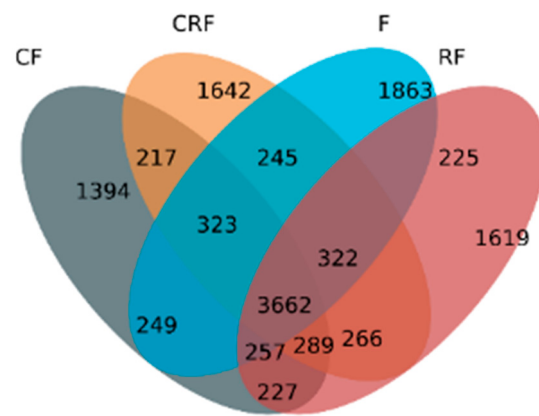
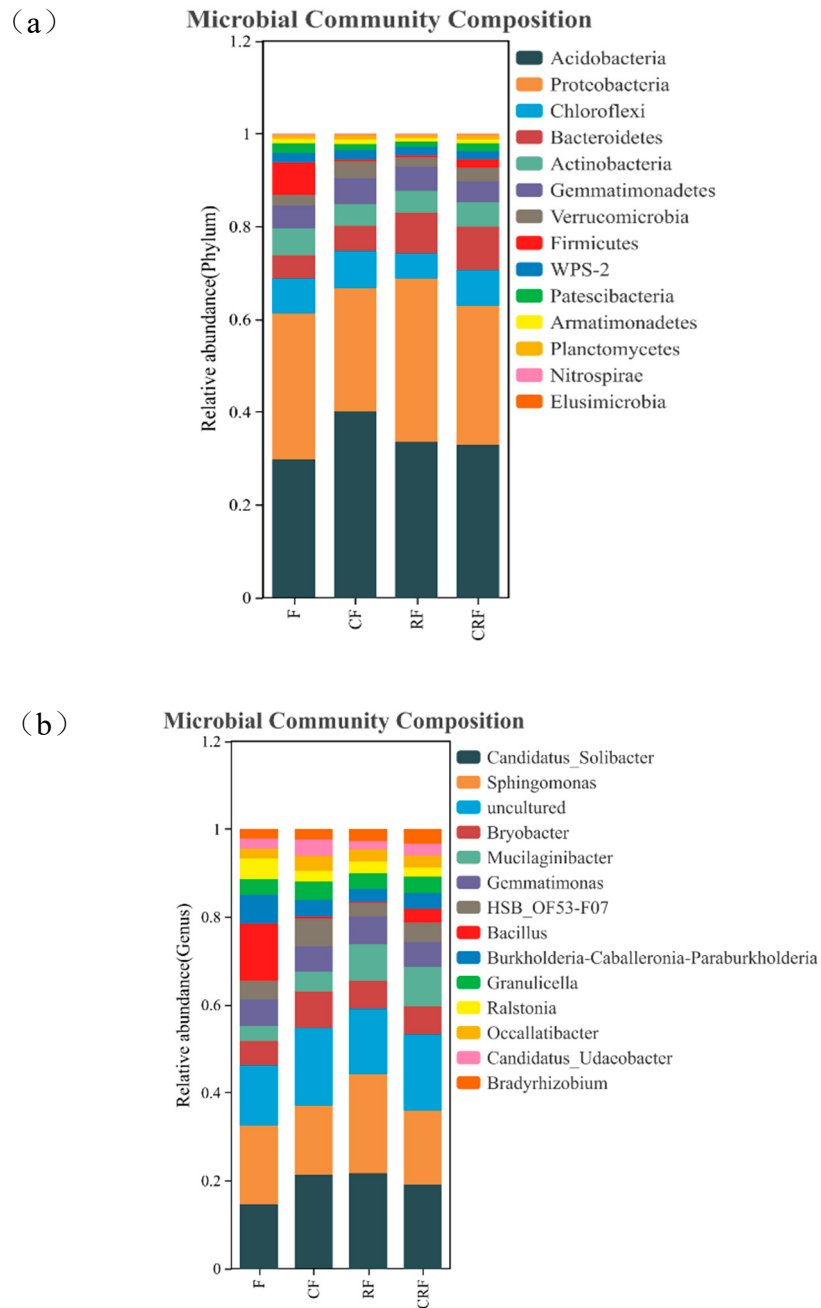
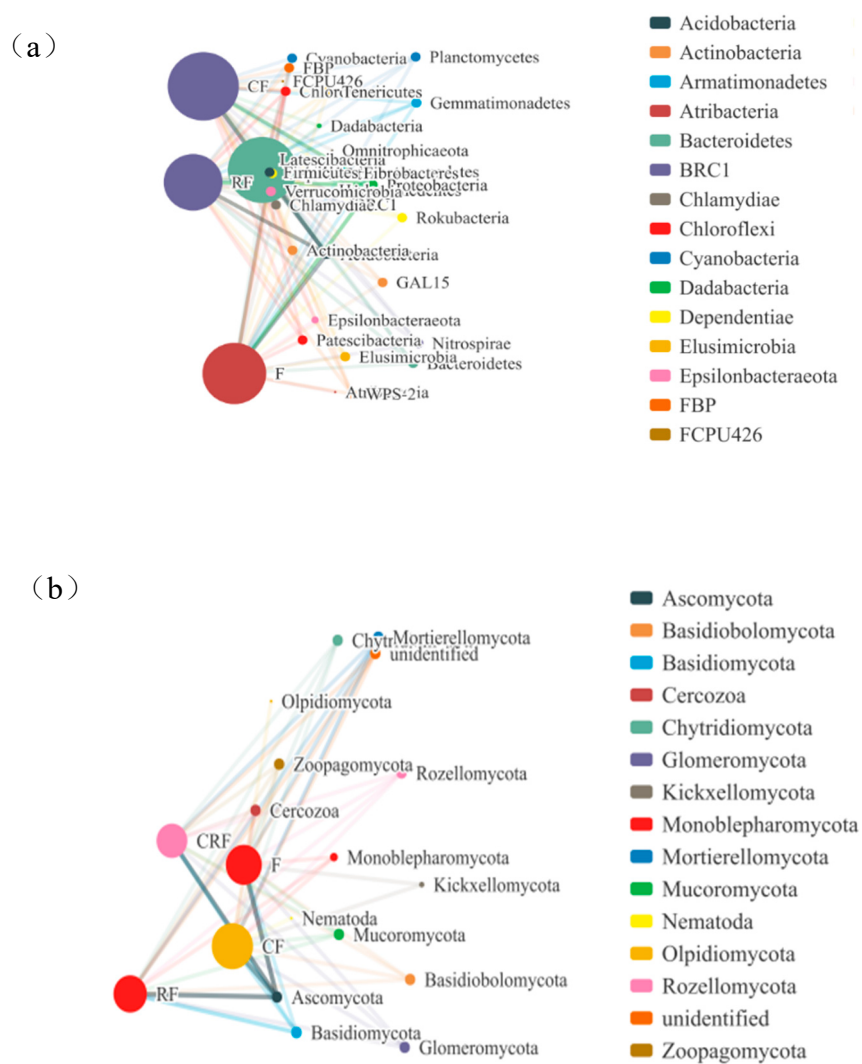




Supplemenatry Figure S1. Venn of common OTU of different treatments



Supplemenatry Figure S2. Changes in the abundance of phylum (a) and genus under different treatments (b)



Supplementary Figure S3. Conetwork analysis of phylum (a) and genus (b) under different treatments

Supplementary Table S1 Changes of soybean mainly agronomic shape under different treatments

Rhizobial strain	Treatment	Plant height (cm)	Root length (cm)	Aboveground fresh weight (g)
HH103	1	45.32 ± 1.36 dC	18.59 ± 0.72 cB	151.53 ± 5.84 cB
	2	46.67 ± 1.42 dC	20.70 ± 0.83 aA	148.40 ± 5.26 dB
	3	44.71 ± 1.31 dC	19.49 ± 0.76 aA	132.85 ± 4.92 cC
	4	52.56 ± 1.57 cB	18.76 ± 0.69 bB	166.83 ± 6.14 aA
	5	55.44 ± 1.68 bA	18.77 ± 0.71 bB	159.93 ± 5.73 bB
	6	62.39 ± 1.92 aA	18.00 ± 0.66 dC	170.94 ± 6.31 aA
	7	59.35 ± 1.78 aA	19.78 ± 0.74 aA	165.09 ± 5.95 aA
TY3-5-1	1	46.34 ± 1.39 cB	20.57 ± 0.78 cB	151.94 ± 5.49 cB
	2	52.14 ± 1.56 bA	16.96 ± 0.65 dC	145.95 ± 5.16 dC
	3	44.93 ± 1.34 dC	22.45 ± 0.86 cB	144.57 ± 5.03 dC
	4	58.43 ± 1.75 aA	24.84 ± 0.93 bB	170.08 ± 6.18 aA
	5	47.33 ± 1.42 cB	23.83 ± 0.88 bB	165.21 ± 5.87 aA
	6	50.55 ± 1.53 bA	30.45 ± 1.12 aA	162.39 ± 5.76 bA
	7	52.80 ± 1.61 bA	26.24 ± 0.97 bB	147.04 ± 5.21 dC

Footnote: Within the same inoculation method, values followed by different uppercase and lowercase letters in the same column differ significantly at $P < 0.01$ and $P < 0.05$, respectively; the same notation applies to subsequent tables.

Supplementary Table S2 Changes of nodulation in soybean under different treatments

Rhizobial strain	Treatment	Nodule number per plant	Fresh nodule weight (g)	Nodule volume (cm ³)
HH103	1	0.00 ± 0.00 dC	0.00 ± 0.00 cC	0.00 ± 0.00 dC
	2	34.7 ± 1.8 cB	0.35 ± 0.03 bB	0.78 ± 0.05 bB
	3	46.1 ± 2.1 aA	0.49 ± 0.04 aA	0.69 ± 0.04 cB
	4	44.6 ± 2.0 bA	0.47 ± 0.03 aA	0.82 ± 0.05 bB
	5	43.3 ± 1.9 bA	0.42 ± 0.03 bB	0.84 ± 0.05 bB
	6	50.2 ± 2.3 aA	0.56 ± 0.04 aA	1.02 ± 0.06 aA
	7	0.00 ± 0.00 dC	0.00 ± 0.00 cC	0.00 ± 0.00 dC
TY3-5-1	1	0.00 ± 0.00 eD	0.00 ± 0.00 bB	0.00 ± 0.00 eD
	2	34.3 ± 1.7 dC	0.56 ± 0.04 aA	0.63 ± 0.04 dC
	3	38.6 ± 1.9 cB	0.59 ± 0.04 aA	0.88 ± 0.05 bA
	4	43.5 ± 2.0 aA	0.62 ± 0.05 aA	0.92 ± 0.05 aA
	5	41.5 ± 1.8 bB	0.59 ± 0.04 aA	0.85 ± 0.05 cA
	6	45.8 ± 2.1 aA	0.66 ± 0.05 aA	0.77 ± 0.04 dB
	7	0.00 ± 0.00 eD	0.00 ± 0.00 bB	0.00 ± 0.00 eD

Supplementary Table S3 Bacterial richness and diversity indexes calculated by QIIME

Treatment	Chao1	ACE	Shannon	Simpson
F	3114.50 ± 86.32 bC	3321.38 ± 94.15 bB	10.00 ± 0.16 bB	0.995 ± 0.002 aA
CF	2906.33 ± 79.47 cD	3028.33 ± 88.26 cC	10.50 ± 0.18 aA	0.997 ± 0.001 aA
RF	3235.50 ± 91.24 bB	3416.33 ± 101.43 bB	9.57 ± 0.15 cB	0.957 ± 0.006 bB
CRF	3603.83 ± 105.68 aA	3937.83 ± 112.36 aA	9.46 ± 0.14 cB	0.929 ± 0.008 cC