

Supplementary Material

1 Supplementary Figures and Tables

1.1 Supplementary Figures

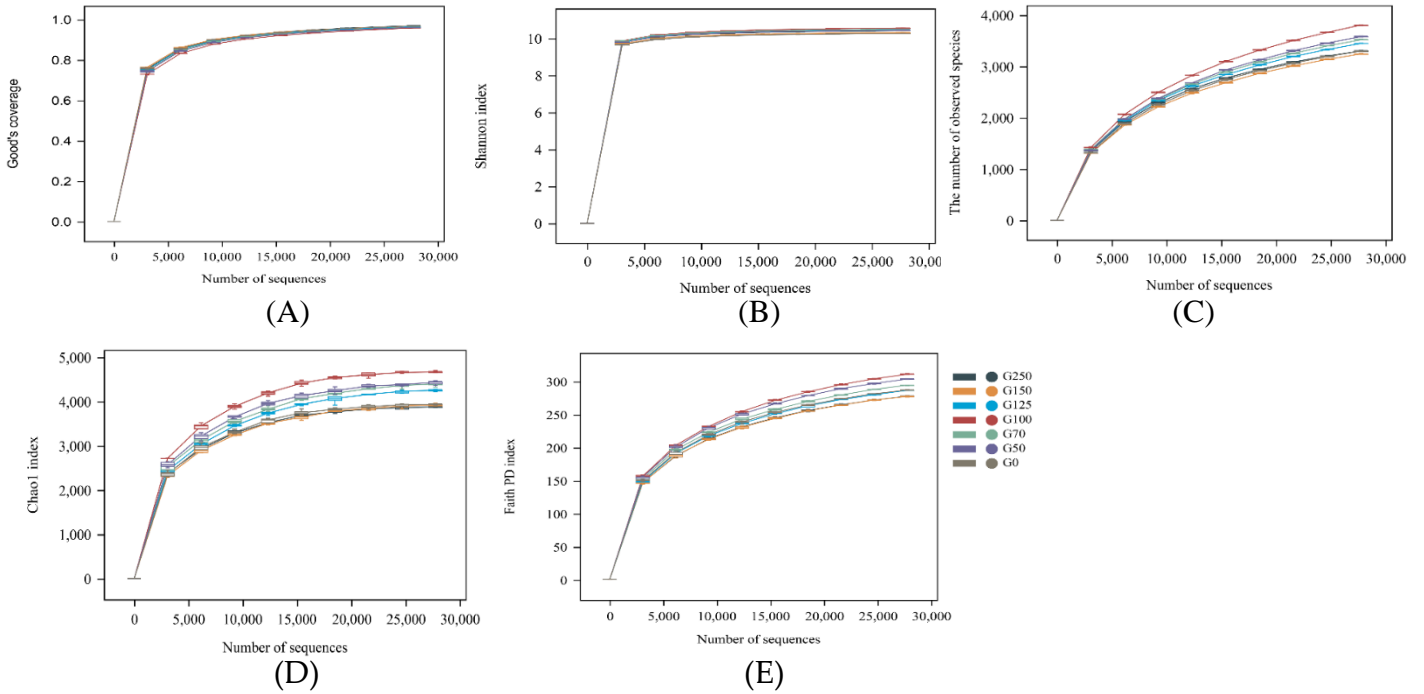


Figure S1. Rarefaction curves of ASVs. (A-E) Rarefaction curves at Good's coverage, Shannon, observed species richness, Chao1 and Faith PD indices level, respectively.

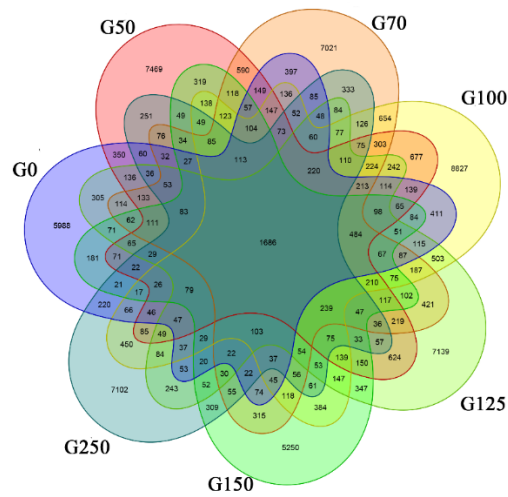


Figure S2. The Venn diagram of ASVs at different-sized forest gaps.

1.2 Supplementary Tables

Table S1. Analysis of similarities (ANOSIM) and permutational multivariate analysis of variance (PERMANOVA) based on weighted Unifrac distance at different gap size gradients

Group1	Group2	F	P	R ²
all	-	1.736	0.001	0.173
G250	G150	2.398	0.021	0.270
G250	G125	3.640	0.003	0.442
G250	G100	1.296	0.029	0.216
G250	G70	2.516	0.02	0.304
G250	G50	1.911	0.047	0.183
G250	G0	1.465	0.28	0.043
G150	G125	1.330	0.077	0.192
G150	G100	1.963	0.02	0.304
G150	G70	1.203	0.106	0.144
G150	G50	1.039	0.326	0.024
G150	G0	1.288	0.107	0.120
G125	G100	3.310	0.001	0.391
G125	G70	1.830	0.03	0.210
G125	G50	1.609	0.174	0.069
G125	G0	1.570	0.018	0.240
G100	G70	1.895	0.035	0.196
G100	G50	0.924	0.428	0.002
G100	G0	1.724	0.033	0.223
G70	G50	0.937	0.504	0.014
G70	G0	1.193	0.064	0.165
G50	G0	1.315	0.128	0.097

Note: the explanation degree(R²) and significance degree (P) of the grouping scheme are calculated on the weighted Unifrac distance matrix, with the number of permutation tests set to 999.

Table S2. Topological characteristics of co-occurrence networks of soil bacteria community in forest gaps and closed forests

Network properties	G250	G150	G125	G100	G70	G50	G0
Total nodes	98	97	100	100	100	100	99
Total edges	529	344	433	330	344	464	326
Positive edges	318 (60.11%)	198 (58.43%)	251 (57.97%)	187 (56.67%)	189 (56.98%)	255 (54.96%)	200 (61.35%)
Negative edges	211 (39.89%)	143 (41.57%)	182 (42.03%)	143 (43.33%)	155 (45.02%)	209 (45.04%)	126 (38.65%)
AD	10.796	7.093	8.66	8.6	7.88	9.28	6.586
Diameter	6	9	8	8	8	8	8
Density	0.111	0.074	0.087	0.068	0.069	0.094	0.067
Modularity	0.481	0.588	0.447	0.571	0.535	0.462	0.604
ACC	0.514	0.499	0.402	0.407	0.383	0.447	0.45
No. modules	4	8	7	7	6	6	7
APL	2.804	3.418	2.992	3.267	3.063	2.872	3.514
N/P cohesion	66.35%	72.22%	72.51%	76.47%	82.01%	81.96%	61.35%

Note: AD, average degree; ACC, average clustering coefficient; APL, average path length; N/P cohesion, negative and positive connection proportions; No. modules, number of modules.

Table S3. Percent variance explained of the composition of soil bacterial community by each gap-related microenvironmental factor.

Factors	Explains %	Contribution %	pseudo-F	P
AP	6.5	12	3.3	0.014
ATH	4.9	9.1	2.7	0.034
Utot	4.5	8.3	2.6	0.034
LAI	4.8	8.9	2.6	0.05
GapSize	4.2	7.7	2.4	0.084
AK	3.1	5.8	2	0.102
INV	2.8	5.2	1.8	0.154
SOM	3	5.4	1.8	0.158
Udif	2.2	4.1	1.5	0.172
ST	2.6	4.8	1.5	0.178
AN	2.6	4.7	1.6	0.182
PHO	2	3.6	1.3	0.29
Udir	1.6	3	1.1	0.31
ReD	1.7	3.2	1.1	0.342
SW	1.8	3.3	1.2	0.348
CO	1.6	2.9	1	0.376
EC	1.6	3	1.1	0.402

RLA	1.1	2.1	0.7	0.548
ADBH	0.8	1.5	0.5	0.706
URE	0.8	1.4	0.5	0.766

Table S4. Percent variance explained of the diversity and network structure of soil bacterial community by each gap-related microenvironmental factor.

Factors	Explains %	Contribution %	pseudo-F	P
ReD	15.9	22.8	9.1	0.002
GapSize	16.8	24.2	11.7	0.002
LAI	7.6	10.9	5.8	0.008
RLA	4.2	6	3.4	0.012
ATH	3	4.3	2.8	0.044
SW	3.4	4.9	2.9	0.062
ST	2.3	3.3	2.2	0.082
EC	2.6	3.7	2.2	0.084
ADBH	2	2.9	1.8	0.148
AK	1.7	2.4	1.6	0.188
Utot	1.8	2.5	1.7	0.208
CO	1.4	2.1	1.4	0.236
AP	1.3	1.9	1.3	0.268
INV	1.2	1.7	1.2	0.324
SOM	1.1	1.6	1.1	0.336
AN	1	1.4	1	0.372
URE	0.9	1.3	0.9	0.418
PHO	0.7	1	0.7	0.552
Udir	0.5	0.7	0.5	0.658
Udif	0.2	0.3	0.2	0.906

Table S5. The SEM's fitting parameters of forest gaps and closed forests for *L. principis-rupprechtii* Mayr plantations after modification

Statistics		Absolute fit index				Baseline Comparisons			
Fitting Index	χ^2 test(χ^2)	Chi-square/ p -value degree of Freedom(χ^2/df)	Goodness of Fit Index (GFI)	Root Mean Square Error of Approximation (RMSEA)	Normed Fit Index (NFI)	Comparative Fit Index (CFI)	Incremental Fit Index (IFI)	Relative Fit Index (RFI)	Non-normed Fit Index (TLI)
	251.55	3.184	0.946	0.021	0.957	0.985	0.977	0.827	0.915
Fitting standards	The smaller the better	<5	≥ 0.80	<0.08	≥ 0.80	≥ 0.80	≥ 0.80	≥ 0.80	≥ 0.80
Ideal value	The smaller the better	<3	>0.90	<0.05	>0.90	>0.90	>0.90	>0.90	>0.90