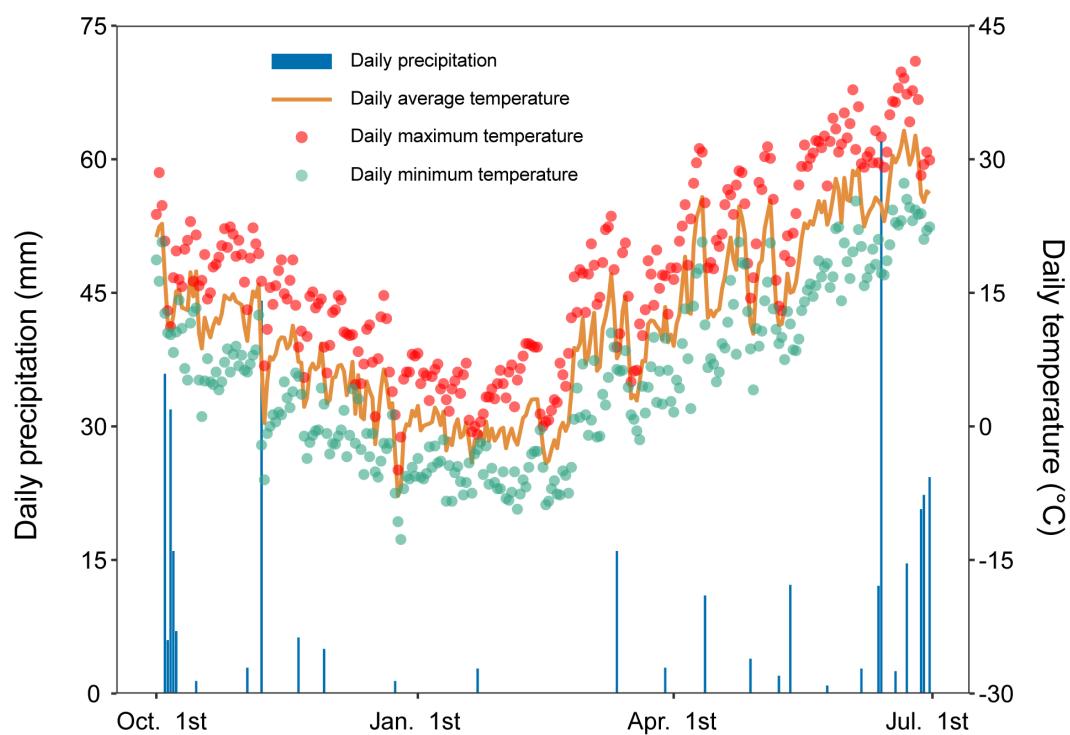


1 Supplementary figures



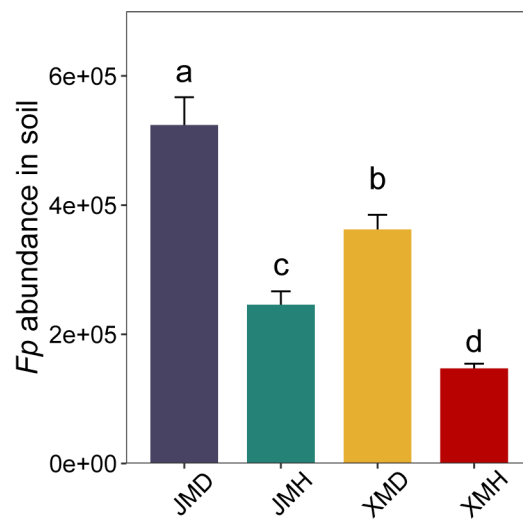
2

3 Supplementary Figure 1

4 Daily precipitation (mm) and temperature (°C) during the 2021–2022 winter wheat growing season.

5 The average temperature is calculated as the mean of the daily maximum and minimum temperatures.

6

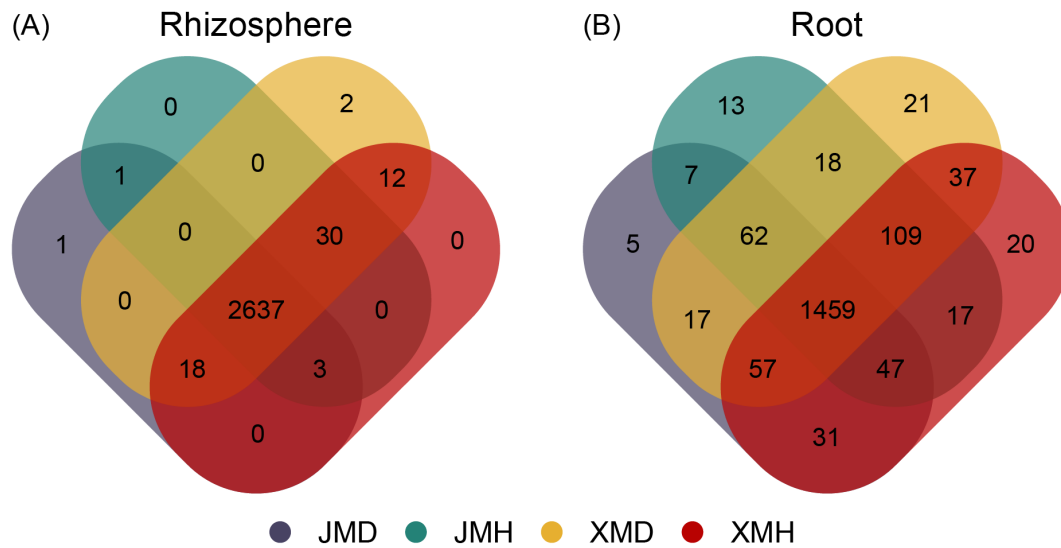


7

8 **Supplementary Figure 2**

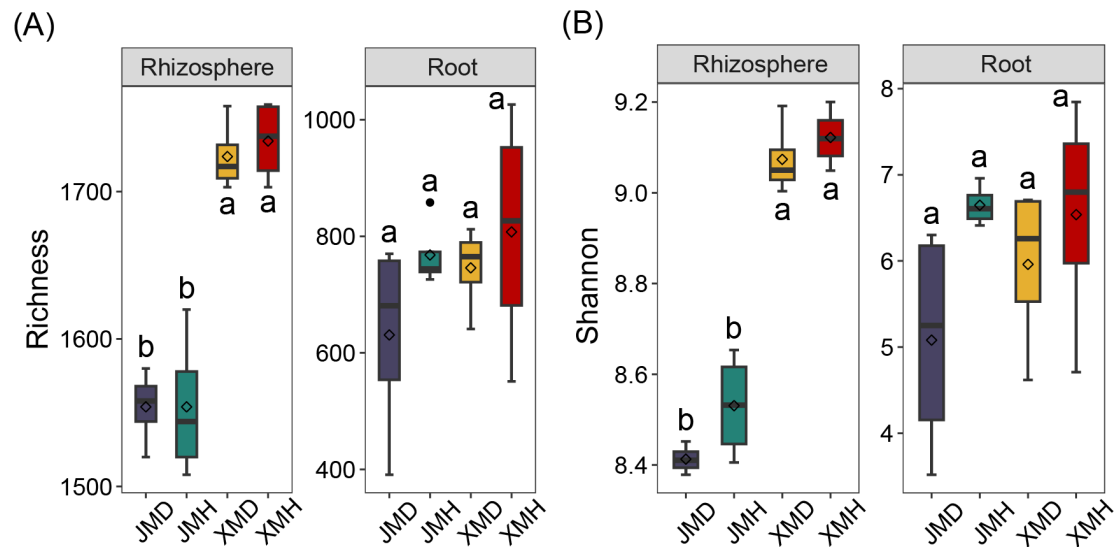
9 Abundance of *Fp* in the rhizosphere soil. Data are shown as mean $\pm$ standard error ($n = 4$). Different
10 lowercase letters indicate significant differences between groups (Duncan's test, $P < 0.05$). JMD and
11 JMH: diseased and healthy samples of cv. JM22, respectively; XMD and XMH: diseased and healthy
12 samples of cv. XM26, respectively.

13



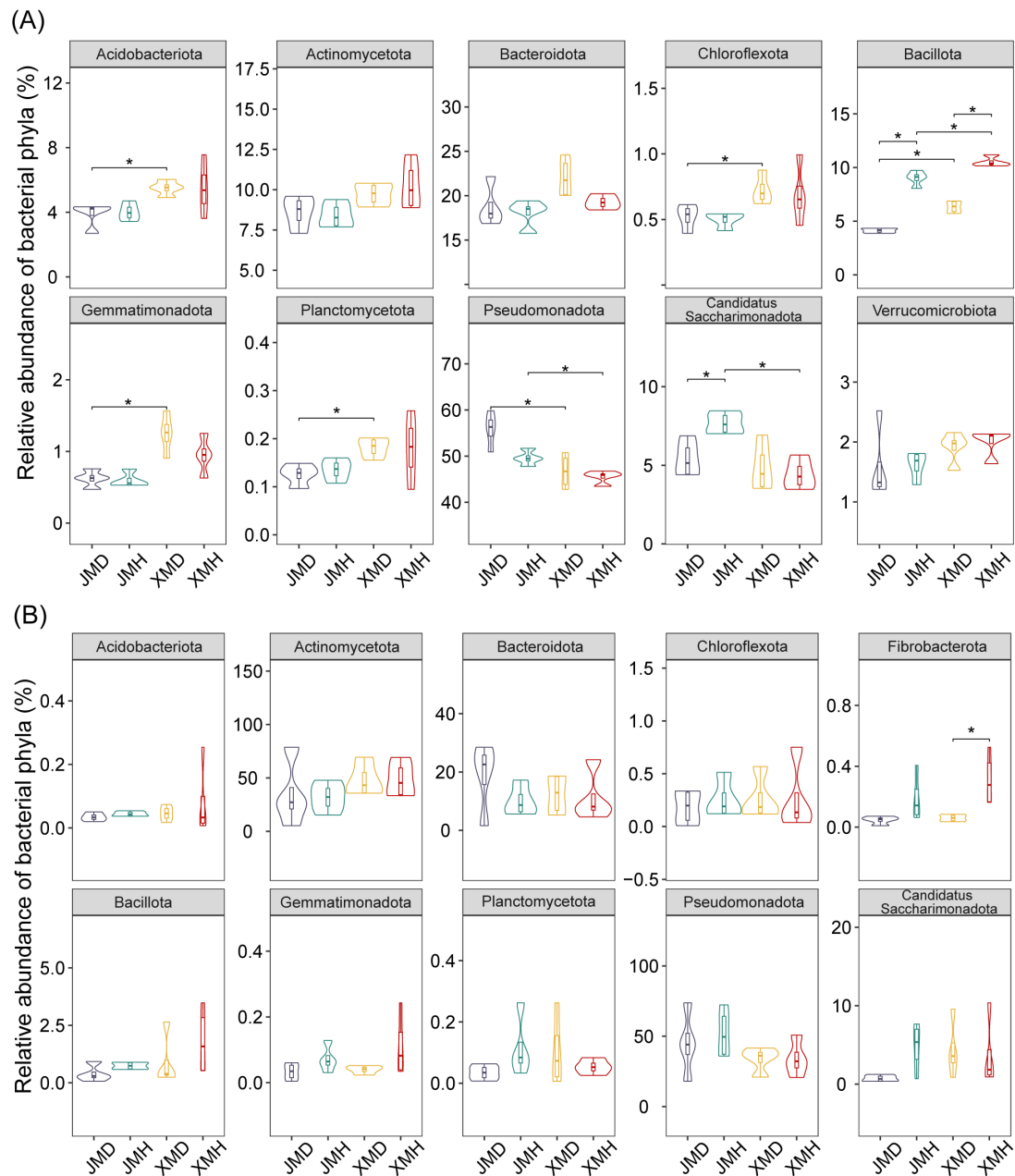
Supplementary Figure 3

Venn diagrams showing the shared and specific bacterial ASVs across different genotypes and health statuses in the rhizosphere (A) and root endosphere (B) microbiome. JMD and JMH: diseased and healthy samples of cv. JM22, respectively; XMD and XMH: diseased and healthy samples of cv. XM26, respectively.



Supplementary Figure 4

Alpha diversity of bacterial communities in the rhizosphere and root endosphere. (A) Comparison of the richness index between groups. (B) Comparison of the Shannon index between groups. Box boundaries represent the 25th and 75th percentiles, the internal line represents the median, and the open diamond indicates the mean. Whiskers extend to the most extreme data points within 1.5 times the interquartile range from the box edges. Black dots beyond the whiskers represent outliers. Different letters indicate significant differences at $P < 0.05$ based on Duncan's test. JMD and JMH: diseased and healthy samples of cv. JM22, respectively; XMD and XMH: diseased and healthy samples of cv. XM26, respectively.

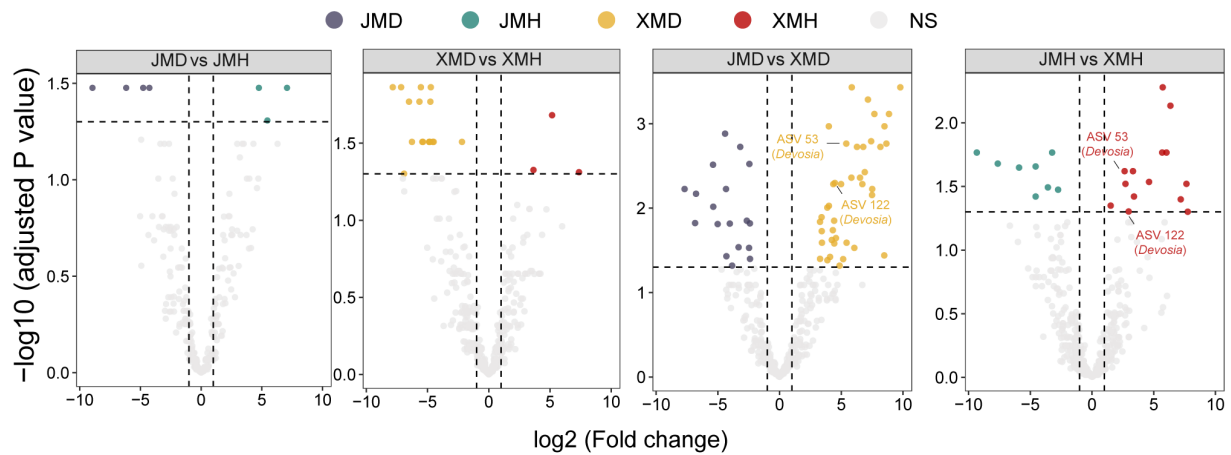


Supplementary Figure 6

Comparison of the relative abundance of bacterial phyla in rhizosphere **(A)** and root endosphere **(B)** communities across cultivars and health statuses. Box boundaries represent the 25th and 75th percentiles, and the internal line represents the median. Whiskers extend to the most extreme data points within 1.5 times the interquartile range from the box edges. The shaded areas surrounding the box plots are violin plots illustrating the distribution of the data. Asterisks indicate statistically significant differences between groups: * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$ (Wilcoxon test). "ns" indicates no significant difference. JMD and JMh: diseased and healthy samples of cv. JM22,

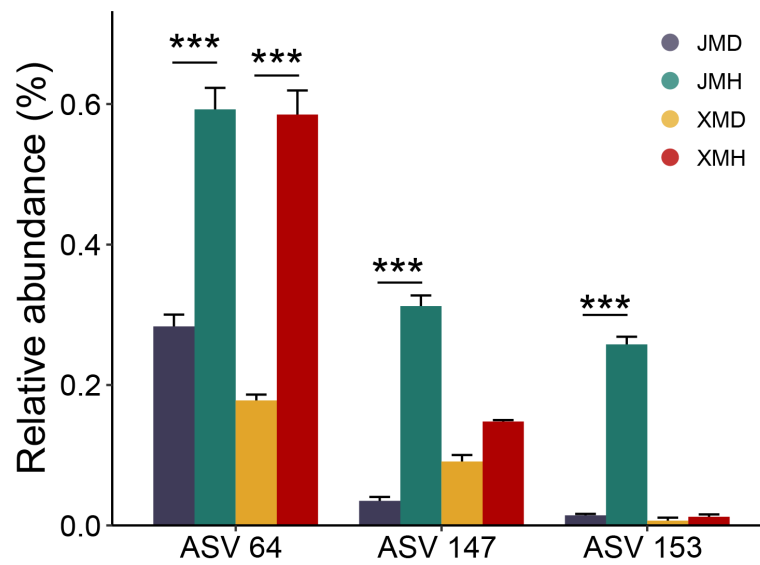
51 respectively; XMD and XMH: diseased and healthy samples of cv. XM26, respectively.

52



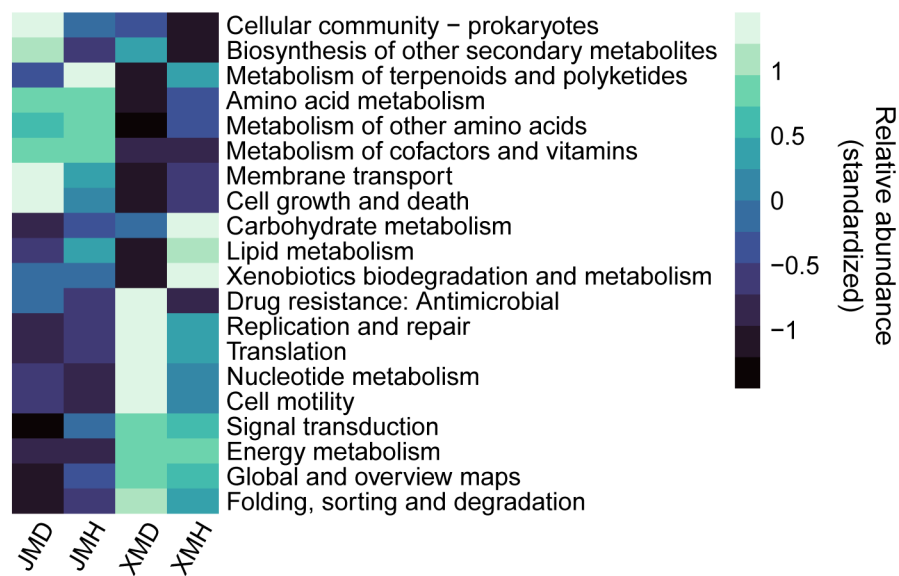
Supplementary Figure 7

Volcano plots displaying enriched and depleted ASVs in the root endosphere microbiome. Colored points represent ASVs with $|\log_2(\text{fold change})| > 1$ and an FDR-adjusted $P < 0.05$. JMD and JMH: diseased and healthy samples of cv. JM22, respectively; XMD and XMH: diseased and healthy samples of cv. XM26, respectively.



Supplementary Figure 8

Comparison of the relative abundance of ASV 64, ASV 147, and ASV 153 in the rhizosphere microbiome. Asterisks indicate statistically significant differences between groups: *** $P < 0.001$ (Student's t-test). JMD and JMH: diseased and healthy samples of cv. JM22, respectively; XMD and XMH: diseased and healthy samples of cv. XM26, respectively.

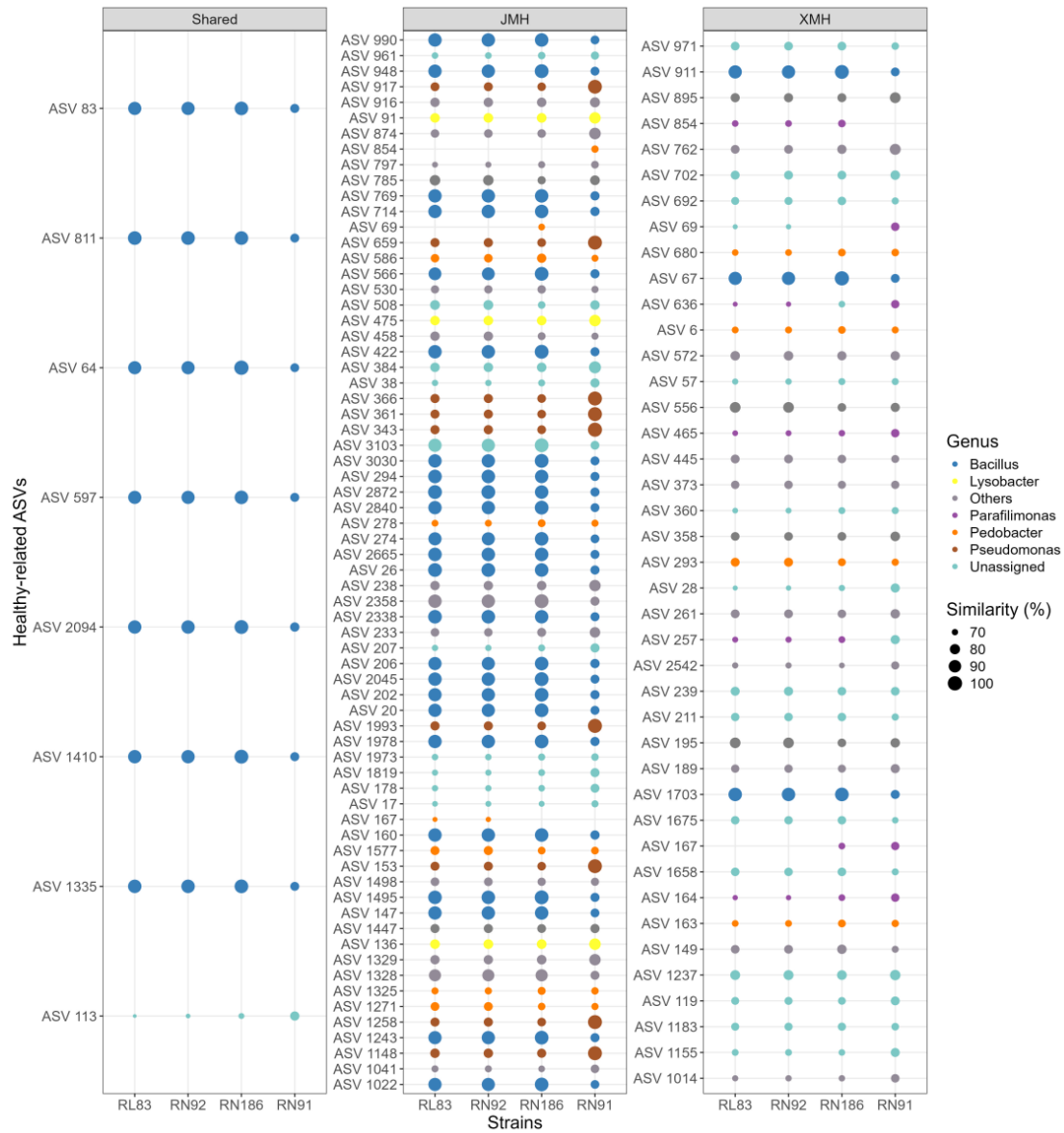


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68 **Supplementary Figure 9**

69 Functional prediction of the rhizosphere microbiome using the Tax4Fun2 package. The relative
 70 abundances of functional pathways are standardized by Z-score method. JMD and JMH: diseased and
 71 healthy samples of cv. JM22, respectively; XMD and XMH: diseased and healthy samples of cv. XM26,
 72 respectively.

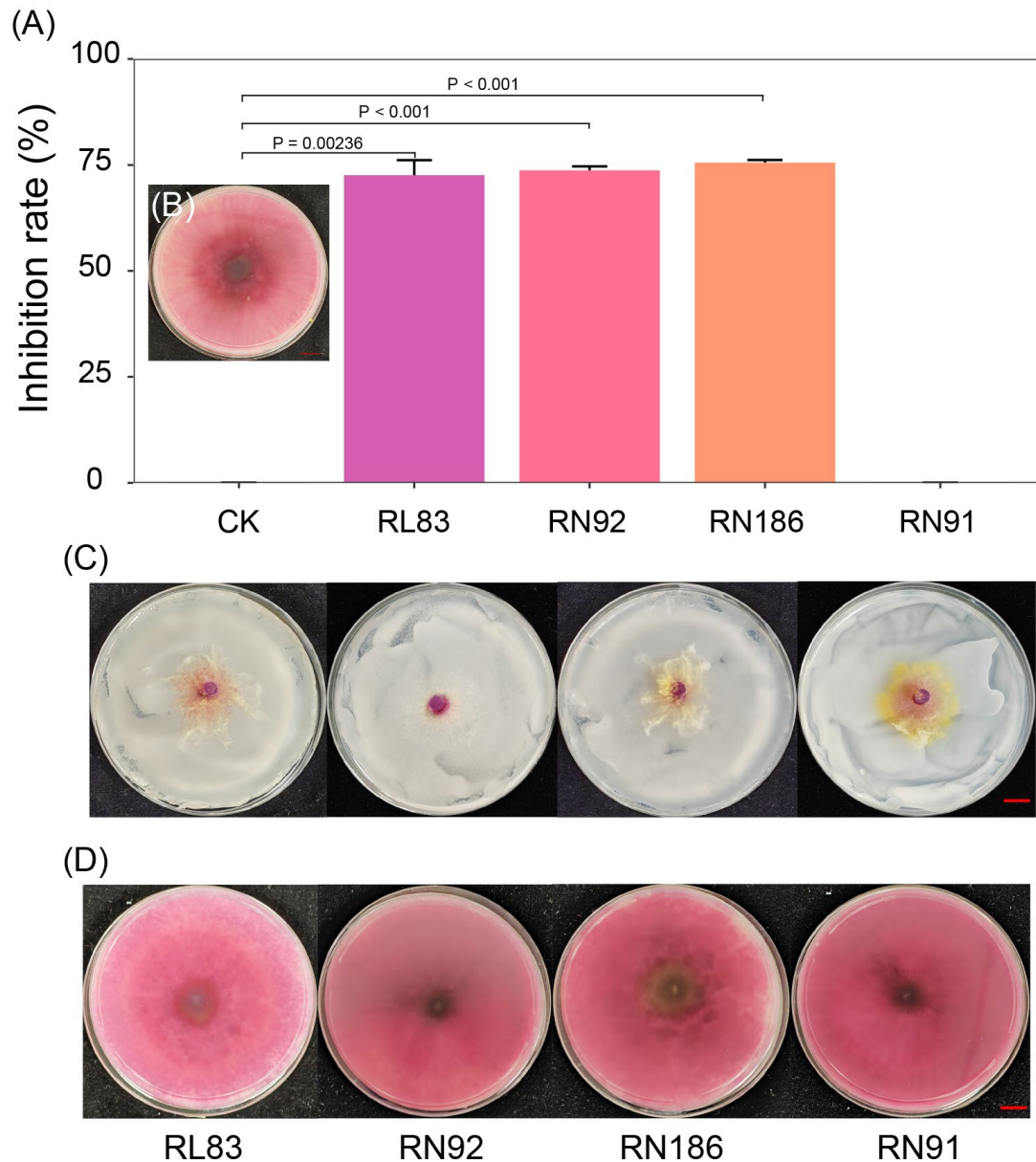
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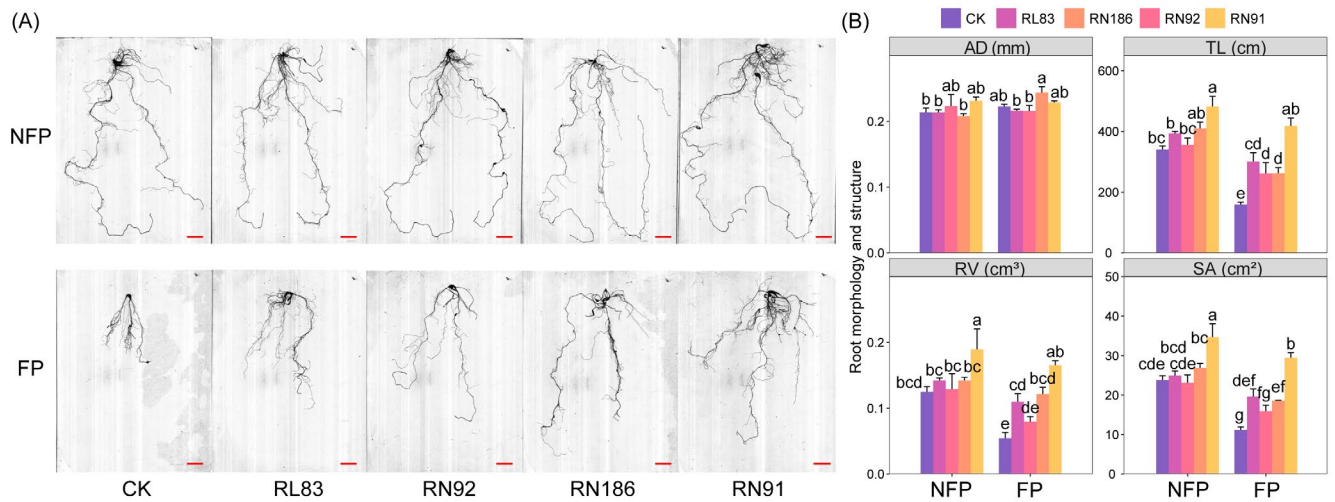
75 **Supplementary Figure 10**

76 Sequence similarity between isolated bacterial strains and ASVs enriched in the healthy wheat
 77 rhizosphere. Facet definitions: Shared, ASVs co-enriched in the healthy rhizosphere of both cultivars;
 78 JMH and XMH, ASVs uniquely enriched in the healthy rhizosphere of cv. JM22 and cv. XM26,
 79 respectively. Bubble color and size represent the bacterial genus and nucleotide similarity,
 80 respectively.



Supplementary Figure 11

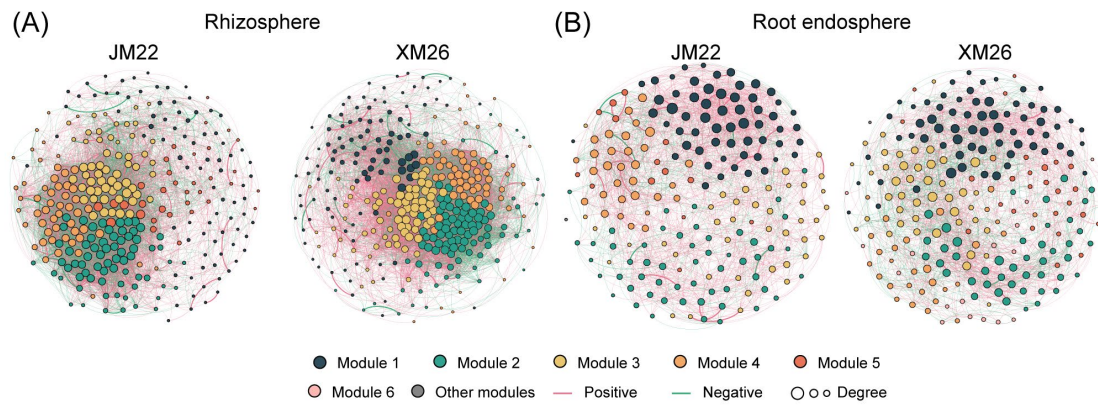
(A) Inhibitory effect of the isolated strains against *Fp* on PDA using a dual-culture assay. (B) *Fp* cultured alone served as the negative control (CK). (C) Antagonistic activity of the bacteria against *Fp* evaluated using a spread-plate assay. (D) Antagonistic activity of the bacteria against *Fp* evaluated using a cell-free supernatant assay. Statistical differences between inoculation treatments and CK are determined using Student's t-test ($P < 0.05$). The red line indicates 1 cm.



Supplementary Figure 12

(A) Scanning images of wheat seedling roots from the pot experiment. The red line represents 2 cm.

(B) Traits of root system architecture extracted from the scanning images. AD: average diameter, TL: total root length, RV: root volume, SA: total surface area. Different lowercase letters indicate significant differences between groups (Duncan's test, $P < 0.05$). FP and NFP: treatments inoculated and non-inoculated with the pathogen *Fp*, respectively. CK: control treatment without isolated strains. RL83, RN186, RN92, and RN91: treatments inoculated with the respective isolated strains.



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Supplementary Figure 13

100

Bacterial co-occurrence network patterns in the rhizosphere (A) and root endosphere (B) of two

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wheat cultivars. Networks were constructed using the same data as in Fig. 4, but nodes are colored

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by network modules. Node size represents degree. Red and green edges indicate positive and

103

negative correlations, respectively, with edge thickness reflecting the strength of the correlation.

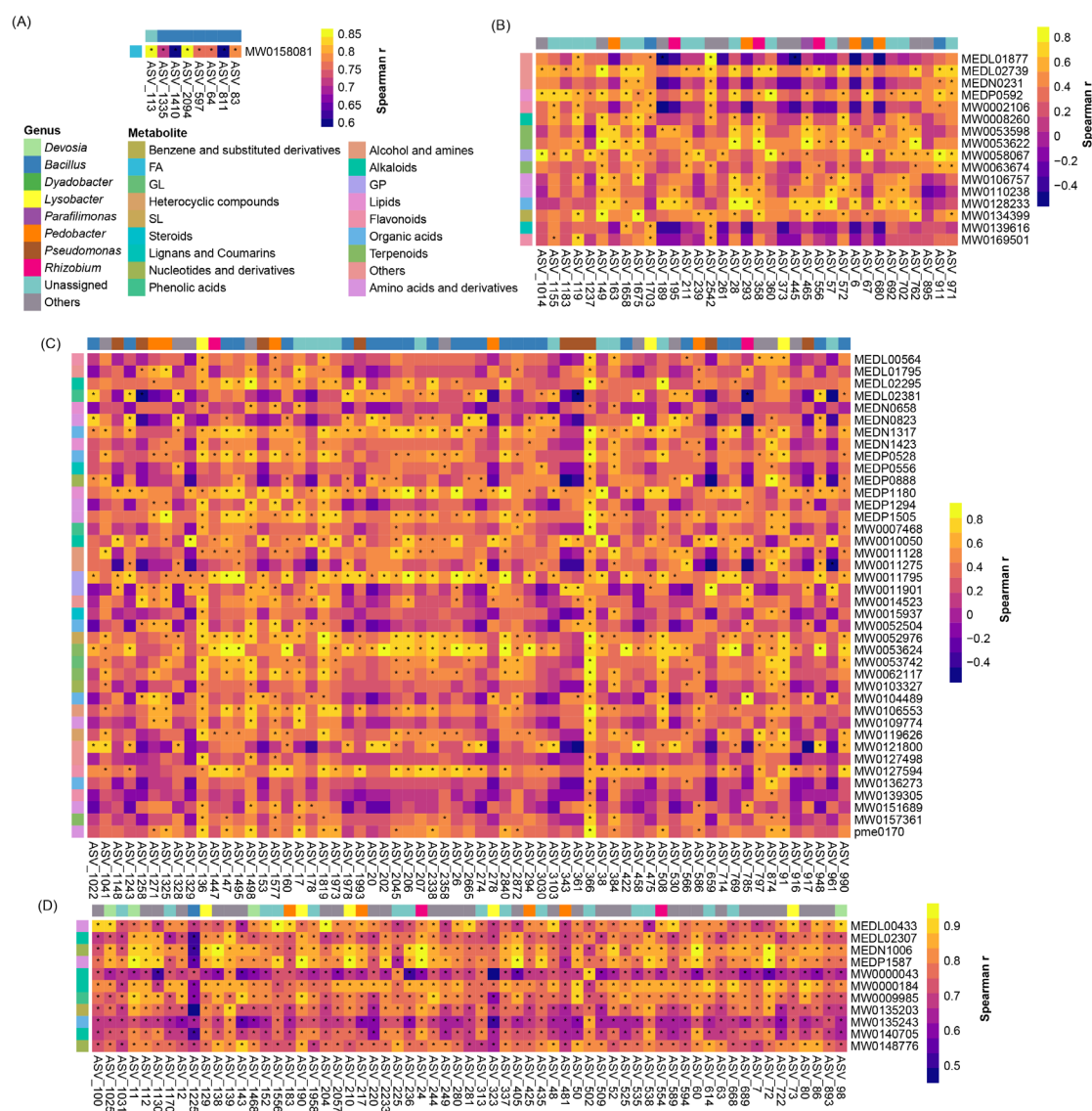
104

(A)



Supplementary Figure 14

Pie charts showing the proportion of different chemical classifications of differentially abundant metabolites (DAMs) in the rhizosphere of healthy JM22 and XM26 plants (A), and specifically in JM22 and XM26 (B).



Supplementary Figure 15

Heatmaps illustrating correlations between enriched ASVs and DAMs. (A) Correlation in the healthy rhizosphere of both cultivars. (B) Correlation in the healthy rhizosphere of XM26. (C) Correlation in the healthy rhizosphere of JM22. (D) Correlation in the rhizosphere of XM26. Asterisks indicate significant correlations (FDR-adjusted $P < 0.05$). Detailed information on DAMs is provided in Supplementary Table 6.

118 **Supplementary tables**

119 **Supplementary Table 1** Primer pairs used in this study.

Gene	Forward primer	Reverse primer
<i>Tri5</i>	5'-GCGCATCGAGAATTTGCA-3'	5'-TGGCGAGGCTGAGCAAAG-3'
<i>WABP</i>	5'-CGCGAGGACAAGATGCTGTA-3'	5'-CACGTCGATCTGCACGCC-3'
<i>PAL</i>	5'-CGTTATGCTCTCCGAACATC-3'	5'-GAAGTTGCCACCATGTAAGG-3'
<i>AOS</i>	5'-TCTCTTCCTCTTCCTTCTCTTCACC-3'	5'-CGCCGGGTATAGTCCTGGTAGATA-3'
338F/806R	5'-ACTCCTACGGGAGGCAGCA-3'	5'-GGACTACHVGGGTWTCTAAT-3'
799F/1193R	5'-AACMGGATTAGATACCCKG-3'	5'-ACGTCATCCCCACCTTCC-3'
27F/1492R	5'-AGRGTTTGATYNTGGCTCAG-3'	5'-TASGGHTACCTTGTTASGACTT-3'

120

121 **Supplementary Table 2** Effects of cultivars, heath status, and their interaction on bacterial community
122 structure in the rhizosphere and root endosphere based on PERMANOVA.

	Rhizosphere		Root	
	R ²	P	R ²	P
Cultivar (C)	0.28	< 0.001	0.09	0.020
Status (S)	0.11	0.015	0.08	0.094
C × S †	0.1	0.013	0.07	0.353

123 PERMANOVA is calculated by Adonis function. † C × S indicate the interaction of cultivars and status.

124

125 **Supplementary Table 3** Differential enrichment analysis of bacterial ASVs across wheat cultivars and
126 health statuses in the rhizosphere.

127

128 **Supplementary Table 4** Characteristics of potentially beneficial strains isolated from the rhizosphere
129 soil of healthy plants.

Strains	Source	Genus
RL83	JMH	<i>Bacillus</i>
RN92	JMH	<i>Bacillus</i>
RN186	JMH	<i>Bacillus</i>
RN91	JMH	<i>Pseudomonas</i>
RN100	XMH	<i>Bacillus</i>
RN80	XMH	<i>Bacillus</i>

130

131 **Supplementary Table 5** Topological parameters of bacterial co-occurrence networks of two winter

132 wheat cultivars in the rhizosphere and root endosphere.

Parameters	Rhizosphere		Root endosphere	
	JM22	XM26	JM22	XM26
Node number	297	337	199	229
Edge number	8142	12328	2207	2331
Average degree	54.83	73.16	22.18	20.36
Clustering coefficient	0.62	0.63	0.51	0.46
Average path length	2.28	2.18	2.45	2.55
Graph diameter	5	5	5	5
Graph density	0.19	0.22	0.11	0.09
Betweenness centralization	0.014	0.007	0.02	0.02
Degree centralization	0.22	0.22	0.15	0.11
Modularity	0.19	0.2	0.42	0.41

133

134 **Supplementary Table 6** Regulatory patterns and characteristics of differentially abundant metabolites
135 (DAMs) in the rhizosphere.

136