SUPPLEMENTARY MATERIAL

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Table S1. PCR components.

Reagent	Negative control	Positive control	Samples
Buffer	4.5 µl	4.5 µl	4.5 µl
MgCl	2.5 µl	2.5 µl	2.5 µl
dNTPs	1.25 µl	1.25 µl	1.25 µl
Primer Fw	2 µl	2 µl	2 µl
Primer Rv	2 µl	2 µl	2 µl
DNA	0 µl	2 µl	2 µl*
Enzima	0.250 µl	0.250 µl	0.250 µl
H_2O	39.5 µl	37.5 µl	37.5 µl

* DNA concentration dilutions: (IS) Initial soil 1:10, (NC) Native consortium 1:20, (EC) Exogenous consortium 1:20, (BNC) Bioaugmentation native consortium final soil 1:10, (BEC) Bioaugmentation exogenous consortium final soil 1:10

Table S2. Normality and homogeneity of variance test*.

		Day 0 (Initial soil)		Day 7		Day 14		Day 21		Day 30	
	Response variable	TPH (mg/kg)	Degrading bacteria (Log10 UFC/g)	TPH (mg/kg)	Degrading bacteria (Log10 UFC/g)	TPH (mg/kg)	Degrading bacteria (Log10 UFC/g)	TPH (mg/kg)	Degrading bacteria (Log10 UFC/g)	TPH (mg/kg)	Degrading bacteria (Log10 UFC/g)
Test	D'Agostino & Pearson (K^2) / Shapiro-Wilk (W)	*W 1.000*	*W 0.9905*	*K^2 1.870*	*K^2 3.242*	*K^2 2.524*	*K^2 4.095*	*K^2 3.956*	*K^2 3.438*	*K^2 3.428*	*K^2 3.500*
		P >0.9999	*P 0.8135*	*P 0.3926*	*P 0.1977*	*P 0.2830*	*P 0.12091*	*P 0.1383*	*P 0.1792*	*P 0.1801*	*P 0.1738*
	Brown-Forsythe (F)	*N/A*	*N/A*	*F 0.8606*	*F 1.621*	*F 2.035*	*F 1.637*	*F 1.300*	*F 2.142*	*F 0.3766*	*F 1.337*
		N/A	*N/A*	*P 0.4998*	*P 0.2598*	*P 0.1876*	*P 0.2564*	*P 0.3394*	*P 0.1730*	*P 0.7725*	*P 0.3289*

*Values of P > 0.05 indicate that data meet the assumptions of normality (D'Agostino–Pearson or Shapiro-Wilk test) and homogeneity of variance (Brown–Forsythe test). α=*0.05*, *N/A*= Not applicable; only one data group was analyzed.

Table S3. Concentration, Purity, and Integrity of DNA Extracts.

	Concentrated DNA			PCR products		
Sample *	**ng/µl**	**A280/A260**	**A260/A230**	**ng/µl**	**A280/A260**	**A260/A230**
IS	219.1	1.55	0.45	65.6	2.30	4.62
NC	62.1	1.86	1.29	59.4	2.19	4.17
EC	24.6	1.81	0.77	52.7	2.55	7.34
NM	95.0	1.71	0.61	44.9	1.84	1.2
BNC	102.5	1.61	0.51	36.6	1.87	0.79
BEC	165.5	1.65	0.57	45.0	1.52	0.57

* IS= Initial soil, NC= Native consortium, EC= Exogenous consortium, NM= Native microbiota final soil, BNC= Bioaugmentation native consortium final soil, BEC= Bioaugmentation exogenous consortium final soil.

Table S4. Relative abundance profile (%) of the 30 predominant bacterial genera in soil samples.

Initial soil (IS)		Native microbiota final soil (NM)		Bioaugmentation native consortium final soil (BNC)		Bioaugmentation exogenous consortium final soil (BEC)	
Nocardioides	36.17	*Pseudomonas*	51.54	*Pseudomonas*	33.93	*Pseudomonas*	29.95
Nocardia	16.03	*Unclassified*	9.38	*Nocardia*	10.02	*Pseudoxanthomonas*	20.27
Streptomyces	13.34	*Sphingobium*	5.98	*Sphingobium*	6.52	*Dietzia*	12.22
Rhodococcus	4.35	*Nocardia*	4.69	*Sedimentibacter*	5.46	*Ramlibacter*	4.93
Pseudomonas	3.13	*Coprococcus*	3.35	*Pseudoxanthomonas*	5.27	*Gordonia*	4.76
Arthrobacter	2.61	*Caloramator*	2.52	*Unclassified*	4.41	*Chryseoglobus*	4.47
Limnobacter	2.26	*Parapedobacter*	2.50	*Pusillimonas*	3.40	*Rhodococcus*	3.65
Sphingomonas	2.10	*Anaerovorax*	1.76	*Achromobacter*	3.40	*Sphingobium*	2.60
Bacillus	1.78	*Achromobacter*	1.28	*Rhodococcus*	2.61	*Achromobacter*	1.92
Metabacillus	1.74	*Sphingomonadaceae Group*	1.26	*Bdellovibrio*	2.10	*Iamia*	1.54
Lysobacter	1.58	*Sedimentibacter*	1.20	*Paracoccus*	1.89	*Paracoccus*	1.53
Peribacillus	1.35	*Phenylobacterium*	1.17	*Parapedobacter*	1.67	*Caloramator*	1.23
Neobacillus	1.07	*Pseudoxanthomonas*	1.01	*Xanthomonas*	1.60	*Phenylobacterium*	1.16
Marmoricola	0.67	*Parapusillimonas*	0.95	*Alkanindiges*	1.31	*Unclassified*	0.91
Aeromicrobium	0.59	*Rhodococcus*	0.70	*Sphingomonadaceae Group*	1.22	*Bacillus*	0.82
Priestia	0.51	*Gracilibacteraceae Group*	0.61	*Bacillus*	1.11	*Xanthomonas*	0.79
Hyphomicrobium	0.51	*Bdellovibrio*	0.53	*Anaerovorax*	1.03	*Mycobacterium*	0.76
Microvirga	0.44	*Sphingopyxis*	0.48	*Phenylobacterium*	0.97	*Sphingomonadaceae_ Group*	0.59
Fictibacillus	0.40	*Paracoccus*	0.41	*Puniceicoccaceae Group*	0.64	*Nocardia*	0.51
Lentzea	0.40	*Bacillus*	0.41	*Ramlibacter*	0.63	*Proteiniclasticum*	0.42
Mycolicibacterium	0.40	*Nocardioides*	0.38	*Gordonia*	0.59	*Rhodobacter*	0.32
Agromyces	0.28	*Caldicoprobacter*	0.37	*Corynebacteriaceae_Group*	0.56	*Sphingosinicella*	0.30
Nitrosospira	0.28	*Altererythrobacter*	0.32	*Microbacterium*	0.51	*Georgenia*	0.27
Sphingosinicella	0.24	*Xanthomonas*	0.32	*Parapusillimonas*	0.49	*Sphingopyxis*	0.25
Hydrogenophaga	0.24	*Lutispora*	0.32	*Luteimonas*	0.47	*Methyloversatilis*	0.22
Kribbella	0.24	*Devosia*	0.31	*Ellin6075 Group*	0.42	*Microbacterium*	0.18
Afipia	0.24	*Luteimonas*	0.31	*Rhodanobacter*	0.30	*Agrobacterium*	0.14
Pseudoxanthomonas	0.20	*Arenimonas*	0.27	*Devosia*	0.27	*Nocardioides*	0.13
Mycobacteroides	0.20	*Dietzia*	0.24	*Luteolibacter*	0.27	*Devosia*	0.12
Frankia	0.20	*Bradyrhizobiaceae Group*	0.23	*Methylophilaceae Group*	0.25	*Parachlamydia*	0.12

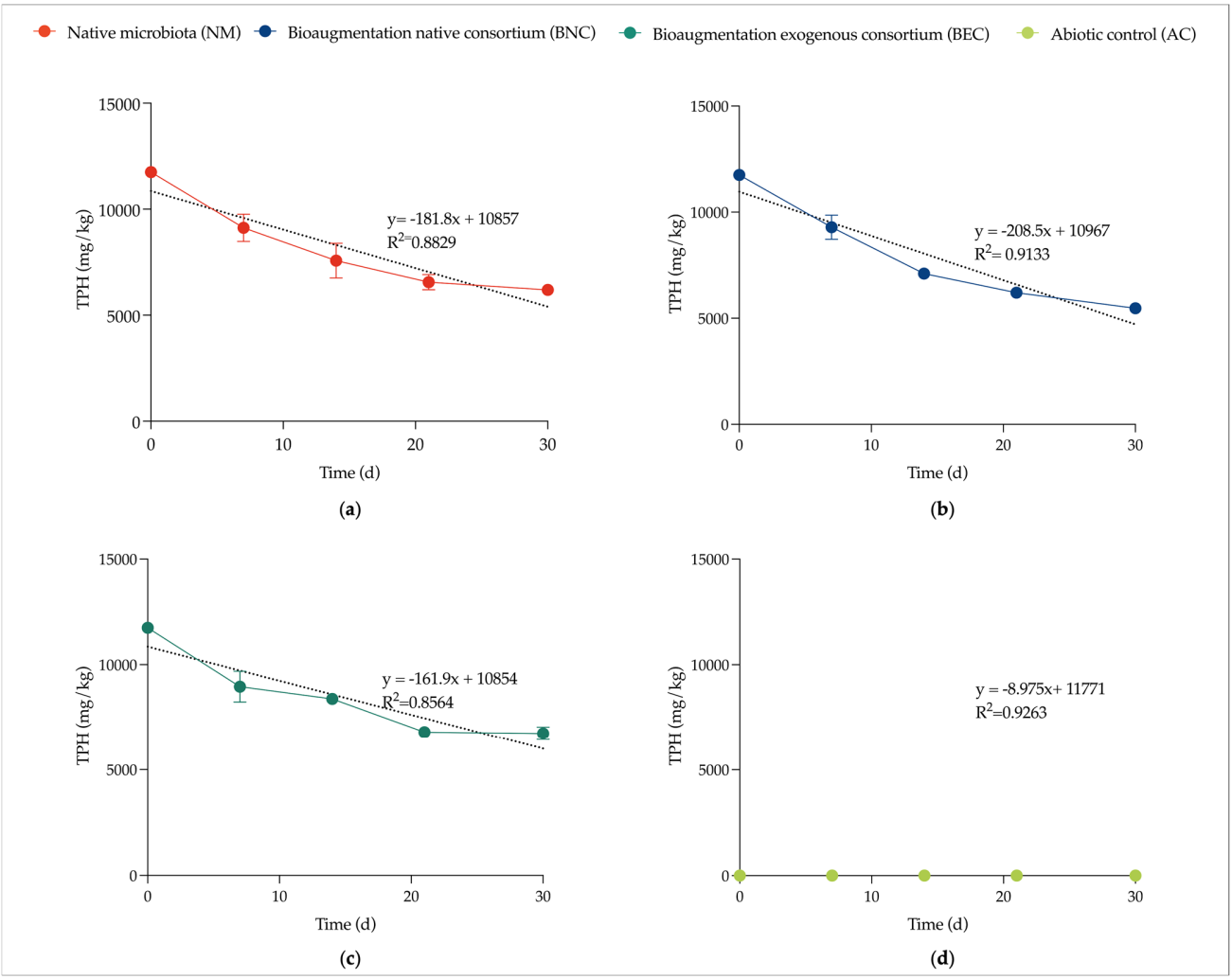


Figure S1. Biodegradation rate prediction. (**a**) Native microbiota (NM), (**b**) Bioaugmentation native consortium (BNC), (**c**) Bioaugmentation exogenous consortium, (**d**) Abiotic control (AC).

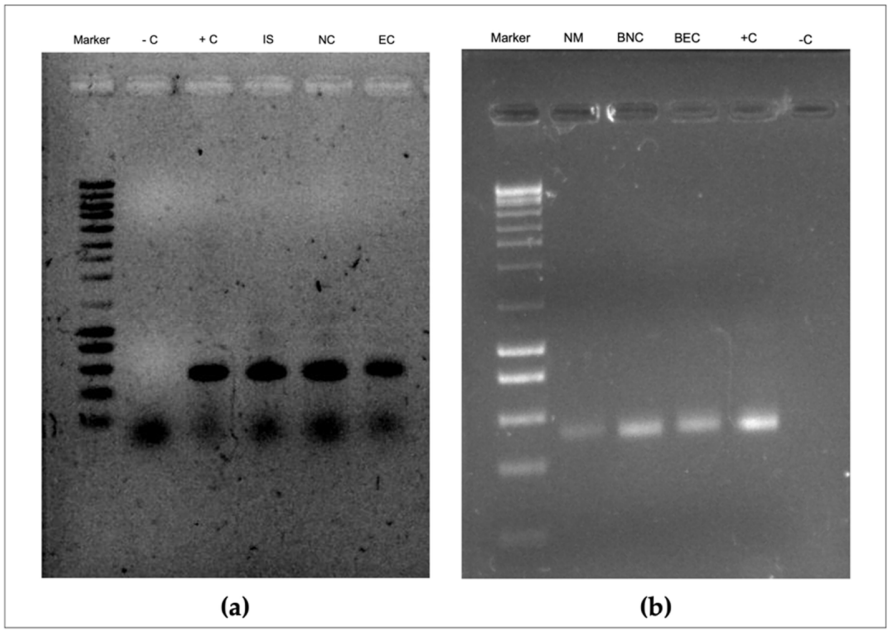


Figure S2. Integrity analysis of PCR amplicons. (**a**) IS= Initial soil, NC= Native consortium, EC= Exogenous consortium, (**b**) NM= Native microbiota final soil, BNC= Bioaugmentation native consortium final soil, BEC= Bioaugmentation exogenous consortium final soil. +C= positive control, -C= negative control

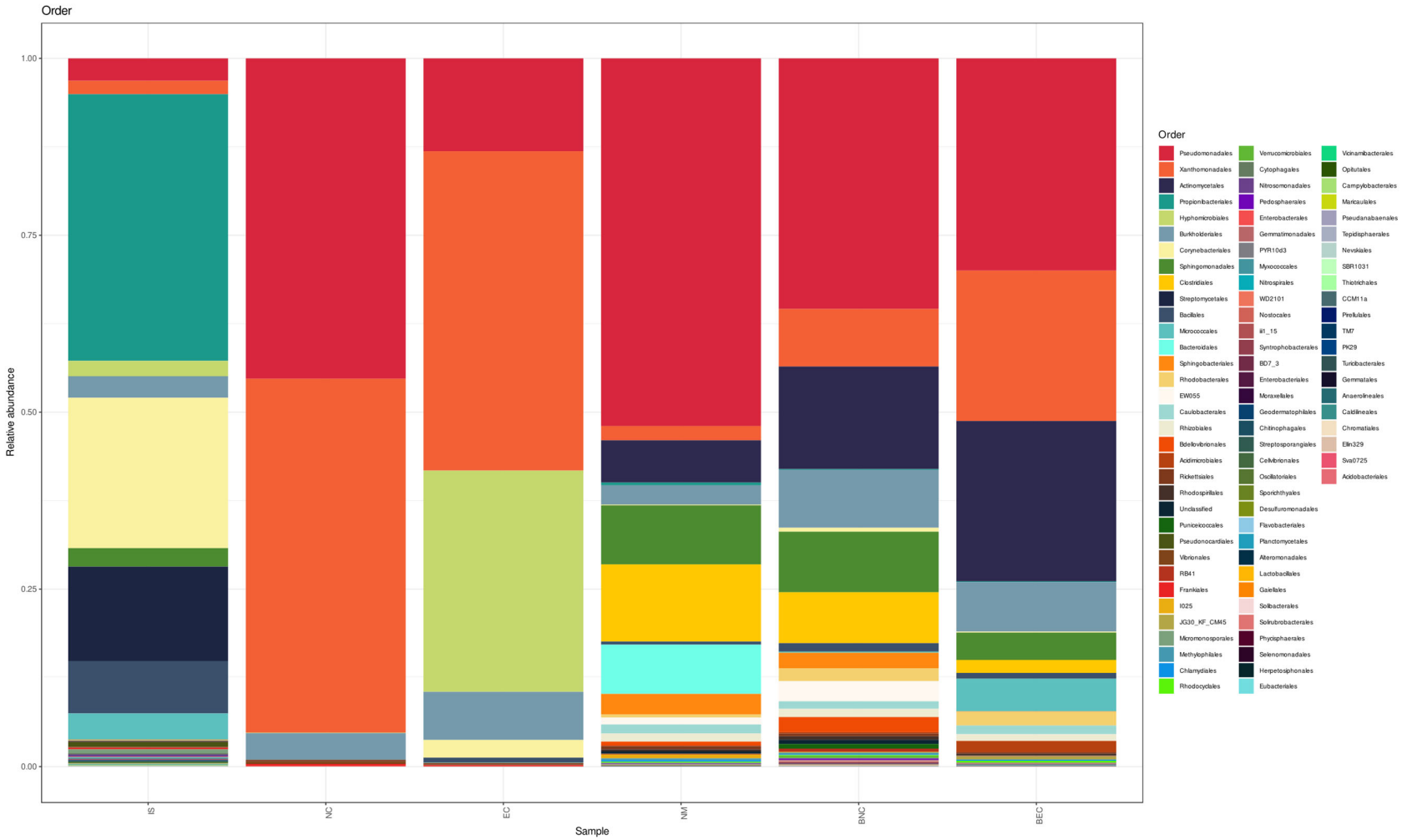


Figure S3. Relative abundance of bacterial taxa at the Order level. The initial soil contained 42 bacterial orders, predominantly *Propionibacteriales* (37.67%) and *Corynebacteriales* (21.25%). The native consortium reduced diversity to 14 orders, mainly *Xanthomonadales* (50.01%) and *Pseudomonadales* (47.27%), while the exogenous consortium showed 17 orders with *Xanthomonadales* (45.13%) and *Hyphomicrobiales* (31.36%) prevailing. Bioremediation with the native microbiota resulted in 49 groups, dominated by *Pseudomonadales* (51.95%), whereas bioaugmentation with the native consortium increased diversity to 60 orders, primarily *Pseudomonadales* (35.42%) and *Actinomycetales* (14.49%). The exogenous consortium-treated soil showed 49 groups with a similar profile, including *Pseudomonadales* (29.99%) and *Actinomycetales* (22.66%).

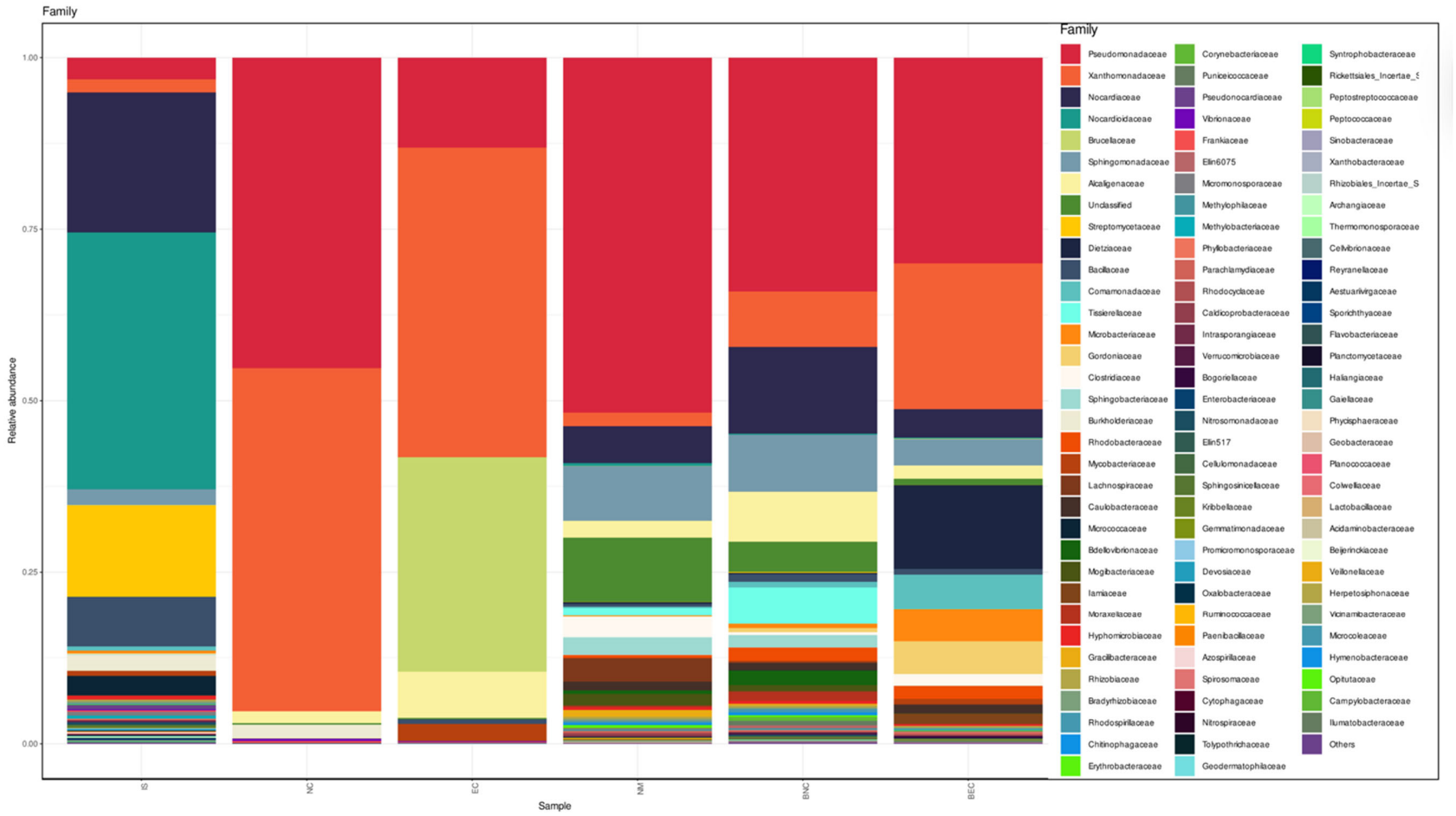


Figure S4. Relative abundance of bacterial taxa at the Family level. The initial soil contained 66 families, mainly *Nocardioidaceae* (37.44%) and *Nocardiaceae* (20.42%). The native consortium comprised 17 families, dominated by *Xanthomonadaceae* (50.01%) and *Pseudomonadaceae* (45.27%), while the exogenous consortium showed a similar structure with *Xanthomonadaceae* (45.13%) and *Brucellaceae* (31.31%). Bioremediated soils exhibited higher diversity (84–96 families), with *Pseudomonadaceae* as the dominant group in all treatments.