Table S1. Effects of forestland conversion to tea plantations on soil physical and chemical properties.

Soil depth /cm	Land-use types	Soil organic matter (g/kg soil)	Available N (mg/kg soil)	Available P (mg/kg soil)	Available K (mg/kg soil)	pH	Available Fe (mg/kg soil)	Exchangeable Ca (cmol/kg soil)	Soil bulk density (g/cm³ soil)
0-20 cm	FDA	52.00±1.57aA	122.33 ±5.51bA	3.30 ±1.27bA	91.33±11.71aA	4.47±0.05aA	81.97±5.25bA	0.77±0.16aA	0.92±0.08cB
	ZC3A	14.07 ±3.58cA	78.00 ±14.01cA	2.97±0.84bA	44.00±8.66 bA	4.37±0.05aA	5.53±0.85cA	0.54±0.09bA	1.20±0.06aA
	ZC30A	37.03±4.43bA	186.67 ±11.59aA	112.00±7.81aA	50.33±5.13 bA	3.77±0.15bA	268.90±32.18aA	0.48 ±0.24bA	1.10±0.06bA
20-40 cm	FDB	27.40±1.67aB	104.02 ±11.15aA	2.03±0.93bA	48.67±4.73aB	4.57±0.12aA	14.60 ±1.05bB	0.45±0.17aB	1.12±0.06abA
	ZC3B	10.13 ±1.65cA	73.67 ±10.78bA	2.63±0.83bA	54.01±11.37aA	4.39±0.15aA	5.40±1.83cA	0.55±0.12aA	1.22±0.04aA
	ZC30B	21.47±4.11bB	129.00±26.21aB	16.00±5.89aB	45.00±8.54aA	3.97±0.20bA	67.97±16.83aB	0.23±0.07bB	1.11±0.03bA
Land-use(L)		121.57**	55.42**	453.29**	2.26^{NS}	18.13**	74.11**	3.37^{NS}	17.62**
Depth(D)		101.46**	40.51**	287.59**	2.25^{NS}	1.17^{NS}	62.35**	4.83^{NS}	10.67*
L×D		16.80**	9.69**	273.64**	0.84^{NS}	0.39^{NS}	27.12**	1.44^{NS}	5.85*

Note: Values are given as means ± standard deviation (n=3). Letters A and B under the "Land-use " column indicate sampled depths of 0-20 cm and 20-40 cm, respectively. Different lowercase letters indicate significant differences between different soil samples at the same sampled soil depth ($p<0.05$) whereas different capital letters indicate significant differences between the same soil type at different sampled depths ($p<0.05$). *, $p< 0.05$. **, $p< 0.01$. NS, not significant. The same below.

Table S2. Primer sets and thermal profiles used in PCR amplification.

Primer	Sequence (5′-3′)	PCR conditions
ITS1F	CTTGGTCATTTAGAGGAAGTAA	initial denaturation at 95℃ for 3 min; 35 cycles of 30 s at 95℃, 30 s at 55℃, and 45 s at 72 ℃; and a final
ITS2R	GCTGCGTTCTTCATCGATGC	extraction at 72 ℃ for 10 min.

Table S3. Key species in soil fungal network under different land use

OTU	Phylum	Order	genus	Land-use types	degree
OTU525	unclassified_k__Fungi	unclassified_k__Fungi	unclassified_k__Fungi	FD	34
OTU2716	Ascomycota	Hypocreales	Trichoderma	FD	34
OTU2686	Mortierellomycota	Mortierellales	Mortierella	FD	34

OTU962	Ascomycota	Pleosporales	unclassified_o__Pleosporales	FD	34
OTU457	Ascomycota	Hypocreales	Ilyonectria	FD	34
OTU149	Ascomycota	Hypocreales	Paecilomyces	FD	34
OTU63	Ascomycota	Archaeorhizomycetales	Archaeorhizomyces	FD	34
OTU760	Ascomycota	unclassified_c__Archaeorhizomycetes	unclassified_c__Archaeorhizomycetes	FD	33
OTU53	Ascomycota	Pleosporales	Paraboeremia	FD	32
OTU2493	Ascomycota	unclassified_c__Archaeorhizomycetes	unclassified_c__Archaeorhizomycetes	FD	32
OTU2463	Ascomycota	Eurotiales	Sagenomella	ZC3	36
OTU2422	Basidiomycota	unclassified_p__Basidiomycota	unclassified_p__Basidiomycota	ZC3	37
OTU1809	Ascomycota	Orbiliales	Dactylella	ZC3	37
OTU2458	Ascomycota	Annulatascales	unclassified_o__Annulatascales	ZC3	36
OTU2468	Ascomycota	Sordariales	Dendrosporium	ZC3	36
OTU989	unclassified_k__Fungi	unclassified_k__Fungi	unclassified_k__Fungi	ZC3	36
OTU2563	Ascomycota	unclassified_p__Ascomycota	unclassified_p__Ascomycota	ZC3	36
OTU2562	Ascomycota	unclassified_p__Ascomycota	unclassified_p__Ascomycota	ZC3	30
OTU2032	Glomeromycota	unclassified_p__Glomeromycota	unclassified_p__Glomeromycota	ZC3	33
OTU2582	Glomeromycota	unclassified_p__Glomeromycota	unclassified_p__Glomeromycota	ZC3	33
OTU2661	Ascomycota	unclassified_p__Ascomycota	unclassified_p__Ascomycota	ZC30	34
OTU1019	Basidiomycota	unclassified_p__Basidiomycota	unclassified_p__Basidiomycota	ZC30	34
OTU2063	Mortierellomycota	Mortierellales	Mortierella	ZC30	34
OTU1580	Mortierellomycota	Mortierellales	Mortierella	ZC30	34
OTU1983	Ascomycota	Hypocreales	Trichoderma	ZC30	34
OTU15	Rozellomycota	unclassified_p__Rozellomycota	unclassified_p__Rozellomycota	ZC30	34
OTU1398	unclassified_k__Fungi	unclassified_k__Fungi	unclassified_k__Fungi	ZC30	34
OTU1355	unclassified_k__Fungi	unclassified_k__Fungi	unclassified_k__Fungi	ZC30	33
OTU1232	unclassified_k__Fungi	unclassified_k__Fungi	unclassified_k__Fungi	ZC30	32

OTU1352	unclassified_k__Fungi		unclassified_k__Fungi		unclassified_k__Fungi	ZC30	32

Note:Top ten nodes with the highest degree, highest closeness centrality, and lowest betweenness centrality were selected as the keystone taxa.

Table S4. Effects of forestland conversion to tea plantations on soil fungal trophic modes.

Soil depth/cm	Land-use types	P	S	Sy	P-S	S-Sy	P-S-Sy	P-Sy
	FDA	7.43±2.20Ab	74.59±6.71Aa	11.86±4.07Ab	4.18±2.08Ab	1.52±0.99Ba	0.28±0.16Aa	0.1±0.06Aa
0-20 cm	ZC3A	7.45±2.05Ab	50.11±9.98Aab	36.09±8.66a	1.53±0.93b	3.88±2.55Aa	0.87±0.28Aa	0.02±0.02Aa
	ZC30A	18.37±5.43Aa	43.19±15.74b	2.02±2.02Bb	29.74±31.14Aa	1.92±1.41Aa	1.41±1.31a	3.31±2.9Aa
	FDB	7.23±3.18Aa	56.78±6.03Ab	9.93±1.8Ab	2.00±0.76Aa	22.46±9.53Aa	0.39±0.37Aa	1.17±1.02Aa
20-40 cm	ZC3B	5.49±7.02Aa	59.03±12.67Ab	32.82±3.79Aa	0.44±0.48Ab	1.86±1.72Ab	0.26±0.33Aa	0.06±0.05Ab
	ZC30B	6.45±2.72Ba	79.25±5.26Aa	7.93±1.7Ab	1.79±0.77Aab	1.41±0.63Ab	0.41±0.26Aa	2.72±1.49Aa
Land-use (L)		3.516[NS]	1.09[NS]	75.235[**]	2.357[NS]	11.06[**]	1.393[NS]	1.746[NS]
Depth(D)		5.646[*]	2.145[NS]	0.013[NS]	2.993[NS]	9.808[**]	3.122[NS]	2.552[NS]
L×D		3.409[NS]	6.325[*]	1.905[NS]	2.13[NS]	14.309[**]	1.317[NS]	1.714[NS]

Note: P: pathotroph; S: saprotroph, Sy: symbiotroph, S-Sy: saprotroph-symbiotroph, P-Sy: pathotroph-symbiotroph, P-S: pathotroph-saprotroph ; P-S-Sy:

pathotroph-saprotroph-symbiotroph.

Table S5. Effects of forestland conversion to tea plantations on soil fungal functional groups (guilds).

Trophic	Guild	Land-use (L)	Depth(D)	L×D
pathotroph	animal pathogen	2.862^{NS}	2.169^{NS}	0.636^{NS}
	plant pathogen	0.524^{NS}	4.68^{NS}	2.114^{NS}
	fungal parasite	2.508^{NS}	2.033^{NS}	2.493^{NS}
saprotroph	soil saprotroph	10.038**	15.758**	6.321**
	undefined saprotroph	0.997^{NS}	5.488*	4.994*
symbiotroph	arbuscular mycorrhizal	56.567**	3.293^{NS}	2.589^{NS}
pathotroph-saprotroph	animal pathogen-endophyte-lichen parasite-plant pathogen-soil saprotroph-wood saprotroph	22.101**	0.237^{NS}	0.261^{NS}
	animal pathogen-plant pathogen-soil saprotroph-undefined saprotroph	8.207**	7.063*	7.458**
	animal pathogen-plant pathogen-undefined saprotroph	3.629^{NS}	6.41*	1.166^{NS}
	fungal parasite-plant pathogen-plant saprotroph	1.263^{NS}	1.237^{NS}	1.244^{NS}
saprotroph-symbiotroph	bryophyte parasite-ectomycorrhizal-ericoid mycorrhizal-undefined saprotroph-wood saprotroph	14.369**	3.178^{NS}	4.443*
	ectomycorrhizal-fungal parasite-soil saprotroph-undefined saprotroph	1.166^{NS}	1.62^{NS}	1.20^{NS}
	endophyte-litter saprotroph-soil saprotroph-undefined saprotroph	0.096^{NS}	4.018^{NS}	4.199^{NS}
	endophyte-litter saprotroph-wood saprotroph	8.067**	0.907^{NS}	0.578^{NS}
	endophyte-soil saprotroph	9.665**	10.709**	10.619**
pathotroph-saprotroph-symbiotroph	fungal parasite-undefined saprotroph	0.445^{NS}	13.626**	1.434^{NS}

Table S6. Pearson correlations between soil properties and fungal alpha diversity.

Diversity index	SOM	AN	AP	AK	pH	AFe	ACa	BK
Sobs	0.264	0.617**	0.629**	-0.716**	-0.174	0.572*	0.181	-0.600**
Shannon	0.226	0.738**	0.751**	-0.743**	0.082	0.490*	0.351	-0.683**
Simpson	-0.130	-0.725**	-0.733**	0.672**	-0.265	-0.402	-0.409	0.585*
ACE	0.234	0.681**	0.691**	-0.754**	-0.141	0.563*	0.238	-0.668**

Chao1	0.02	0.992**	0.991**	-0.881**	0.322	0.178	0.568*	-0.735**

Note: SOM, Soil organic matter. AN, available N. AP, available P. AK, available K. AFe, available Fe. ACa, exchangeable calcium. BK, soil bulk density. *, $p< 0.05$. **, $p< 0.01$. The same below.

Table S7. Correlations between soil fungal community and soil properties.

Factors	phylum		genus	
	R²	*P*-values	R²	*P*-values
AN	0.478	0.01	0.5848	0.001
AP	0.2069	0.162	0.3663	0.045
AK	0.4233	0.012	0.2794	0.091
pH	0.2791	0.082	0.2854	0.084
ACa	0.367	0.042	0.1062	0.45
BK	0.2584	0.101	0.4779	0.012

Table S8. Pearson correlations between soil properties and fungal trophic modes.

Parameter	SOM	AN	AP	AK	pH	AFe	ACa	BK
pathogen	0.334	0.403	0.750**	0.196	-0.417	0.781**	-0.155	-0.103
saprotroph	0.166	0.161	-0.414	-0.006	0.032	-0.186	0.106	-0.209
symbiotroph	-0.650**	-0.720**	-0.534*	-0.04	0.396	-0.644**	0.182	0.495*
pathotroph-saprotroph	0.283	0.351	0.705**	-0.01	-0.393	0.568*	-0.175	-0.248
saprotroph-symbiotroph	-0.042	-0.136	-0.23	-0.002	0.429	-0.279	-0.05	0.111
pathotroph-saprotroph-symbiotroph	0.097	0.172	0.530*	-0.111	-0.472*	0.604**	0.019	0.184
pathotroph-symbiotroph	0.116	0.33	0.608**	-0.129	-0.575*	0.542*	-0.205	0.015

(a)

■ FDA
■ ZC3A
■ ZC30A

(b)

■ FDB
■ ZC3B
■ ZC30B

■ a : c__Sordariomycetes
■ b : g__Pseudopestalotiopsis
■ c : g__Neopestalotiopsis
■ d : o__Hypocreales
■ e : g__Fusarium
■ f : g__Dactylaria
■ g : o__unclassified_c__Archaeorhizomycetes
■ h : f__unclassified_c__Archaeorhizomycetes
■ i : g__unclassified_c__Archaeorhizomycetes
■ j : c__Eurotiomycetes
■ k : o__Eurotiales
■ l : o__unclassified_c__Eurotiomycetes
■ m : f__unclassified_c__Eurotiomycetes
■ n : c__unclassified_c__Eurotiomycetes
■ o : p__Glomeromycota
■ p : c__unclassified_p__Glomeromycota

■ q : o__unclassified_p__Glomeromycota
■ r : f__unclassified_p__Glomeromycota
■ s : g__unclassified_p__Glomeromycota
■ t : c__Glomeromycetes
■ u : o__Glomerales
■ v : c__Agaricomycetes
■ w : o__Agaricales
■ x : f__unclassified_o__Agaricales
■ y : g__unclassified_o__Agaricales
■ z : c__unclassified_p__Rozellomycota
■ a1 : o__unclassified_p__Rozellomycota
■ b1 : f__unclassified_p__Rozellomycota
■ c1 : g__unclassified_p__Rozellomycota

■ a : o__Venturiales
■ b : f__unclassified_o__Venturiales
■ c : g__unclassified_o__Venturiales
■ d : o__Sordariales
■ e : f__Sordariales_fam_Incertae_sedis
■ f : g__Dendrosporium
■ g : f__Nectriaceae
■ h : g__Fusarium
■ i : g__unclassified_f__Clavicipitaceae
■ j : o__Annulatascales
■ k : f__unclassified_o__Annulatascales
■ l : g__unclassified_o__Annulatascales
■ m : g__Xylogone
■ n : o__unclassified_c__Archaeorhizomycetes
■ o : f__unclassified_c__Archaeorhizomycetes
■ p : g__unclassified_c__Archaeorhizomycetes
■ q : o__GS31
■ r : f__unclassified_o__GS31
■ s : g__unclassified_o__GS31

■ t : o__Archaeorhizomycetales
■ u : f__Archaeorhizomycetaceae
■ v : g__Archaeorhizomyces
■ w : f__unclassified_o__Phaeomoniellales
■ x : g__unclassified_o__Phaeomoniellales
■ y : f__Trichocomaceae
■ z : g__Talaromyces
■ a1 : f__Glomeraceae
■ b1 : g__unclassified_f__Glomeraceae
■ c1 : c__Agaricomycetes
■ d1 : o__Agaricales
■ e1 : f__unclassified_o__Agaricales
■ f1 : g__unclassified_o__Agaricales
■ g1 : c__Geminibasidiomycetes
■ h1 : o__Geminibasidiales
■ i1 : f__Geminibasidiaceae
■ j1 : g__Geminibasidium
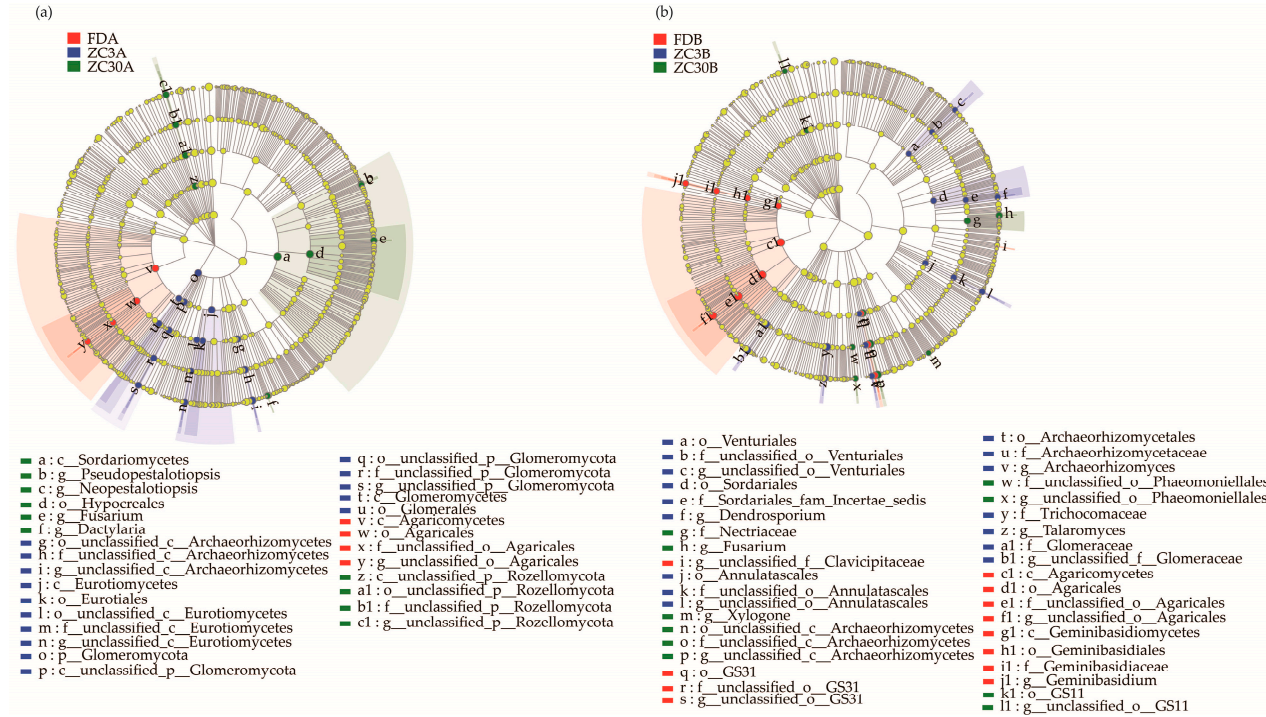■ k1 : o__GS11
■ l1 : g__unclassified_o__GS11

Figure S1. LEfSe indicating differences in the fungal taxa among forestland and tea garden samples. Different colored bars indicate taxa were enrichment among forestland and tea garden samples.
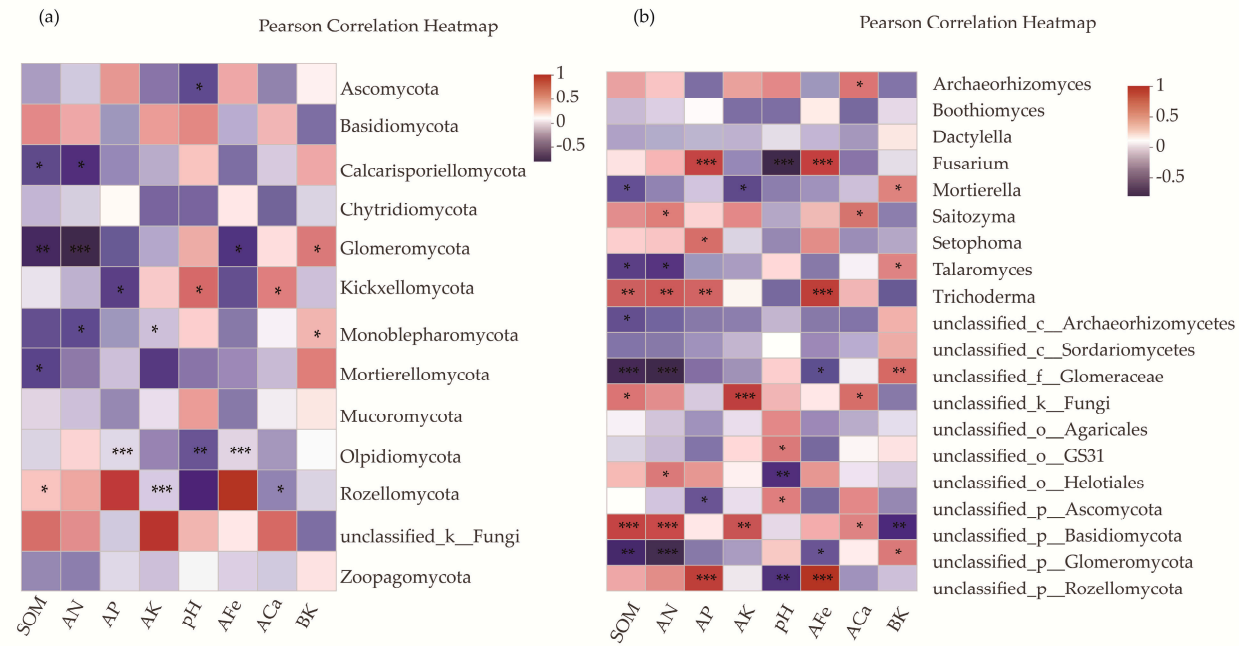
Figure S2. Pearson correlations between soil properties and abundant fungal phyla (a) or fungal genera (b).