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Supplementary Materials for

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804 **Rhizosphere *Streptomyces* confers dual-mode resistance to root-knot**

805 **nematodes through nematicidal metabolites and JA-mediated**

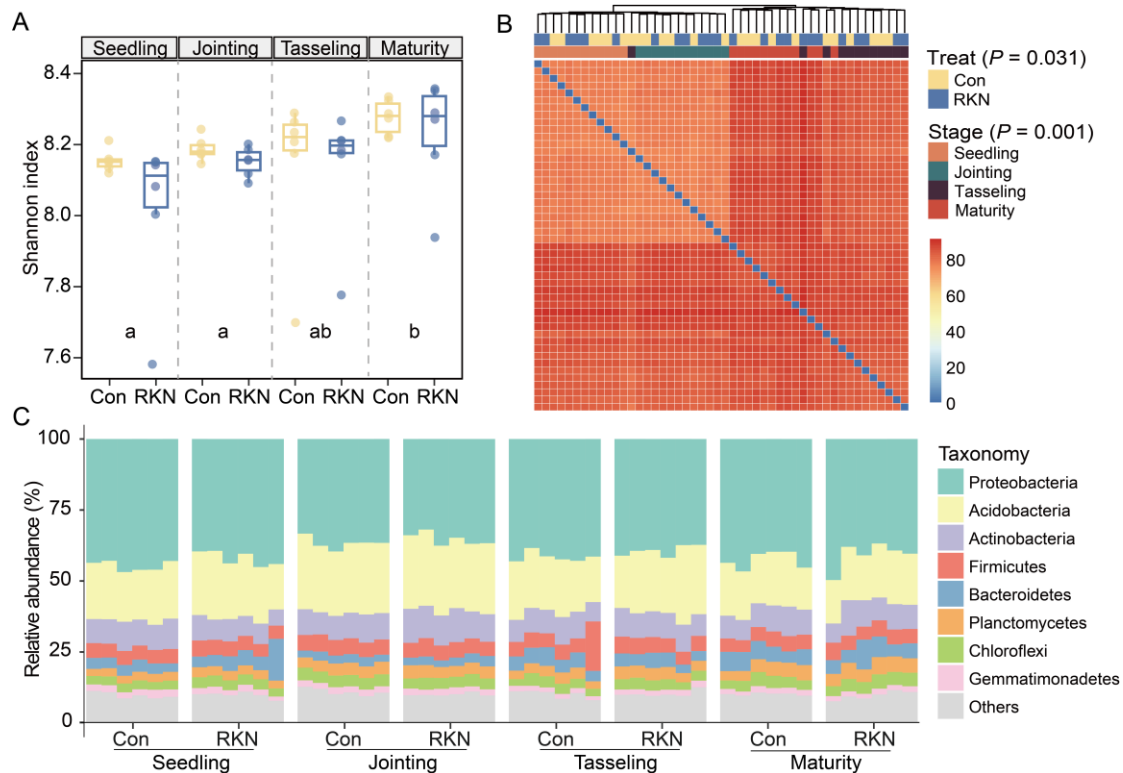
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immunity in maize

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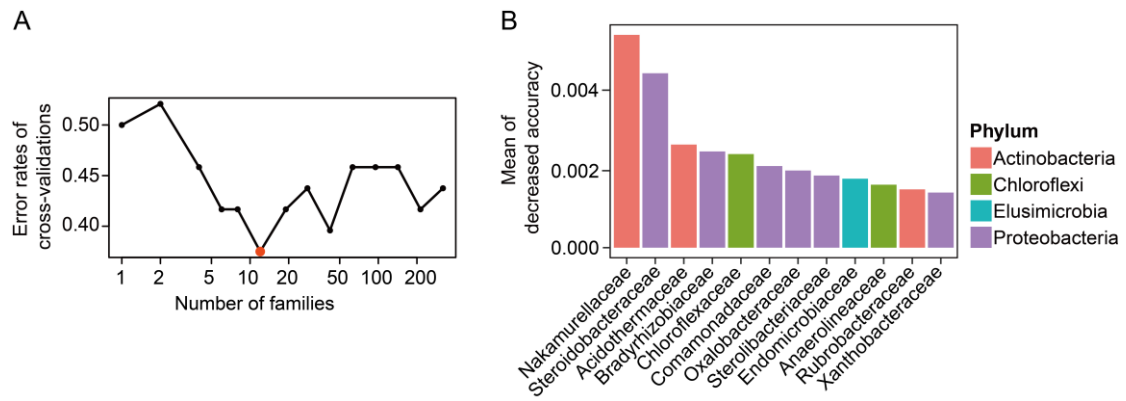
Zheng et al.

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810 **Fig. S1 Composition of the rhizosphere microbiome across maize developmental**
 811 **stages. (A)** Shannon diversity index of rhizosphere bacterial communities in healthy
 812 (Con) and RKN-infected (RKN) maize plants at the seedling, jointing, tasseling, and
 813 maturity stages (mean \pm SD; $n = 6$). Boxes represent the interquartile range (IQR; 25th
 814 to 75th percentiles), and individual data points denote biological replicates. Different
 815 letters indicate statistically significant differences between developmental stages
 816 (Kruskal–Wallis test; $P < 0.05$). “n.s.” indicates there was not significant between Con
 817 and RKN treatments (Wilcoxon test). **(B)** Heatmap based on Euclidean distance
 818 illustrating differences in rhizosphere bacterial community composition between Con
 819 and RKN treatments across the four maize growth stages. Each square represents an
 820 individual replicate. 999 permutational multivariate analysis of variance
 821 (PERMANOVA, adonis) was used to analysis the significance in developmental stages
 822 and treat. **(C)** Relative abundance (%) of the top eight bacterial phyla in the rhizosphere
 823 across all maize developmental stages.
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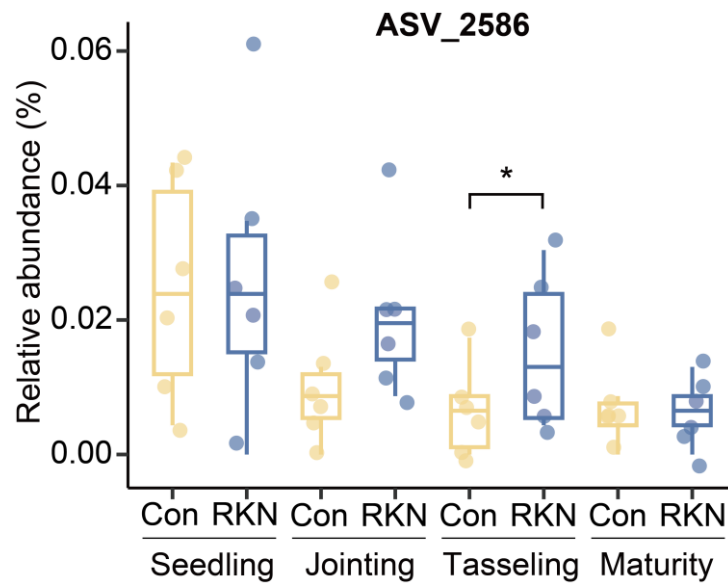


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826 **Fig. S2 Key rhizosphere bacterial families identified from healthy and RKN-**
 827 **infected maize across the full growth period by Random Forest. (A)** Number of
 828 bacterial families selected by Random Forest as key discriminators between healthy
 829 (Con) and RKN-infected (RKN) treatments across the full growth period ($n = 12$). **(B)**
 830 Model classification accuracy of Random Forest based on the selected 12 bacterial
 831 families.

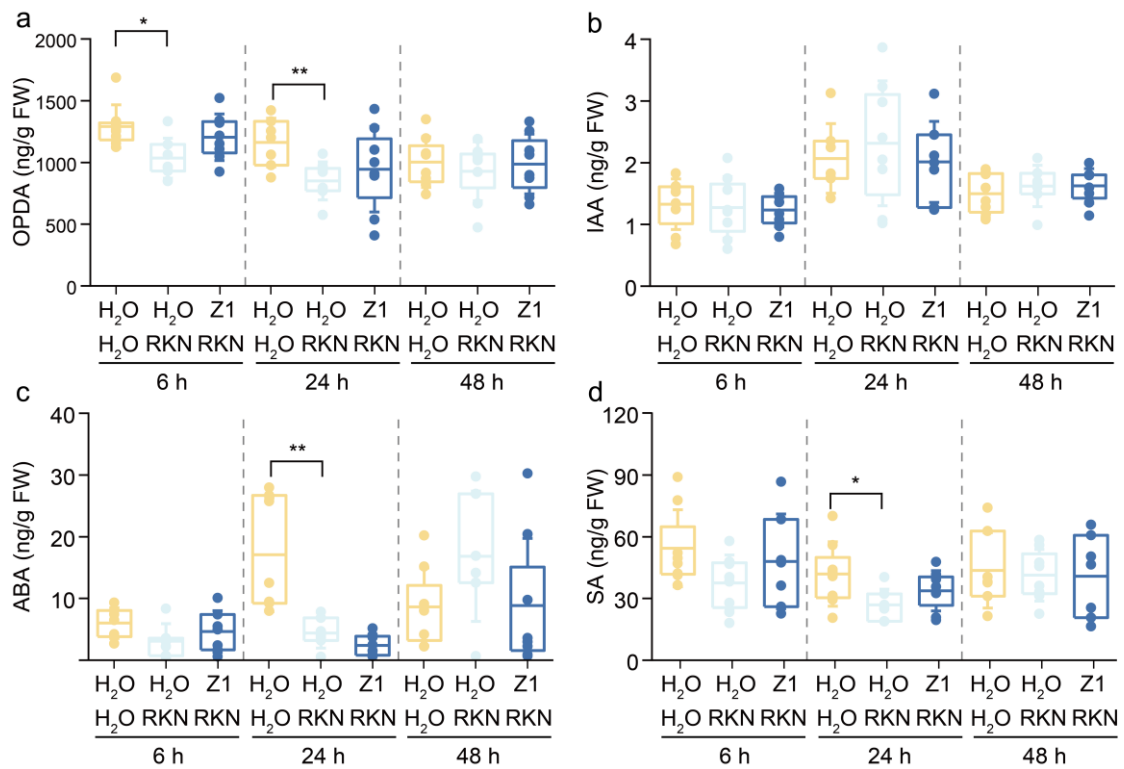
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835 **Fig. S3 Relative abundance of ASV_2586 in healthy and RKN-infected maize**
836 **rhizospheres across four developmental stages.** Relative abundance (%) of
837 ASV_2586 in the rhizosphere of healthy (Con) and RKN -infected (RKN) maize at the
838 seedling, jointing, tasseling, and maturity stages (mean \pm SD, $n = 6$). Asterisks indicate
839 statistically significant differences between treatments at each stage (two-sided Welch's
840 t -test; $P < 0.05$).
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844 **Fig. S4 Phytohormone dynamics in maize roots following RKN infection under Z1**
 845 **inoculation. (A–D)** Concentrations of phytohormones measured at 6, 24, and 48 hours
 846 after RKN infection in maize roots inoculated with Z1: (A) 12-oxo-phytodienoic acid
 847 (OPDA), (B) indole-3-acetic acid (IAA), (C) abscisic acid (ABA), and (D) salicylic
 848 acid (SA) (mean \pm SD, $n = 6-8$). Boxes represent the interquartile range (IQR; 25th to
 849 75th percentiles), and data points indicate individual biological replicates. Asterisks
 850 denote statistically significant differences between treatments (two-sided Student's t -
 851 test; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).
 852

Genus	Difference in mean proportions (%)	Mean proportion (%) (Control)	Mean proportion (%) (RKN-infected)	statistic	p.value	parameter	conf.low	conf.high	method	alternative
<i>Magnetospirillum</i>	0.8391	3.1366	2.2975	4.4665	0.0022	7.8514	0.4045	1.2738	Welch Two Sample t-test	two.sided
<i>Gaiella</i>	0.6917	2.3518	1.6601	3.8901	0.0033	9.5684	0.2931	1.0904	Welch Two Sample t-test	two.sided
<i>Caballeronia</i>	0.4757	1.5826	1.1069	4.7994	0.0012	8.2787	0.2485	0.7030	Welch Two Sample t-test	two.sided
<i>Solimonas</i>	0.3577	0.8220	0.4642	2.8423	0.0249	7.0152	0.0603	0.6552	Welch Two Sample t-test	two.sided
<i>Arenimonas</i>	0.3323	0.8205	0.4882	4.1338	0.0048	6.7044	0.1405	0.5241	Welch Two Sample t-test	two.sided
<i>Paraburkholderia</i>	0.2673	1.0713	0.8041	2.8258	0.0208	8.5878	0.0517	0.4828	Welch Two Sample t-test	two.sided
<i>Haliangium</i>	0.2645	0.6495	0.3850	5.4466	0.0003	9.4925	0.1555	0.3735	Welch Two Sample t-test	two.sided
<i>Methyloversatilis</i>	0.2627	1.2374	0.9748	2.9186	0.0189	8.1855	0.0559	0.4694	Welch Two Sample t-test	two.sided
<i>Delftia</i>	0.1614	0.2028	0.0414	4.8385	0.0037	5.4858	0.0779	0.2450	Welch Two Sample t-test	two.sided
<i>Nocardioides</i>	0.1604	0.4547	0.2943	3.4634	0.0063	9.7330	0.0568	0.2640	Welch Two Sample t-test	two.sided
<i>Actinomarinicola</i>	0.1204	0.6236	0.5032	2.6219	0.0264	9.5658	0.0175	0.2234	Welch Two Sample t-test	two.sided
<i>Chondromyces</i>	0.1196	0.2405	0.1209	2.6056	0.0460	5.2144	0.0030	0.2361	Welch Two Sample t-test	two.sided
<i>Racemicystis</i>	0.1110	0.2716	0.1607	8.7019	0.0001	7.0115	0.0808	0.1411	Welch Two Sample t-test	two.sided
<i>Solirubrobacter</i>	0.1081	0.2892	0.1811	3.2732	0.0109	8.2347	0.0323	0.1839	Welch Two Sample t-test	two.sided
<i>Panacagrimonas</i>	0.1065	0.2607	0.1541	2.7446	0.0276	7.3039	0.0155	0.1976	Welch Two Sample t-test	two.sided
<i>Marmoricola</i>	0.0942	0.2581	0.1639	4.8397	0.0018	7.1120	0.0483	0.1400	Welch Two Sample t-test	two.sided
<i>Sorangium</i>	0.0820	0.1078	0.0258	4.7130	0.0015	7.9690	0.0418	0.1221	Welch Two Sample t-test	two.sided
<i>Kofleria</i>	0.0741	0.1435	0.0694	4.7614	0.0031	6.0434	0.0361	0.1121	Welch Two Sample t-test	two.sided
<i>Azospirillum</i>	0.0603	0.1435	0.0832	4.5427	0.0011	9.8604	0.0307	0.0899	Welch Two Sample t-test	two.sided
<i>Blastococcus</i>	0.0600	0.1527	0.0927	2.8701	0.0170	9.8170	0.0133	0.1067	Welch Two Sample t-test	two.sided
<i>Nocardia</i>	0.0520	0.0839	0.0319	3.3393	0.0089	8.8373	0.0167	0.0874	Welch Two Sample t-test	two.sided
<i>Byssovorax</i>	0.0375	0.0754	0.0378	3.2138	0.0116	8.3654	0.0108	0.0643	Welch Two Sample t-test	two.sided
<i>Ferrovibrio</i>	0.0232	0.0452	0.0220	4.7210	0.0030	6.2166	0.0113	0.0352	Welch Two Sample t-test	two.sided
<i>Enhygromyxa</i>	0.0221	0.0605	0.0384	2.6587	0.0364	6.2022	0.0019	0.0423	Welch Two Sample t-test	two.sided
<i>Microbacterium</i>	0.0201	0.0404	0.0203	2.4357	0.0411	7.9372	0.0010	0.0392	Welch Two Sample t-test	two.sided

<i>Conexibacter</i>	0.0165	0.0230	0.0065	3.1414	0.0181	6.4671	0.0039	0.0292	Welch Two Sample t-test	two.sided
<i>Ornithinibacter</i>	0.0154	0.0304	0.0150	2.6740	0.0239	9.7250	0.0025	0.0283	Welch Two Sample t-test	two.sided
<i>Simplicispira</i>	0.0144	0.0315	0.0171	2.4700	0.0474	6.1563	0.0002	0.0287	Welch Two Sample t-test	two.sided
<i>Methylophilus</i>	-0.0107	0.0118	0.0225	-3.1984	0.0100	9.5942	-0.0182	-0.0032	Welch Two Sample t-test	two.sided
<i>Acidiferrimicrobium</i>	-0.0138	0.0047	0.0185	-2.6943	0.0365	5.8977	-0.0264	-0.0012	Welch Two Sample t-test	two.sided
<i>Tellurimicrobium</i>	-0.0166	0.0409	0.0575	-2.7543	0.0203	9.9967	-0.0300	-0.0032	Welch Two Sample t-test	two.sided
<i>Luteitalea</i>	-0.0230	0.0367	0.0598	-2.7201	0.0249	8.4781	-0.0424	-0.0037	Welch Two Sample t-test	two.sided
<i>Geofilum</i>	-0.0278	0.0253	0.0531	-2.4357	0.0383	8.7741	-0.0537	-0.0019	Welch Two Sample t-test	two.sided
<i>Sediminibacterium</i>	-0.0602	0.0453	0.1055	-2.4428	0.0498	6.0756	-0.1202	-0.0001	Welch Two Sample t-test	two.sided
<i>Rhizorhapis</i>	-0.0621	0.1427	0.2048	-2.3217	0.0471	8.4501	-0.1232	-0.0010	Welch Two Sample t-test	two.sided
<i>Hyphomonas</i>	-0.0652	0.1074	0.1726	-4.1071	0.0021	9.9576	-0.1006	-0.0298	Welch Two Sample t-test	two.sided
<i>Aiffella</i>	-0.0699	0.1089	0.1787	-2.6451	0.0283	8.3810	-0.1303	-0.0094	Welch Two Sample t-test	two.sided
<i>Lacipirellula</i>	-0.0855	0.1671	0.2526	-3.1196	0.0128	8.7264	-0.1477	-0.0232	Welch Two Sample t-test	two.sided
<i>Thermomarinilinea</i>	-0.0855	0.3838	0.4693	-2.8325	0.0229	7.7219	-0.1555	-0.0154	Welch Two Sample t-test	two.sided
<i>Bradyrhizobium</i>	-0.0929	0.2671	0.3600	-2.9079	0.0184	8.4994	-0.1658	-0.0200	Welch Two Sample t-test	two.sided
<i>Aggregatilinea</i>	-0.0944	0.2585	0.3529	-2.9467	0.0151	9.6801	-0.1660	-0.0227	Welch Two Sample t-test	two.sided
<i>Litorilinea</i>	-0.1486	0.3668	0.5154	-3.1399	0.0113	9.3858	-0.2550	-0.0422	Welch Two Sample t-test	two.sided
<i>Acidibacter</i>	-0.1695	1.0494	1.2190	-2.7076	0.0222	9.8992	-0.3092	-0.0298	Welch Two Sample t-test	two.sided
<i>Ferruginibacter</i>	-0.2425	0.3062	0.5487	-4.8863	0.0011	8.2166	-0.3564	-0.1286	Welch Two Sample t-test	two.sided
<i>Terrimonas</i>	-0.2947	0.4724	0.7671	-5.0506	0.0008	8.6678	-0.4274	-0.1619	Welch Two Sample t-test	two.sided
<i>Rhodoplanes</i>	-0.2994	0.8112	1.1105	-3.4185	0.0066	10.0000	-0.4945	-0.1042	Welch Two Sample t-test	two.sided
<i>Spingomonas</i>	-0.7029	1.6831	2.3860	-2.4194	0.0441	7.4530	-1.3815	-0.0243	Welch Two Sample t-test	two.sided

853 **Table S1 Differential genus between the healthy (Con) and RKN-infected (RKN) maize rhizosphere at the seedling stage by STAMP**
854 **analysis.**

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Genus	Difference in mean proportions (%)	Mean proportion (%) (Control)	Mean proportion (%) (RKN-infected)	statistic	p.value	parameter	conf.low	conf.high	method	alternative
<i>Nitrospira</i>	0.8095	2.8511	2.0417	2.6339	0.0339	6.9560	0.0818	1.5371	Welch Two Sample t-test	two.sided
<i>Limnobacter</i>	0.0906	0.2794	0.1888	2.9691	0.0184	7.7928	0.0199	0.1612	Welch Two Sample t-test	two.sided
<i>Minicystis</i>	0.0394	0.0722	0.0328	3.9976	0.0063	6.3967	0.0157	0.0632	Welch Two Sample t-test	two.sided
<i>Rhizorhapis</i>	0.0362	0.0994	0.0631	2.9186	0.0194	7.9738	0.0076	0.0648	Welch Two Sample t-test	two.sided
<i>Nitrosospora</i>	0.0357	0.2088	0.1731	3.1386	0.0106	9.9798	0.0103	0.0610	Welch Two Sample t-test	two.sided
<i>Niveibacterium</i>	0.0199	0.0564	0.0365	2.9533	0.0181	8.0756	0.0044	0.0355	Welch Two Sample t-test	two.sided
<i>Desulfofundulus</i>	0.0178	0.0278	0.0100	4.9357	0.0008	9.1833	0.0097	0.0259	Welch Two Sample t-test	two.sided
<i>Allospingosinicella</i>	0.0156	0.0273	0.0118	2.8256	0.0181	9.9339	0.0033	0.0278	Welch Two Sample t-test	two.sided
<i>Delftia</i>	0.0122	0.0267	0.0145	3.1416	0.0105	9.9455	0.0035	0.0208	Welch Two Sample t-test	two.sided
<i>Paradevosia</i>	0.0121	0.0132	0.0011	2.5635	0.0458	5.5453	0.0003	0.0239	Welch Two Sample t-test	two.sided
<i>Polaromonas</i>	0.0061	0.0079	0.0017	2.3433	0.0499	7.3415	0.0000	0.0123	Welch Two Sample t-test	two.sided
<i>Spiribacter</i>	-0.0197	0.0253	0.0450	-2.4065	0.0377	9.6675	-0.0380	-0.0014	Welch Two Sample t-test	two.sided
<i>Nonomuraea</i>	-0.0273	0.0183	0.0456	-2.5914	0.0349	7.2266	-0.0520	-0.0025	Welch Two Sample t-test	two.sided
<i>Chloroflexus</i>	-0.0306	0.0661	0.0966	-2.7363	0.0307	6.6228	-0.0573	-0.0038	Welch Two Sample t-test	two.sided
<i>Acidiferrimicrobium</i>	-0.0369	0.0296	0.0665	-2.6058	0.0315	7.9429	-0.0696	-0.0042	Welch Two Sample t-test	two.sided
<i>Desulfomonile</i>	-0.0443	0.2004	0.2448	-2.7899	0.0193	9.8738	-0.0798	-0.0089	Welch Two Sample t-test	two.sided
<i>Niastella</i>	-0.0676	0.0935	0.1611	-3.4506	0.0127	6.2576	-0.1151	-0.0202	Welch Two Sample t-test	two.sided
<i>Steroidobacter</i>	-0.1066	0.5254	0.6320	-3.0888	0.0115	9.9630	-0.1835	-0.0297	Welch Two Sample t-test	two.sided
<i>Actinomarinicola</i>	-0.1221	0.6241	0.7462	-2.7786	0.0226	8.5287	-0.2224	-0.0219	Welch Two Sample t-test	two.sided

856 **Table S2 Differential genus between the healthy (Con) and RKN-infected (RKN) maize rhizosphere at the jointing stage by STAMP**
857 **analysis.**