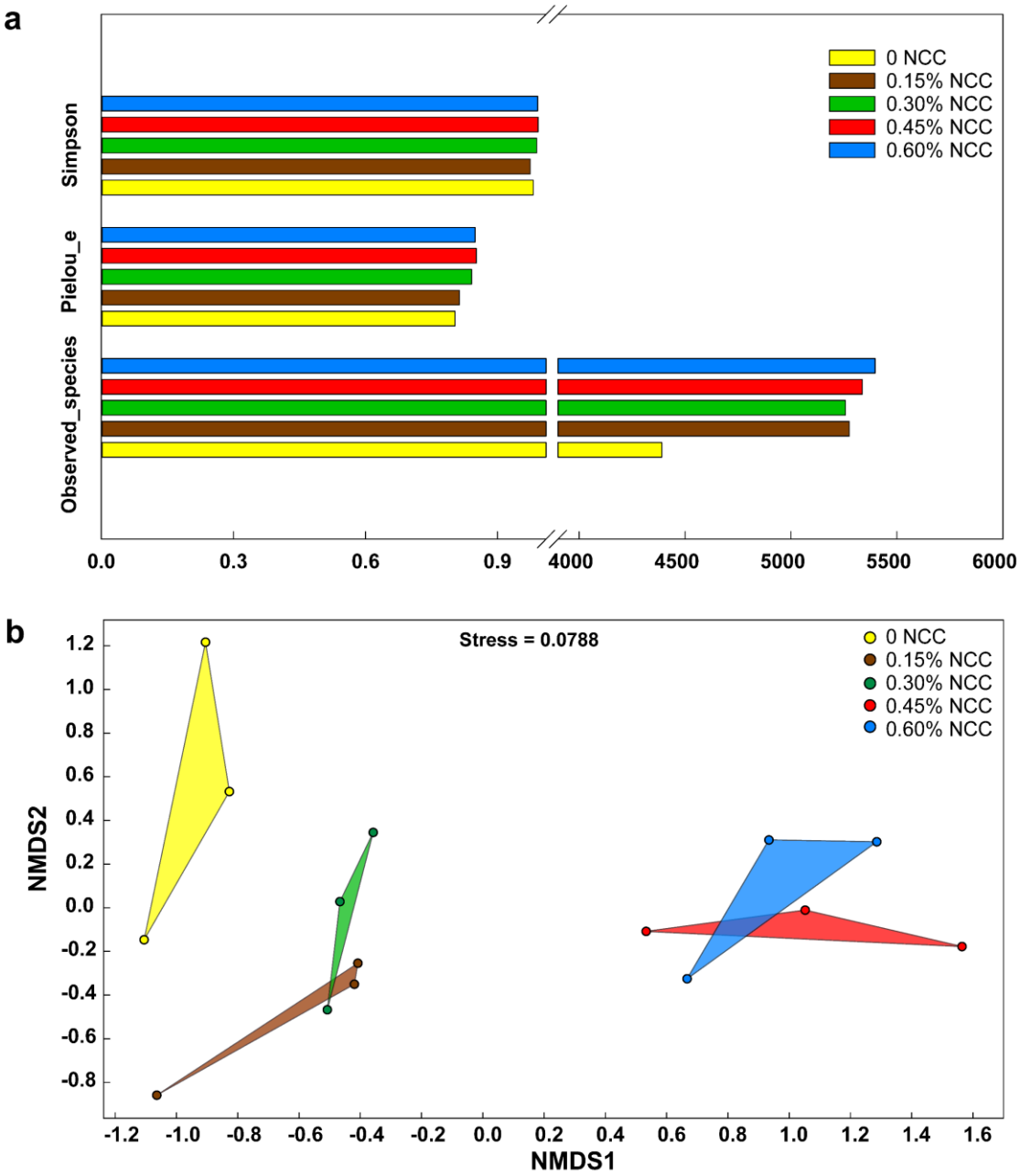

Fig. s4 Observed_species, Pielou_e and Simpson index of soil microbial communities (a). NMDS analysis of soil microbial communities based on the Bray-Curtis distance algorithm.

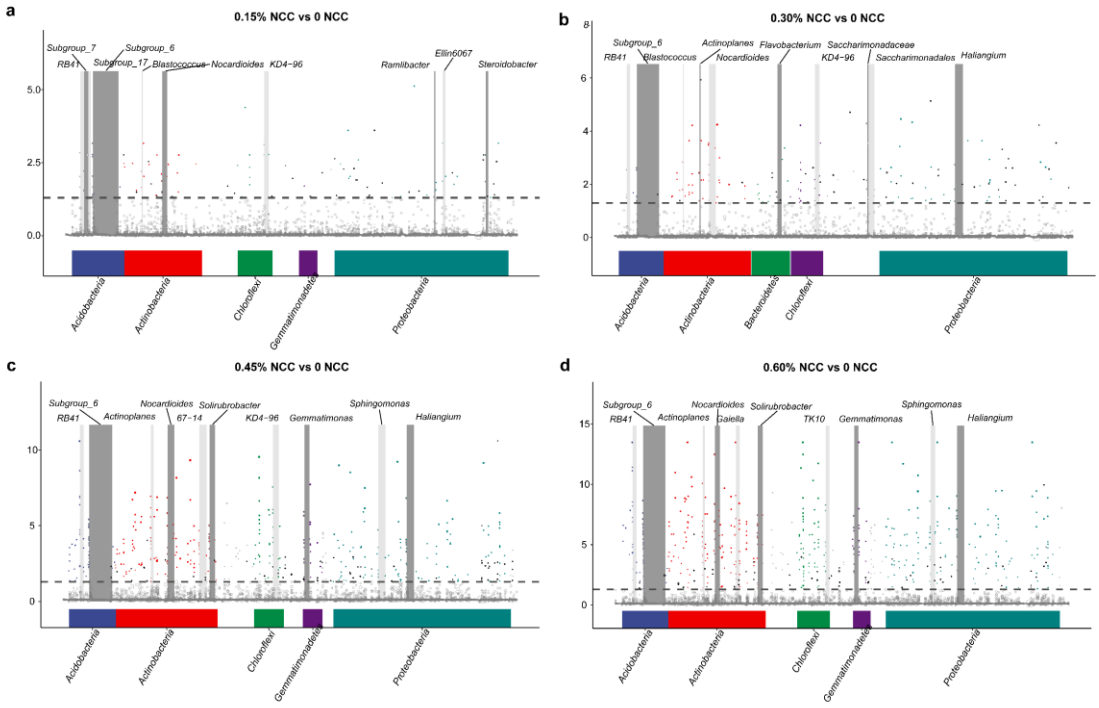

Fig. s5 MetagenomeSeq analysis of NCC treatments vs 0 NCC. The results of metagenomeSeq analyses were filtered using ASV/OTU with a frequency of occurrence greater than or equal to 0.3 (default value) in each treatment as a condition. The horizontal coordinate is the ordering of ASVs/OTUs according to their taxonomic information names (information from phylum to species); the vertical coordinate is the -log10 (adj-Pvalue) value, the more significant the difference, the higher the position of the Y-axis. Each dot or circle within the coordinate system represents 1 ASV/OTU, and the size represents its relative abundance (in log2(CPM/n); CPM: copy per million; n: sample number), and the dashed line separates the significantly different (above) from the non-significant ASVs/OTUs, with the points of significant differences marked by colored dots or circles, and the non-significant ones are indicated by gray circles, and those that are significantly up-regulated within that subgroup are shown by colored solid dots. In the figure, the color of the dots identifies their gate level name and is labeled at the bottom of the figure (gates in the top 5 of significantly up-regulated points); a grayscale background is added for genera ranked in the top 10 of significantly up-regulated points (the default value).

Tables

Table s1 Phylum-level species scores based on OPLS-DA analysis

Name	PC1	PC2	PC3
Proteobacteria	0.71806	0.119828	0.033714
Firmicutes	-0.63491	0.061278	0.085827
Chloroflexi	-0.11645	0.545747	0.178262
Actinobacteria	0.021619	-0.6046	-0.29658
Planctomycetes	-0.07434	0.153366	0.022096
Bacteroidetes	-0.06766	-0.28345	0.591275
Entotheonellaeota	0.104531	0.072089	0.084535
Rokubacteria	0.060765	0.267539	0.040479
Gemmatimonadetes	-0.13777	0.155899	-0.66037
Latescibacteria	0.037068	0.168642	-0.02691

Table s2 Genus-level species scores based on OPLS-DA analysis

Name	PC1	PC2	PC3
Bacillus	-0.40305	0.271206	0.107889
KD4-96	0.149538	0.17595	-0.16026
RB41	0.199224	0.057705	-0.04838
Actinoplanes	0.153874	-0.09426	0.182249
Nocardioides	0.118923	-0.10736	-0.09016
Lysobacter	-0.07339	-0.14049	-0.04095
Subgroup_6	0.185587	0.190207	-0.09662
Pedobacter	-0.07779	-0.10262	-0.07196
Gaiella	0.100747	0.077801	0.043546
Dongia	0.077386	0.097433	-0.0114

Field experiment sampling

Soil samples were collected from the 0-20 cm and 20-40 cm inter-root layers of wheat, with three sample points selected from each plot. Duplicate samples were collected from each plot. Following this, the samples were mixed and dried in the shade at room temperature. Once dry, the samples were sieved through a 1 mm sieve to determine AP content and ALP activity. Plant samples were obtained from above-ground sources and a total of 30 samples were taken from each plot of the same replication. All samples from the same replication were combined and separated into three categories: stems (including leaf sheaths), leaves, and spikes. These samples were then dried and pulverized using a grinder. The resulting powdered samples were sieved through a 1 mm sieve and placed in a sealed bag for future use.

Wheat inter-root soil samples were collected at five points within each plot on three occasions: May 2 (0 d after anthesis), May 23 (20 d after anthesis), and June 12 (40 d after anthesis) in 2022. The duplicate samples from each treatment area were thoroughly mixed and stored in liquid nitrogen. They were then transferred to a -80°C refrigerator for storage and subsequently transported to Shanghai Paysono

Biotechnology Co. for the determination of soil microbial community diversity.

Determination of soil microbial community diversity

Total soil RNA was extracted using the OMEGA Soil DNA Kit (Omega Bio-Tek, Norcross, GA, USA), and the quality of the extracted DNA was verified by: 1) molecular size determination using 0.8% agarose gel electrophoresis; 2) DNA quantification using an ultramicro UV spectrophotometer (NanoDrop one C Thermo Fisher Scientific, USA) for DNA quantification.

The highly variable region (V3V4) of the bacterial 16S rRNA gene was sequenced using a sequencing platform (Illumina Novaseq-PE250). PCR amplification was performed using NEB Q5 DNA high-fidelity polymerase, and primers specific for the V3-V4 region of bacterial 16S rRNA were selected for amplification with the following sequences:

F = 5'- ACTCCTACGGGGAGGCAGCA-3'

R = 5'- GGACTACHVGGGGTWTCTAAT-3'

The amplification results were subjected to 2% agarose gel electrophoresis, and the target fragments were excised and then recovered using the Axygen Gel Recovery Kit.

The PCR products were quantified on a microplate reader (BioTek, FLx800) using the Quant-iT PicoGreen dsDNA Assay Kit, and then library construction was performed using the TruSeq Nano DNA LT Library Prep Kit (Illumina, USA). After quality control and quantification, the library gradient was diluted to 2 nM, and then samples were mixed proportionally according to the required sequencing throughput, and the mixed library was denatured with 0.1 N NaOH to single-strand for 2×250 bp double-ended sequencing on the Illumina NovaSeq machine using the NovaSeq 6000 SP Reagent Kit (500 cycles).

Microbiome biological information was analyzed using QIIME2 version 2019.4.