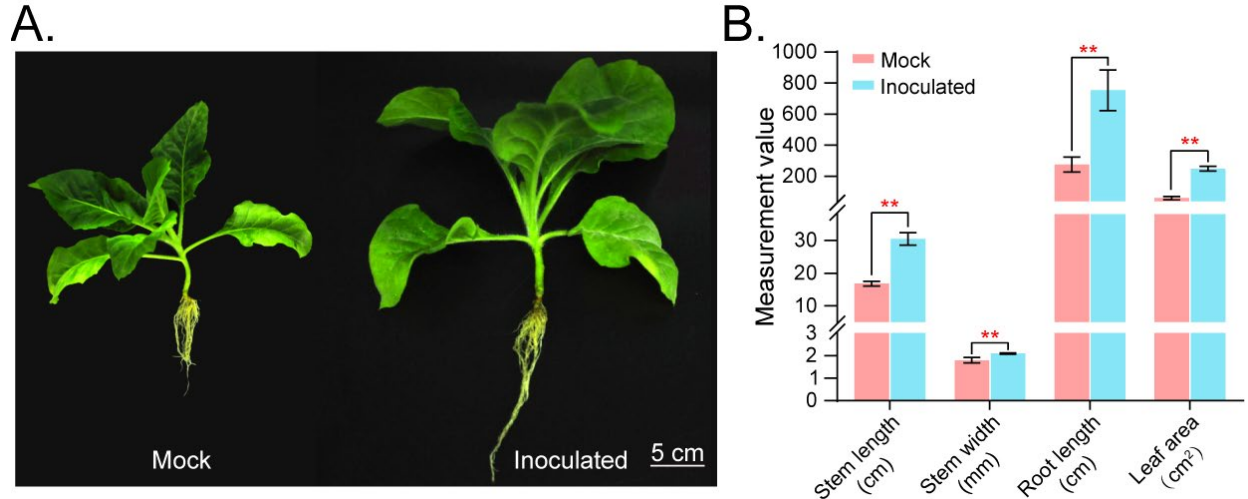
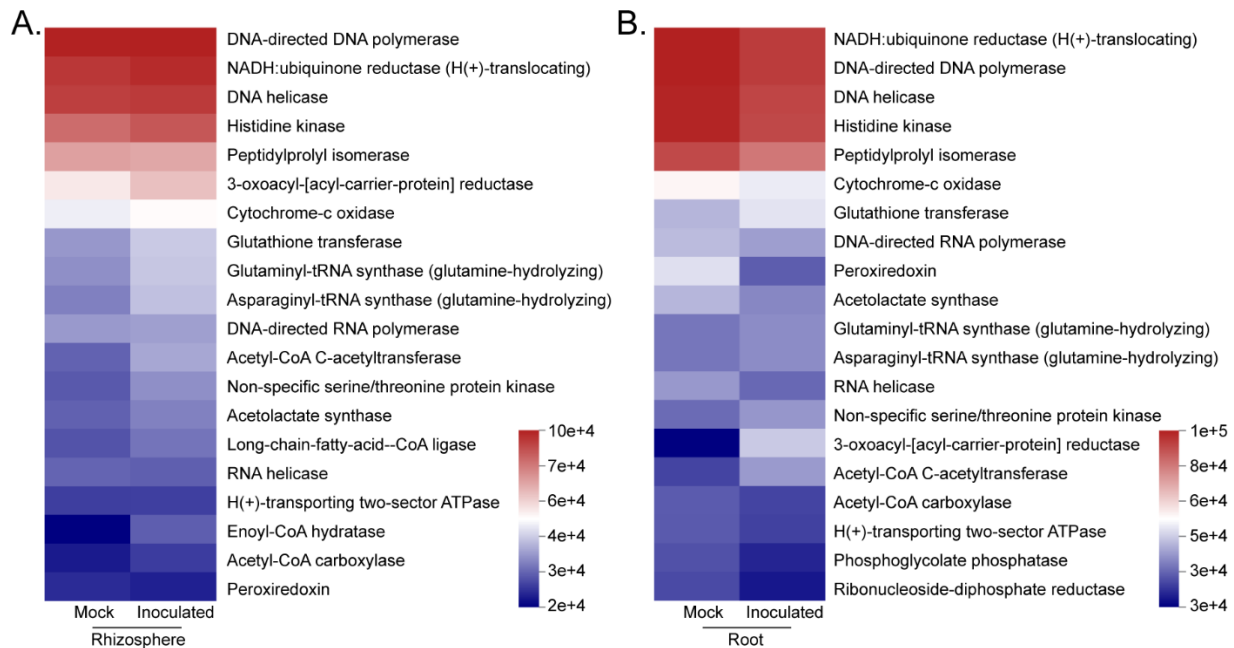


## Supplementary Material

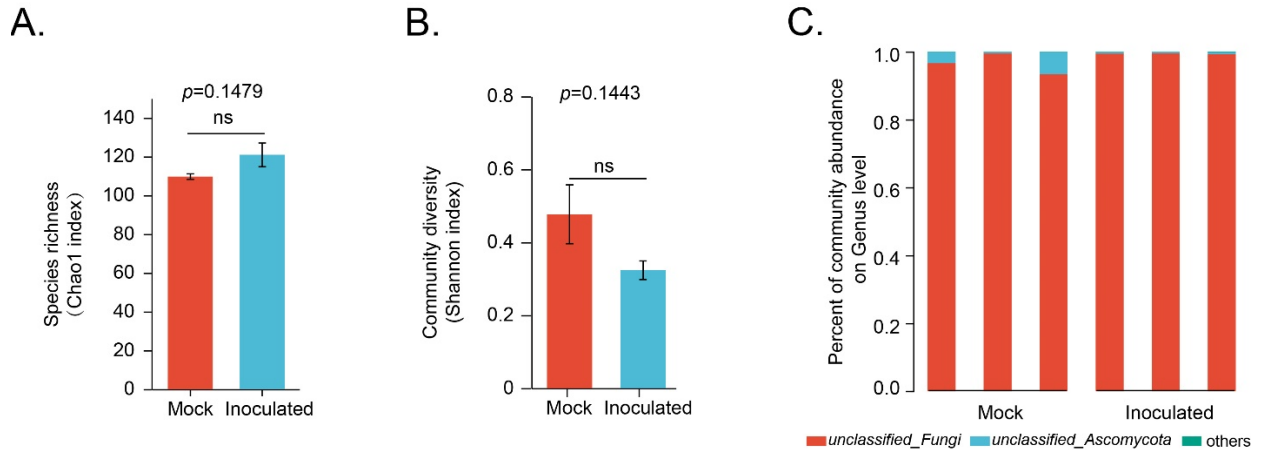
### 1. Supplementary Figures



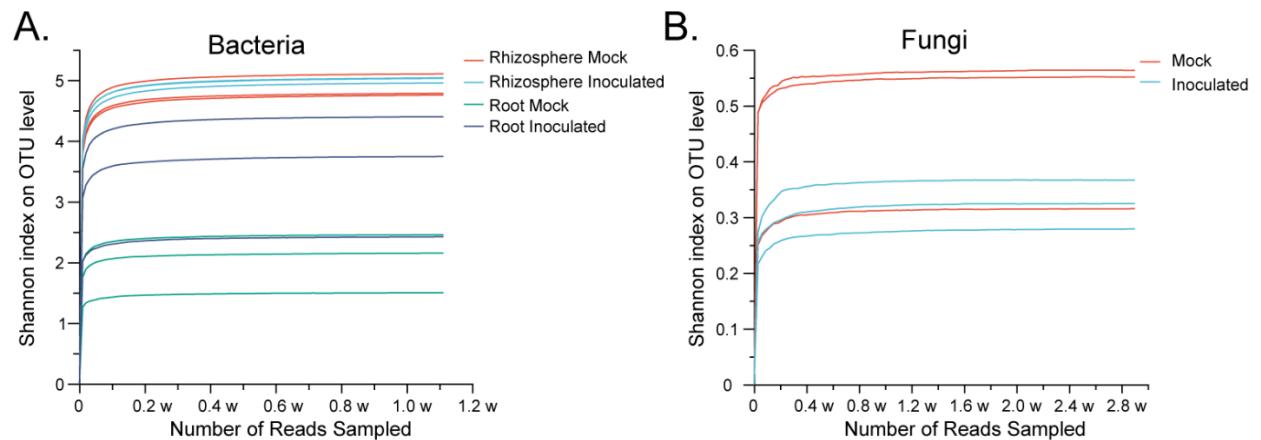
**Supplementary Fig. S1 Plant phenotype inoculated with *Bacillus paralicheniformis* RP01.** (A.) Phenotypic differences in tobacco (*Nicotiana glauca* K326) after inoculated with RP01 and without (Mock group). Scale bar represent 5 cm. (B.) The biomass of pakchoi cabbage (*Brassica chinensis*) after inoculated with RP01 and without. Leaf area is measured as the area of the third leaf from the top bud. The asterisk (\*) indicates a significant difference  $P < 0.05$  and (\*\*) indicates  $P < 0.01$ . One-way analysis of variance (ANOVA) followed by Bonferroni's post-hoc test ( $N=30$ , bars represent Mean  $\pm$  Standard error)



**Supplementary Fig. S2 Heatmap of enzyme in KEGG by PICRUSt2 function prediction.** Functional differences at rhizosphere microbiomes (A.) and cotton roots microbiomes (B.) for *B. paralicheniformis* RP01 inoculation.



**Supplementary Fig. S3 Differences in root fungal microorganism.** Chao1 index for species richness (A.) and Shannon index for community diversity (B.) of the test group. Variance analysis between groups using the Student's *t*-test. "ns" means no significant difference here. Other indexes of alpha diversity were shown in **Supplementary Table S3C**. (C.) Relative abundance at the genus level in different samples.



**Supplementary Fig. S4 Microbiota rarefaction curves.** Shannon index plot at the operational taxonomic unit (OTU) level with 97% similarity for bacteria (A.) and fungi (B.).

## 2 Supplementary Tables

**Table S1: The solubilization ability test of Phosphate-solubilizing bacteria.**

Strain	Soluble phosphorus content/(mg/L)	pH
CK	26.8±5.18 d	6.02 a
P1(RP01)	129±11.89 a	4.26 b
P2	45.2±5.03 c	4.38 b
P3	48.2±6.40 c	4.42 b
P4	84.9±7.65 b	4.43 b
P5	41.0±2.42 c	4.44 b
P6	45.9±5.24 c	4.30 b

Note: Different letters (a, b, and c) indicate a significant difference at  $P < 0.05$ , and the same letter indicate no significant difference here between groups it represents (n=3, bars represent the mean ± standard error, statistical tests: one-way ANOVA by Bonferroni's post-hoc test).

**Table S2: Physiological and biochemical characteristics of *B. paralicheniformis* RP01.**

Strain	RP01
Catalase test	+
Starch hydrolysis test	-
D-glucose produced acid test	+
D-xylose produced acid test	+
D-glucose produced gas test	-
methyl red test	-
Voges-Proskauer test	+
Citrate utilization test	+
gelatin liquefaction test	+
phenylalanine deaminase test	-

All test strains were cultivated for 16 h at 37 °C. Note: “+”present positive reaction, “-”present negative reaction.

**Table S3: Alpha diversity indexes after inoculated with *B. paralicheniformis* RP01. for rhizosphere bacteria (A.), root bacteria (B.) and root fungi (C.). See excel file named Supplementary file Table S3.**

**Table S4: Significant differences on genus level after inoculated with *B. paralicheniformis* RP01. At rhizosphere (A.) and cotton roots (B.). See excel file named Supplementary file Table S4.**

**Table S5: Gene annotations blasted in 6 major databases (NR, Swiss-Prot, Pfam, EggNOG, GO and KEGG). (A.) Gene count statistics for six databases. (B.) Gene detail tables summarized from six databases. See excel file named Supplementary file Table S5.**

**Table S6: Carbohydrate-active enzyme annotation prediction in RP01. (A.) Carbohydrate-active enzyme categorical statistics in RP01. (B.) Gene detail tables of carbohydrate-active**

enzyme prediction. See excel file named Supplementary file Table S6.

**Table S7: Secondary metabolites biosynthetic gene clusters prediction in RP01. (A.)**

Statistics of secondary metabolites synthesis gene clusters. **(B.)** Gene detail table of secondary metabolites synthesis gene clusters. See excel file named Supplementary file Table S7.

**Table S8: Antibiotic Resistance prediction of RP01. (A.)** Classification statistics of antibiotic resistance genes. **(B.)** Detail table of antibiotic resistance genes. See excel file named Supplementary file Table S8.

**Table S9: The homologous genes and unique genes in the genome of RP01 compared with the other three strains. (A.)** The homologous genes in the genome of the four strains. **(B.)** The unique genes in the genome of RP01 compared with the other three strains. See excel file named Supplementary file Table S9.

**Table S10: Primers for qRT-PCR.**

Gene name	Forward primer (5'--3')	Reverse primer (5'-3')
<i>Histone3</i>	GCCAAGCGTGTGTCACAATTATGC	ACATCACATTGAACCTACCACTA
<i>YUCCA4</i>	TCTGGTCTAGCAACATCCGC	TGAGGGAAACCAAGGAGTGG
<i>AUX1</i>	TTAACCCTTCCATCCGCTTC	TCTCCACACGAAGTACAATG
<i>GA20ox</i>	TTTACAAGAGCCGCTTGAC	ACAAAGCCCAGCATTGTCC
<i>GA3ox</i>	ATGGAACCAACGCGACGATA	GTCGGGACAAGCTGGGTAAT
<i>BES1</i>	GGCTTGAGGCAATACGGTAATT	AGGCGGCTAGCACATCGTT
<i>ICS1</i>	ATGGATGAATGGGTGCGAAGG	AAGAATGCCAGAGGTAAGAGGA
<i>EDS1</i>	GCAGCAACAGCTCCTCTACCTCA	GGCAGACCAAGACGCTACAGATA
<i>AOC1</i>	CTCCCAAGCCCACAAAAGTT	ACAGAGTCCAGCCGTGATGC
<i>OPR3</i>	TGGAAGATGATTGTGGATGCTG	GAGATGGGTTTGTGTTGAGGA
<i>TCP</i>	CATCCGAACCCAGATATGG	TGTAAGGGTGCTTGCAATGTG
<i>PDF1.2</i>	CTGTGGTAGCGGATGGTGATAAG	GTGCAGACGCATTTGCGAAGGA
<i>ERF1</i>	CCAAGTTCCGACAATGTTATGC	CCAACAGCTCGTCCGACAA
<i>PAD4</i>	GGATGGAAGAATGGAAAGAAAT	GAAGTAGGAAAGCAGACTAAGG