Supplementary Materials

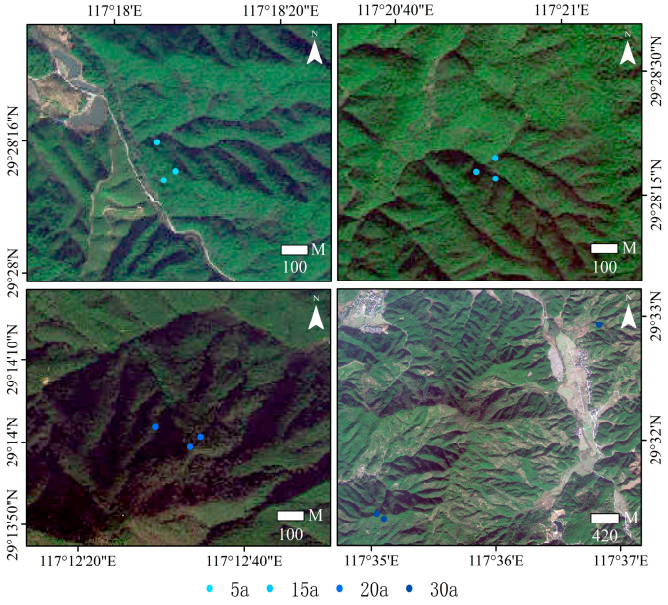

Figure S1. Spatial distribution of long-term forest monitoring plots representing four stand development stages (5, 15, 20, and 30 years) within the study area. Colors correspond to distinct stand-age classes as shown in the legend. Plot symbols are exaggerated for visibility at this cartographic scale.

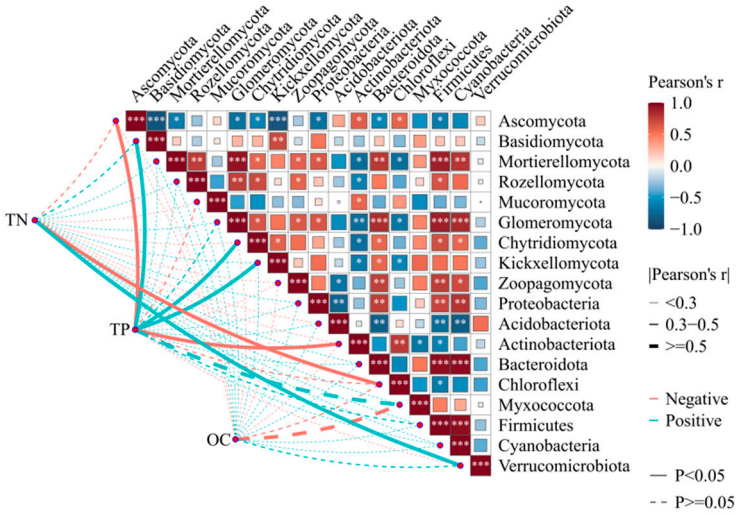

Figure S2. Network Correlation Heatmap of Soil Nutrients and Microbial Community Structurein Monoculture Chinese Fir Plantations. The heatmap displays Pearson correlation coefficients between major fungal phyla (e.g., Ascomycota) and bacterial phyla (e.g., Proteobacteria) with key environmental factors (TN: total nitrogen, TP: total phosphorus, OC: organic carbon). Color intensity indicates the strength of correlation (see color bar: red for positive, blue for negative). Only statistically significant correlations ($p < 0.05$) are shown. Microbial taxa are ordered by cluster analysis (Euclidean distance, complete linkage). Asterisks indicate statistical significance: $p < 0.05$.

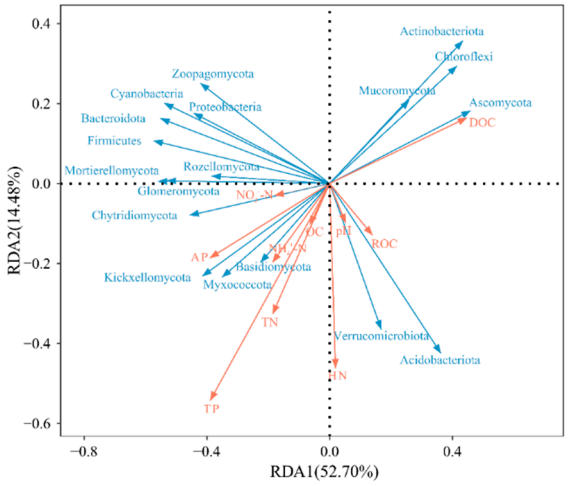

Figure S3. Redundancy Analysis of Soil Physicochemical Properties and Microbial Community Composition in Monoculture Chinese Fir Plantations. The RDA ordination plot illustrates the influence of soil environmental factors on the bacterial community structure. Blue arrows represent dominant phyla of fungi and bacteria, while red arrows denote different soil environmental factors. The length of the arrows indicates the strength of the influence of each factor on the community distribution, and the angles between arrows reflect the correlations among factors. The first two RDA axes collectively explain 67.18% of the total variance in the community data. The Monte Carlo permutation test indicates that the entire model is significant.

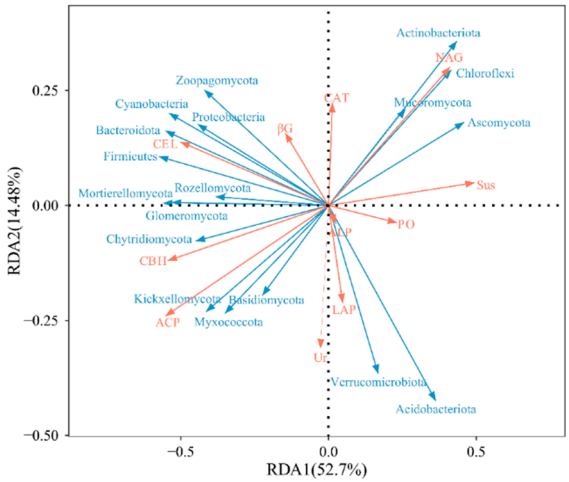

Figure S4. Redundancy Analysis of Soil Enzyme Activities and Microbial Community Composition in Monoculture Chinese Fir Plantations. The RDA ordination plot demonstrates the effects of soil environmental factors on bacterial community structure. Blue arrows represent dominant bacterial and fungal phyla, while red arrows indicate different enzymes. Arrow length reflects the strength of influence of each factor on community distribution, and the angles between arrows represent correlations among factors. The first two RDA axes collectively explain 67.18% of the total variance in community data. The Monte Carlo permutation test shows the overall model is significant.

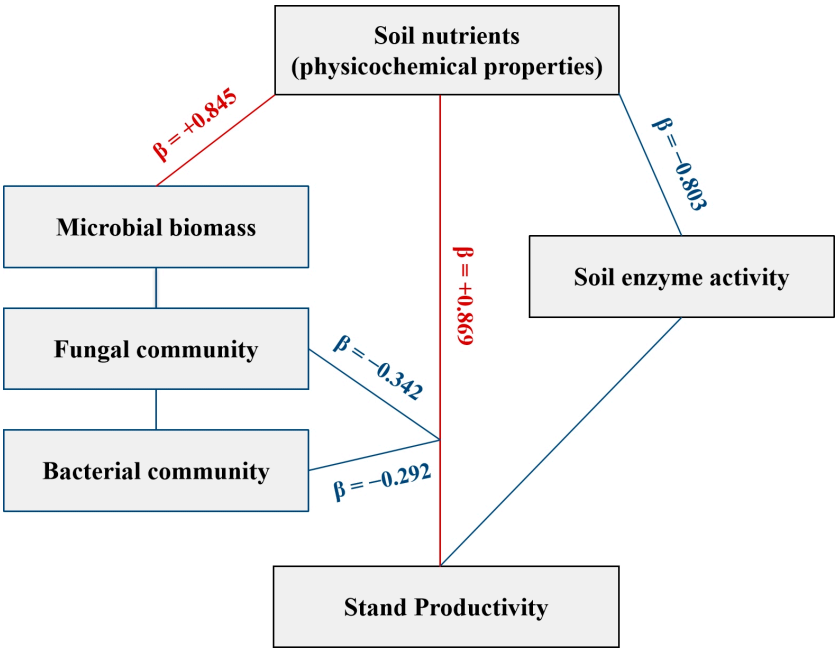

Figure S5. Conceptual representation of the dual-effect mechanism by which soil nutrients regulate stand productivity in Chinese fir plantations. Soil nutrients exert a strong direct positive influence on stand productivity while simultaneously producing indirect negative effects by stimulating microbial biomass accumulation, restructuring fungal and bacterial communities, suppressing soil enzyme activity, and intensifying microbially mediated competition for limiting nutrients. These opposing pathways—promotion versus inhibition—jointly determine the net productivity outcome, consistent with the structural relationships revealed by the PLS-SEM analysis.