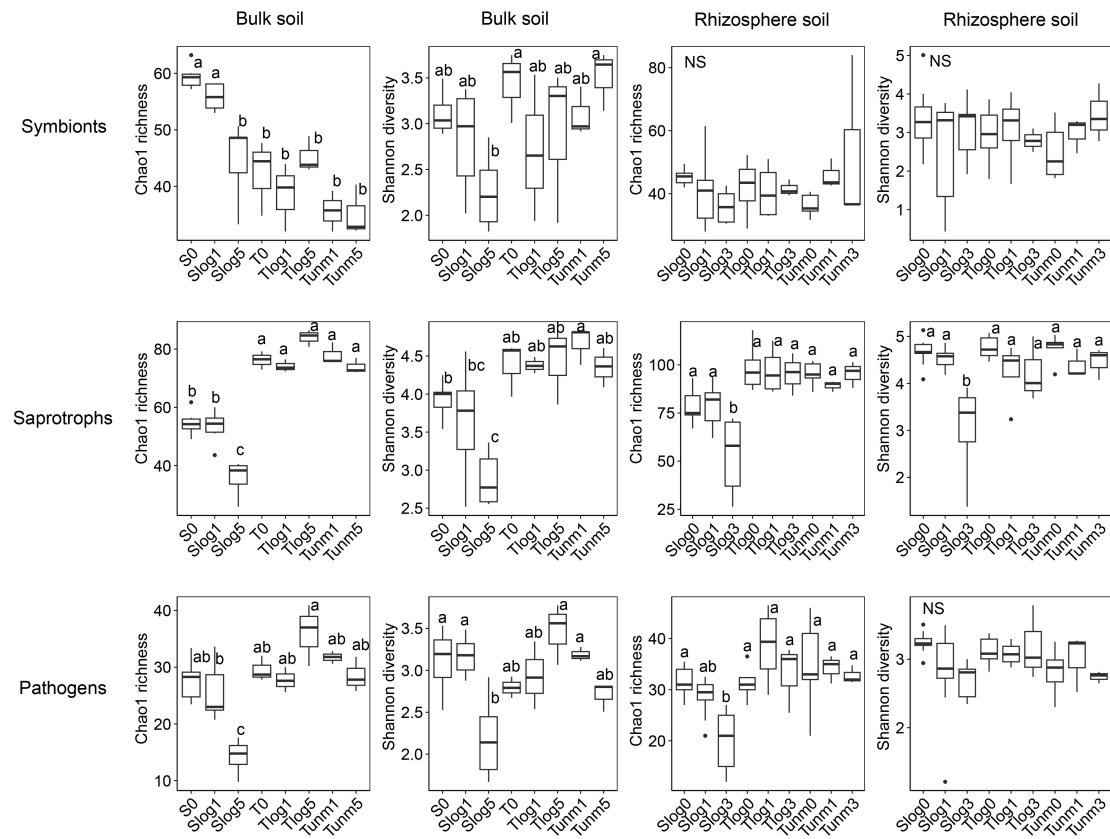# Supplemental materials

Figure S1. Alpha diversity of trophic groups of soil fungi. Letters represent difference among infected years and treatments at the significance level (*P* < 0.05). NS represent no significant difference among infected years or treatments. S, forest plots in Suichang County; T, forest plots in Taishun County; 0, uninfected plot; log1, logged plot or pine individuals after 1-year disease infection; log5, logged plot after 5-year disease infection; log3, logged pine individuals after 3-year disease infection; unm3, unmanaged pine individuals after 3-year disease infection.

Table S1. Relative abundance of bacterial phylum taxa in all samples of bulk soil and Masson pine rhizosphere soil.

Phylum taxa	Relative abundance in bulk soil (%)	Relative abundance in rhizosphere soil (%)
Acidobacteriota	42.3	41.2
Proteobacteria	30.4	34.1
Actinobacteriota	12.4	5.3
Verrucomicrobiota	5.6	6.4
Unclassified	4.2	5.0
Chloroflexi	1.9	1.4
Planctomycetota	1.6	3.0
Myxococcota	1.2	1.1
Others	2.3	2.3

Table S2. Relative abundance of fungal phylum taxa in all samples of bulk soil and Masson pine rhizosphere soil.

Phylum taxa	Relative abundance in bulk soil (%)	Relative abundance in rhizosphere soil (%)
Ascomycota	49.4	56.0
Basidiomycota	43.1	34.3
Unclassified	3.9	5.4
Mortierellomycota	2.3	2.9
Others	1.1	1.7

Table S3. Analysis of covariance on microbial alpha diversity in bulk soil, with PWD-infected years and management treatments (logging vs unmanaged) as fixed factor, and NMDS axis of woody plant community (NMDS1 and NMDS2) as covariate. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

Sites	Factors	Bacterial Chao1 richness	Bacterial Shannon diversity	Fungal Chao1 richness	Fungal Shannon diversity
Suichang	Years	0.13	0.43	8.12**	1.57
	NMDS1	1.00	2.79	0.38	0.60
	NMDS2	31.18***	8.71*	52.95***	7.84*
Taishun	Years	1.13	0.25	4.62*	0.43
	NMDS1	0.58	0.16	0.00	0.14
	NMDS2	0.32	0.09	0.04	0.31
Taishun	Treatments	2.88	4.25*	6.99*	0.71
	NMDS1	0.89	0.28	0.00	0.14
	NMDS2	0.50	0.16	0.05	0.33