

Supplemental information for **Effects of microbial communities on elevational gradient adaptation strategies of *Pinus yunnanensis* Franch. and *Pinus densata* Mast. in a mixed zone**

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The following supporting information is available for this article:

**Supplemental Figure S1.** Workflow of sample collection.

**Supplemental Figure S2.** Sampling sites.

**Supplemental Figure S3.** Morphological features of pine needles at different elevations.

**Supplemental Figure S4.** Raincloud plot showing needle morphological features at different elevations.

**Supplemental Figure S5.** Rarefaction curves for different groups of samples.

**Supplemental Figure S6.** Composition and relative abundance of microbial communities at the phylum and genus levels.

**Supplemental Figure S7.** The distribution of samples at different altitudes on the PC1 axis analysed by PCoA.

**Supplemental Figure S8.** Variation in OTU abundance with altitudinal gradient.

**Supplemental Figure S9.** The different groups between the two types of pines at the OTU level and functions of bacteria at the KEGG 2 level.

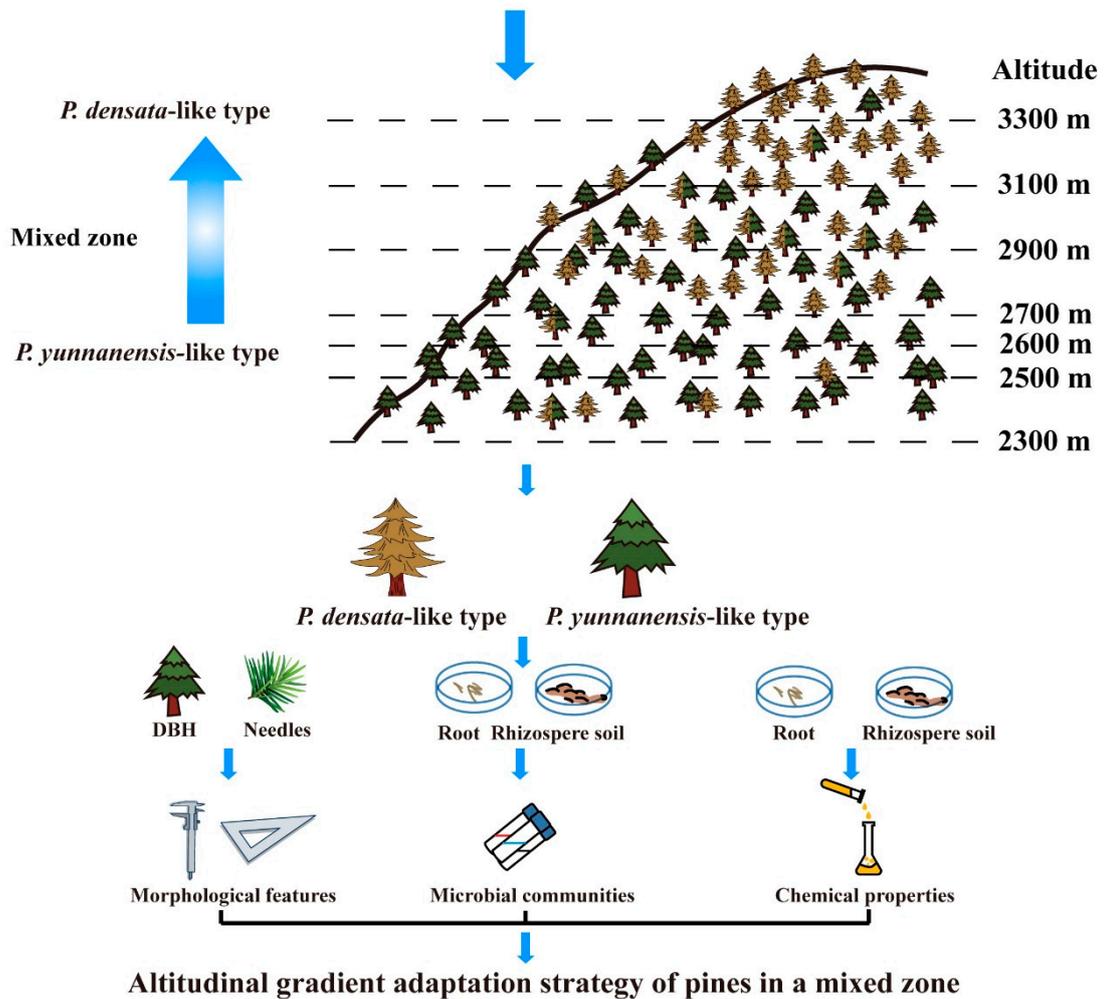
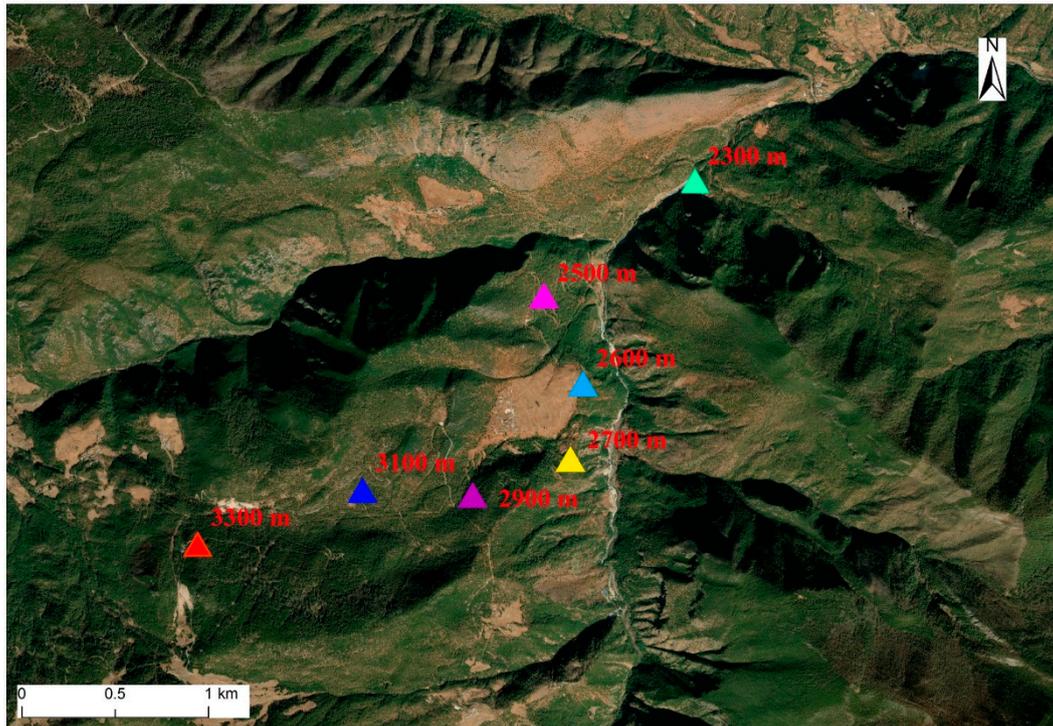
**Supplemental Figure S10.** The different groups between rhizosphere soil and roots at the OTU level and functions of bacteria at the KEGG 2 level.

**Supplemental Figure S11.** RDA/CCA of the microbial communities of different pine types.

**Supplemental Figure S12.** RDA/CCA of the microbial communities of rhizosphere soil and roots.

**Supplementary Table S1.** Sampling site information.

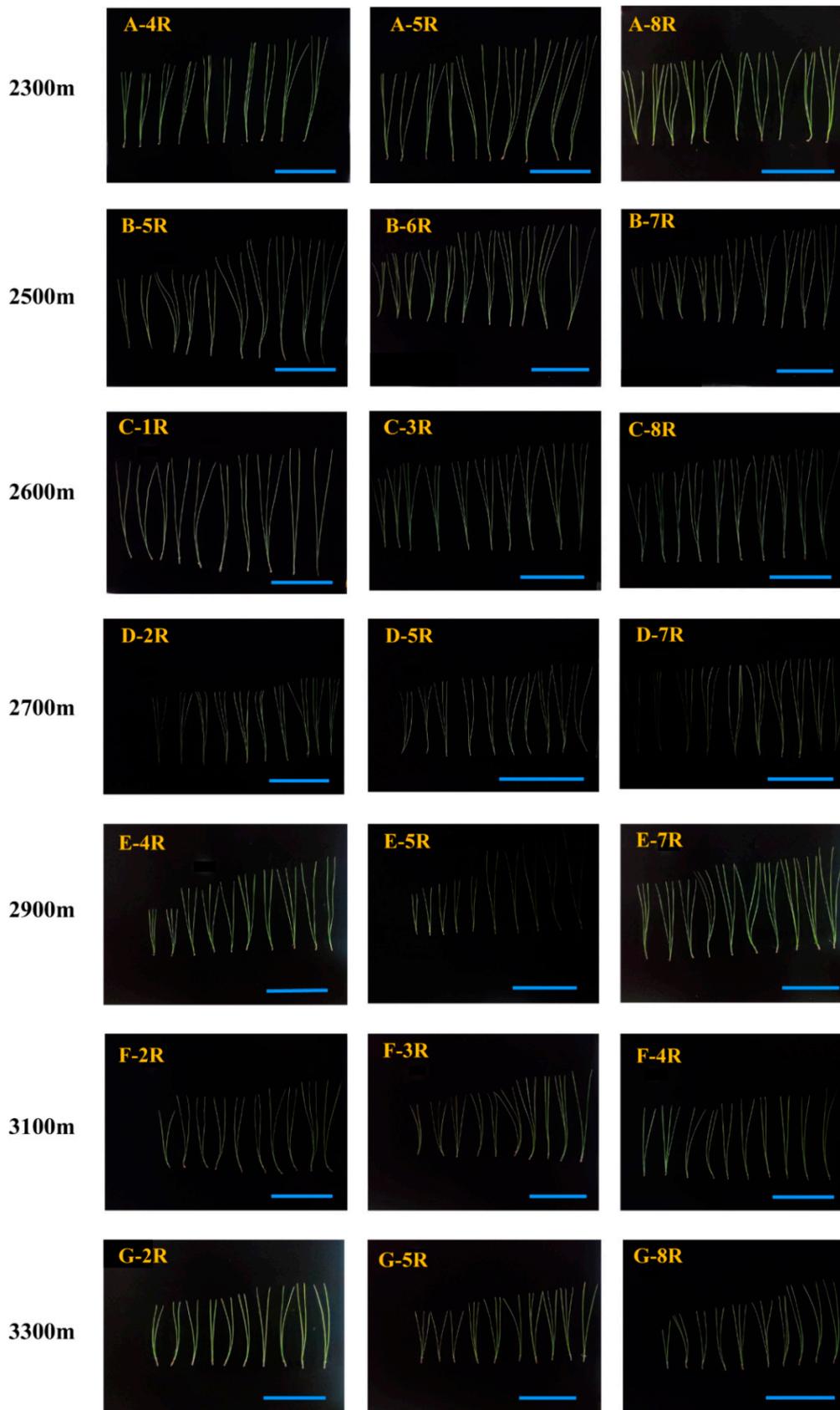
**Supplementary Table S2.** Plant information for sampling sites at different elevations.



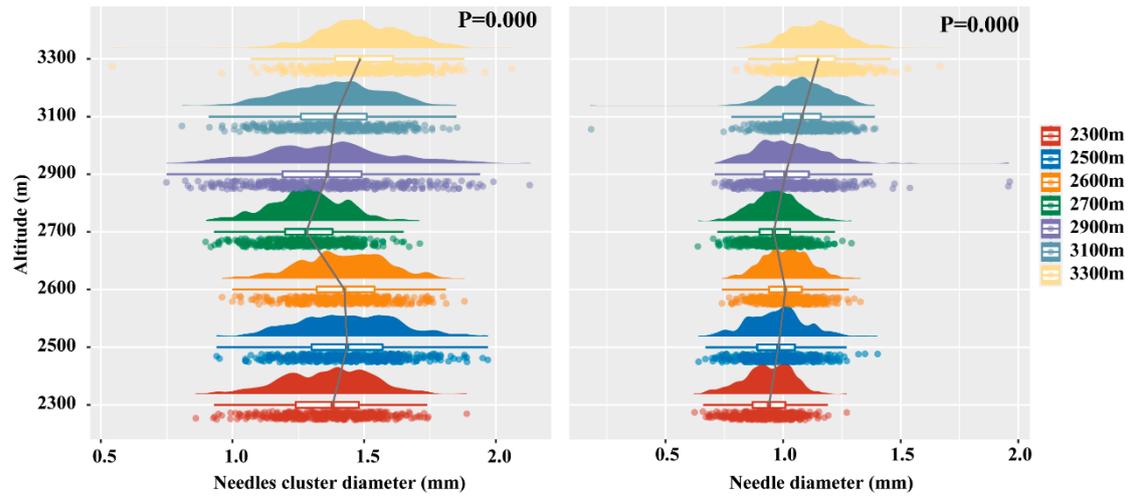
Supplemental Figure S1. Workflow of sample collection.



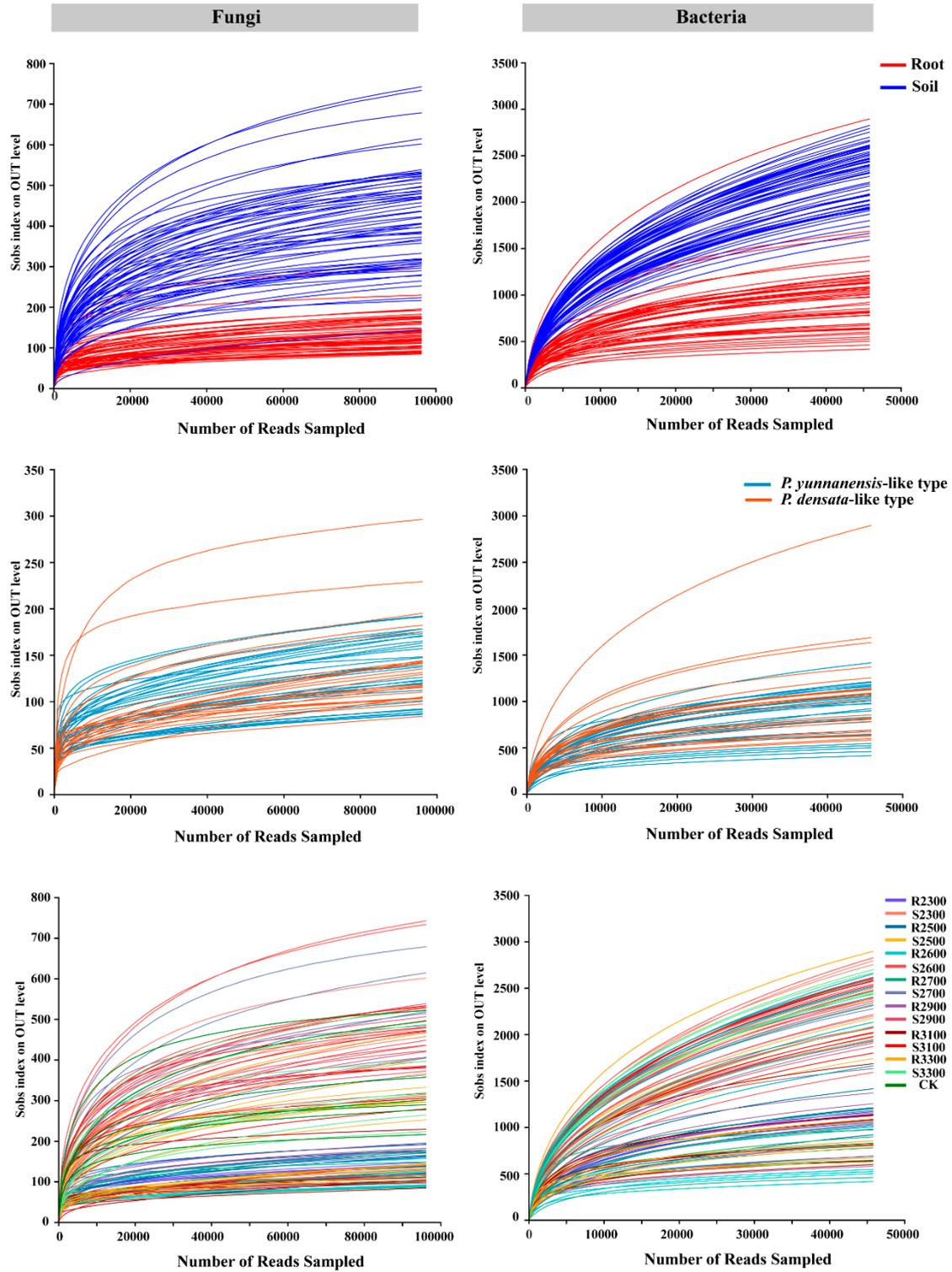
**Supplemental Figure S2. Sampling sites.** A, B, C: The pine forests used for sampling. D, E, F: The pine trees used to collect fine roots and rhizosphere soil. G, H: Fine roots and rhizosphere soil were collected.



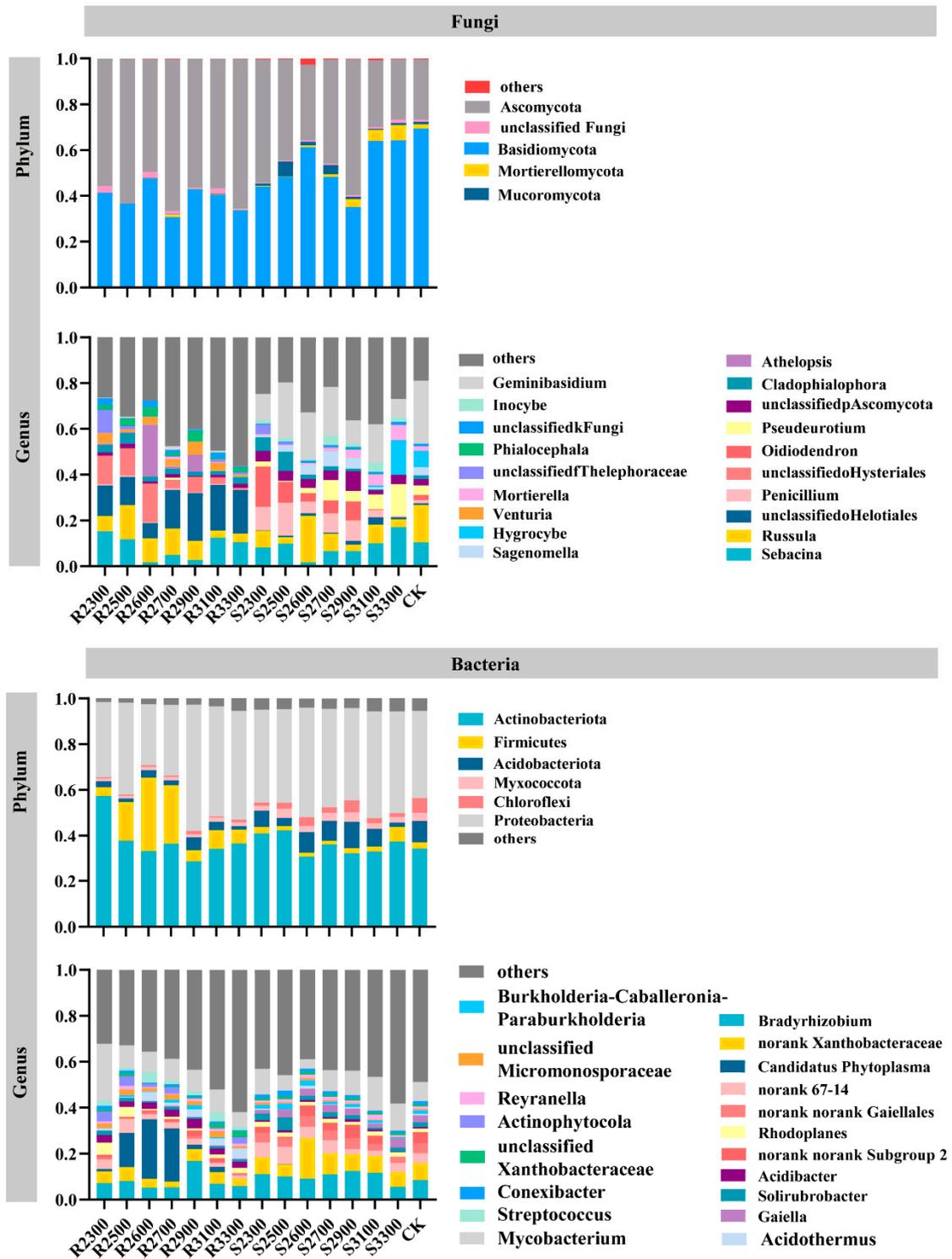
**Supplemental Figure S3. Morphological features of pine needles at different elevations.** The scale bars represent 10 cm.



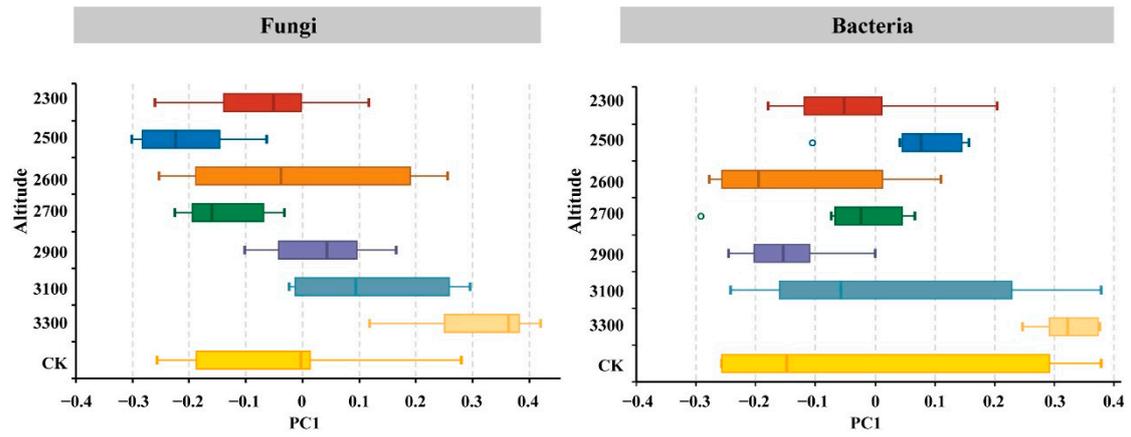
**Supplemental Figure S4. Raincloud plot showing needle morphological features at different elevations.** The half-violin diagram (cloud) shows the kernel density of the data distribution, and the scatter diagram (rain) shows the degree of dispersion. The raincloud plot also includes a box plot (umbrella) and lines (thunder) that link the medians of different groups.



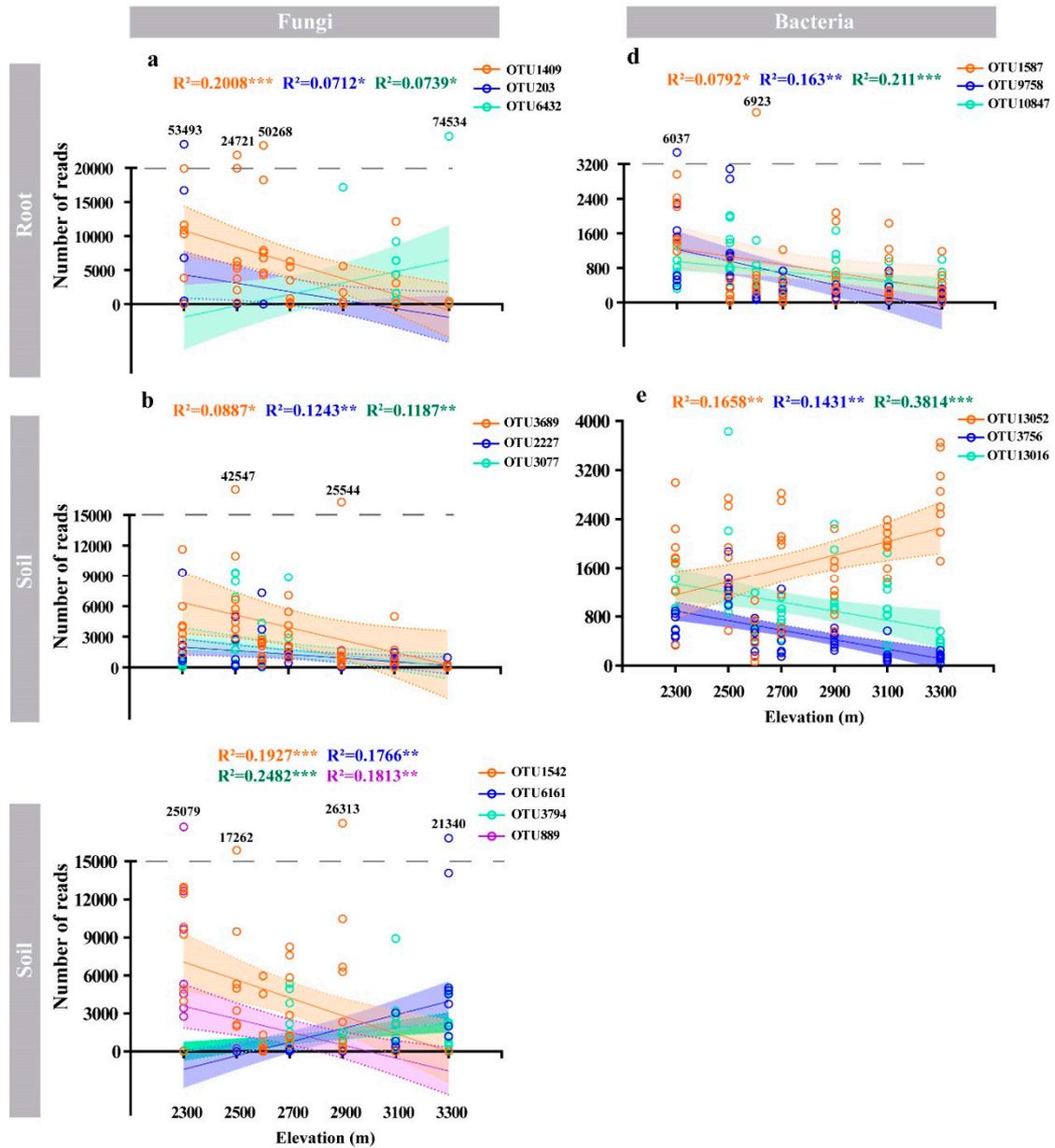
Supplemental Figure S5. Rarefaction curves for different groups of samples.



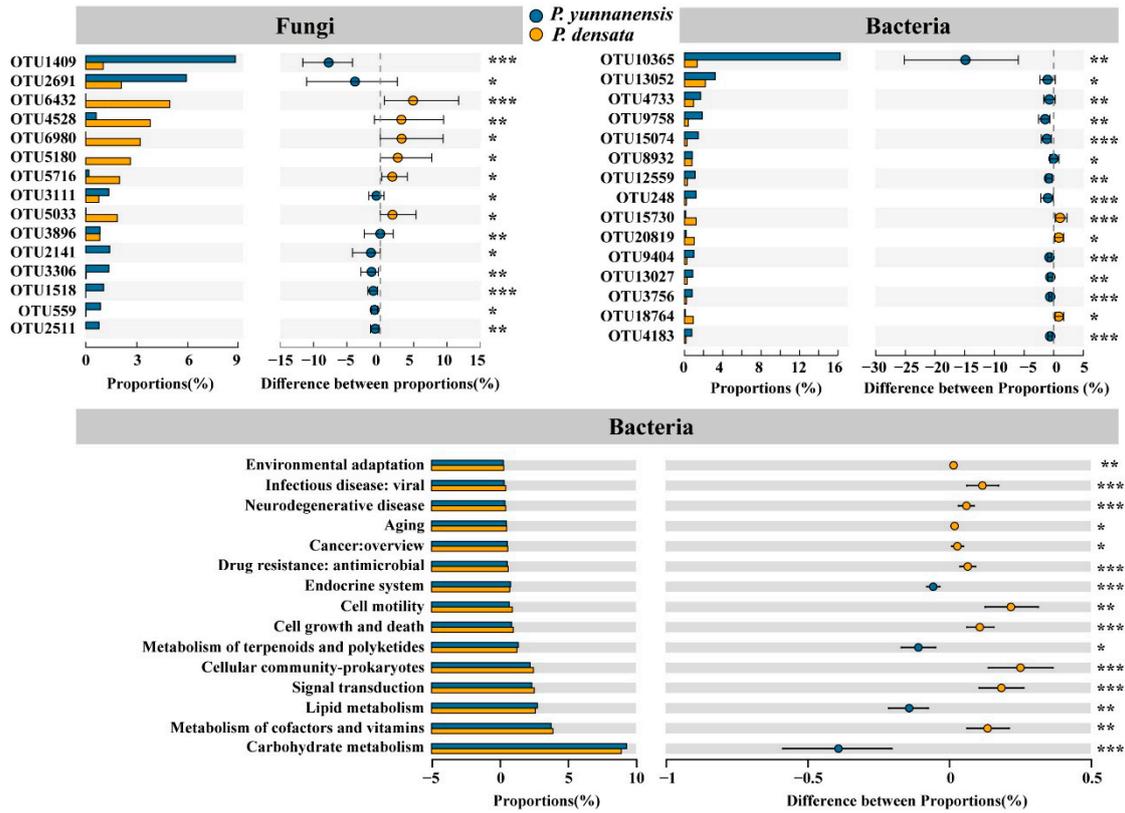
**Supplemental Figure S6. Composition and relative abundance of microbial communities at the phylum and genus levels.** Others represent the sum of the phyla or genera with a relative abundance less than 0.01.



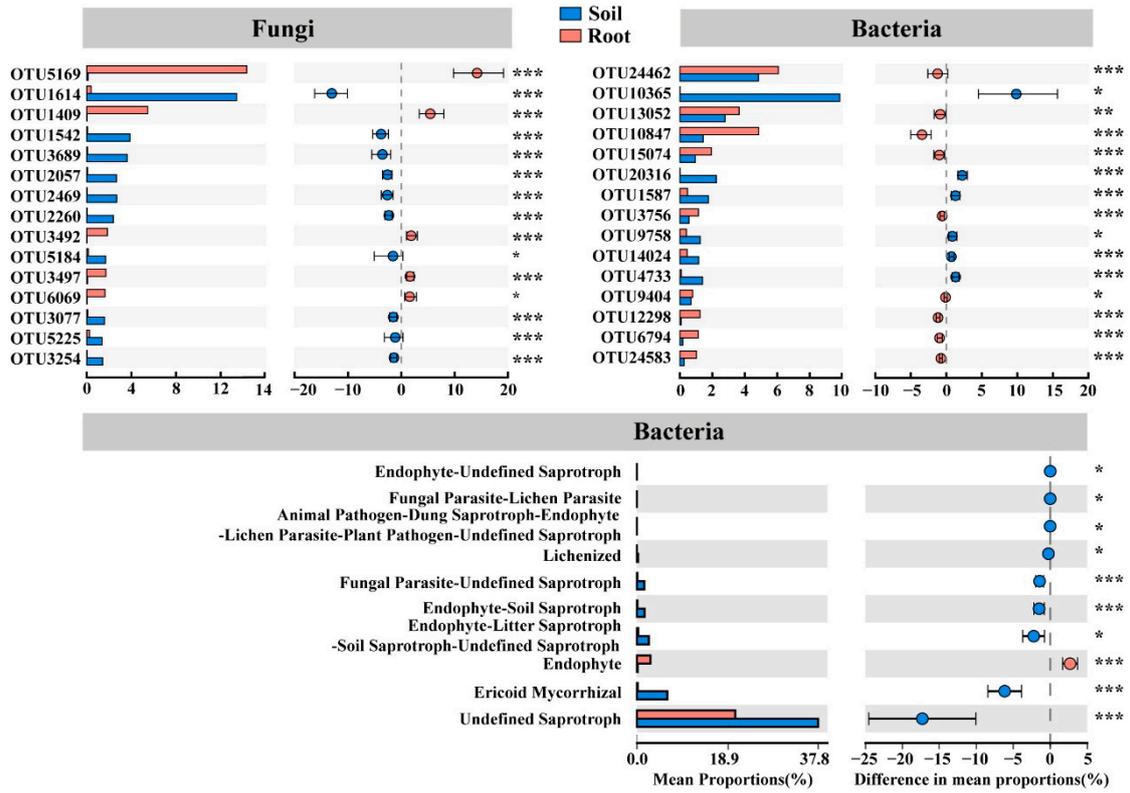
**Supplemental Figure S7. The distribution of samples at different elevations on the PC1 axis analysed by PCoA.**



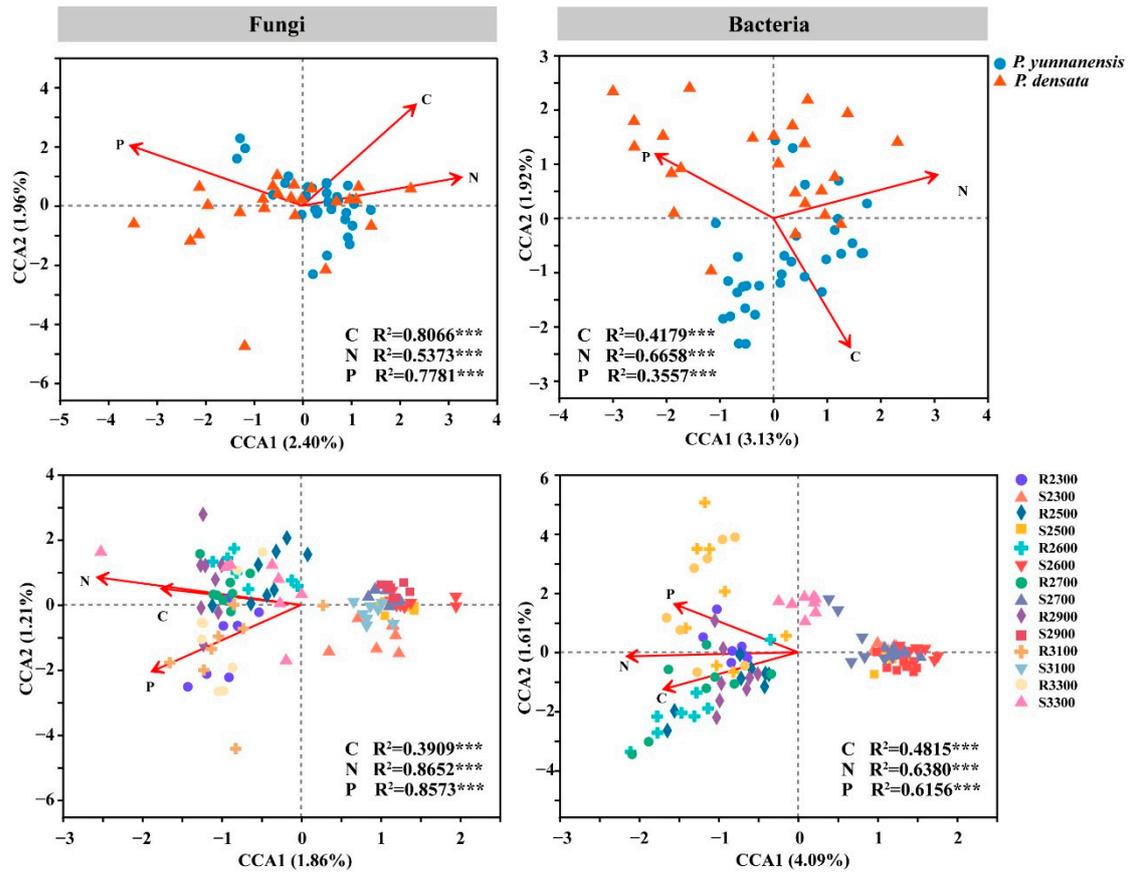
**Supplemental Figure S8. Variation in OTU abundance with altitudinal gradient.** The line indicates the linear regression fit, and the shaded band represents the 95% confidence level.  $R^2$  was employed to determine the models that fit the whole altitudinal gradient. Significant difference: \*  $P \leq 0.05$ , \*\*  $P \leq 0.01$ , \*\*\*  $P \leq 0.001$ .



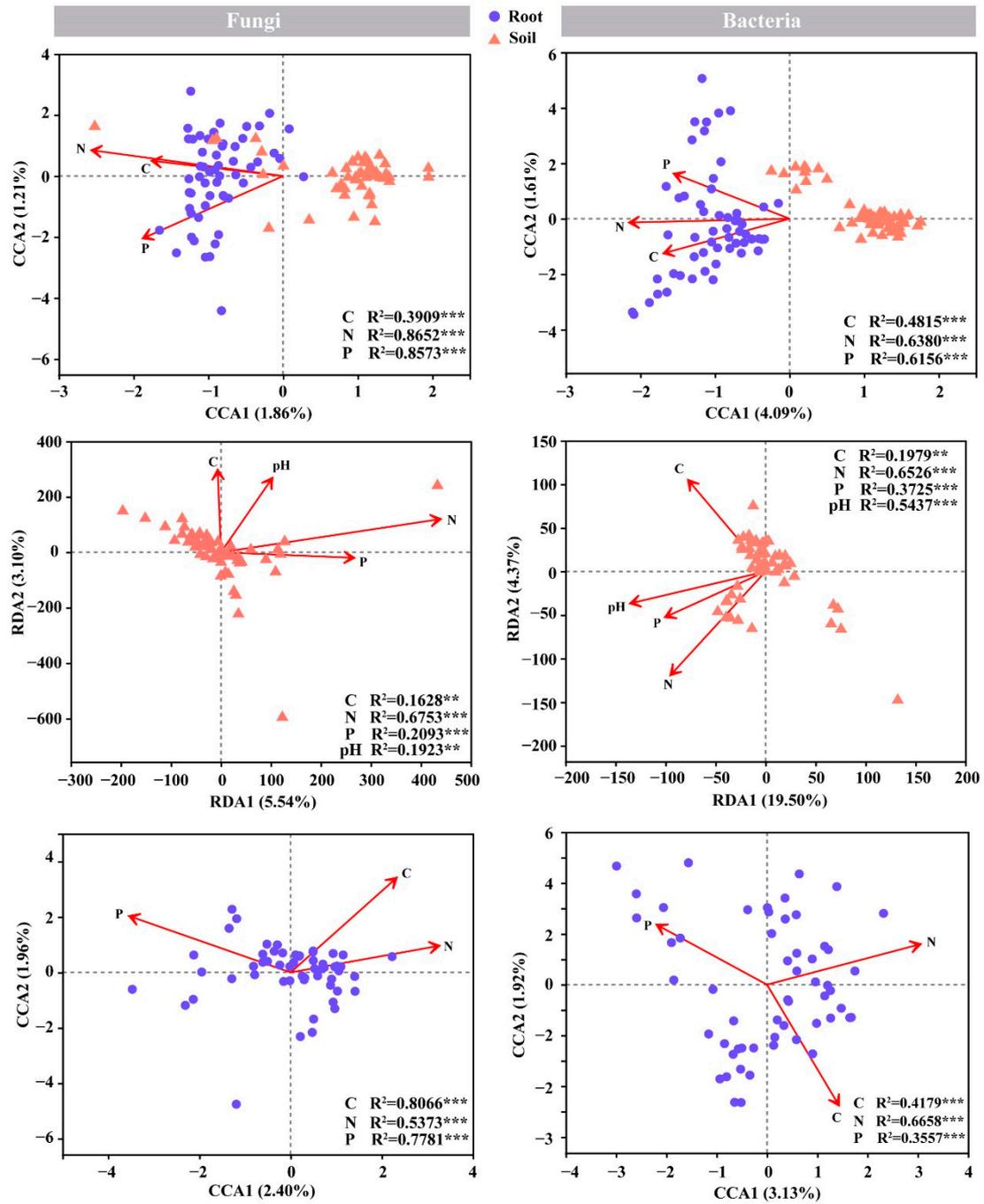
**Supplemental Figure S9. The different groups between the two types of pines at the OTU level and functions of bacteria at the KEGG 2 level.** Mann–Whitney U tests were used to evaluate differences in the abundance and functions of pine root endophytes. Significant difference: \*  $P \leq 0.05$ , \*\*  $P \leq 0.01$ , \*\*\*  $P \leq 0.001$ .



**Supplemental Figure S10. The different groups between rhizosphere soil and roots at the OTU level and functions of bacteria at the KEGG 2 level.** Mann–Whitney U tests were used to evaluate differences in the abundance and functions of pine root endophytes. Significant difference: \*  $P \leq 0.05$ , \*\*  $P \leq 0.01$ , \*\*\*  $P \leq 0.001$ .



**Supplemental Figure S11. RDA/CCA of the microbial communities of different pine types.** Soil properties and plant nutrient contents with significant relationships ( $P < 0.05$ ) are indicated by red arrows, and the  $R^2$  values are shown. Significant difference:  $*** P \leq 0.001$ .



**Supplemental Figure S12. RDA/CCA of the microbial communities of rhizosphere soil and roots.** Soil properties and plant nutrient contents with significant relationships ( $P < 0.05$ ) are indicated by red arrows, and the  $R^2$  values are shown. Significant difference: \*\*  $P \leq 0.01$ , \*\*\*  $P \leq 0.001$ .

**Supplementary Table S1. Sampling site information.**

Sampling sites	Longitude (E)	Latitude (N)	Elevation (m)
1	100°5'38.91"	27°45'44.42"	2300
2	100°4'51.76"	27°45'7.51"	2500
3	100°5'3.61"	27°44'39.69"	2600
4	100°5'0.32"	27°44'15.94"	2700
5	100°4'29.37"	27°44'4.31"	2900
6	100°3'55.51"	27°44'5.73"	3100
7	100°3'2.93"	27°43'49.49"	3300

**Supplementary Table S2. Plant information for sampling sites at different elevations.**

Species	Family	Cover degree (%)						
		2300m	2500m	2600m	2700m	2900m	3100m	3300m
<i>Pinus yunnanensis</i> -like type	Pinaceae	50	50	30	70	0	0	0
<i>Pinus densata</i> -like type	Pinaceae	0	0	0	0	30	50	30
<i>Quercus semecarpifolia</i>	Fagaceae	1	<1	<1	10	0	0	30
<i>Quercus aliena</i>	Fagaceae	1	0	0	0	0	0	0
<i>Coriaria nepalensis</i>	Coriariaceae	<1	<1	0	0	0	0	0
<i>Rhododendron simsii</i>	Ericaceae	1	<1	<1	5	0	40	<1
<i>Vaccinium fragile</i>	Ericaceae	20	10	25	10	10	0	0
<i>Indigofera tinctoria</i>	Leguminosa	1	0	0	0	0	0	0
<i>Campylotropis hirtella</i>	Leguminosa	10	15	5	3	0	0	0
<i>Quercus monimotricha</i>	Fagaceae	0	0	0	0	5	5	0
<i>Vaccinium</i> sp.	Ericaceae	0	0	0	0	<1	3	<1
<i>Pinus armandii</i>	Pinaceae	0	0	0	0	0	0	<1