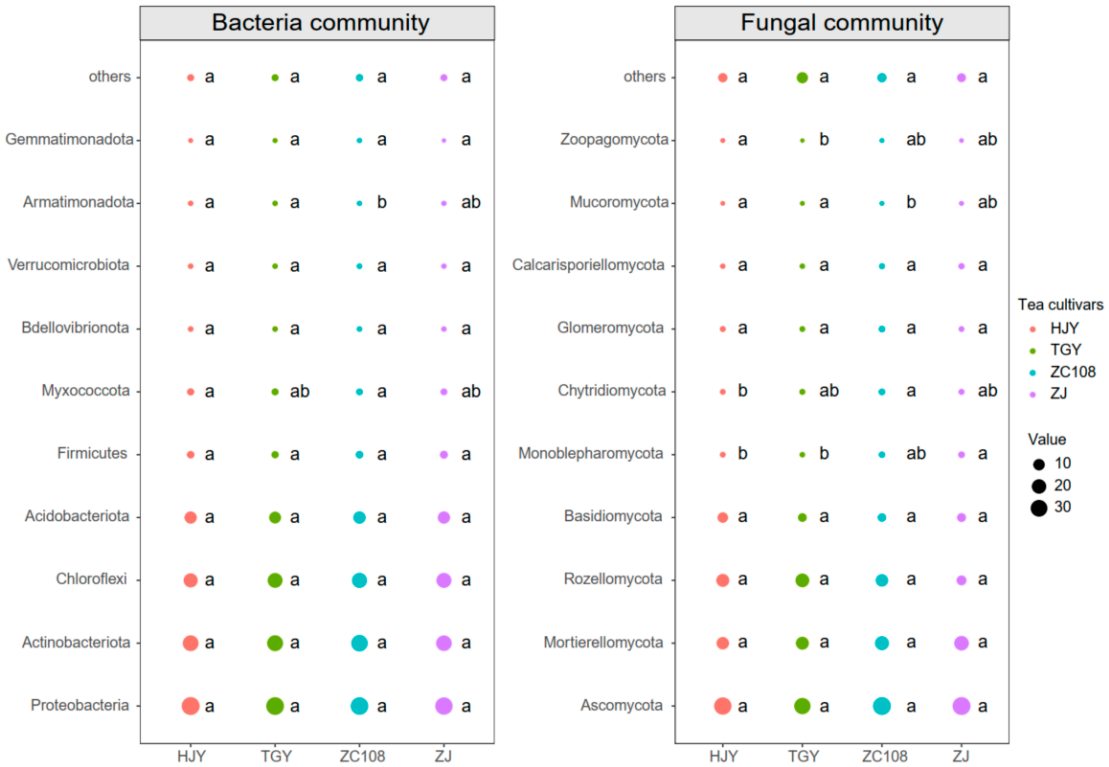# Supplemental materials

Figure. S1 Bubble plots shows the relative abundance of the top 10 bacterial (left panel) and fungal composition (right panel) at the phylum levels in the tea plantation soils under different tea cultivars. The size of the bubble corresponds to the relative abundance of microbial taxa. Different lowercase letters on the right of the bubbles indicate significant differences among the treatments (one-way ANOVA test, $p < 0.05$).
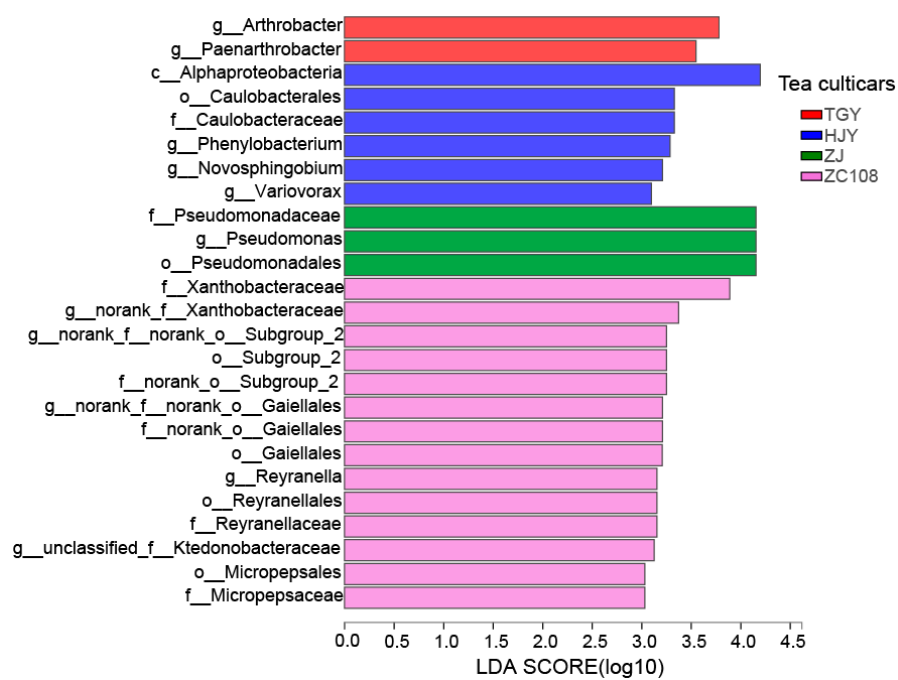
Figure S2 Histogram of the LDA scores computed for differentially abundant of soil bacteria under different tea cultivars planting.
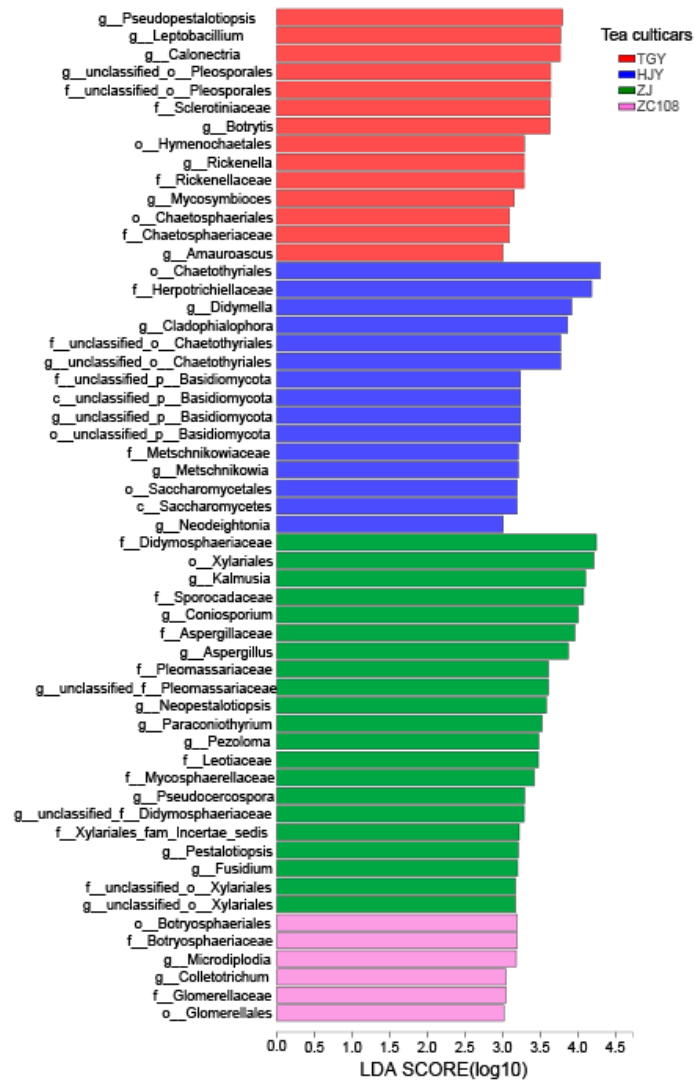
Figure S3 Histogram of the LDA scores computed for differentially abundant of soil fungi under different tea cultivars planting.

Table S1 The correlations of bacterial and fungal community composition at the phylum levels.

Parameters	Ascmycota	Mortierellomycota	Rozellomycota	Basidiomycota	Monoblepharomycota	Chytridiomycota	Glomeromycota	Calcarisporiellomycota	Mucoromycota	Zoopagomycota
Proteobacteria	-0.36	-0.16	**0.423***	0.04	-0.08	-0.26	-0.33	0.16	0.23	0.23
Actinobacteriota	0.34	-0.12	-0.13	0.07	0.18	0.18	0.33	-0.00	**-0.42***	0.15
Chloroflexi	0.069	0.27	-0.36	0.02	-0.22	0.10	0.07	-0.21	0.02	-0.38
Acidobacteriota	**-0.42***	-0.05	**0.49***	-0.31	0.17	-0.03	-0.28	0.19	0.35	0.11
Firmicutes	**0.41***	0.16	-0.36	-0.01	**0.44***	-0.13	-0.16	0.08	0.30	0.34
Myxococcota	-0.15	**-0.55****	0.38	0.29	**-0.44***	**-0.65****	0.11	0.01	-0.05	-0.01
Bdellovibrionota	-0.12	**-0.57****	**0.48***	0.20	-0.25	**-0.54****	0.07	0.28	-0.02	0.10
Verrucomicrobiota	**-0.42***	-0.09	0.32	-0.05	-0.27	-0.19	-0.13	0.18	0.03	-0.28
Armatimonadota	-0.29	**-0.60****	**0.50***	0.23	-0.20	-0.47*	-0.04	0.02	0.00	-0.14
Gemmatimonadota	0.03	-0.36	0.26	0.15	-0.05	-0.03	0.09	0.09	-0.12	0.19

Significant correlations (**, $p < 0.01$ and *, $p < 0.05$) are shown in bold

Table S2 The correlations of Chao1, Shannon index and composition (phylum level) of soil bacterial community with soil properties.

Parameters	pH	NH$_4^+$	NO$_3^-$	AP	AK	TP	TK	SOC	TN	C/N	SFI
Chao1	0.06	-0.20	0.19	0.21	0.21	-0.19	0.21	**0.53****	**0.42***	**0.52***	-0.38
Shannon	0.27	-0.31	-0.29	0.29	**0.44***	-0.09	**0.50***	**0.61****	**0.64****	0.34	-0.15
Proteobacteria	-0.02	**-0.42***	-0.38	**0.58****	**0.41***	0.10	0.33	0.28	0.33	0.11	0.02
Actinobacteriota	-0.38	-0.28	0.07	0.16	-0.33	0.30	0.05	0.06	0.11	-0.07	0.24
Chloroflexi	**0.44***	**0.73****	0.25	**-0.73****	0.02	-0.36	**-0.55****	**-0.47***	**-0.54****	-0.20	-0.01
Acidobacteriota	-0.18	**-0.49***	-0.11	**0.42***	0.08	-0.12	**0.56****	**0.46***	0.42*	0.39	-0.36
Firmicutes	**-0.45***	-0.23	-0.09	0.25	-0.37	**0.58****	0.22	0.19	0.28	-0.01	-0.25
Myxococcota	**0.72****	0.34	-0.24	-0.01	**0.57****	0.02	0.08	-0.01	-0.03	0.03	-0.01
Bdellovibrionota	0.29	-0.09	**-0.49***	**0.41***	**0.46***	0.24	0.30	0.15	0.18	0.07	-0.04
Verrucomicrobiota	0.40	-0.12	-0.02	0.24	**0.55****	-0.28	0.22	0.20	0.21	0.15	-0.19
Armatimonadota	0.34	-0.10	-0.21	0.32	**0.47***	0.03	0.22	0.12	0.07	0.16	-0.18
Gemmatimonadota	-0.21	-0.32	-0.12	0.30	-0.16	0.27	0.27	0.27	0.24	0.20	0.10

Significant correlations (**, $p < 0.01$ and *, $p < 0.05$) are shown in bold.

Table S3 The correlations of Chao1, Shannon index and composition (phylum level) of soil fungal community with soil properties.

Parameters	pH	NH_4^+	NO_3^-	AP	AK	TP	TK	SOC	TN	C/N	SFI
Chao1	**0.50***	0.15	-0.16	0.08	**0.56****	-0.33	0.25	0.34	0.30	0.29	-0.18
Shannon	-0.09	0.13	0.02	-0.19	-0.16	-0.18	-0.16	**-0.47***	**-0.48***	-0.29	-0.01
Ascomycota	-0.13	0.05	-0.30	-0.07	-0.40	0.39	-0.04	-0.13	-0.03	-0.23	0.03
Mortierellomycota	-0.36	0.09	**0.43***	-0.10	-0.23	-0.25	-0.11	-0.33	-0.21	-0.38	-0.07
Rozellomycota	0.22	-0.15	-0.23	0.24	0.37	-0.08	0.21	**0.49***	0.31	**0.58****	-0.06
Basidiomycota	0.22	0.05	-0.08	-0.19	0.28	-0.05	0.05	-0.40	-0.30	**-0.46***	0.40
Monoblepharomycota	**-0.67****	-0.31	0.06	0.07	**-0.59****	0.11	-0.06	-0.15	-0.18	-0.06	-0.36
Chytridiomycota	**-0.54****	-0.15	**0.49***	-0.18	**-0.41***	**-0.44***	-0.19	-0.21	-0.27	-0.07	-0.31
Glomeromycota	0.35	0.38	-0.16	**-0.43***	0.21	-0.04	-0.23	0.09	0.12	-0.02	0.23
Calcarisporiellomycota	-0.25	-0.28	-0.28	0.16	-0.47*	0.15	0.15	0.04	-0.00	0.10	-0.14
Mucoromycota	-0.18	0.08	-0.08	0.30	-0.06	0.00	**0.52****	0.07	0.16	-0.07	-0.12
Zoopagomycota	-0.40	-0.33	0.09	**0.52****	-0.04	0.20	0.34	0.13	0.26	-0.10	0.06

Significant correlations (**, $p < 0.01$ and *, $p < 0.05$) are shown in bold.

Table S4 The correlations of bacterial predicted function and fungal predicted function with soil properties.

Parameters	Bacterial predicted function			Fungal predicted function		
	C-cycling	N-cycling	S-cycling	Pathotroph	Saprotroph	Symbiotroph
pH	**-0.66****	**0.51***	0.31	-0.03	-0.02	-0.10
NH_4^+	-0.20	0.10	0.26	0.26	-0.02	-0.01
NO_3^-	0.12	-0.09	0.09	-0.01	-0.19	-0.29
AP	0.01	-0.14	-0.11	-0.08	-0.25	0.13
AK	**-0.76****	**0.59****	**0.41***	-0.16	-0.28	-0.22
TP	0.35	-0.38	0.02	-0.12	0.32	-0.04
TK	-0.28	0.24	0.04	-0.02	-0.20	0.33
SOC	-0.11	-0.02	-0.16	**-0.52***	0.03	0.22
TN	-0.19	0.123	0.05	**-0.47***	0.17	0.14
C/N	0.05	-0.24	**-0.44***	**-0.43***	-0.17	0.25
SFI	-0.02	-0.04	0.28	-0.02	0.08	0.14

Significant correlations (**, $p < 0.01$ and *, $p < 0.05$) are shown in bold.

Table S5 The correlations of bacterial predicted function and fungal predicted function with community composition of soil bacteria and fungi.

Parameters	Bacterial predicted function			Fungal predicted function		
	C-cycling	N-cycling	S-cycling	Pathotroph	Saprotroph	Symbiotroph
Bacterial community composition						
Proteobacteria	-0.39	0.26	-0.01	-0.13	-0.23	-0.07
Actinobacteriota	**0.42***	-0.2	0.28	0.04	0.13	0.18
Chloroflexi	-0.09	0.06	-0.01	0.19	0.16	-0.07
Acidobacteriota	-0.15	-0.01	**-0.47***	-0.31	-0.32	-0.08
Firmicutes	**0.44***	**-0.46***	-0.19	-0.03	0.29	-0.01
Myxococcota	**-0.49***	0.36	0.11	-0.01	-0.25	-0.22
Bdellovibrionota	**-0.41***	0.28	0.08	0.01	-0.33	-0.09
Verrucomicrobiota	**-0.68****	**0.49***	0.18	-0.23	-0.25	-0.07
Armatimonadota	**-0.42***	0.26	-0.12	0.30	**-0.45***	-0.07
Gemmatimonadota	0.09	-0.02	0.24	0.04	0.01	**0.44***
Fungal community composition						
Ascomycota	0.39	-0.23	-0.13	0.23	**0.62****	0.27
Mortierellomycota	0.20	-0.23	0.12	-0.05	0.03	-0.19
Rozellomycota	-0.34	0.22	-0.15	-0.32	**-0.44***	0.05
Basidiomycota	-0.16	0.29	0.35	0.4	0.02	-0.07
Monoblepharomycota	**0.67****	**-0.53****	-0.34	0.09	0.05	-0.17
Chytridiomycota	0.33	-0.14	-0.04	-0.04	-0.18	-0.07
Glomeromycota	-0.09	0.2	0.28	-0.04	0.16	-0.10
Calcarisporiellomycota	0.27	-0.16	-0.25	0.00	0.16	0.18
Mucoromycota	-0.22	0.10	0.01	0.07	-0.15	0.28
Zoopagomycota	0.16	-0.13	-0.06	-0.19	-0.11	-0.12

Significant correlations (**, $p < 0.01$ and *, $p < 0.05$) are shown in bold