Supplementary Materials:

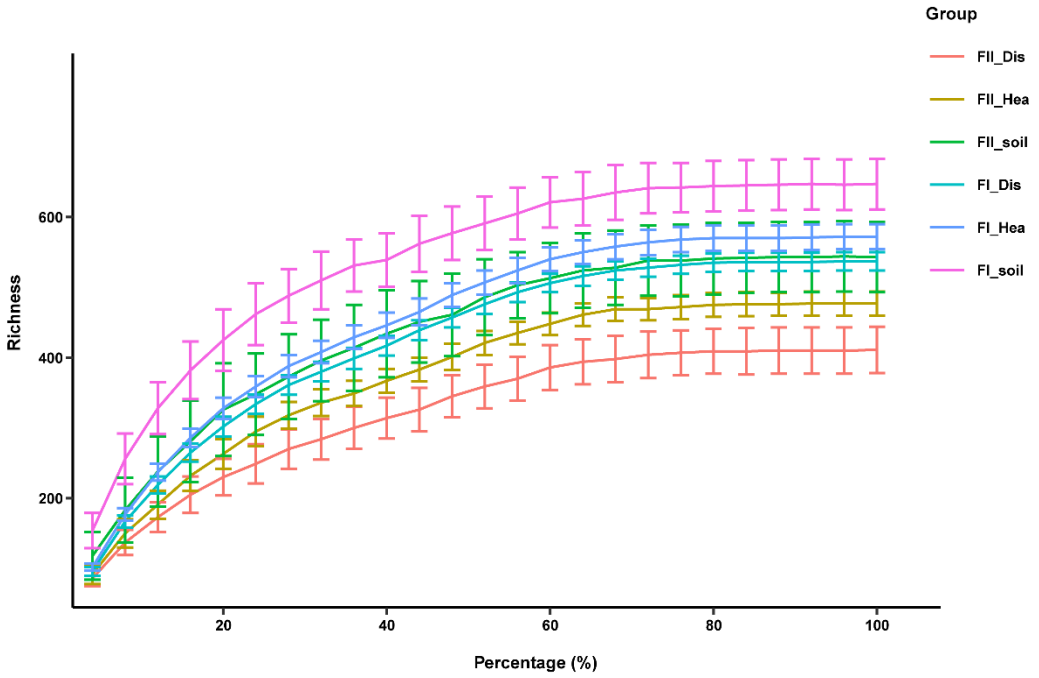


Figure S1. Rarefaction curves showing OTU richness of microbial communities in the *F. tataricum* rhizosphere.

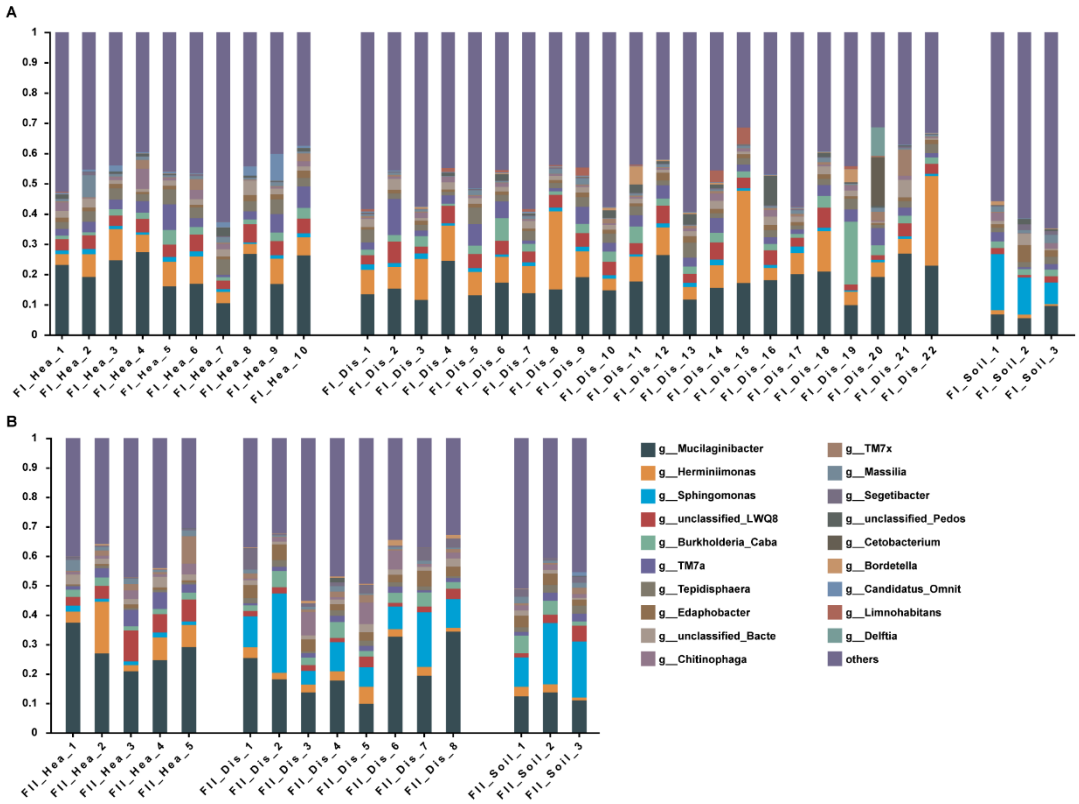


Figure S2. Cumulative analysis of the relative abundance of rhizosphere microbial communities at the genus level in Field I and

Field II. The numbers above each box represent OTU richness (i.e., the number of OTUs) in each sample. (A) In Field I; (B) In Field II.

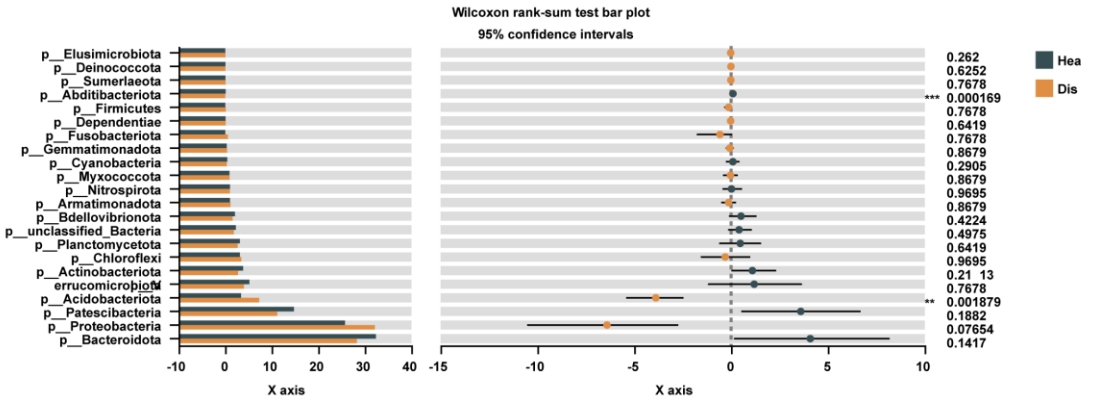


Figure S3. Taxonomic characteristics of differential bacteria at the phylum level between healthy and diseased rhizosphere microbiota. Statistical comparisons were conducted using the Wilcoxon rank-sum test. Asterisks (*) denote a significant difference with a p-value < 0.05.

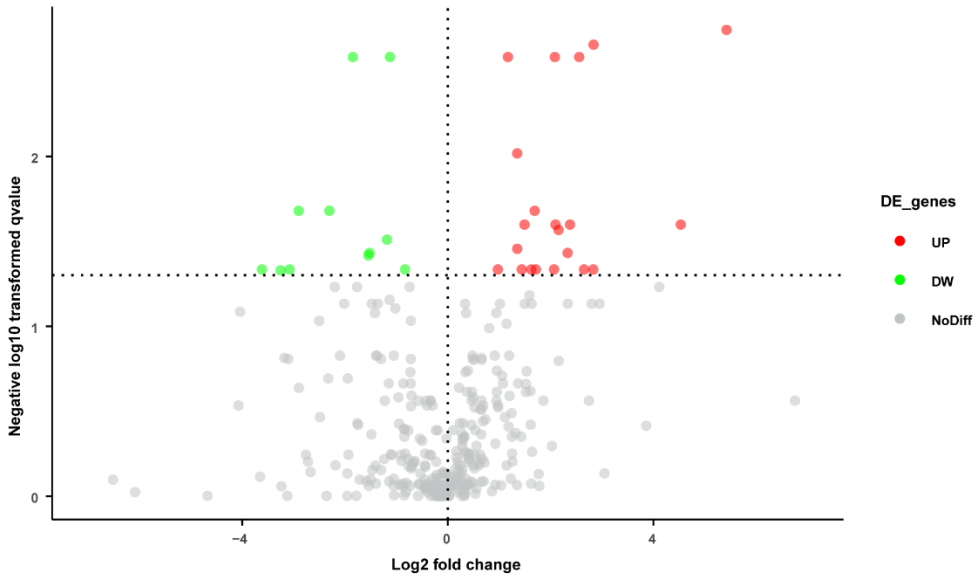


Figure S4. Volcano plot of taxonomic characteristics of differential bacteria at the genus level between healthy and diseased rhizosphere microbiota. Statistical comparisons were conducted using the Wilcoxon rank-sum test. Red indicates bacterial genera enriched in the healthy rhizosphere, while green represents those enriched in the diseased rhizosphere. Gray points represent no significant difference between the two groups. A p-value < 0.05 denotes a significant difference.

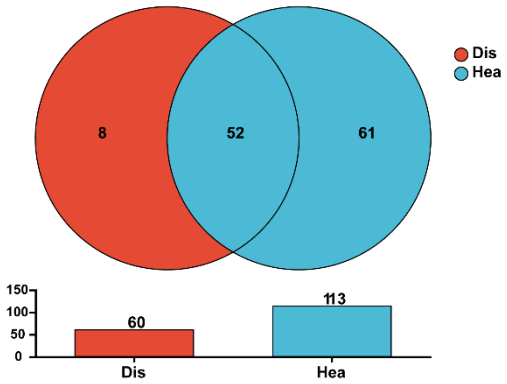


Figure S5. Venn diagram illustrating the OTUs shared across all samples. The Venn diagram presents the distribution and overlap of operational taxonomic units (OTUs) among all samples included in this study.

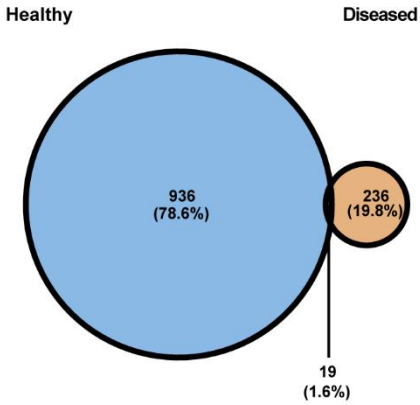


Figure S6. Comparison of unique and overlapping interaction edges detected between the healthy and diseased groups, illustrating group-specific and shared network connectivity patterns.

Table S1. Overview of statistics for PacBio filtered Circular Consensus Sequence (CCS) reads across multiple sample sets.

Sample	Raw CCS	Clean CCS	Effective CCS	AvgLen(bp)	Effective(%)	Group1	Group2	Coverage
FI_Dis_1	11887	11864	11394	1449	95.85	Dis	FI	1.00
FI_Dis_10	12955	12946	12431	1452	95.96	Dis	FI	1.00
FI_Dis_11	10873	10864	10435	1454	95.97	Dis	FI	1.00
FI_Dis_12	11169	11159	10743	1446	96.19	Dis	FI	1.00
FI_Dis_13	12976	12959	12407	1449	95.61	Dis	FI	1.00
FI_Dis_14	8360	8356	7941	1448	94.99	Dis	FI	1.00
FI_Dis_15	8737	8733	8495	1454	97.23	Dis	FI	1.00
FI_Dis_16	13059	13037	12533	1452	95.97	Dis	FI	1.00
FI_Dis_17	13009	12994	12717	1446	97.76	Dis	FI	0.99
FI_Dis_18	9990	9977	9602	1448	96.12	Dis	FI	1.00
FI_Dis_19	13021	13009	12626	1456	96.97	Dis	FI	1.00
FI_Dis_2	11766	11756	11279	1447	95.86	Dis	FI	1.00
FI_Dis_20	13056	13044	12844	1449	98.38	Dis	FI	1.00
FI_Dis_21	10424	10416	10100	1449	96.89	Dis	FI	1.00
FI_Dis_22	12951	12934	12623	1455	97.47	Dis	FI	1.00
FI_Dis_3	9341	9330	9099	1451	97.41	Dis	FI	1.00
FI_Dis_4	8261	8252	8000	1454	96.84	Dis	FI	1.00
FI_Dis_5	12975	12959	12473	1448	96.13	Dis	FI	1.00
FI_Dis_6	13004	12979	12413	1452	95.46	Dis	FI	1.00
FI_Dis_7	13020	12990	12659	1454	97.23	Dis	FI	1.00
FI_Dis_8	13009	13003	12600	1456	96.86	Dis	FI	1.00
FI_Dis_9	8642	8631	8317	1447	96.24	Dis	FI	1.00
FI_Hea_1	12997	12985	12351	1449	95.03	Hea	FI	0.98
FI_Hea_10	11633	11618	11142	1446	95.78	Hea	FI	1.00
FI_Hea_2	8055	8044	7730	1448	95.97	Hea	FI	1.00
FI_Hea_3	8741	8735	8441	1449	96.57	Hea	FI	1.00
FI_Hea_4	10589	10575	10138	1448	95.74	Hea	FI	1.00
FI_Hea_5	13006	12995	12483	1450	95.98	Hea	FI	1.00
FI_Hea_6	9638	9622	9152	1448	94.96	Hea	FI	1.00
FI_Hea_7	12999	12983	12323	1455	94.8	Hea	FI	1.00
FI_Hea_8	13048	13027	12516	1449	95.92	Hea	FI	1.00
FI_Hea_9	13003	12995	12400	1444	95.36	Hea	FI	1.00
FI_soil_1	13025	13016	12468	1446	95.72	Soil	FI	1.00
FI_soil_2	13005	12984	12895	1441	99.15	Soil	FI	0.99
FI_soil_3	12990	12974	12752	1444	98.17	Soil	FI	0.99
FII_Dis_1	10456	10448	10095	1447	96.55	Dis	FII	1.00
FII_Dis_2	12940	12885	12652	1440	97.77	Dis	FII	1.00
FII_Dis_3	12934	12923	12843	1442	99.3	Dis	FII	1.00
FII_Dis_4	12983	12979	12259	1445	94.42	Dis	FII	1.00
FII_Dis_5	13039	13012	12470	1444	95.64	Dis	FII	1.00
FII_Dis_6	13070	13045	12767	1449	97.68	Dis	FII	1.00
FII_Dis_7	12979	12954	12665	1446	97.58	Dis	FII	1.00
FII_Dis_8	13000	12944	12585	1446	96.81	Dis	FII	1.00
FII_Hea_1	13159	13151	12892	1454	97.97	Hea	FII	1.00
FII_Hea_2	9278	9272	8919	1449	96.13	Hea	FII	1.00
FII_Hea_3	13019	13007	12368	1440	95.00	Hea	FII	1.00
FII_Hea_4	12656	12656	12032	1444	95.07	Hea	FII	1.00
FII_Hea_5	10829	10819	10474	1445	96.72	Hea	FII	1.00
FII_soil_1	13026	13019	12931	1440	99.27	Soil	FII	0.99
FII_soil_2	12955	12941	12703	1443	98.05	Soil	FII	1.00
FII_soil_3	13004	12991	12459	1442	95.81	Soil	FII	1.00

Table S2. Statistical analysis of the interaction frequency among taxa at the phylum level in the healthy network.

Phylum	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15	P16	P17	P18	P19	P20
Abditibacteriota	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Acidobacteriota	1	7	11	1	8	1	18	0	0	0	0	5	4	1	8	11	18	1	8	20
Actinobacteriota	0	11	20	0	29	6	10	0	0	0	0	1	4	0	43	3	24	0	8	7
Armatimonadota	0	1	0	0	4	0	0	0	0	1	0	0	0	0	0	0	3	0	0	1
Bacteroidota	0	8	29	4	15	7	11	3	0	0	0	4	4	1	38	9	40	0	11	12
Bdellovibrionota	0	1	6	0	7	1	5	0	0	0	0	0	0	0	11	2	6	0	8	3
Chloroflexi	1	18	10	0	11	5	34	0	0	0	0	8	4	0	39	11	28	1	6	11
Cyanobacteria	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
Dependentiae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Elusimicrobiota	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Firmicutes	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0
Gemmatimonadota	0	5	1	0	4	0	8	0	0	0	1	1	1	3	4	6	10	0	2	7
Myxococcota	0	4	4	0	4	0	4	0	0	0	1	1	1	4	3	3	14	0	1	7
Nitrospirota	0	1	0	0	1	0	0	0	0	0	0	3	4	2	3	3	5	0	2	4
Patescibacteria	0	8	43	0	38	11	39	0	0	1	1	4	3	3	32	10	19	0	11	12
Planctomycetota	0	11	3	0	9	2	11	0	0	0	0	6	3	3	10	5	10	0	8	12
Proteobacteria	0	18	24	3	40	6	28	1	1	0	0	10	14	5	19	10	49	1	11	26
Sumerlaeota	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	1
unclassified_Bacteria	0	8	8	0	11	8	6	0	0	0	0	2	1	2	11	8	11	0	2	16
Verrucomicrobiota	0	20	7	1	12	3	11	1	0	0	0	7	7	4	12	12	26	1	16	16

* P1–P20 represent phyla as follows — P1: Abditibacteriota; P2: Acidobacteriota; P3: Actinobacteriota; P4: Armatimonadota; P5: Bacteroidota; P6: Bdellovibrionota; P7: Chloroflexi; P8: Cyanobacteria; P9: Dependentiae; P10: Elusimicrobiota; P11: Firmicutes; P12: Gemmatimonadota; P13: Myxococcota; P14: Nitrospirota; P15: Patescibacteria; P16: Planctomycetota; P17: Proteobacteria; P18: Sumerlaeota; P19: Unclassified Bacteria; P20: Verrucomicrobiota.

Table S3. Statistical analysis of the interaction frequency among taxa at the phylum level in the diseased network.

Phylum	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15
Acidobacteriota	14	0	0	12	0	6	3	2	0	2	2	17	2	4	1
Actinobacteriota	0	3	0	1	0	16	1	0	0	0	0	0	0	1	0
Armatimonadota	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Bacteroidota	12	1	2	12	1	2	1	3	0	3	1	12	1	1	2
Bdellovibrionota	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
Chloroflexi	6	16	0	2	1	72	8	1	0	1	2	3	0	0	1
Gemmatimonadota	3	1	0	1	0	8	0	0	1	0	0	0	0	0	0
Myxococcota	2	0	0	3	0	1	0	0	0	0	0	3	0	0	0
Nitrospirota	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Patescibacteria	2	0	0	3	0	1	0	0	0	5	0	0	0	1	1
Planctomycetota	2	0	0	1	0	2	0	0	0	0	1	3	0	1	1
Proteobacteria	17	0	0	12	0	3	0	3	0	0	3	8	1	5	3
Sumerlaeota	2	0	0	1	0	0	0	0	0	0	0	1	0	0	0
unclassified_Bacteria	4	1	0	1	0	0	0	0	0	1	1	5	0	2	0
Verrucomicrobiota	1	0	0	2	0	1	0	0	0	1	1	3	0	0	2

* P1–P15 represent phyla as follows — P1: Acidobacteriota; P2: Actinobacteriota; P3: Armatimonadota; P4: Bacteroidota; P5: Bdellovibrionota; P6: Chloroflexi; P7: Gemmatimonadota; P8: Myxococcota; P9: Nitrospirota; P10: Patescibacteria; P11: Planctomycetota; P12: Proteobacteria; P13: Sumerlaeota; P14: Unclassified Bacteria; P15: Verrucomicrobiota.