Supplementary Information

Table S1. Relative abundance of the most abundant bacterial phyla (>1%) present in the different planting ages tea plantations[1]

Phylum	Y0[2]	Y6	Y12	Y23	Y35
Acidobacteria	28.34 a[3]	9.41 c	9.41 c	21.08 b	25.12 ab
Proteobacteria	20.96 c	39.71 ab	41.40 a	37.54 ab	34.02 b
Chloroflexi	13.27 a	9.50 a	3.35 b	8.64 a	10.08 a
Firmicutes	12.44 a	12.49 a	16.03 a	8.27 b	6.39 b
Bacteroidetes	9.45 bc	10.99 ab	13.80 a	7.44 cd	6.05 d
GAL15	4.30 a	0.08 b	0.01 b	0.20 b	0.16 b
Verrucomicrobia	2.79 a	1.41 b	1.60b	2.37 ab	2.14 ab
Actinobacteria	2.37 c	11.52 a	8.01 b	6.65 b	7.31 b
Rokubacteria	1.48 a	0.02 b	0.02 b	0.05 b	0.23 b
Planctomycetes	1.41 a	0.61 b	0.36 b	1.42 a	1.62 a
Gemmatimonadetes	1.19 ab	0.23 b	0.09 b	1.70 a	2.20 a
WPS-2	0.61 b	2.02 a	2.90 a	1.99 a	2.14 a

[1]Data are mean values ± standard deviation ($n = 4$); [2] Y0 represent wood land; Y6, Y12, Y23 and Y35 represent tea planting for 6, 12, 23 and 35 years; [3] Lowercase letters indicate significant differences between restoration ages at $p < 0.05$.

Table S2. Relative abundance of the most abundant fungal phyla (>1%) present in the different planting ages tea plantations[1]

Phylum	Y0[2]	Y6	Y12	Y23	Y35
Ascomycota	53.53 a	54.14 a	55.27 a	39.27 a	38.63 a
Basidiomycota	39.13 a	33.45 a	29.17 a	19.45 a	35.32 a
Mortierellomycota	1.8 b	7.52 ab	8.62 a	10.1 a	5.3 ab
Rozellomycota	0.12 a	0.88 a	1.07 a	4.59 a	7.41 a

[1]Data are mean values ± standard deviation ($n = 4$); [2] Y0 represent wood land; Y6, Y12, Y23 and Y35 represent tea planting for 6, 12, 23 and 35 years;[3] Lowercase letters indicate significant differences between restoration ages at $p < 0.05$.

Table S3. Bacterial function group (Top10) present in the different planting ages tea plantations[1]

Function group	Y0[2]	Y6	Y12	Y23	Y35
chemoheterotrophy	32.75c	37.04a	34.78b	34.36bc	35.12b
fermentation	24.74a	16.03b	22.19a	14.93b	13.75b
aerobic_chemoheterotrophy	9.95c	22.26a	14.66b	20.77a	22.69a
animal_parasites_or_symbionts	9.82a	5.07bc	6.64b	4.87bc	4.24c
nitrate_reduction	4.57a	3.56ab	4.31a	2.81b	2.59b
cellulolysis	1.51b	2.92ab	1.61b	2.36ab	3.22a
human_gut	2.93a	1.85b	2.79a	1.98b	1.70b
mammal_gut	2.93a	1.85b	2.79a	1.98b	1.70b
nitrogen_fixation	1.29b	2.66a	1.08b	3.10a	2.96a
others	9.51a	8.79b	7.66ab	7.36ab	6.76ab

[1]Data are mean values $\pm$ standard deviation (n = 4); [2] Y0 represent wood land; Y6, Y12, Y23 and Y35 represent tea planting for 6, 12, 23 and 35 years; [3] Lowercase letters indicate significant differences between restoration ages at p < 0.05.

Table S4. Fungal function group present in the different planting ages tea plantations[1]

Function group	Y0[2]	Y6	Y12	Y23	Y35
Saprotroph	50.07ab	61.52a	62.05a	58.37ab	30.83b
Pathotroph	14.51b	26.17ab	29.73a	28.13ab	37.03a
Symbiotroph	35.42a	12.31ab	8.21b	13.50ab	32.14a

[1]Data are mean values ± standard deviation ($n = 4$); [2] Y0 represent wood land; Y6, Y12, Y23 and Y35 represent tea planting for 6, 12, 23 and 35 years;[3] Lowercase letters indicate significant differences between restoration ages at $p < 0.05$.
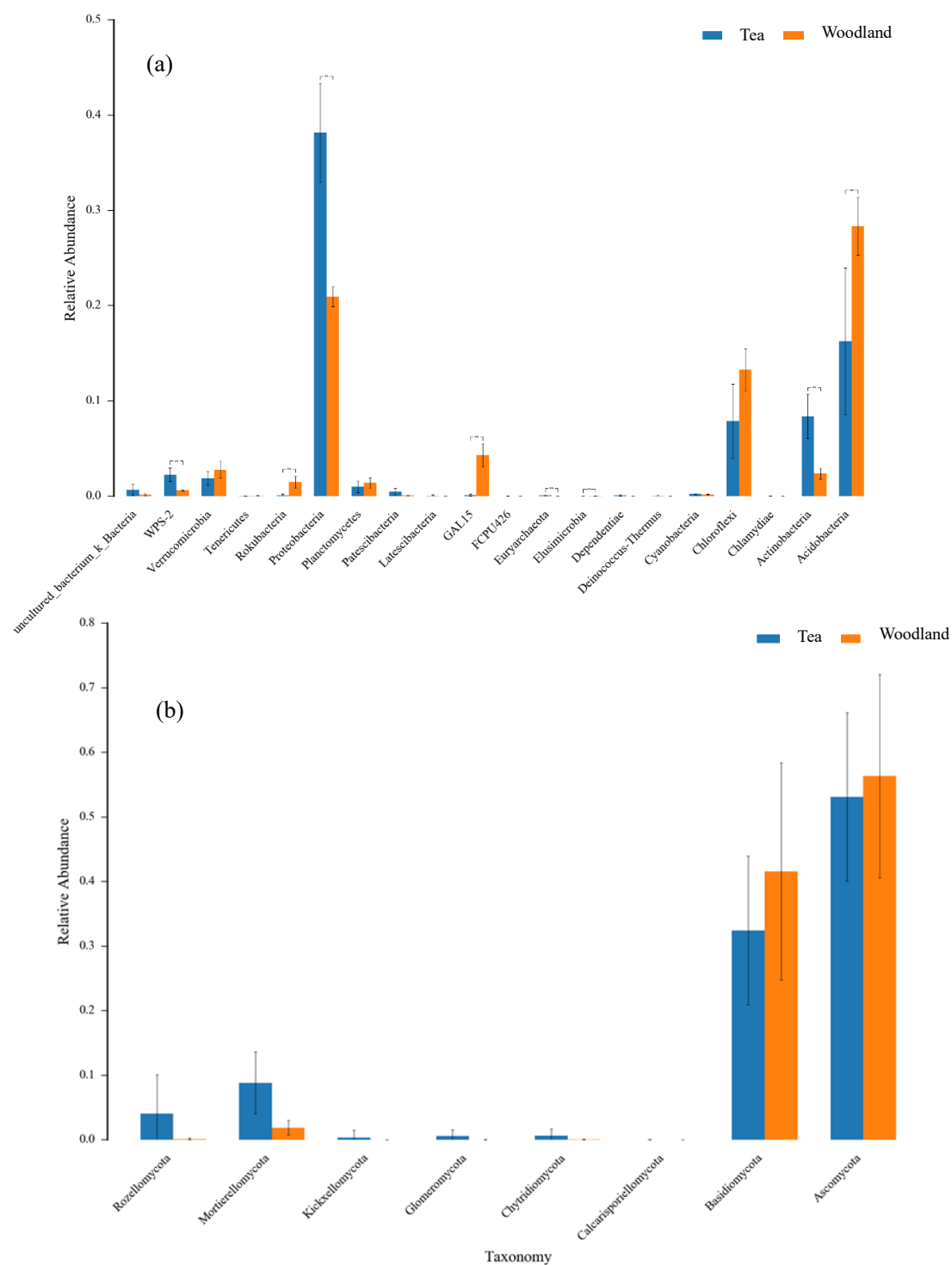
Figure S1. Analysis of variance analyses (ANOVA) showing the differential distribution of soil bacterial (**a**) and fungal (**b**) community between tea plantations and wood land.
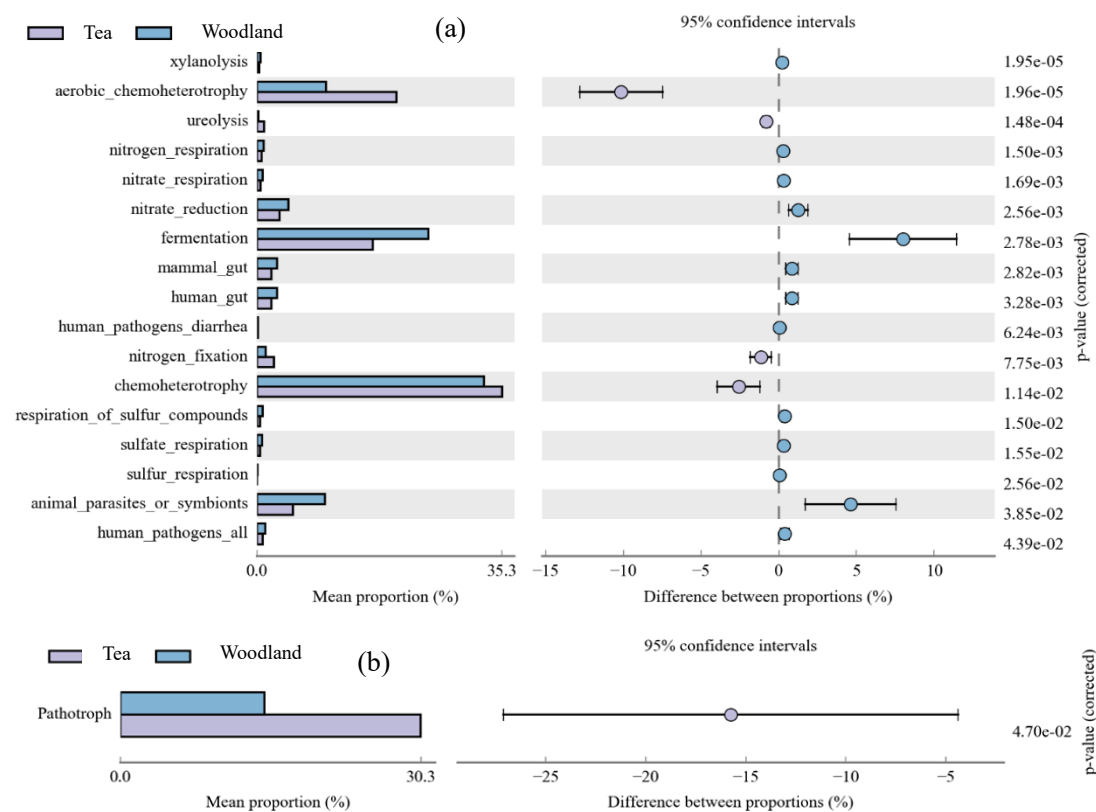
Figure S2. Statistically significant differences in the bacterial (**a**) and fungal (**b**) function group between tea plantations and wood land.