Supporting Information

Supplementary Table 1. General description of all, abundant, and rare OTUs datasets at 97% sequence identity level.

Category	OTU number	Sequence number	Chao1	ACE
All	17409	14703300	17713±30	17688±62
Abundant	338（2.23%）	9853872（67.02%）		
Rare	13010（74.73%）	343981（2.34%）		

Supplementary Table 2. Linear mixed effects models (LMMs) show the effects of year, depth and radius on the alpha-diversity of abundant and rare bacteria. Year indicates four successional stages, including farmland, Y10-Forest, Y20-Forest and Y30-Forest stages. Depth denotes top (10 cm, 20 cm and 40 cm), middle (60 cm, 80 cm and 100 cm), and deep (150 cm, 200 cm, 250 cm and 300 cm) soils layers. Abundant, abundant bacteria; Rare, rare bacteria. Bold font means the significance at P < 0.05 level.

	Abundant		Rare	
	F	*P*	*F*	*P*
Year				
Richness	**28.185**	<0.001	**33.584**	< 0.001
Shannon	**28.645**	<0.001	**45.923**	< 0.001
Depth				
Richness	**12.619**	<0.001	**6.525**	< 0.01
Shannon	**22.662**	< 0.001	**4.113**	< 0.05
Radius				
Richness	0.382	0.683	0.876	0.417
Shannon	0.833	0.436	0.770	0.464

Supplementary Table 3. Spearman correlation between alpha-diversity of abundant and rare bacteria and environmental variables. Abundant, abundant bacteria; Rare, rare bacteria. The abbreviations of environmental variables are defined in *Methods*. Significance was tested using 999 permutations. **p < .05, **p < .01, ***p < .001.*

	pH	OM	NO3	TP	AP	AK
Abundant						
Richness	-0.362***	-0.109	0.385***	-0.550***	-0.497***	0.223***
Shannon	-0.356***	-0.024	0.464***	-0.521***	-0.529***	0.281***
Rare						
Richness	-0.269***	-0.152**	0.351***	-0.623***	-0.562***	0.112
Shannon	-0.281***	-0.185**	0.320***	-0.610***	-0.474***	0.082

Supplementary Table 4. Analysis of similarity (ANOSIM) of different reforestation stages across different layers. Abundant, abundant bacteria; Rare, rare bacteria. Top, top soil; Mid, middle soil; Deep, deep soil.

	Abundant		Rare	
	R	*P*	*R*	*P*
Reforestation-Top	0.896	<0.001	0.920	<0.001
Reforestation-Mid	0.827	<0.001	0.909	<0.001
Reforestation-Deep	0.756	<0.001	0.847	<0.001

Supplementary Table 5. Analysis of similarity (ANOSIM) of different reforestation stages across different radius. Abundant, abundant bacteria; Rare, rare bacteria. R30, 30 cm radius around the trunk; R60, 60 cm radius around the trunk; R90, 90 cm radius around the trunk.

	Abundant		Rare	
	R	*P*	*R*	*P*
Reforestation-R30	0.728	<0.001	0.938	<0.001
Reforestation-R60	0.691	<0.001	0.879	<0.001
Reforestation-R90	0.638	<0.001	0.750	<0.001

Supplementary Table 6. Mantel and partial Mantel tests for correlations between bacterial community similarity and edaphic and geographic factors in successional soils based on Spearman's correlation coefficient. Significance was tested using 999 permutations. **p < .05, **p < .01.*

	Effect	Controlling for	Farmland	Y10-Forest	Y20-Forest	Y30-Forest
Abundant	Environmental		0.175*	0.211***	0.071	0.137**
	Spatial		0.538***	0.304***	0.026	0.118**
	Environmental	Spatial	0.1154	0.150**	0.067	0.123*
	Spatial	Environmental	0.526***	0.268***	0.011	0.102**
Rare	Environmental		-0.062	0.223***	0.098*	0.099*
	Spatial		0.118	0.216***	0.020	0.036
	Environmental	Spatial	-0.081	0.181**	0.096*	0.096*
	Spatial	Environmental	0.128	0.173***	-0.001	0.013

Supplementary Table 7. Environmental fitness (Envfit) of abundant and rare bacteria correlated with NMDS ordinations during reforestation. Abundant, abundant bacteria; Rare, rare bacteria. The abbreviations of environmental variables are defined in *Methods*.

	Abundant		Rare	
Factor	R^2	*p*-value	R^2	*p*-value
TP	0.7613	0.006	0.7189	0.006
AP	0.5505	0.006	0.5220	0.006
AK	0.1729	0.006	0.1679	0.006
pH	0.1318	0.006	0.1340	0.006
NO3	0.0535	0.012	0.0208	0.294
OM	0.0061	1.000	0.0206	0.228

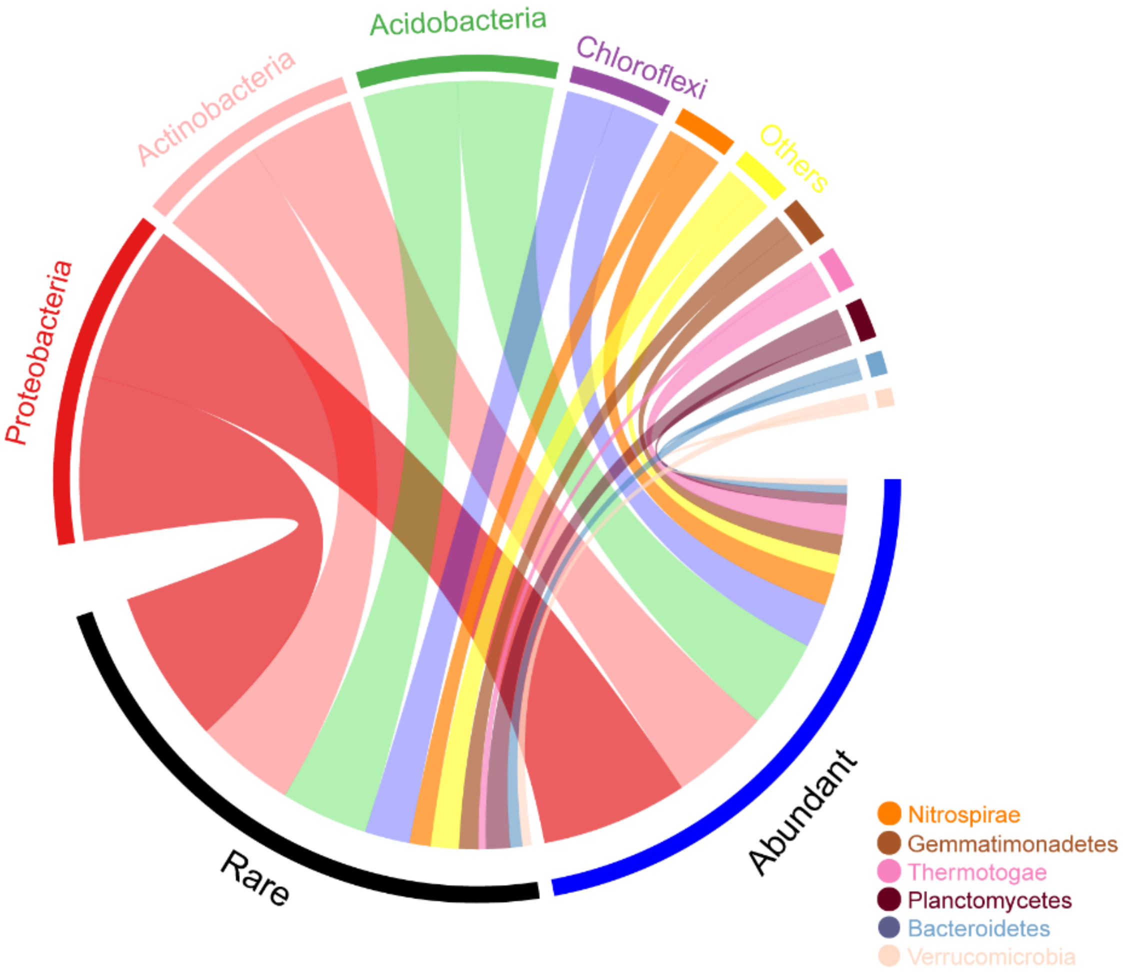
Supplementary Table 8. ANOVA of environmental factors correlated with soil bacterial *β*-diversity of abundant and rare communities during reforestation. Abundant, abundant bacteria; Rare, rare bacteria. The abbreviations of environmental variables are defined in *Method`s*.

	Factor	df	Variance	Pseudo-F	p-value
Abundant	TP	1	0.791	39.772	0.006
	AP	1	0.291	14.621	0.006
	pH	1	0.241	12.136	0.006
	NO3	1	0.151	7.581	0.006
	OM	1	0.147	7.372	0.006
	AK	1	0.117	5.874	0.006
	Residual	293	5.825		0.006
Rare	TP	1	3.813	10.244	0.006
	AP	1	1.913	5.139	0.006
	pH	1	1.344	3.612	0.006
	NO3	1	0.866	2.326	0.006
	OM	1	1.106	2.973	0.006
	AK	1	1.199	3.221	0.006
	Residual	293	109.047		

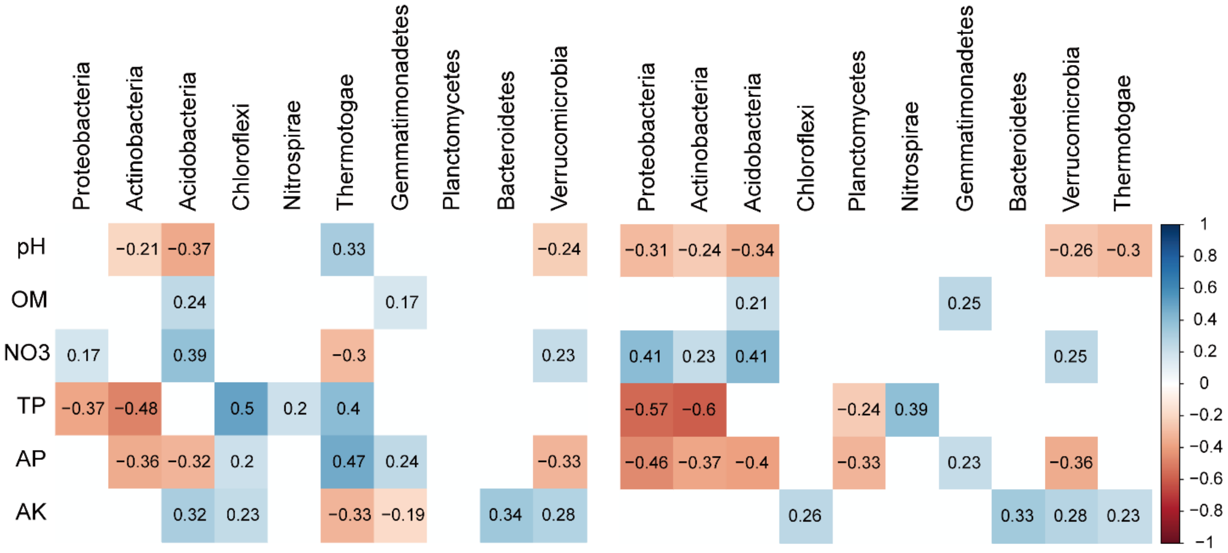
Supplementary Table 9. Partial Mantel Test results showing relationship between phylogenetic turnover (*β*NTI) versus soil TP and spatial and environmental distances for abundant/rare subcommunities after controlling for the other two explanatory distance constant in all soil samples. **p < .05, **p < .01, ***p < .001*

Variables	Controlling for	Abundant	Rare
TP	Environment (excluding TP)	**0.166*****	**0.384*****
	Spatial	**0.167*****	**0.387*****
Environment (excluding TP)	TP	0.010	0.042
	Spatial	0.021	0.042
Spatial	TP	-0.025	0.103***
	Environment (excluding TP)	-0.027	0.088***

Supplementary Figure 1. Taxonomic distribution of abundant and rare taxa at phylum level shown as circos plot. The thickness of each ribbon represents the number of abundant and rare taxa assigned to different phyla.



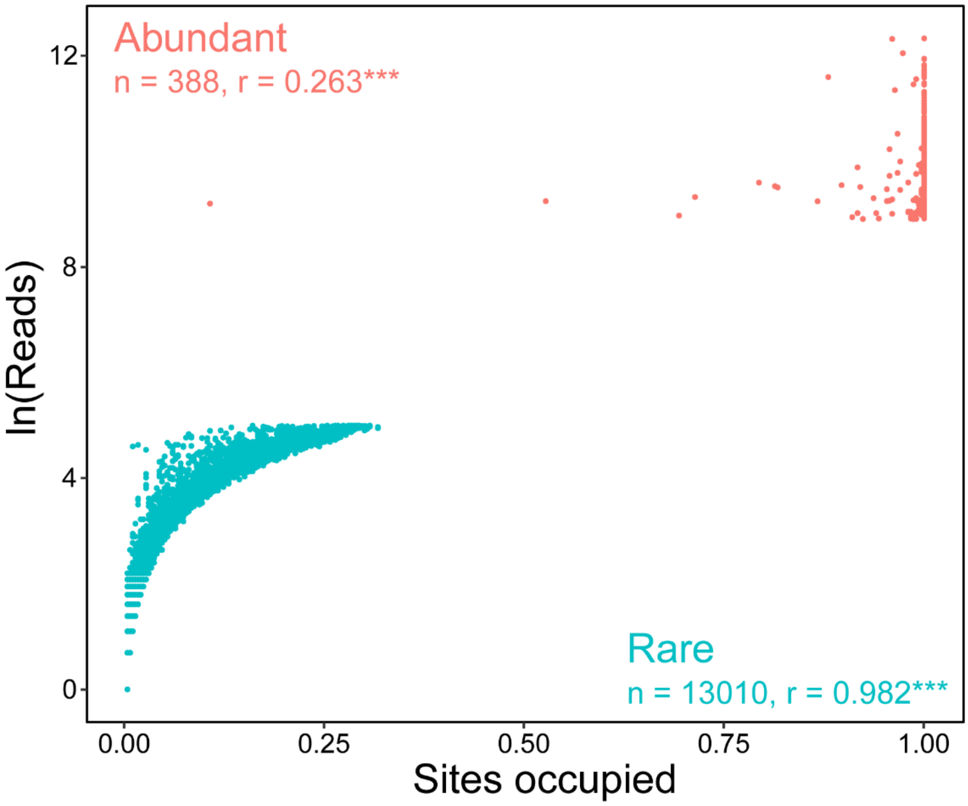
Supplementary Figure 2. The top 10 phylum in the rare and abundant sub-communities and their environmental preferences (e.g., positive or negative). The abbreviations of environmental variables are defined in *Methods*.



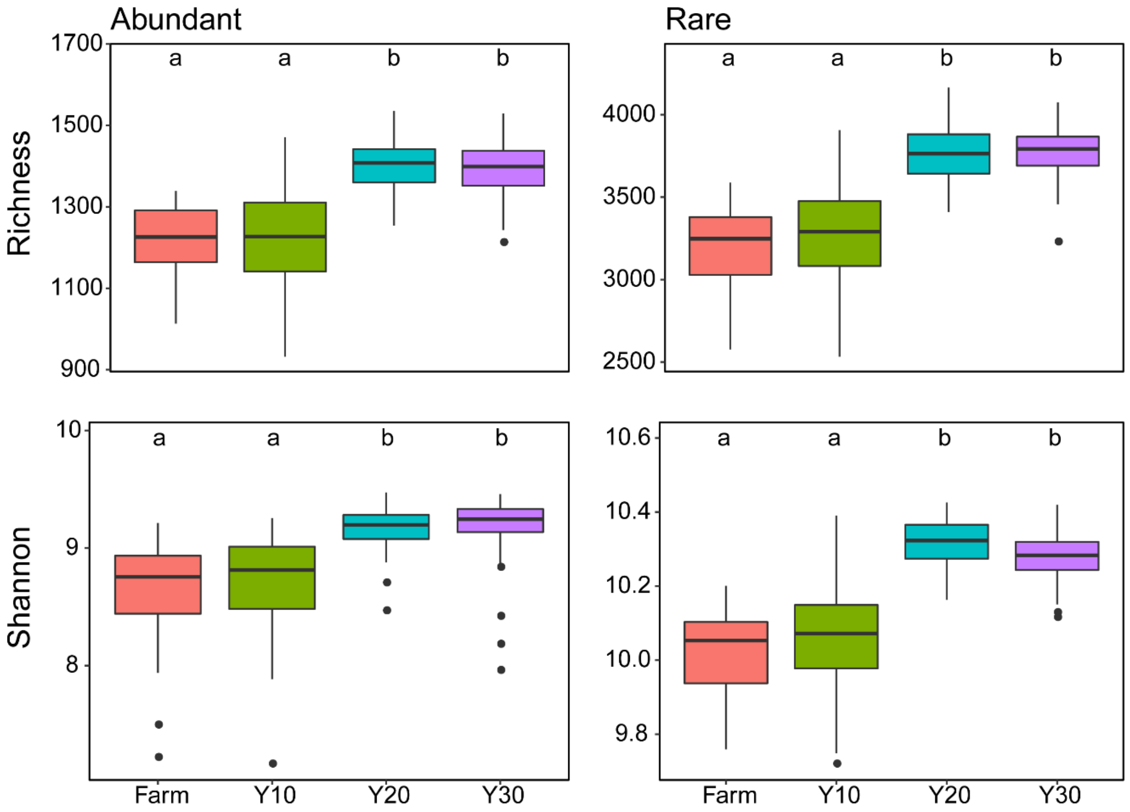
	Proteobacteria	Actinobacteria	Acidobacteria	Chloroflexi	Nitrospirae	Thermotogae	Gemmatimonadetes	Planctomycetes	Bacteroidetes	Verrucomicrobia
pH		−0.21	−0.37			0.33				−0.24
OM			0.24				0.17			
NO3	0.17		0.39			−0.3				0.23
TP	−0.37	−0.48		0.5	0.2	0.4				
AP		−0.36	−0.32	0.2		0.47	0.24			−0.33
AK			0.32	0.23		−0.33	−0.19		0.34	0.28

	Proteobacteria	Actinobacteria	Acidobacteria	Chloroflexi	Planctomycetes	Nitrospirae	Gemmatimonadetes	Bacteroidetes	Verrucomicrobia	Thermotogae
pH	−0.31	−0.24	−0.34						−0.26	−0.3
OM			0.21				0.25			
NO3	0.41	0.23	0.41						0.25	
TP	−0.57	−0.6			−0.24	0.39				
AP	−0.46	−0.37	−0.4		−0.33		0.23		−0.36	
AK				0.26				0.33	0.28	0.23

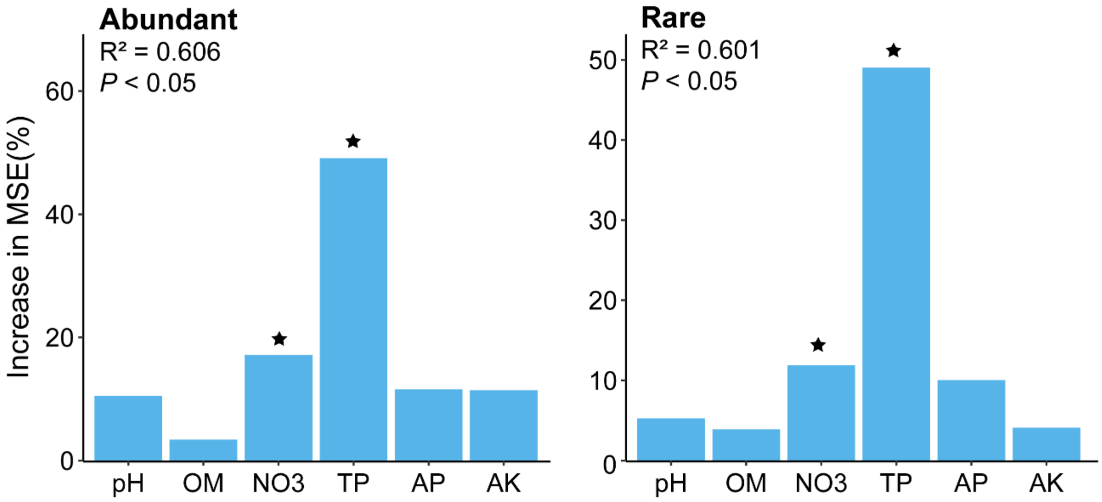
Supplementary Figure 3. Abundance-occupancy relationship of abundant and rare bacterial taxa. Spearman's rank correlation between mean relative abundance of abundant and rare bacteria and number of samples occupied (n is the number of OTUs). Abundant, abundant bacteria; Rare, rare bacteria.



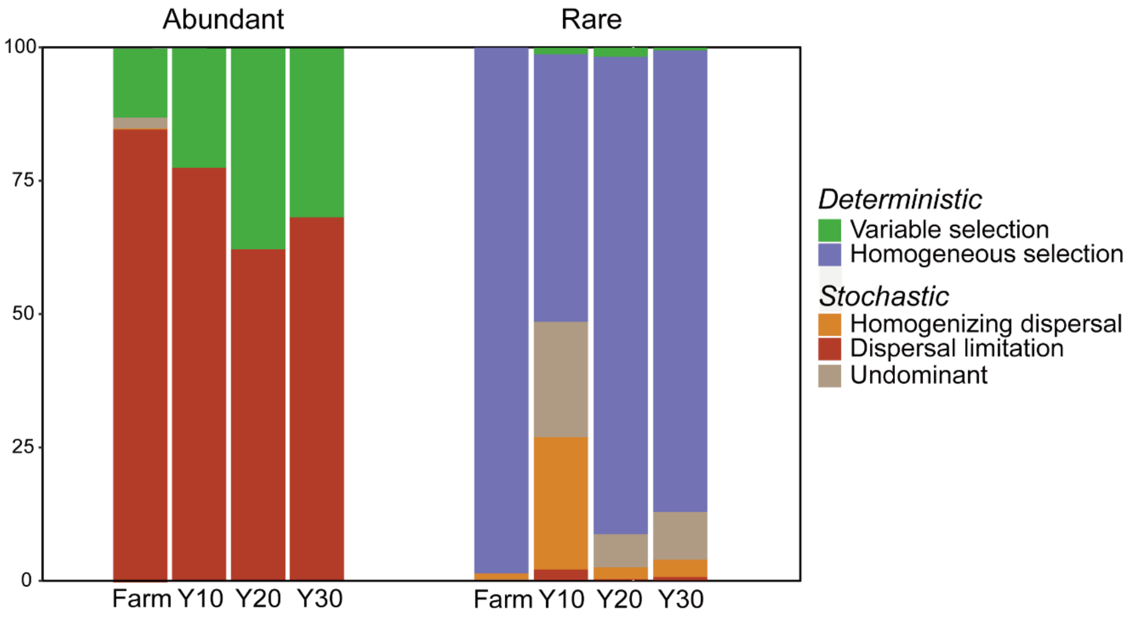
Supplementary Figure 4. Variation in alpha-diversity through succession. LMMs was used to compare the differences among different succession stages. Abundant, abundant bacteria; Rare, rare bacteria. Farm, farmland; Y10, Y10-Forest; Y20, Y20-Forest; Y30, Y30-Forest.



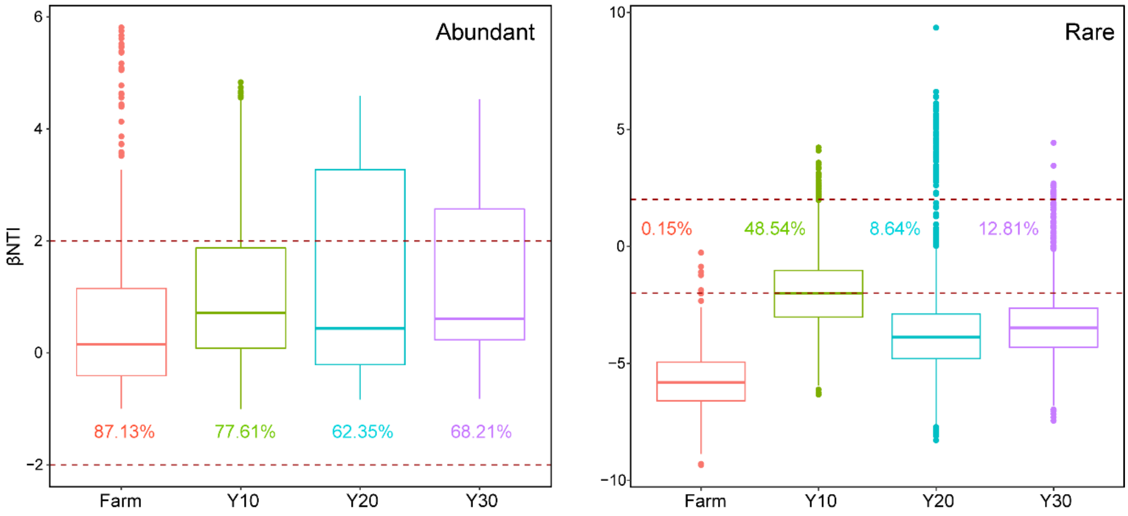
Supplementary Figure 5. Potential drivers of alpha-diversity variation of abundant and rare communities in reforested ecosystems. Percentage increases in the MSE (mean squared error) of variables were used to estimate the importance of these predictors, and higher MSE% values imply more important predictors. Significance levels are as follows: **P* < 0.05. MSE, mean squared error. Abundant, abundant bacteria; Rare, rare bacteria.



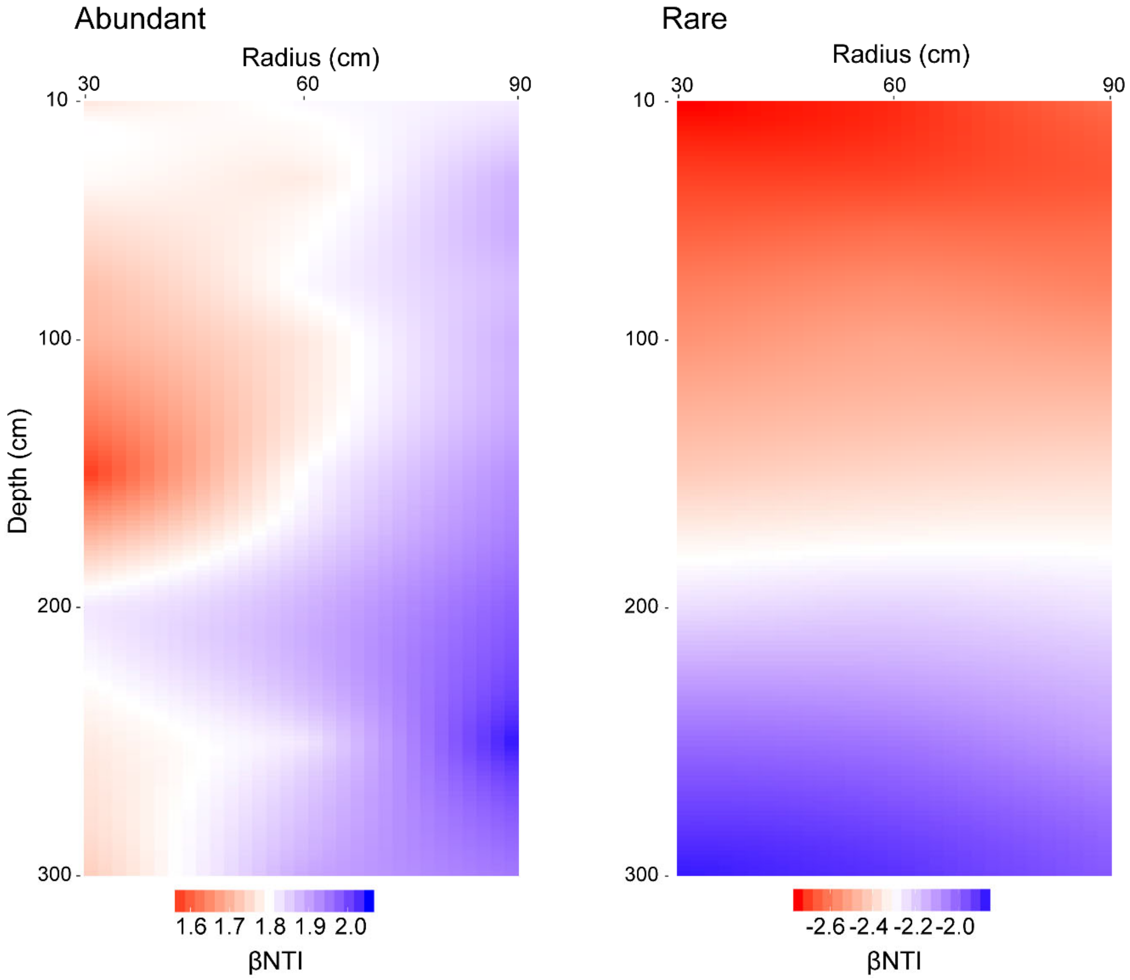
Supplementary Figure 6. The per cent of turnover in abundant and rare bacterial community assembly governed primarily by various deterministic, including homogeneous and variable selection, and stochastic processes, including dispersal limitations and homogenizing dispersal, as well as the fraction that was not dominated by any single process ('Undominated') in four successional stages soils. Farm, farmland; Y10, Y10-Forest; Y20, Y20-Forest; Y30, Y30-Forest. Abundant, abundant bacteria; Rare, rare bacteria.



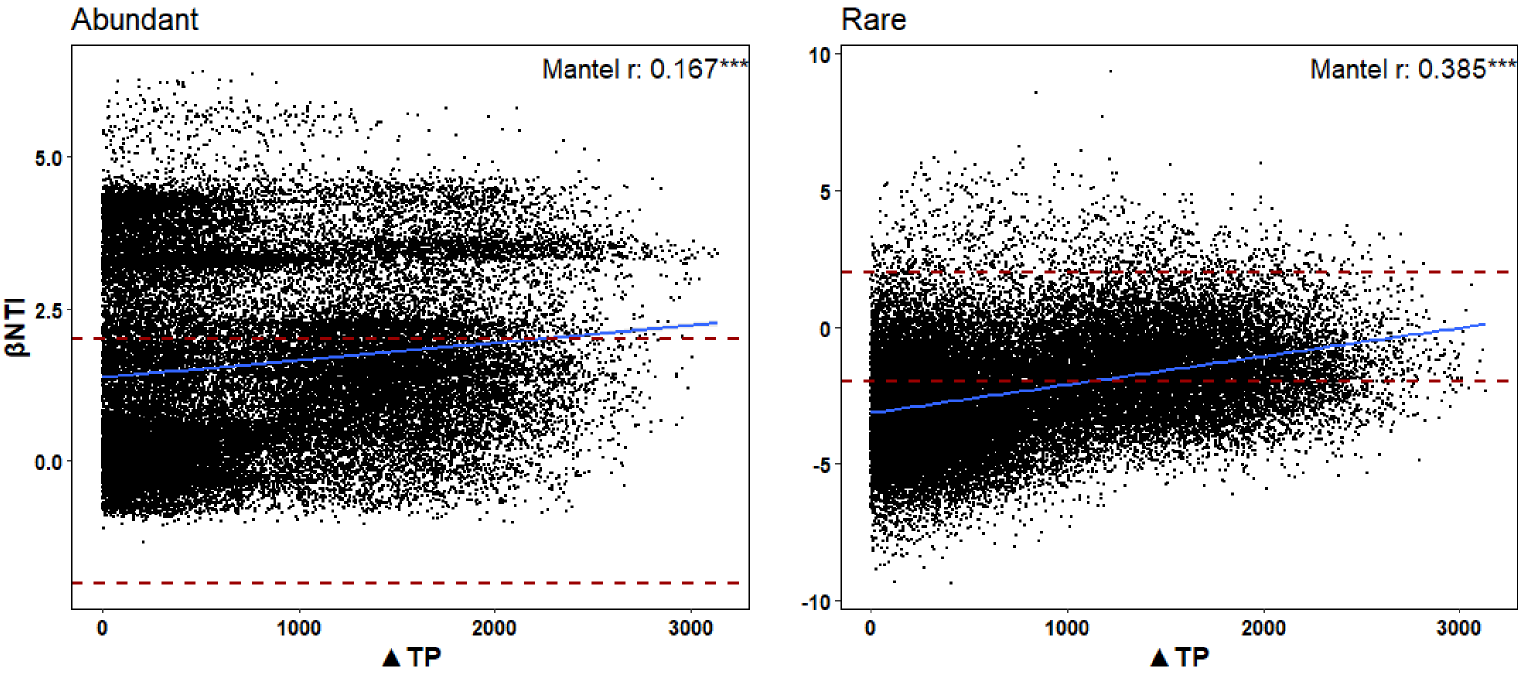
Supplementary Figure 7. Boxplots showed the variation in *β*NTI across successional stages. Farm, farmland; Y10, Y10-Forest; Y20, Y20-Forest; Y30, Y30-Forest. Abundant, abundant bacteria; Rare, rare bacteria. Horizontal dashed lines indicate the *β*NTI significance thresholds of +2 and −2.



Supplementary Figure 8. Variation in *β*NTI of abundant and rare communities in the horizontal and vertical soil profiles. Abundant, abundant bacteria; Rare, rare bacteria.



Supplementary Figure 9. Relative influences of deterministic and stochastic assembly processes in shaping abundant and rare sub-communities in reforestation successional soils. Relationships between β-nearest taxon index (βNTI) and differences in soil total phosphorus (TP) for the abundant and rare sub-communities. Linear regressions models (shown as blue lines) and associated correlation coefficients are provided on each panel. Horizontal dashed lines indicate the βNTI significance thresholds of +2 and −2. Abundant, abundant bacteria; Rare, rare bacteria.



Supplementary Figure 10. Boxplots showed the variation in *β*NTI across low, medium ('Med') and high categories of soil TP. Abundant, abundant bacteria; Rare, rare bacteria. Horizontal dashed lines indicate the *β*NTI significance thresholds of +2 and −2. Data that do not share a letter are significantly different between treatments ($P < 0.05$; multiple comparison with Kruskal-Wallis tests)