

Supplementary for:

**Tea plantation intercropping legume improves soil ecosystem
multifunctionality and tea quality by regulating rare bacterial taxa**

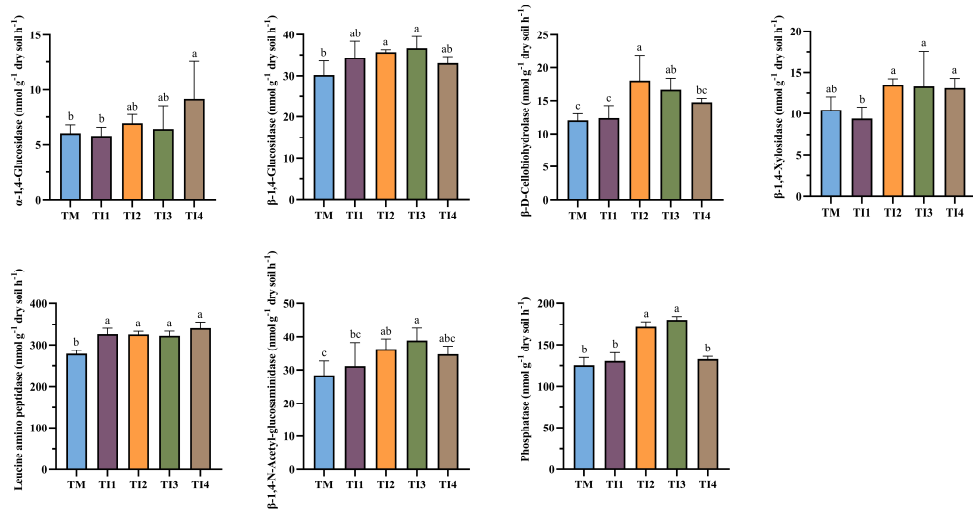


Figure S1: Levels of multiple soil functions based on enzyme activities in the different treatments. Different letters represent significant differences of value between treatments ($P < 0.05$). Treatments include tea plant monoculture (TM), tea intercropping with soybean (TI1), tea intercropping with soybean + milk vetch (TI2), tea intercropping with soybean + red clover (TI3), and tea intercropping with soybean + smooth vetch (TI4).

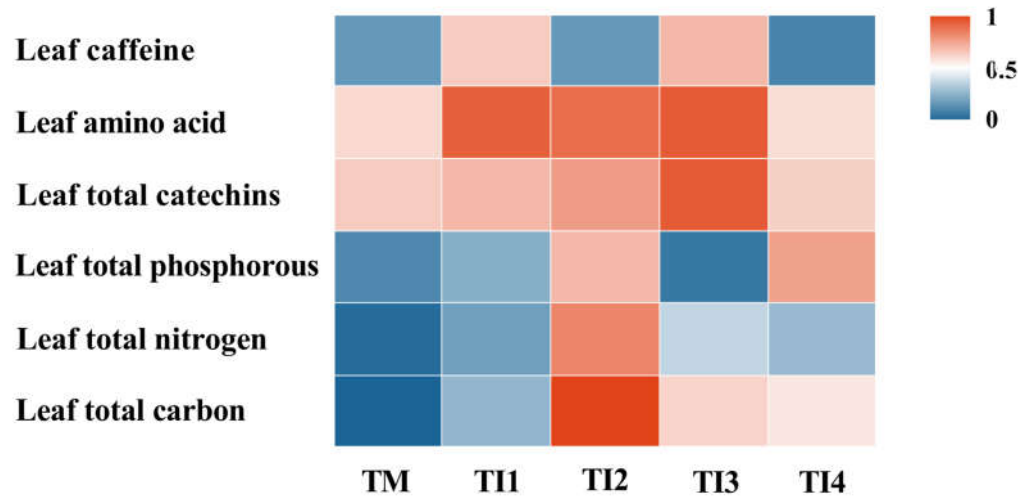


Figure S2: Heat map showing the changes in tea performance (Min-Max normalization value) including total carbon content, nutrient content, and secondary metabolite content in tea leaves under different treatments. Treatments include tea plant monoculture (TM), tea intercropping with soybean (TI1), tea intercropping with soybean + milk vetch (TI2), tea intercropping with soybean + red clover (TI3), and tea intercropping with soybean + smooth vetch (TI4).

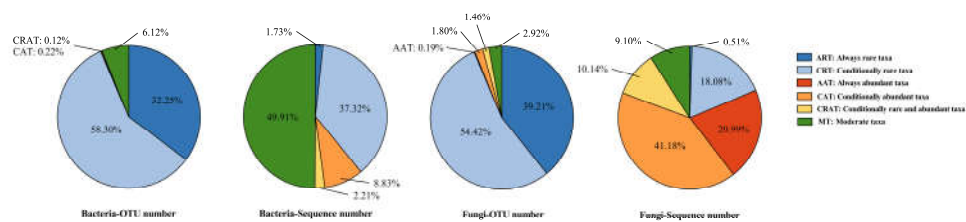


Figure S3: Proportion of six categories of microbial taxa to the overall OTUs and sequence numbers.

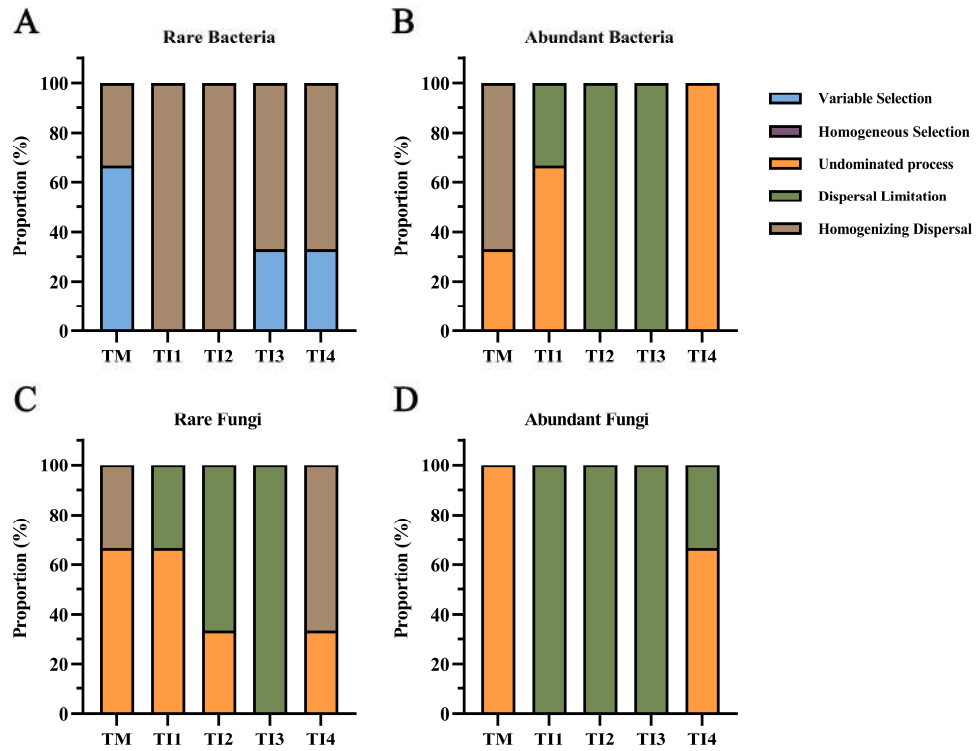


Figure S4: The percentage of (A) rare and (B) abundant bacterial, (C) rare and (D) abundant fungal communities with different assembly processes. Treatments include tea plant monoculture (TM), tea intercropping with soybean (TI1), tea intercropping with soybean + milk vetch (TI2), tea intercropping with soybean + red clover (TI3), and tea intercropping with soybean + smooth vetch (TI4).

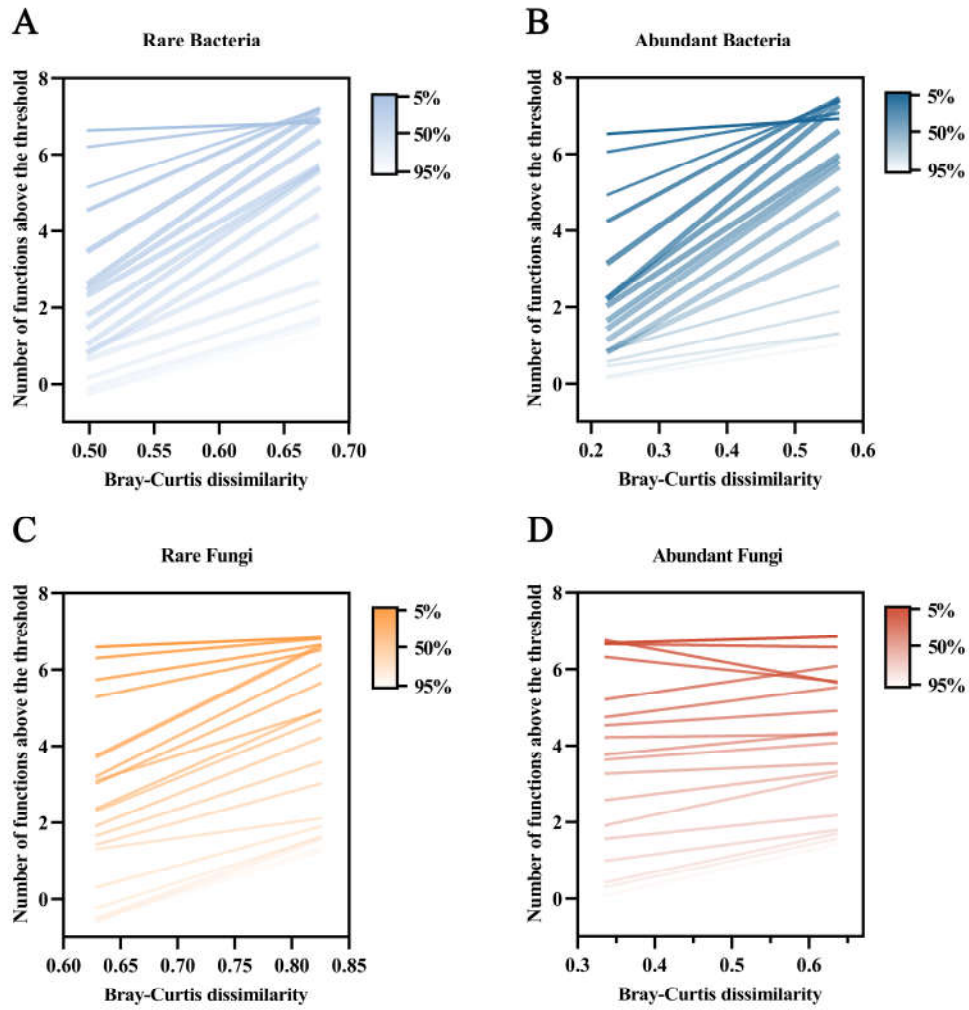


Figure S5: The relationships between the number of functions beyond threshold and (A) rare and (B) abundant bacterial and (C) rare and (D) abundant fungal community Bray–Curtis dissimilarities. The color of the line changing from light to dark represents a threshold from 5% to 95%, and the thick line represents ordinary least squares linear regressions $P < 0.05$.

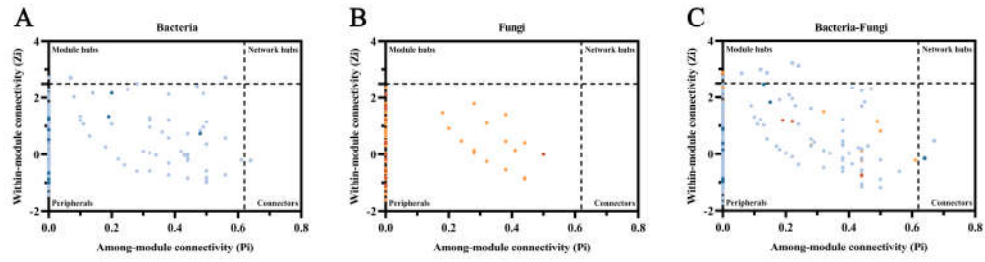


Figure S6: Zi-Pi plot shows the distribution of OTUs based on their topological roles for bacteria, fungi, and bacteria-fungi. Light and dark blue nodes represent rare and abundant bacterial OTUs, while light and dark orange nodes represent rare and abundant fungal OTUs, respectively. The keystone OTUs are represented by square nodes.

Table S1 Soil properties under different intercropping practices in tea plantation

Soil properties	TM	TI1	TI2	TI3	TI4
pH	4.96±0.01a	4.84±0.02c	4.65±0.03d	4.41±0.02e	4.92±0.05b
TC (g/kg)	13.24±0.55b	13.38±0.41b	13.47±0.69b	13.51±0.6b	14.51±0.4a
TN (g/kg)	1.78±0.12b	1.83±0.09ab	1.97±0.19ab	2.01±0.16ab	2.1±0.24a
TP (g/kg)	0.59±0.04a	0.52±0.06b	0.51±0.04b	0.39±0.01d	0.45±0.01c
NH ₄ ⁺ -N (mg/kg)	10.89±0.37e	13.43±0.35c	18.56±1.23a	17.32±0.93b	12.06±0.47d
NO ₃ ⁻ -N (mg/kg)	42.41±1.11c	53.16±3.47b	71.37±12.63a	78.99±5.26a	73.33±5.46a
AP (mg/kg)	59.68±1.77a	45.05±3.22c	53.52±6.15b	37.03±1.95d	58.29±2.28ab

Note: Different lowercase letters in the same row indicate significant difference between treatments at $P < 0.05$. Treatments include tea plant monoculture (TM), tea intercropping with soybean (TI1), tea intercropping with soybean + milk vetch (TI2), tea intercropping with soybean + red clover (TI3), and tea intercropping with soybean + smooth vetch (TI4).

Table S2 Impacts of edaphic factors on rare and abundant communities (Monte Carlo permutation test)

Factors	Bacteria				Fungi			
	Rare		Abundant		Rare		Abundant	
	<i>R</i>	<i>P</i>	<i>R</i> ²	<i>P</i>	<i>R</i> ²	<i>P</i>	<i>R</i> ²	<i>P</i>
pH	0.693	0.001	0.804	0.001	0.741	0.001	0.650	0.001
TC	0.219	0.153	0.081	0.494	0.285	0.078	0.384	0.014
TN	0.182	0.205	0.307	0.041	0.292	0.073	0.321	0.045
TP	0.563	0.001	0.616	0.002	0.731	0.001	0.256	0.087
NH ₄ ⁺ -N	0.599	0.001	0.674	0.002	0.813	0.001	0.588	0.001
NO ₃ ⁻ -N	0.385	0.018	0.622	0.002	0.794	0.001	0.622	0.001
AP	0.291	0.061	0.457	0.010	0.460	0.011	0.318	0.039

Note: TC, soil total carbon; TN, soil total nitrogen; TP, soil total phosphorus; NH₄⁺-N, soil ammonium nitrogen; NO₃⁻-N, soil nitrate nitrogen; and AP, soil available phosphorus.

Table S3 R^2 and P values corresponding to the regressions in Fig S5

Threshold	Bacteria				Fungi			
	Rare		Abundant		Rare		Abundant	
	R^2	P	R^2	P	R^2	P	R^2	P
5%	0.017	0.626	0.043	0.439	0.016	0.643	0.007	0.765
10%	0.017	0.626	0.043	0.439	0.016	0.643	0.007	0.765
15%	0.111	0.209	0.147	0.144	0.034	0.495	0.001	0.919
20%	0.230	0.060	0.239	0.055	0.030	0.523	0.040	0.461
25%	0.322	0.022	0.344	0.017	0.044	0.433	0.011	0.702
30%	0.628	<0.001	0.620	<0.001	0.255	0.046	0.021	0.594
35%	0.734	<0.001	0.736	<0.001	0.224	0.064	0.014	0.661
40%	0.751	<0.001	0.687	<0.001	0.223	0.065	0.004	0.812
45%	0.681	<0.001	0.662	<0.001	0.128	0.174	0.000	0.960
50%	0.763	<0.001	0.649	<0.0001	0.222	0.065	0.010	0.711
55%	0.752	<0.001	0.570	<0.001	0.163	0.121	0.005	0.795
60%	0.720	<0.001	0.487	0.003	0.149	0.141	0.002	0.878
65%	0.619	<0.001	0.449	0.005	0.113	0.203	0.015	0.651
70%	0.592	<0.001	0.442	0.005	0.126	0.177	0.075	0.304
75%	0.399	0.009	0.194	0.087	0.041	0.454	0.021	0.591
80%	0.373	0.012	0.114	0.201	0.151	0.137	0.035	0.491
85%	0.341	0.018	0.055	0.384	0.233	0.058	0.098	0.238
90%	0.457	0.004	0.125	0.180	0.402	0.008	0.127	0.175
95%	0.385	0.010	0.094	0.248	0.350	0.016	0.176	0.106