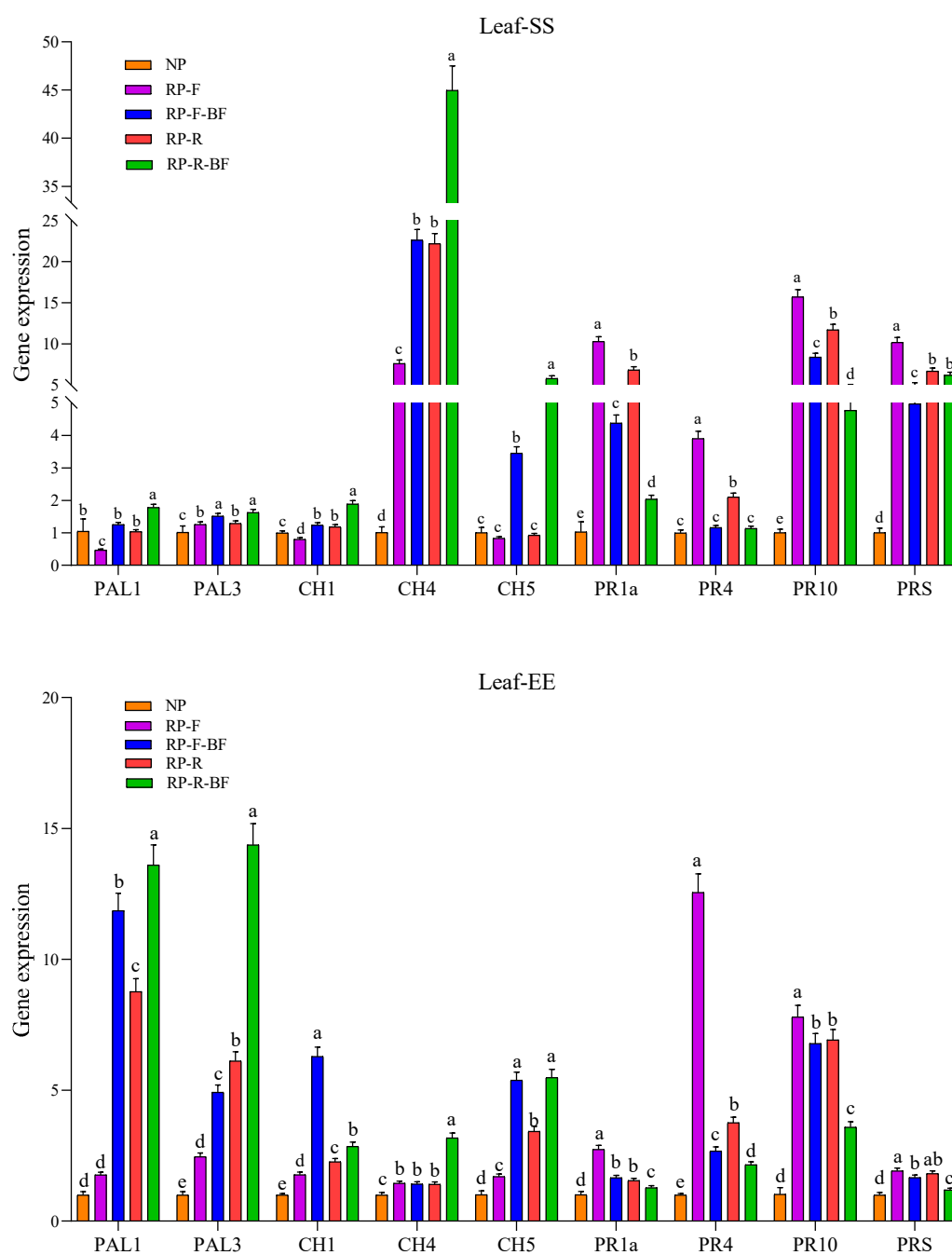


Figure S1. Schematic diagram of soil treatments of *R. pseudostellariae* in 2019 and 2020. NP: the newly planting *Radix pseudostellariae*. RP-F: the keeping soil fallow after harvesting *Radix pseudostellariae*. RP-F-BF: applying bio-microbial fertilizer in fallow soil before the next planting period of *Radix pseudostellariae*. RP-R: *Radix pseudostellariae* rotated with rice. RP-R-BF: applying bio-microbial fertilizer in the soil after harvesting the rice rotated with *Radix pseudostellariae*.



Figure S2. Appearance and morphology of *R. Pseudostellariae* root tubers under different treatments. Treatments are the same as those given in Figure S1.



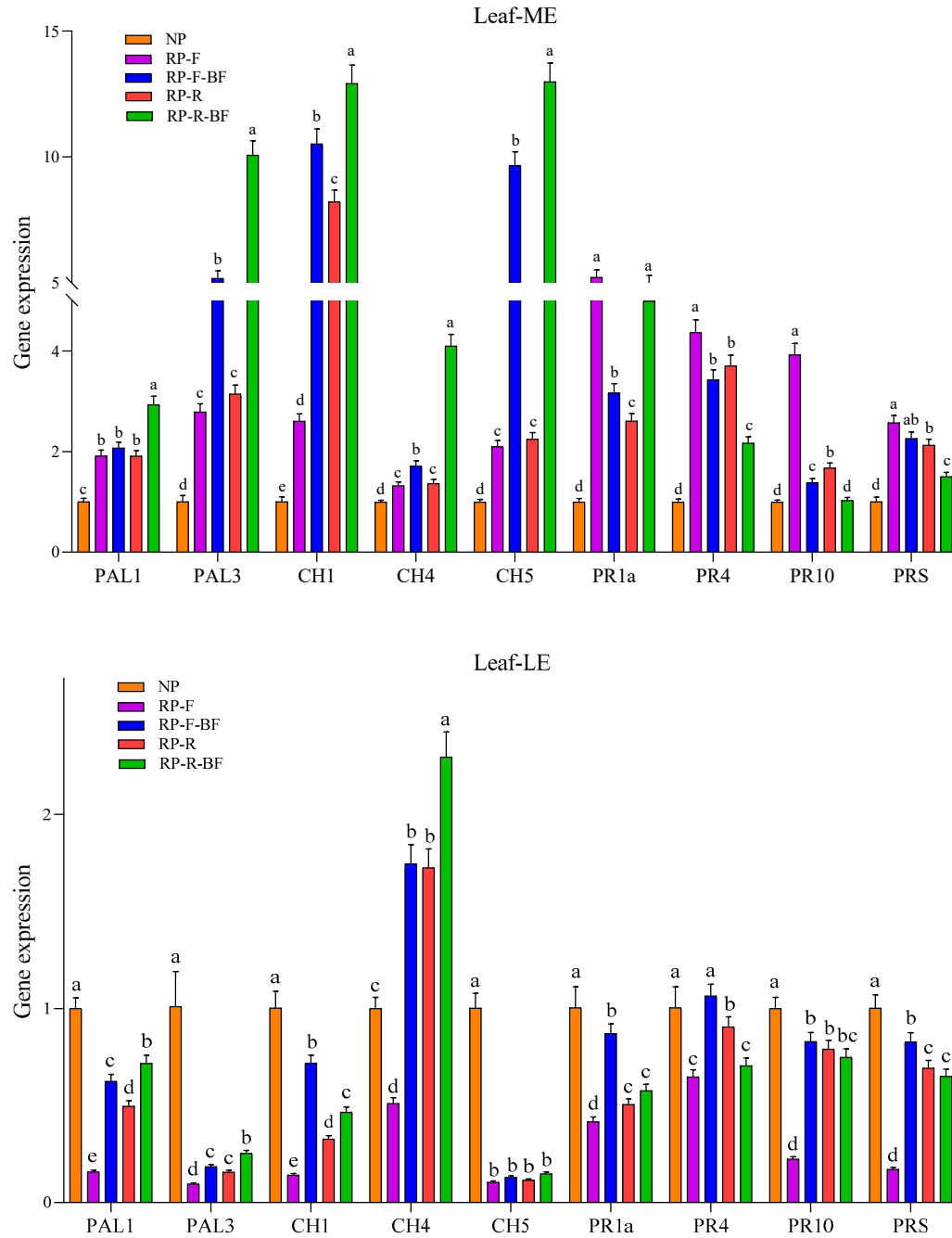
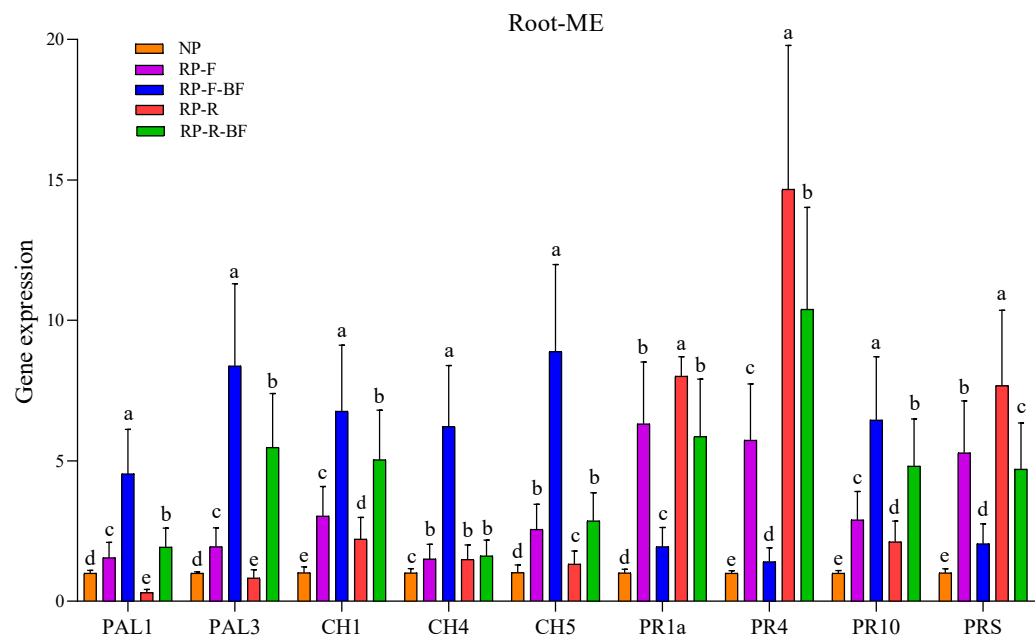
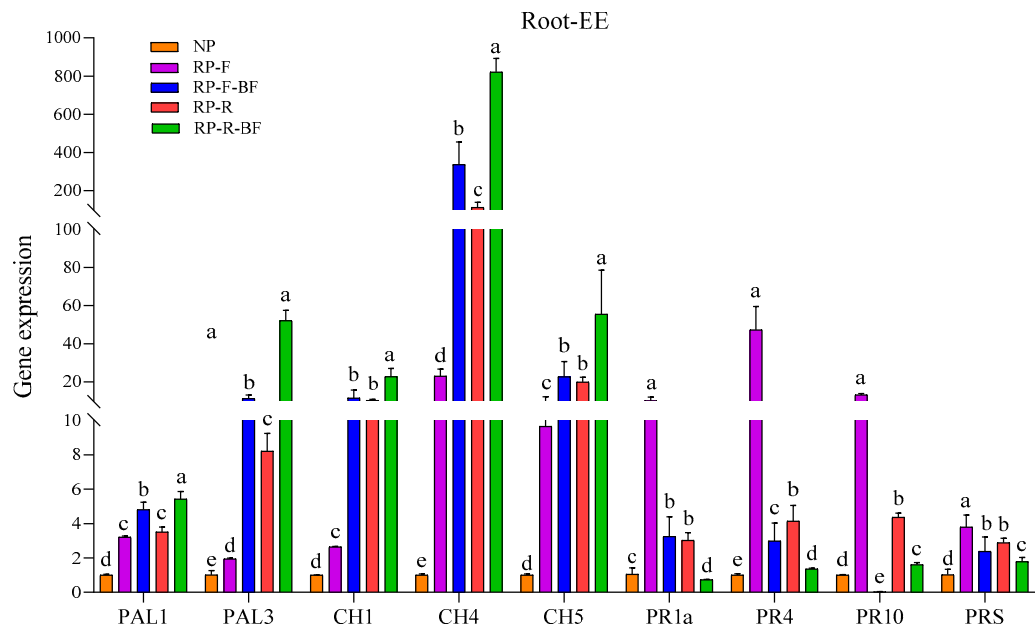


Figure S3. Differential expression of disease resistance and defense related genes in the leaves of *R. pseudostellariae* under different treatments. Treatments are the same as those given in Figure S1. SS: the seedling stage. EE: the early expanding stage of tuber roots. ME: the middle expanding stage of tuber roots. LE: the late expanding stage of tuber roots. Different lowercase letters indicate significant differences between different treatments at $p < 0.05$.



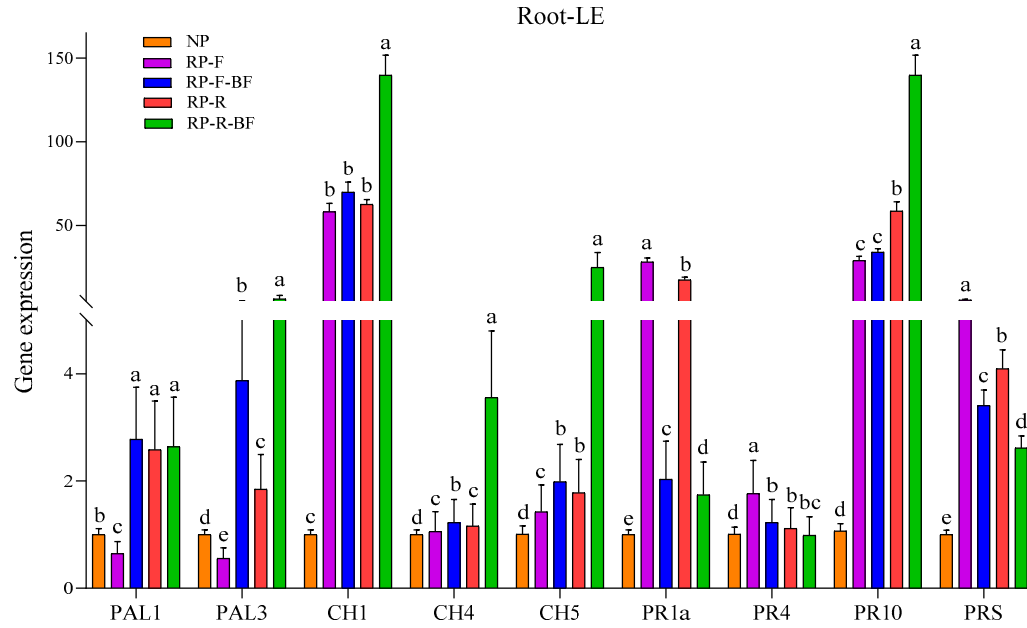


Figure S4. Differential expression of disease resistance and defense related genes in the root tubers of *R. pseudostellariae* under different treatments. Treatments are the same as those given in Figure S1. SS: the seedling stage. EE: the early expanding stage of tuber roots. ME: the middle expanding stage of tuber roots. LE: the late expanding stage of tuber roots. Different lowercase letters indicate significant differences between different treatments at $p < 0.05$.

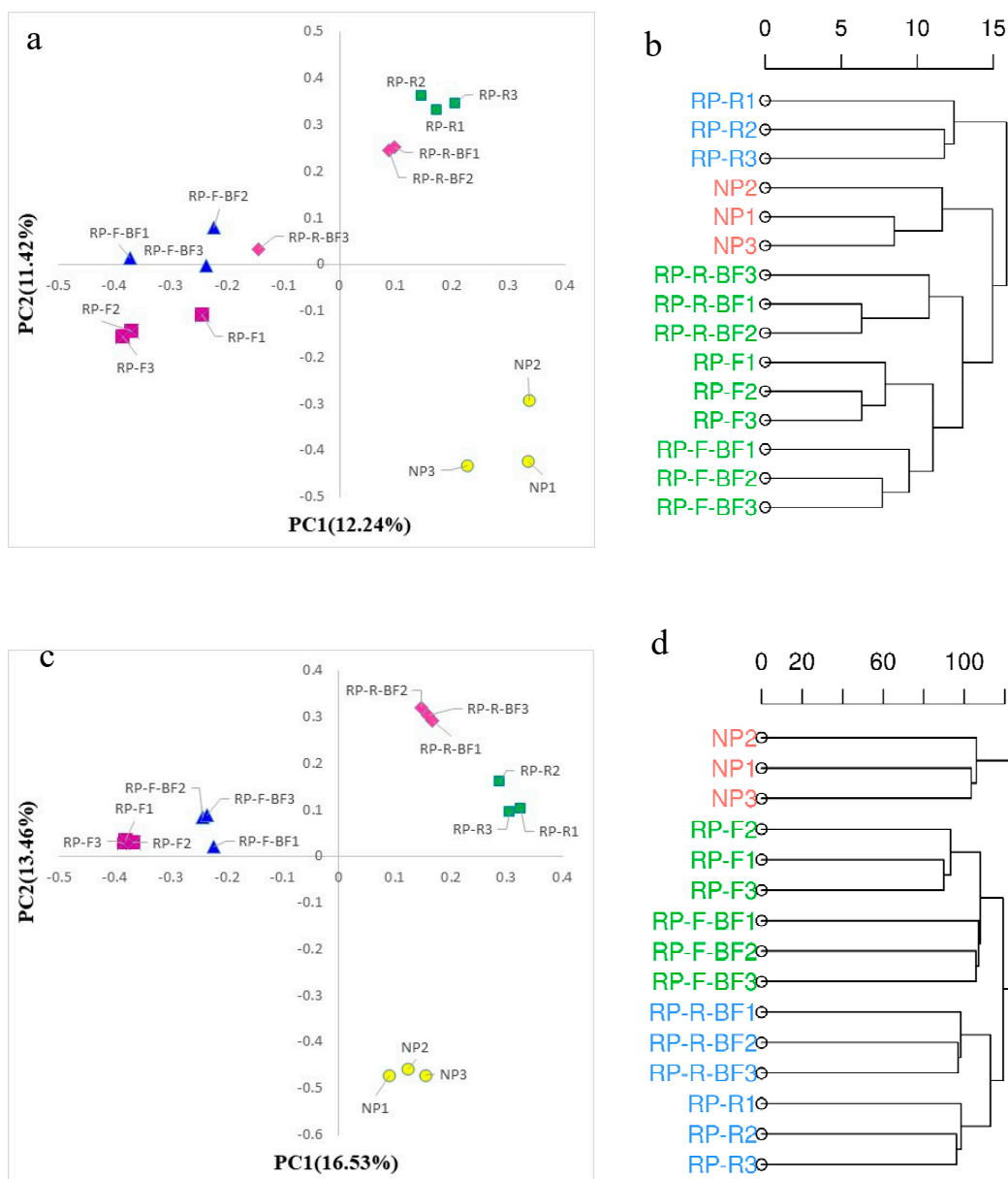


Figure S5. Principal component analysis and cluster analysis of microbial communities in the rhizosphere soil of *R. pseudostellariae* under different treatments. Treatments are the same as those given in Figure S1. **(a and b)** show principal component analysis and cluster analysis of fungal communities, and **(c and d)** show principal component analysis and cluster analysis of bacterial communities.

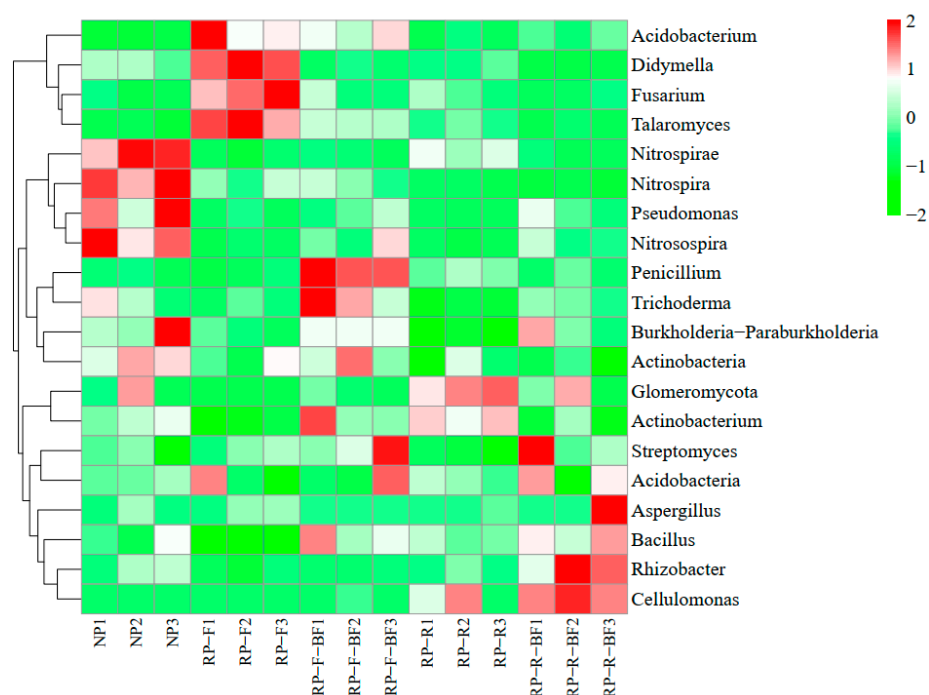


Figure S6. The abundance of microbial species in the rhizosphere soil of *R. pseudostellariae* under different treatments. Treatments are the same as those given in Figure S1.

Table S1. Primer sequence of defense related genes.

Function name	Primer ID	Primer Sequence (5'-3')	Products
Chitinase 1	CH1-F	CCCAATCCAACCTG	232 bp
	CH1-R	ACTTGACACGGCTCCTAA	
Chitinase class IV	CH4-F	CTCTAGTTACCCTAGTTTCG	298 bp
	CH4-R	TCAGTAGCCAAGATTTC	
chitinase 5-like	CH5-F	TTCTTATGCTCCTAATCACCC	145 bp
	CH5-R	CGAGTAGTCCCACAGTATCCA	
pathogenesis-related protein -4	PR4-F	AGGTGATGTACTCCGAGGCG	299 bp
	PR4-R	GCAACGAGGTATTCAGAAGCAG	
pathogenesis-related protein 10	PR10-F	GTGGAGTTACCCCAGCAAG	136 bp
	PR10-R	CAGAGTCAACGTCACCCTCA	
pathogenesis-related protein STH-21	PRS-F	AACAATACGCAAACGAAAG	233 bp
	PRS-R	AACCAAGACGAACCGAGT	
pathogenesis-related protein 1a	PR1a-F	TATGCCTAGTTGTCGGTGGT	278 bp
	PR1a-R	GTTGTTTGTGCTCCTGTTCC	
phenylalanine ammonia-lyase 1	PAL1-F	CAACCACTCATCAGACCCAC	252 bp
	PAL1-R	GAGCCACTGTCAATGTTTCC	
phenylalanine ammonia-lyase 3	PAL3-F	ATGTTGGAAGCCATCACC	128 bp
	PAL3-R	AGCCCAGCAATGTAGGAG	