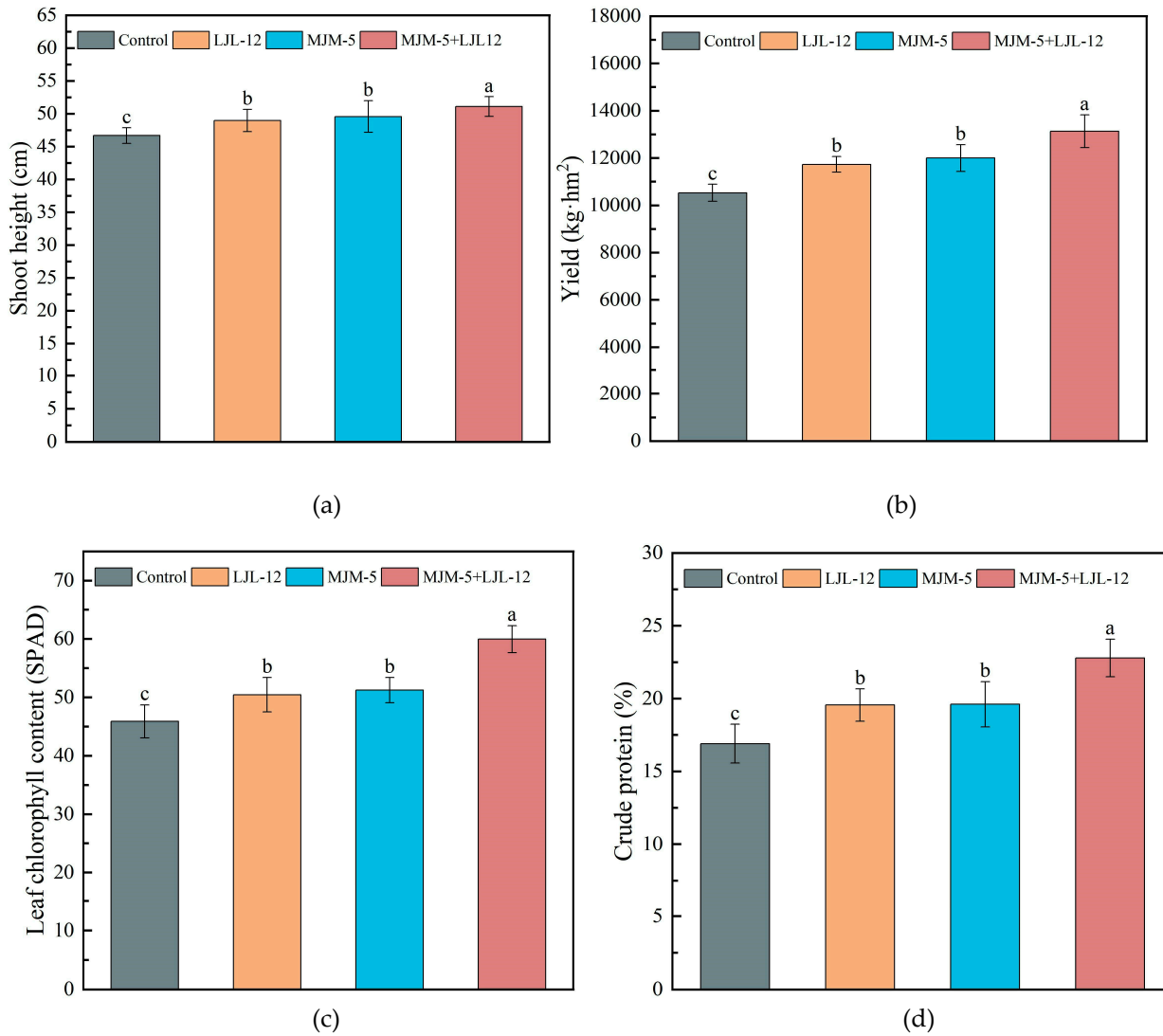
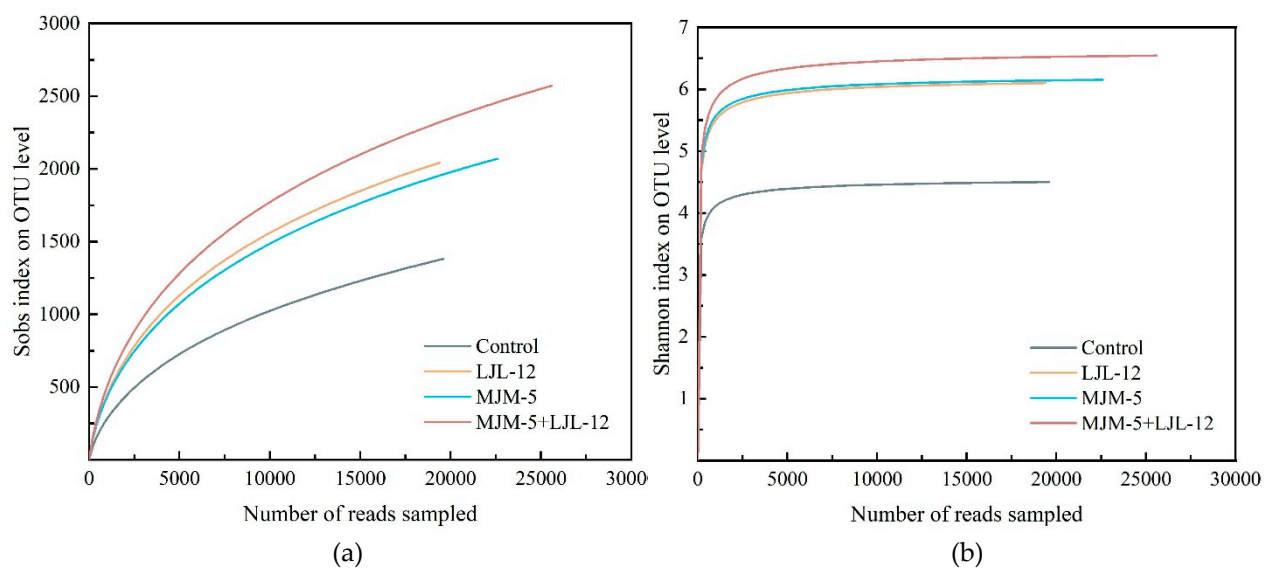


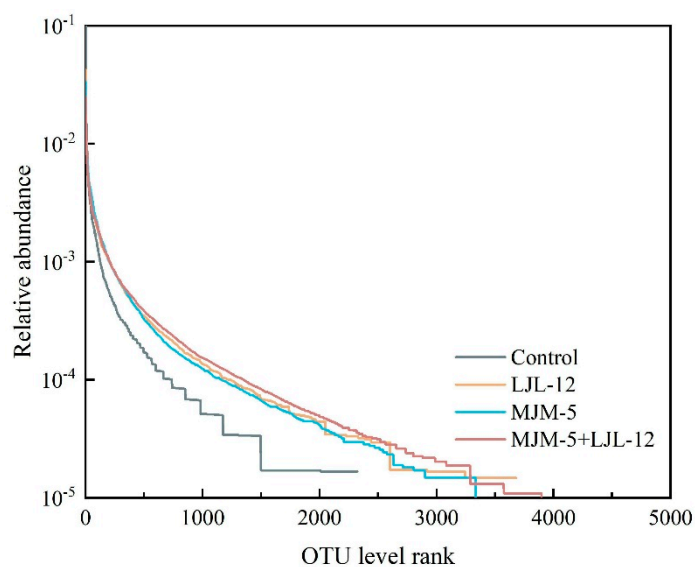
### Supplementary materials



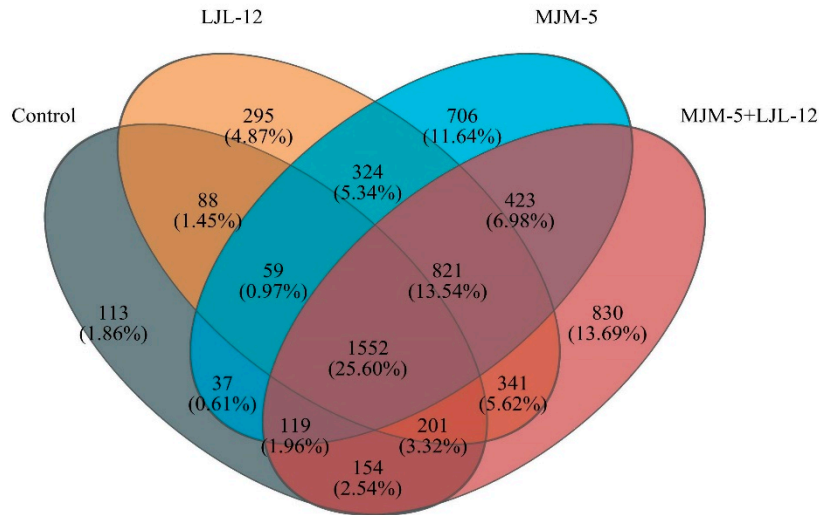
**Supplementary Figure S1.** Agronomic characteristics of alfalfa under Control, LJL-12, MJM-5, and MJM-5+LJL-12 treatments, including (a) shoot height, (b) yield, (c) leaf chlorophyll content, (d) crude protein. Lowercase letters indicate significant differences among the treatments ( $P < 0.05$ ).



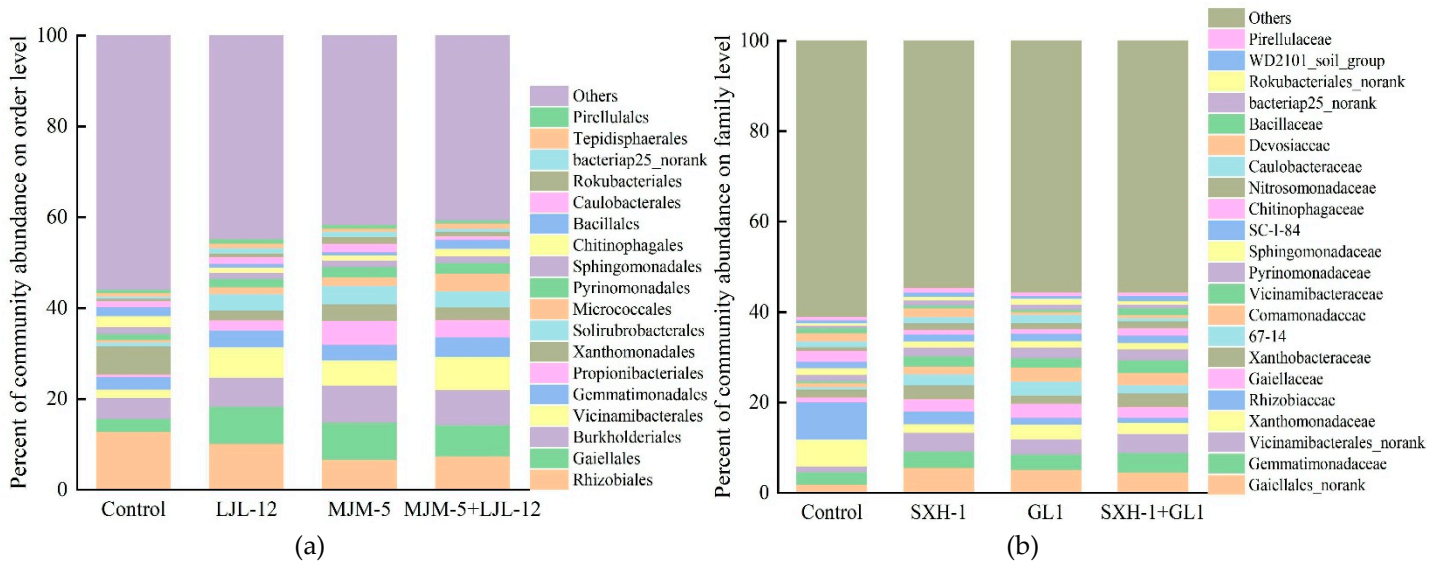
**Supplementary Figure S2.** Rarefaction curves of bacterial community in the rhizosphere of alfalfa under Control, LJL-12, MJM-5, and MJM-5+LJL-12 treatments, based on (a) Sobs and (b) Shannon indexes.



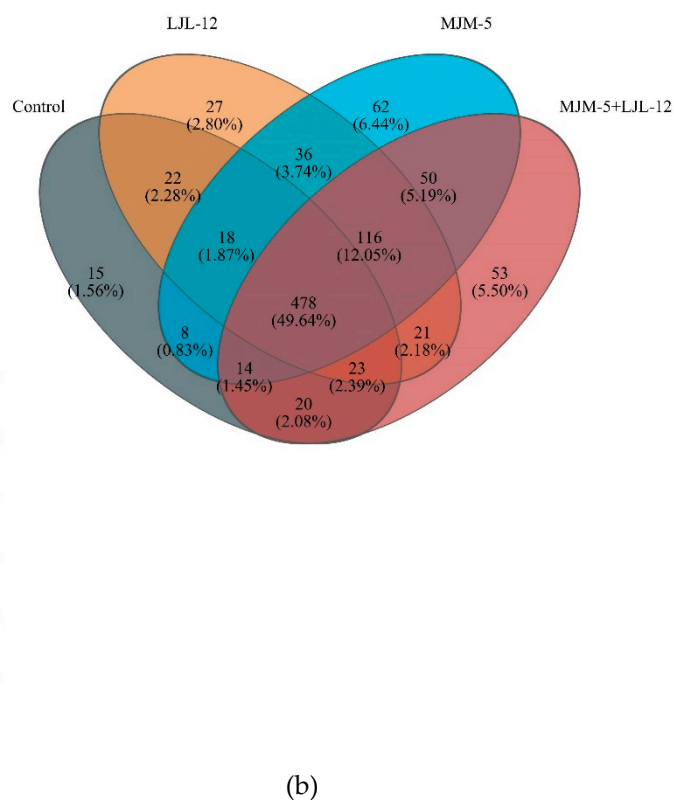
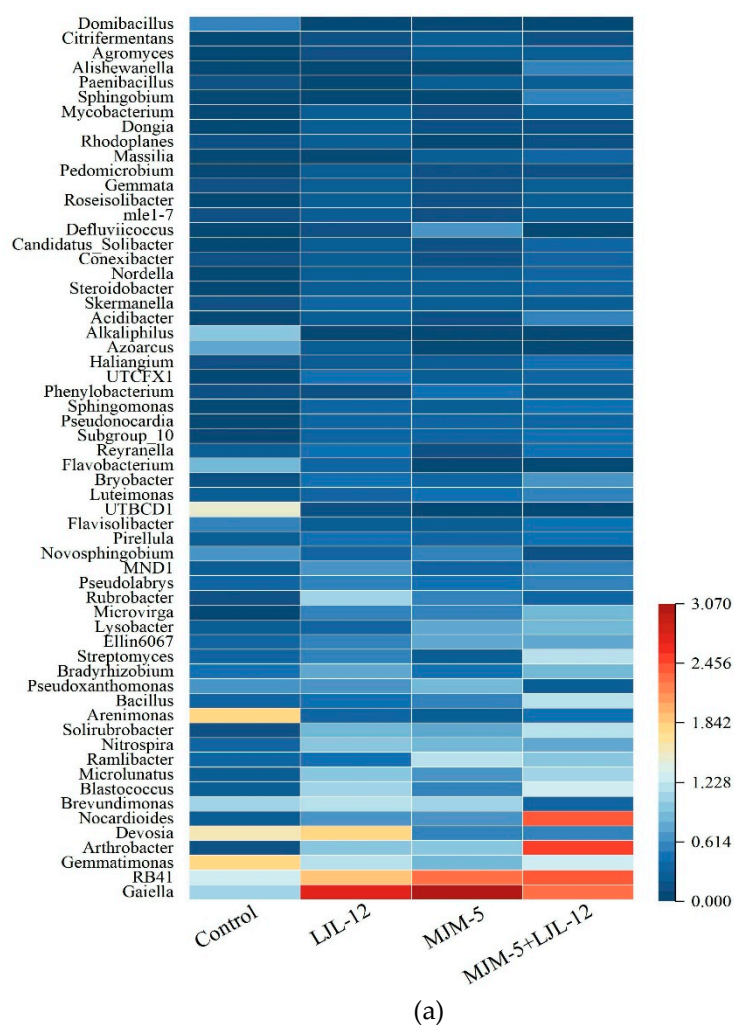
**Supplementary Figure S3.** Rank-abundances of bacterial community in the rhizosphere of alfalfa under Control, LJL-12, MJM-5, and MJM-5+LJL-12 treatments.



**Supplementary Figure S4.** Venn diagram of OTUs level of bacterial community in the rhizosphere of alfalfa under Control, LJL-12, MJM-5, and MJM-5+LJL-12 treatments. The figure shows the number of shared and unique OTUs and their relative percentage among treatments.



**Supplementary Figure S5.** Bacterial community composition in the rhizosphere of alfalfa under Control, LJL-12, MJM-5, and MJM-5+LJL-12 treatments at **(a)** the order (others: relative abundance < 0.5%) and **(b)** the family levels (others: relative abundance < 0.5%).



**Supplementary Figure S6. (a)** Top 60 bacterial genera in abundance of alfalfa rhizosphere under Control, LJJ-12, MJM-5, and MJM-5+LJJ-12 treatments. Different color boxes represent the relative abundance change of bacterial taxa. The color bar on the right of the heatmap shows the range of relative changes; **(b)** Venn diagram of bacterial genera in the rhizosphere of alfalfa. Different values in the Venn diagram represent the number and percentage of bacterial genera that were either shared or unique among treatments.



**Supplementary Figure S7.** Field experiment area of the alfalfa planting.

**Supplementary Table S1.** Relative abundance of bacterial phyla in the rhizosphere of alfalfa under Control, LJL-12, MJM-5, and MJM-5+LJL-12 treatments.

<b>Taxon</b>	<b>Relative abundance (%)</b>			
<b>Phylum</b>	<b>Control</b>	<b>LJL-12</b>	<b>MJM-5</b>	<b>MJM-5+LJL-12</b>
Proteobacteria	57.686	29.134	27.809	26.952
Actinobacteriota	7.377	23.987	30.452	27.228
Acidobacteriota	4.56	12.145	12.384	14.633
Chloroflexi	2.722	8.523	7.048	8.312
Gemmatimonadota	4.182	4.402	4.055	4.737
Bacteroidota	6.522	2.591	2.855	2.854
Firmicutes	7.174	1.732	1.711	3.167
Planctomycetota	2.307	3.474	2.568	3.504
Cyanobacteria	0.158	5.401	3.318	0.503
Myxococcota	0.812	2.160	1.852	2.236
Desulfobacterota	4.223	1.577	0.837	0.414
Methylomirabilota	0.525	0.808	1.520	0.914
Bacteria_unclassified	0.412	1.038	0.750	1.289
Nitrospirota	0.351	0.982	0.867	0.782
Armatimonadota	0.427	0.688	0.498	0.842
Latescibacterota	0.117	0.182	0.221	0.439
Others	0.444	1.175	1.257	1.194

**Supplementary Table S2.** Relative abundance of bacterial classes in the rhizosphere of alfalfa under Control, LJL-12, MJM-5, and MJM-5+LJL-12 treatments.

<b>Taxon</b>	<b>Relative abundance (%)</b>			
<b>Class</b>	<b>Control</b>	<b>LJL-12</b>	<b>MJM-5</b>	<b>MJM-5+LJL-12</b>
Gammaproteobacteria	39.159	12.15	12.982	14.319
Alphaproteobacteria	18.527	16.978	14.819	12.631
Thermoleophilia	3.886	12.072	12.575	10.724
Actinobacteria	2.625	7.726	9.816	13.036
Vicinamibacteria	1.883	6.803	6.000	7.510
Gemmatimonadetes	2.775	3.763	3.532	4.361
Bacteroidia	5.971	2.326	2.600	2.723
Blastocatellia	1.537	2.499	2.970	3.145
Chloroflexia	0.595	3.175	1.950	2.674
MB-A2-108	0.412	1.260	3.698	1.426
Planctomycetes	1.452	2.282	1.719	2.143
Bacilli	2.364	1.043	0.984	2.462
Acidobacteriae	0.655	1.518	0.962	2.153
KD4-96	0.489	1.258	1.321	1.714
Anaerolineae	0.444	1.572	1.416	1.314
Methylomirabilia	0.525	0.808	1.520	0.914
Phycisphaerae	0.806	1.074	0.698	1.171
bacteriap25	0.501	1.176	1.125	0.766
Bacteria_unclassified	0.412	1.038	0.750	1.289
Others	14.985	19.480	18.563	13.524

**Supplementary Table S3.** Relative abundance of bacterial orders in the rhizosphere of alfalfa under Control, LJL-12, MJM-5, and MJM-5+LJL-12 treatments.

<b>Taxon</b>	<b>Relative abundance (%)</b>			
<b>Order</b>	<b>Control</b>	<b>LJL-12</b>	<b>MJM-5</b>	<b>MJM-5+LJL-12</b>
Rhizobiales	12.772	10.137	6.657	7.365
Gaiellales	2.968	8.247	8.245	6.978
Burkholderiales	4.559	6.427	8.057	7.662
Vicinamibacterales	1.832	6.615	5.555	7.3
Gemmatimonadales	2.775	3.763	3.532	4.361
Propionibacterales	0.532	2.128	5.206	3.79
Xanthomonadales	6.217	2.181	3.660	2.776
Solirubrobacterales	0.862	3.689	4.066	3.566
Micrococcales	0.553	1.476	1.838	3.821
Pyrinomonadales	1.302	1.913	2.279	2.394
Sphingomonadales	1.508	1.305	1.470	1.470
Chitinophagales	2.410	1.123	1.137	1.654
Bacillales	2.016	0.859	0.702	1.985
Caulobacterales	1.301	1.434	1.871	0.741
Rokubacterales	0.525	0.804	1.508	0.912
bacteriap25_norank	0.501	1.176	1.125	0.766
Tepidisphaerales	0.714	1.003	0.626	1.134
Pirellulales	0.766	1.011	0.824	0.718
Others	55.888	44.708	41.640	40.605

**Supplementary Table S4.** Relative abundance of bacterial families in the rhizosphere of alfalfa under Control, LJL-12, MJM-5, and MJM-5+LJL-12 treatments.

<b>Taxon</b>	<b>Relative abundance (%)</b>			
<b>Family</b>	<b>Control</b>	<b>LJL-12</b>	<b>MJM-5</b>	<b>MJM-5+LJL-11</b>
Gaiellales_norank	1.857	5.534	5.092	4.566
Gemmatimonadaceae	2.775	3.763	3.532	4.361
Vicinamibacterales_norank	1.275	4.076	3.321	4.195
Xanthomonadaceae	5.919	1.933	3.249	2.419
Rhizobiaceae	4.346	6.781	7.488	9.121
Gaiellaceae	1.077	2.676	3.064	2.329
Xanthobacteraceae	1.703	3.073	1.875	2.975
67-14	0.560	2.537	3.112	1.862
Comamonadaceae	0.809	1.563	3.057	2.652
Vicinamibacteraceae	0.524	2.386	2.117	2.866
Pyrinomonadaceae	1.302	1.913	2.279	2.394
Sphingomonadaceae	1.508	1.305	1.470	1.470
SC-I-84	2.485	1.584	1.654	1.639
Chitinophagaceae	5.393	1.013	1.005	1.536
Nitrosomonadaceae	0.782	1.417	1.296	1.534
Caulobacteraceae	1.294	1.429	1.869	0.740
Devosiaceae	5.751	1.865	0.594	0.610
Bacillaceae	1.201	0.681	0.541	1.406
bacteriap25_norank	6.501	1.176	1.025	0.066
Rokubacterales_norank	0.517	0.734	1.262	0.837

WD2101_soil_group	0.700	0.963	0.611	1.092
Pirellulaceae	0.766	1.011	0.024	0.718
Others	50.956	50.588	50.562	48.621

**Supplementary Table S5.** Some unique bacterial genera in the rhizosphere of alfalfa under LJL-12, MJM-5, and MJM-5+LJL-12 treatments.

Taxa	LJL-12	Taxa	MJM-5	Taxa	MJM-5+LJL-12
Derxia	0.032	Oscillatoria_PCC-6304	0.999	Acinetobacter	0.061
Aquiflexum	0.031	Lentimicrobium	0.012	Mumia	0.014
Deferrisoma	0.027	BSV13	0.010	MM2	0.010
CK06-06-Mud-MAS4B-21	0.003	Candidatus_Methyloirab ilis	0.009	Paludibacter	0.009
Desulfovira	0.003	Pseudofulvimonas	0.008	E1B-B3-114	0.006
Microcoleus_Es-Yyy1400	0.003	Methylobacter	0.007	Kouleothrix	0.005
1174-901-12	0.002	Pleomorphomonas	0.006	Saccharothrix	0.005
Anaerocolumna	0.002	Rubritepida	0.005	OM60NOR5_clade	0.004
DEV114	0.002	Tagaea	0.005	Jeongeupia	0.004
Parvibium	0.002	Hydrocarboniphaga	0.004	Nostoc_PCC-73102	0.003
Phormidium_SAG_37.90	0.002	Nibrella	0.004	Clostridium_sensu_stric to_6	0.003
Microseira_Carmichael- Alabama	0.001	Pelagibius	0.004	Deinococcus	0.003
Crocinitomix	0.001	Oscillatoria	0.003	Desulfitobacterium	0.002
Leadbetterella	0.001	Candidatus_Glomeribacter	0.003	Aneurinibacillus	0.002
SWB02	0.001	Isosphaera	0.002	Sphingobacterium	0.002
Propionivibrio	0.001	Anaerosinus	0.002	Endomicrobium	0.001

**Supplementary Table S6.** LEfSe analysis of bacterial community in the rhizosphere of alfalfa under Control and LJL-12 treatments and the bacterial taxa were significantly enriched in the LJL-12 treatment.

Species	Mean	LDA value	P value
p__Actinobacteriota	5.380	4.906	0.0495
c__Thermoleophilia	5.082	4.579	0.0495
p__Acidobacteriota	5.084	4.565	0.0495
p__Chloroflexi	4.931	4.491	0.0495
o__Gaiellales	4.916	4.412	0.0495
c__Actinobacteria	4.888	4.399	0.0495
c__Vicinamibacteria	4.833	4.380	0.0495
o__Vicinamibacterales	4.821	4.367	0.0495
g__norank_f__norank_o__Gaiellales	4.743	4.236	0.0495
f__norank_o__Gaiellales	4.743	4.226	0.0495
f__norank_o__Vicinamibacterales	4.610	4.145	0.0495
g__norank_f__norank_o__Vicinamibacterales	4.610	4.133	0.0495
c__Chloroflexia	4.502	4.131	0.0495
o__Solirubrobacterales	4.567	4.109	0.0495
f__Vicinamibacteraceae	4.378	3.927	0.0495
f__67-14	4.404	3.904	0.0495
g__norank_f__67-14	4.404	3.895	0.0495

f__Gaiellaceae	4.427	3.882	0.0495
g__norank_f__Vicinamibacteraceae	4.289	3.856	0.0495
g__norank_f__Gemmatimonadaceae	4.309	3.855	0.0495
o__Propionibacteriales	4.328	3.854	0.0495
g__Gaiella	4.427	3.854	0.0495
c__Acidimicrobiia	4.263	3.829	0.0495
o__Frankiales	4.248	3.797	0.0495
p__Myxococcota	4.334	3.790	0.0495
c__Anaerolineae	4.196	3.758	0.0495
o__Thermomicrobiales	4.177	3.749	0.0495
p__Planctomycetota	4.541	3.726	0.0495
g__Arthrobacter	4.000	3.672	0.0495
o__Microtrichales	4.075	3.670	0.0495
f__Micrococcaceae	4.018	3.669	0.0495
g__norank_f__AKIW781	3.838	3.668	0.0495
f__Propionibacteriaceae	4.116	3.663	0.0495
f__AKIW781	3.838	3.656	0.0495
o__Rubrobacterales	4.029	3.643	0.0495
o__Kallotenuales	3.838	3.642	0.0495
f__JG30-KF-CM45	4.115	3.640	0.0495
g__norank_f__JG30-KF-CM45	4.115	3.630	0.0495
g__Rubrobacter	4.029	3.626	0.0495
o__Chloroflexales	3.992	3.621	0.0495
f__Rubrobacteriaceae	4.029	3.618	0.0495
c__Rubrobacteria	4.029	3.595	0.0495
f__Geodermatophilaceae	4.077	3.594	0.0495
o__norank_c__MB-A2-108	4.100	3.593	0.0495
g__norank_f__Roseiflexaceae	3.945	3.584	0.0495
c__MB-A2-108	4.100	3.576	0.0495
f__Roseiflexaceae	3.954	3.569	0.0495
f__norank_o__norank_c__KD4-96	4.100	3.539	0.0495
f__Nitrosomonadaceae	4.151	3.568	0.0495
c__Nitrospira	3.991	3.566	0.0495
f__Solirubrobacteraceae	4.048	3.562	0.0495
c__Planctomycetes	4.358	3.556	0.0495
g__Blastococcus	4.040	3.553	0.0495
f__Anaerolineaceae	3.921	3.552	0.0495
f__norank_o__norank_c__MB-A2-108	4.100	3.550	0.0495
g__norank_f__norank_o__norank_c__MB-A2-108	4.100	3.548	0.0495
p__Nitrospirota	3.992	3.547	0.0495
f__norank_o__norank_c__KD4-96	4.100	3.539	0.0495
g__norank_f__norank_o__norank_c__KD4-96	4.100	3.532	0.0495
c__KD4-96	4.100	3.532	0.0495
o__Nitrospirales	3.991	3.528	0.0495
g__Microlunatus	4.000	3.524	0.0495
o__Anaerolineales	3.921	3.524	0.0495
g__Nitrospira	3.991	3.520	0.0495
f__Nitrospiraceae	3.991	3.519	0.0495
c__bacteriap25	4.071	3.503	0.0495
c__TK10	3.921	3.496	0.0495
g__norank_f__norank_o__norank_c__bacteriap25	4.071	3.494	0.0495
f__norank_o__norank_c__bacteriap25	4.071	3.485	0.0495



g__unclassified_k__norank_d__Bacteria	4.016	3.474	0.0495
p__unclassified_k__norank_d__Bacteria	4.016	3.473	0.0495
o__norank_c__bacteriap25	4.071	3.473	0.0495
o__norank_c__TK10	3.921	3.471	0.0495
g__Solirubrobacter	3.923	3.470	0.0495
g__norank_f__norank_o__norank_c__TK10	3.921	3.460	0.0495
o__unclassified_k__norank_d__Bacteria	4.016	3.435	0.0495
f__norank_o__norank_c__TK10	3.921	3.428	0.0495
f__unclassified_k__norank_d__Bacteria	4.016	3.424	0.0495
f__Ilumatobacteraceae	3.803	3.402	0.0495
f__Nocardioideaceae	3.915	3.398	0.0495
c__unclassified_k__norank_d__Bacteria	4.016	3.396	0.0495
f__Beijerinckiaceae	3.990	3.390	0.0495
g__norank_f__Xanthobacteraceae	4.005	3.361	0.0495
g__Clostridium_sensu_stricto_12	1.919	3.353	0.0369
c__Polyangia	3.793	3.340	0.0495
g__Bryobacter	3.680	3.329	0.0495
g__Nocardioideae	3.832	3.325	0.0495
o__Bryobacteriales	3.680	3.316	0.0495
f__Bryobacteraceae	3.680	3.316	0.0495
g__Microvirga	3.740	3.302	0.0495
f__norank_o__Subgroup_7	3.780	3.296	0.0495
o__Azospirillales	3.835	3.262	0.0495
g__UTCFX1	3.640	3.261	0.0495
o__Subgroup_7	3.780	3.239	0.0495
c__Holophagae	3.780	3.230	0.0495
f__norank_o__IMCC26256	3.701	3.227	0.0495
g__unclassified_f__Vicinamibacteraceae	3.618	3.223	0.0495
o__IMCC26256	3.701	3.220	0.0495
p__Verrucomicrobiota	3.560	3.216	0.0495
c__Verrucomicrobiae	3.553	3.214	0.0495
o__Gemmatales	3.843	3.208	0.0495
g__norank_f__norank_o__Subgroup_7	3.780	3.208	0.0495
o__Micromonosporales	3.831	3.204	0.0495
g__norank_f__norank_o__Microtrichales	3.597	3.200	0.0495
f__Gemmataceae	3.843	3.198	0.0495
g__Sphingomonas	3.570	3.191	0.0495
g__norank_f__Ilumatobacteraceae	3.621	3.188	0.0495
f__Micromonosporaceae	3.831	3.175	0.0495
g__norank_f__WD2101_soil_group	3.984	3.175	0.0495
o__Thermoanaerobaculales	3.525	3.174	0.0495
f__Pseudonocardiaceae	3.695	3.169	0.0495
g__MND1	3.805	3.168	0.0495
g__norank_f__norank_o__IMCC26256	3.701	3.164	0.0495
f__Thermoanaerobaculaceae	3.525	3.163	0.0495
f__Steroidobacteraceae	3.567	3.163	0.0495
g__Subgroup_10	3.525	3.162	0.0495
o__Pseudonocardiales	3.695	3.160	0.0495
g__Pirellula	3.706	3.157	0.0495
o__Blastocatellales	3.589	3.148	0.0495
o__Steroidobacterales	3.570	3.136	0.0495
c__Thermoanaerobaculia	3.525	3.134	0.0495

f__norank_o__Microtrichales	3.597	3.133	0.0495
o__Opitutales	3.363	3.129	0.0495
o__Tepidisphaerales	4.002	3.127	0.0495
f__Blastocatellaceae	3.589	3.125	0.0495
f__norank_o__norank_c__Gitt-GS-136	3.674	3.120	0.0495
g__norank_f__norank_o__C0119	3.504	3.115	0.0495
f__norank_o__C0119	3.504	3.102	0.0495
o__Solibacterales	3.339	3.091	0.0495
o__C0119	3.504	3.088	0.0495
f__TRA3-20	3.572	3.086	0.0495
o__Caldilineales	3.501	3.085	0.0495
g__Pseudonocardia	3.607	3.081	0.0495
f__Caldilineaceae	3.501	3.073	0.0495
g__Candidatus_Solibacter	3.339	3.070	0.0495
f__norank_o__OPB41	2.181	3.069	0.0369
f__Opitutaceae	3.363	3.068	0.0495
g__norank_f__TRA3-20	3.572	3.067	0.0495
g__norank_f__norank_o__norank_c__Gitt-GS-136	3.674	3.062	0.0495
f__Methylogiellaceae	3.538	3.049	0.0495
f__WD2101_soil_group	3.984	3.047	0.0495
o__norank_c__Gitt-GS-136	3.674	3.045	0.0495
c__Gitt-GS-136	3.674	3.041	0.0495
f__Solibacteraceae	3.339	3.041	0.0495
g__Opitutus	3.286	3.040	0.0495
o__Myxococcales	3.558	3.033	0.0495
g__norank_f__norank_o__Azospirillales	3.478	3.013	0.0495
g__Synechococcus_IR11	3.179	3.013	0.0369
g__Ohtaekwangia	2.617	3.007	0.0369
g__Pir4_lineage	3.426	3.007	0.0495
f__norank_o__Azospirillales	3.478	3.005	0.0495

**Supplementary Table S7.** LEfSe analysis of bacterial community in the rhizosphere of alfalfa under Control and MJM-5 treatments and the bacterial taxa were significantly enriched in the MJM-5 treatment.

Species	Mean	LDA value	P value
p__unclassified_k__norank_d__Bacteria	3.875	3.257	0.0495
c__Acidimicrobiia	4.575	4.232	0.0495
o__Defluviicoccales	3.804	3.542	0.0495
f__norank_o__Gaiellales	4.707	4.235	0.0495
p__Methyloirabilota	4.182	3.719	0.0495
f__Nocardioidaceae	4.066	3.587	0.0495
f__Gaiellaceae	4.486	3.956	0.0495
o__norank_c__Gitt-GS-136	3.925	3.487	0.0495
f__Geminicoccaceae	4.318	3.965	0.0495
c__Chloroflexia	4.290	3.817	0.0495
c__Anaerolineae	4.151	3.654	0.0495
o__Nitrospirales	3.926	3.386	0.0495
c__Polyangia	3.655	3.139	0.0495
o__Solirubrobacterales	4.609	4.201	0.0495
o__Anaerolineales	3.945	3.599	0.0495
g__norank_f__Gemmatimonadaceae	4.300	3.843	0.0495

f__Anaerolineaceae	3.945	3.618	0.0495
f__norank_o__norank_c__bacteriap25	4.051	3.545	0.0495
f__norank_o__Vicinamibacterales	4.521	4.054	0.0495
p__Cyanobacteria	4.521	4.097	0.0495
g__norank_f__Gimesiaceae	2.022	3.280	0.0369
f__Blastocatellaceae	3.682	3.264	0.0495
o__Rubrobacterales	3.747	3.336	0.0495
f__norank_o__Subgroup_7	4.205	3.856	0.0495
c__MB-A2-108	4.568	4.214	0.0495
g__Massilia	3.470	3.156	0.0495
f__Steroidobacteraceae	3.692	3.314	0.0495
f__Latescibacteraceae	2.096	3.351	0.0369
o__Thermomicrobiales	3.936	3.342	0.0495
f__Defluviicoccaceae	3.797	3.484	0.0495
f__Oxalobacteraceae	3.886	3.492	0.0495
f__Rubrobacteriaceae	3.747	3.334	0.0495
o__Subgroup_17	3.645	3.299	0.0495
g__unclassified_f__Propionibacteriaceae	4.525	4.197	0.0369
f__norank_o__norank_c__norank_p__MBNT15	3.444	3.078	0.0495
c__Actinobacteria	4.992	4.501	0.0495
o__Thermosynechococcales	3.524	3.104	0.0369
c__Nitrospiria	3.926	3.431	0.0495
g__Subgroup_10	3.593	3.132	0.0495
c__unclassified_k__norank_d__Bacteria	3.875	3.233	0.0495
g__norank_f__Geminicoccaceae	4.298	3.978	0.0495
f__WX65	3.391	3.066	0.0495
g__Noviherbaspirillum	3.363	3.012	0.0495
f__Solirubrobacteraceae	3.967	3.472	0.0495
f__Methyloiligellaceae	3.831	3.450	0.0495
g__norank_f__norank_o__Vicinamibacterales	4.521	4.038	0.0495
g__Synechococcus_IR11	3.524	3.132	0.0369
f__Microbacteriaceae	3.757	3.404	0.0495
c__Methyloirabilia	4.182	3.687	0.0495
c__Rubrobacteria	3.747	3.331	0.0495
g__norank_f__norank_o__norank_c__Gitt-GS-136	3.925	3.502	0.0495
p__Actinobacteriota	5.484	5.043	0.0495
o__norank_c__norank_p__MBNT15	3.444	3.119	0.0495
g__norank_f__norank_o__Actinomarinales	3.538	3.256	0.0463
c__Thermoleophilia	5.100	4.600	0.0495
f__JG30-KF-CM45	3.881	3.314	0.0495
p__Chloroflexi	4.848	4.342	0.0495
o__Thermoanaerobaculales	3.593	3.116	0.0495
o__Vicinamibacterales	4.745	4.278	0.0495
f__unclassified_o__Cyanobacteriales	3.984	3.571	0.0369
g__norank_f__norank_o__Rokubacteriales	4.101	3.577	0.0495
o__Microtrichales	4.401	4.070	0.0495
g__Solirubrobacter	3.878	3.453	0.0495
g__norank_f__norank_o__Gaiellales	4.707	4.221	0.0495
g__Microvirga	3.770	3.333	0.0495
p__Myxococcota	4.268	3.714	0.0495
c__bacteriap25	4.051	3.493	0.0495
g__norank_f__Methyloiligellaceae	3.822	3.452	0.0495

g__norank_f__norank_o__norank_c__MB-A2-108	4.568	4.182	0.0495
c__Thermoanaerobaculia	3.593	3.190	0.0495
o__norank_c__KD4-96	4.121	3.658	0.0495
p__Acidobacteriota	5.093	4.636	0.0495
p__Nitrospirota	3.938	3.472	0.0495
o__Propionibacteriales	4.717	4.369	0.0495
g__norank_f__Sutterellaceae	3.619	3.281	0.0495
g__norank_f__norank_o__IMCC26256	3.877	3.433	0.0495
g__norank_f__norank_o__norank_c__bacteriap25	4.051	3.512	0.0495
f__Micrococcaceae	4.035	3.591	0.0495
o__IMCC26256	3.877	3.439	0.0495
f__norank_o__norank_c__KD4-96	4.121	3.651	0.0495
f__Comamonadaceae	4.485	4.058	0.0495
g__norank_f__norank_o__norank_c__norank_p__MBNT15	3.444	3.120	0.0495
o__Blastocatellales	3.682	3.260	0.0495
f__Sutterellaceae	3.619	3.314	0.0495
g__norank_f__Vicinamibacteraceae	4.221	3.796	0.0495
f__Vicinamibacteraceae	4.326	3.908	0.0495
f__Ilumatobacteraceae	3.703	3.345	0.0495
g__Rubrobacter	3.747	3.308	0.0495
o__norank_c__MB-A2-108	4.568	4.186	0.0495
g__norank_f__WX65	3.391	3.057	0.0495
f__unclassified_k__norank_d__Bacteria	3.875	3.232	0.0495
g__unclassified_k__norank_d__Bacteria	3.875	3.270	0.0495
c__Gitt-GS-136	3.925	3.522	0.0495
g__Fluviicola	3.421	3.164	0.0369
p__MBNT15	3.444	3.118	0.0495
o__Steroidobacterales	3.697	3.339	0.0495
f__norank_o__Microtrichales	4.275	3.960	0.0495
g__UTCFX1	3.406	3.009	0.0495
g__norank_f__norank_o__Subgroup_7	4.205	3.859	0.0495
g__norank_f__Anaerolineaceae	3.690	3.355	0.0495
f__Nitrospiraceae	3.926	3.403	0.0495
g__unclassified_o__Cyanobacteriales	3.984	3.611	0.0369
g__Defluviicoccus	3.797	3.525	0.0495
g__Microlunatus	3.837	3.348	0.0495
o__Gaiellales	4.916	4.444	0.0495
o__norank_c__bacteriap25	4.051	3.486	0.0495
f__Thermosynechococcaceae	3.524	3.157	0.0369
g__norank_f__67-14	4.493	4.082	0.0495
g__Steroidobacter	3.409	3.001	0.0495
g__unclassified_f__Gemmatimonadaceae	3.631	3.227	0.0495
o__unclassified_k__norank_d__Bacteria	3.875	3.192	0.0495
o__Rokubacteriales	4.178	3.673	0.0495
c__KD4-96	4.121	3.638	0.0495
o__Subgroup_7	4.205	3.847	0.0495
o__Cyanobacteriales	4.398	4.001	0.0495
c__norank_p__MBNT15	3.444	3.116	0.0495
g__Ramlibacter	4.076	3.606	0.0495
o__Actinomarinales	3.538	3.223	0.0463
f__Propionibacteriaceae	4.607	4.254	0.0495
f__norank_o__Actinomarinales	3.538	3.189	0.0463

f__norank_o__Subgroup_17	3.645	3.293	0.0495
f__norank_o__norank_c__MB-A2-108	4.568	4.198	0.0495
g__unclassified_f__Comamonadaceae	4.180	3.775	0.0495
c__Holophagae	4.206	3.853	0.0495
g__Gaiella	4.486	3.985	0.0495
g__Nitrospira	3.926	3.432	0.0495
o__Tistrellales	4.318	3.975	0.0495
f__Hyphomicrobiaceae	3.669	3.094	0.0495
f__norank_o__IMCC26256	3.877	3.443	0.0495
f__norank_o__Rokubacteriales	4.101	3.596	0.0495
g__Arthrobacter	3.998	3.598	0.0495
f__norank_o__norank_c__Gitt-GS-136	3.925	3.497	0.0495
g__norank_f__norank_o__norank_c__KD4-96	4.121	3.617	0.0495
g__Agromyces	3.421	3.083	0.0495
g__norank_f__norank_o__Subgroup_17	3.645	3.305	0.0495
g__Lysobacter	3.886	3.457	0.0495
g__unclassified_f__Vicinamibacteraceae	3.569	3.168	0.0495
g__norank_f__Ilumatobacteraceae	3.573	3.199	0.0495
g__norank_f__norank_o__Microtrichales	4.275	3.943	0.0495
f__67-14	4.493	4.102	0.0495
f__Thermoanaerobaculaceae	3.593	3.165	0.0495
g__norank_f__Steroidobacteraceae	3.370	3.037	0.0495
g__norank_f__JG30-KF-CM45	3.881	3.280	0.0495

**Supplementary Table S8.** LEfSe analysis of bacterial community in the rhizosphere of alfalfa under Control and MJM-5+LJL-12 and the bacterial taxa were significantly enriched in the MJM-5+LJL-12 treatment.

Species	Mean	LDA value	P value
p__Actinobacteriota	5.435	5.024	0.0495
c__Actinobacteria	5.115	4.713	0.0495
p__Acidobacteriota	5.165	4.689	0.0495
c__Thermoleophilia	5.030	4.517	0.0495
c__Vicinamibacteria	4.876	4.424	0.0495
o__Vicinamibacteriales	4.863	4.413	0.0495
p__Chloroflexi	4.920	4.409	0.0495
o__Burkholderiales	4.884	4.282	0.0495
o__Micrococcales	4.582	4.269	0.0495
o__Gaiellales	4.844	4.240	0.0495
o__Propionibacteriales	4.579	4.230	0.0495
g__norank_f__norank_o__Vicinamibacteriales	4.623	4.157	0.0495
f__norank_o__Vicinamibacteriales	4.623	4.143	0.0495
f__norank_o__Gaiellales	4.660	4.137	0.0495
o__Solirubrobacteriales	4.552	4.127	0.0495
f__Micrococcaceae	4.415	4.101	0.0495
g__Arthrobacter	4.391	4.095	0.0495
g__norank_f__norank_o__Gaiellales	4.660	4.073	0.0495
f__Nocardiodaceae	4.424	4.072	0.0495
f__Vicinamibacteraceae	4.457	4.060	0.0495
g__Nocardioidea	4.378	4.048	0.0495
c__Chloroflexia	4.427	4.027	0.0495
f__Comamonadaceae	4.424	3.984	0.0495
g__norank_f__Vicinamibacteraceae	4.349	3.962	0.0495

o__Frankiales	4.322	3.950	0.0495
c__Blastocatellia	4.498	3.911	0.0495
g__norank_f__Gemmatimonadaceae	4.365	3.885	0.0495
g__unclassified_f__Comamonadaceae	4.168	3.847	0.0495
f__Xanthobacteraceae	4.473	3.847	0.0495
c__Acidimicrobiia	4.227	3.843	0.0495
f__Solirubrobacteraceae	4.223	3.832	0.0495
p__Myxococcota	4.349	3.823	0.0495
f__67-14	4.270	3.817	0.0495
c__KD4-96	4.234	3.807	0.0495
g__Gaiella	4.367	3.805	0.0495
g__norank_f__67-14	4.270	3.804	0.0495
g__norank_f__norank_o__norank_c__KD4-96	4.234	3.804	0.0495
f__norank_o__norank_c__KD4-96	4.234	3.800	0.0495
f__Geodermatophilaceae	4.171	3.799	0.0495
c__Acidobacteriae	4.333	3.791	0.0495
g__RB41	4.379	3.774	0.0495
f__Gaiellaceae	4.367	3.771	0.0495
p__Planctomycetota	4.545	3.771	0.0495
o__norank_c__KD4-96	4.234	3.760	0.0495
g__Solirubrobacter	4.067	3.736	0.0495
o__Pyrinomonadales	4.379	3.731	0.0495
g__Blastococcus	4.115	3.714	0.0495
o__Thermomicrobiales	4.143	3.711	0.0495
f__Pyrinomonadaceae	4.379	3.689	0.0495
o__Chloroflexales	4.080	3.683	0.0495
f__Propionibacteriaceae	4.055	3.682	0.0495
g__norank_f__norank_o__norank_c__MB-A2-108	4.154	3.677	0.0495
f__norank_o__norank_c__MB-A2-108	4.154	3.672	0.0495
c__MB-A2-108	4.154	3.662	0.0495
c__Polyangia	4.014	3.661	0.0495
g__Bacillus	4.081	3.661	0.0495
g__Microlunatus	4.051	3.661	0.0495
g__Streptomyces	4.081	3.652	0.0495
o__norank_c__MB-A2-108	4.154	3.651	0.0495
f__Streptomycetaceae	4.083	3.650	0.0495
o__Microtrichales	3.972	3.649	0.0495
f__JG30-KF-CM45	4.082	3.647	0.0495
f__Roseiflexaceae	4.056	3.645	0.0495
g__norank_f__Roseiflexaceae	4.040	3.643	0.0495
p__unclassified_k__norank_d__Bacteria	4.110	3.642	0.0495
o__Streptomycetales	4.083	3.638	0.0495
g__Microvirga	3.937	3.634	0.0495
c__Planctomycetes	4.331	3.631	0.0495
f__Oxalobacteraceae	3.983	3.629	0.0495
g__norank_f__JG30-KF-CM45	4.082	3.628	0.0495
c__unclassified_k__norank_d__Bacteria	4.110	3.609	0.0495
g__unclassified_k__norank_d__Bacteria	4.110	3.602	0.0495
f__unclassified_k__norank_d__Bacteria	4.110	3.597	0.0495
o__unclassified_k__norank_d__Bacteria	4.110	3.596	0.0495
c__Anaerolineae	4.119	3.588	0.0495
g__Sphingobium	3.769	3.561	0.0495

f__Intrasporangiaceae	3.867	3.529	0.0495
f__Ilumatobacteraceae	3.816	3.513	0.0495
f__Nitrosomonadaceae	4.186	3.510	0.0495
g__Lysobacter	3.926	3.502	0.0495
c__TK10	3.973	3.501	0.0495
f__norank_o__norank_c__TK10	3.973	3.499	0.0495
o__norank_c__TK10	3.973	3.498	0.0495
g__norank_f__norank_o__norank_c__TK10	3.973	3.462	0.0495
f__Anaerolineaceae	3.865	3.462	0.0495
g__Bryobacter	3.809	3.445	0.0495
f__Bryobacteraceae	3.809	3.444	0.0495
f__Steroidobacteraceae	3.756	3.435	0.0495
o__Anaerolineales	3.865	3.435	0.0495
o__Bryobacteriales	3.809	3.434	0.0495
f__Micromonosporaceae	3.916	3.432	0.0495
o__Steroidobacteriales	3.760	3.425	0.0495
o__Micromonosporales	3.916	3.414	0.0495
g__norank_f__Xanthobacteraceae	4.053	3.405	0.0495
g__norank_f__norank_o__Subgroup_7	3.889	3.403	0.0495
g__Nitrospira	3.892	3.394	0.0495
c__Holophagae	3.889	3.393	0.0495
o__Subgroup_7	3.889	3.389	0.0495
g__Subgroup_10	3.702	3.385	0.0495
o__Gammaproteobacteria_Incertae_Sedis	3.776	3.385	0.0495
f__Microbacteriaceae	3.667	3.377	0.0495
o__Nitrospirales	3.892	3.373	0.0495
f__norank_o__Subgroup_7	3.889	3.371	0.0495
f__unclassified_o__Gammaproteobacteria_Incertae_Sedis	3.776	3.371	0.0495
c__Thermoanaerobaculia	3.702	3.363	0.0495
o__Azospirillales	3.804	3.361	0.0495
o__Thermoanaerobaculales	3.702	3.359	0.0495
p__Nitrospirota	3.893	3.358	0.0495
g__Acidibacter	3.755	3.357	0.0495
f__Gemmataceae	3.895	3.352	0.0495
g__norank_f__WD2101_soil_group	4.038	3.352	0.0495
f__Thermoanaerobaculaceae	3.702	3.344	0.0495
g__unclassified_f__Vicinamibacteraceae	3.735	3.332	0.0495
o__Pseudonocardiales	3.755	3.328	0.0495
o__Tepidisphaerales	4.055	3.328	0.0495
c__Nitrospira	3.892	3.326	0.0495
o__Gemmatales	3.895	3.325	0.0495
o__Polyangiales	3.664	3.318	0.0495
g__Ellin6067	3.866	3.317	0.0495
o__IMCC26256	3.778	3.311	0.0495
f__Pseudonocardiaceae	3.755	3.308	0.0495
f__Nitrospiraceae	3.892	3.308	0.0495
f__WD2101_soil_group	4.038	3.307	0.0495
g__norank_f__Intrasporangiaceae	3.602	3.305	0.0495
g__norank_f__norank_o__IMCC26256	3.778	3.287	0.0495
f__unclassified_p__Actinobacteriota	2.245	3.287	0.0369
o__Haliangiales	3.673	3.269	0.0495
f__Haliangiaceae	3.673	3.269	0.0495

f__norank_o__IMCC26256	3.778	3.265	0.0495
g__Haliangium	3.673	3.261	0.0495
c__Phycisphaerae	4.069	3.259	0.0495
g__Steriodobacter	3.605	3.254	0.0495
o__Myxococcales	3.640	3.251	0.0495
p__Armatimonadota	3.925	3.245	0.0495
p__Verrucomicrobiota	3.674	3.245	0.0495
c__Myxococcia	3.640	3.242	0.0495
o__Solibacterales	3.597	3.237	0.0495
g__Candidatus_Solibacter	3.597	3.231	0.0495
c__Verrucomicrobiae	3.668	3.231	0.0495
g__unclassified_o__Cyanobacteriales	1.523	3.221	0.0369
g__norank_f__norank_o__Micavibrionales	2.483	3.201	0.0463
f__Solibacteraceae	3.597	3.200	0.0495
f__norank_o__mle1-27	2.386	3.198	0.0463
g__UTCFX1	3.573	3.196	0.0495
g__Sphingomonas	3.617	3.195	0.0495
f__norank_o__C0119	3.597	3.195	0.0495
g__Massilia	3.503	3.190	0.0495
p__Cyanobacteria	3.702	3.190	0.0495
g__norank_f__norank_o__C0119	3.597	3.188	0.0495
o__C0119	3.597	3.187	0.0495
g__Pseudonocardia	3.580	3.179	0.0495
g__unclassified_f__Gemmatimonadaceae	3.620	3.151	0.0495
f__Rhizobiales_Incertae_Sedis	3.639	3.146	0.0495
f__Myxococcaceae	3.546	3.138	0.0495
f__unclassified_c__Polyangia	1.523	3.136	0.0369
g__Agromyces	3.409	3.136	0.0495
g__unclassified_f__Oxalobacteraceae	3.518	3.136	0.0495
g__unclassified_c__Polyangia	1.523	3.133	0.0369
g__Conexibacter	3.601	3.132	0.0495
g__norank_f__norank_o__norank_c__Gitt-GS-136	3.642	3.124	0.0495
g__Ilumatobacter	3.390	3.119	0.0495
f__unclassified_o__Bacillales	3.482	3.115	0.0495
g__unclassified_o__Bacillales	3.482	3.106	0.0495
o__norank_c__Gitt-GS-136	3.642	3.089	0.0495
g__norank_f__Gemmataceae	3.638	3.088	0.0495
f__norank_o__norank_c__Gitt-GS-136	3.642	3.088	0.0495
g__Candidatus_Ovatusbacter	2.035	3.085	0.0369
g__norank_f__Chitinophagaceae	3.534	3.082	0.0495
f__Rubrobacteriaceae	3.530	3.082	0.0495
f__Nakamurellaceae	2.809	3.079	0.0495
g__Noviherbaspirillum	3.412	3.079	0.0495
g__Pelomonas	2.788	3.068	0.0369
g__Rubrobacter	3.530	3.068	0.0495
o__unclassified_c__Polyangia	1.523	3.059	0.0369
g__Roseisolibacter	3.478	3.058	0.0495
g__Tepidisphaera	1.630	3.058	0.0369
g__norank_f__Ilumatobacteraceae	3.391	3.053	0.0495
c__Rubrobacteria	3.530	3.052	0.0495
c__Gitt-GS-136	3.642	3.049	0.0495
g__Tundrisphaera	1.630	3.049	0.0369



g__unclassified_f__Micromonosporaceae	3.494	3.049	0.0495
o__Rubrobacterales	3.530	3.042	0.0495
g__Nordella	3.490	3.041	0.0495
g__MND1	3.739	3.040	0.0495
o__mle1-27	2.386	3.019	0.0463
f__norank_o__Frankiales	3.314	3.018	0.0495
g__norank_f__norank_o__Frankiales	3.314	3.017	0.0495
f__unclassified_o__Vicinamibacterales	3.378	3.013	0.0495
f__unclassified_o__Cyanobacterales	1.523	3.011	0.0369
g__unclassified_o__Vicinamibacterales	3.378	3.000	0.0495

**Supplementary Table S9.** Growth-promoting traits of plant growth promoting rhizobacteria (PGPR) in this study.

Tested trait	LJL-12	MJM-5
Phosphate solubilization ( $\mu\text{g}\cdot\text{mL}^{-1}$ )	$275.3 \pm 6.1$	$281.3 \pm 24.0$
ACCD activity ( $\mu\text{mol}\cdot\alpha\text{-KA}\cdot\text{mg}^{-1}\text{ h}^{-1}$ )	$16.4 \pm 1.9$	$17.2 \pm 1.3$
IAA production ( $\mu\text{g}\cdot\text{mL}^{-1}$ )	$10.3 \pm 0.1$	$8.7 \pm 0.5$
Siderophore (A/Ar)	$0.7 \pm 0.01$	$0.8 \pm 0.02$

**Supplementary Table S10.** Correlation analysis between the physio-chemical properties of alfalfa rhizosphere soil and major bacterial taxa under the Control treatment.

Taxa/Properties	MC	BD	OM	AN	AP	AK
Actinobacteriota	0.663	0.749	0.018	0.994	-0.995	0.990
Proteobacteria	0.911	-0.854	-0.950	0.397	-0.390	0.157
Acidobacteriota	-0.522	0.622	-0.192	-0.960	0.962	-0.999*
Chloroflexi	-1.000**	0.994	0.726	-0.751	0.746	-0.563
Gemmatimonadota	-0.127	0.005	0.764	0.573	-0.579	0.758
Planctomycetota	0.933	-0.970	-0.444	0.933	-0.930	0.814
Myxococcota	-0.062	0.183	-0.629	-0.717	0.722	-0.867
Armatimonadota	-0.268	0.383	-0.454	-0.846	0.850	-0.952
Actinobacteria	0.683	-0.766	-0.009	0.997	-0.997*	0.986
Gammaproteobacteria	-0.351	0.462	-0.375	-0.889	0.893	-0.975
Alphaproteobacteria	0.589	-0.683	0.112	0.979	-0.981	0.999*
Thermolephilia	0.688	-0.771	-0.017	0.997*	-0.998*	0.985
Vicinamibacteria	-0.674	0.759	-0.003	-0.996	0.996	-0.988
Gemmatimonadetes	-0.052	-0.070	0.713	0.633	-0.639	0.805
Arthrobacter	-0.998*	0.983	0.778	-0.697	0.691	-0.497
Sphingomonas	0.645	-0.733	0.041	0.991	-0.992	0.993
Bacillus	-0.785	0.854	0.159	-0.998*	0.997*	-0.949
Streptomyces	0.921	-0.962	-0.416	0.943	-0.941	0.831
Bradyrhizobium	0.987	-0.960	-0.836	0.622	-0.616	0.409

MC: moisture content. BD: bulk density. OM: organic matter. AN: available nitrogen. AP: available phosphorus. AK: available potassium. The values in the Table represent the correlation coefficient of the Pearson analysis. \*  $P < 0.05$ ; \*\*  $P < 0.01$ .

**Supplementary Table S11.** Correlation analysis between the physio-chemical properties of alfalfa rhizosphere soil and major bacterial taxa under the LJL-12 treatment.

Taxa/Properties	MC	BD	OM	AN	AP	AK
Actinobacteriota	0.510	0.360	0.037	0.953	-0.760	-0.208
Proteobacteria	-0.962	0.381	-0.715	-0.899	0.104	-0.523
Acidobacteriota	0.999*	-0.585	0.858	0.773	0.130	0.707
Chloroflexi	0.995	-0.540	0.829	0.807	0.076	0.667
Gemmatimonadota	0.520	-0.993	0.865	-0.180	0.930	0.961
Planctomycetota	0.270	0.590	-0.223	0.842	-0.903	-0.454
Myxococcota	0.143	0.689	-0.347	0.765	-0.951	-0.566
Armatimonadota	0.157	-0.873	0.610	-0.539	1.000**	0.785
Actinobacteria	0.621	0.232	0.171	0.985	-0.666	-0.075
Gammaproteobacteria	-0.837	0.087	-0.473	-0.989	0.397	-0.244
Alphaproteobacteria	-0.997*	0.560	-0.841	-0.793	-0.099	-0.684
Thermolephilia	0.487	0.385	0.011	0.945	-0.777	-0.233
Vicinamibacteria	0.667	0.172	0.230	0.994	-0.620	-0.014
Gemmatimonadetes	0.455	-0.981	0.825	-0.253	0.955	0.938
Arthrobacter	0.996	-0.682	0.915	0.688	0.253	0.790
Sphingomonas	0.704	-0.993	0.958	0.054	0.820	0.999*
Bacillus	-0.321	-0.545	0.170	-0.870	0.878	0.405
Streptomyces	0.007	-0.790	0.484	-0.660	0.986	0.683
Bradyrhizobium	-0.345	-0.524	0.145	-0.882	0.866	0.382

MC: moisture content. BD: bulk density. OM: organic matter. AN: available nitrogen. AP: available phosphorus. AK: available potassium. The values in the Table represent the correlation coefficient of the Pearson analysis. \*  $P < 0.05$ ; \*\*  $P < 0.01$ .

**Supplementary Table S12.** Correlation analysis between the physio-chemical properties of alfalfa rhizosphere soil and major bacterial taxa under the MJM-5 treatment.

Taxa/Properties	MC	BD	OM	AN	AP	AK
Actinobacteriota	-0.464	-0.381	0.992	-0.732	0.060	0.551
Proteobacteria	0.599	0.229	-0.958	0.831	0.099	-0.412
Acidobacteriota	0.924	-0.300	-0.679	0.998*	0.593	0.111
Chloroflexi	-0.701	0.997	-0.427	-0.425	-0.969	-0.963
Gemmatimonadota	0.520	0.321	-0.981	0.774	0.004	-0.497
Planctomycetota	-0.409	0.962	-0.715	-0.084	-0.822	-0.997
Myxococcota	0.433	-0.969	0.696	0.110	0.836	0.998*
Armatimonadota	0.616	0.209	-0.952	0.842	0.119	-0.393
Actinobacteria	-0.809	0.068	0.832	-0.958	-0.388	0.125
Gammaproteobacteria	0.468	0.377	-0.991	0.734	-0.057	-0.548
Alphaproteobacteria	0.888	-0.922	0.124	0.686	0.998*	0.831
Thermolephilia	-0.232	-0.597	0.993	-0.541	0.305	0.740
Vicinamibacteria	0.999*	-0.606	-0.389	0.958	0.831	0.442
Gemmatimonadetes	0.488	0.356	-0.988	0.750	-0.034	-0.529
Arthrobacter	-0.912	0.271	0.700	-0.996	-0.569	-0.081
Sphingomonas	0.903	-0.249	-0.716	0.994	0.550	0.059
Bacillus	-0.636	-0.184	0.944	-0.855	-0.145	0.369

Streptomyces	0.443	0.403	-0.994	0.715	-0.085	-0.572
Bradyrhizobium	0.311	0.529	-0.999*	0.608	-0.226	-0.683

MC: moisture content. BD: bulk density. OM: organic matter. AN: available nitrogen. AP: available phosphorus. AK: available potassium. The values in the Table represent the correlation coefficient of the Pearson analysis. \*  $P < 0.05$ ; \*\*  $P < 0.01$ .

**Supplementary Table S13.** Correlation analysis between the physio-chemical properties of alfalfa rhizosphere soil and major bacterial taxa under the MJM-5+LJL-12 treatment.

Taxa/Properties	MC	BD	OM	AN	AP	AK
Actinobacteriota	-1.000**	-0.487	0.818	-0.679	-0.987	-0.936
Proteobacteria	0.700	-0.285	-0.160	1.000*	0.805	0.906
Acidobacteriota	-0.893	-0.039	0.469	-0.937	-0.953	-0.994
Chloroflexi	-0.064	0.841	-0.524	-0.775	-0.222	-0.409
Gemmatimonadota	0.534	0.998*	-0.924	-0.256	0.393	0.205
Planctomycetota	-0.785	-0.923	0.999*	-0.080	-0.676	-0.519
Myxococcota	-1.000*	-0.503	0.828	-0.665	-0.984	-0.930
Armatimonadota	0.746	0.944	-0.994	0.019	0.631	0.467
Actinobacteria	-0.844	-0.879	0.999*	-0.180	-0.747	-0.602
Gammaproteobacteria	0.780	-0.168	-0.276	0.989	0.870	0.950
Alphaproteobacteria	0.397	-0.610	0.206	0.943	0.538	0.693
Thermolephilia	0.235	0.964	-0.753	-0.553	0.077	-0.120
Vicinamibacteria	-0.688	-0.968	0.981	0.064	-0.564	-0.391
Gemmatimonadetes	0.547	0.997*	-0.930	-0.241	0.407	0.220
Arthrobacter	-0.778	-0.927	0.998*	-0.068	-0.667	-0.509
Sphingomonas	-0.051	0.849	-0.535	-0.767	-0.209	-0.397
Bacillus	0.477	-0.537	0.117	0.969	0.611	0.754
Streptomyces	-0.986	-0.334	0.710	-0.792	-1.000**	-0.982
Bradyrhizobium	-0.383	0.622	-0.220	-0.938	-0.526	-0.682

MC: moisture content. BD: bulk density. OM: organic matter. AN: available nitrogen. AP: available phosphorus. AK: available potassium. The values in the Table represent the correlation coefficient of the Pearson analysis. \*  $P < 0.05$ ; \*\*  $P < 0.01$ .