

Supplementary Files

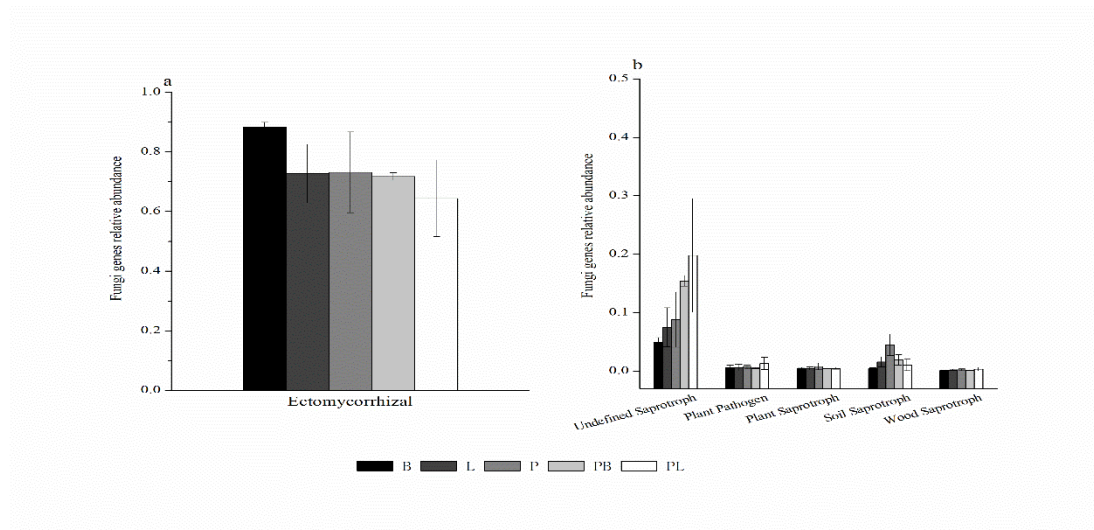


Figure S1. The abundance of fungi functional identified based on FunGuild database.

Table S1 Microbiological Co-occurrent Network Analysis Group

Microbial Co-occurrent Network	Tree Species	Abbreviation
Monoculture plantation	<i>Pinus sibirica</i>	P-L-B
	<i>Larix gmlinii</i>	
	<i>Betula platyphylla</i>	
Coniferous mixed	<i>Pinus sibirica</i>	P-L-PL
	<i>Larix gmlinii</i>	
	<i>Pinus sibirica-Larix gmlinii</i>	
Coniferous-angiosperms mixed	<i>Pinus sibirica</i>	P-B-PB
	<i>Betula platyphylla</i>	
	<i>Pinus sibirica-Betula platyphylla</i>	

Table S2 ANOSIM analysis results, based on the rank of the distance between monoculture groups and all groups.

ANOSIM	Fungal		Bacterial	
	P-value	R-value	P-value	R-value
P-L-B	0.024	0.613	0.003	0.473
PL-L	0.1	0.333	0.2	0.481
PB-B	0.1	1	0.1	0.926
L-PL-PB-P-B	0.001	0.52	0.002	0.508

Table S3 Number of nodes and edges in bacterial-fungal co-occurrence network.
⁺, represents positive correlation; ⁻, represents negative correlation.

	P-L-B	P-L-PL	P-B-PB
Nodes	129	147	149
Bacterial nodes	76	94	95
Fungal nodes	53	53	54

Edges	156	180	274
Fungal-Fungal	13 ⁺ ; 16 ⁻	12 ⁺ ; 6 ⁻	21 ⁺ ; 12 ⁻
Fungal-Bacterial	20 ⁺ ; 24 ⁻	32 ⁺ ; 29 ⁻	56 ⁺ ; 48 ⁻
Bacterial- Bacterial	44 ⁺ ; 39 ⁻	56 ⁺ ; 45 ⁻	75 ⁺ ; 62 ⁻
Network density	0.019	0.017	0.025
Clustering coefficient	0.244	0.185	0.30
