

SUPPLEMENTARY MATERIALS

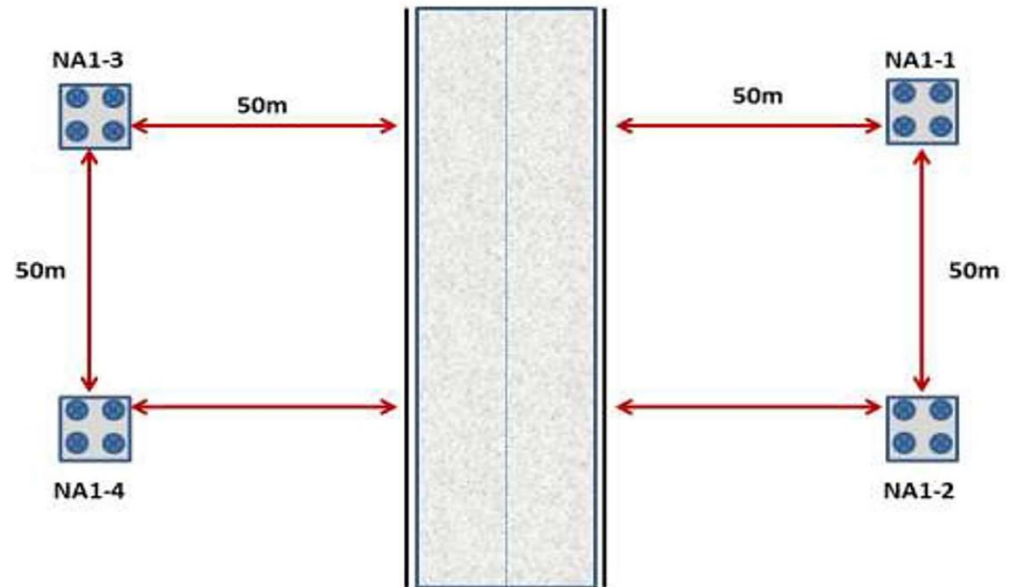


Figure S1. Covering area of each sampling site and its corresponding features (not to scale). Each sampling site was represented by an area of approximately. 100 m × 50 m with four independent sample locations (a virtual 1 m² quadrant) at the corners of the oblong. It is crossed in its length by a road of ca. 6 m wide. At each of the four independent sample locations, four topsoil cores (2 cm in diameter and 5 cm in depth) (pseudo-replicate samples) were collected, pooled together, and homogenized into a composite sample of approximately 25 g (replicate sample). Four independent replicate samples (4 × 25 g) obtained from four sample locations at each sampling site were kept in a labeled sterile plastic bag and formed an independent soil sample (Taken from Gnangui et al., 2021 [1]).

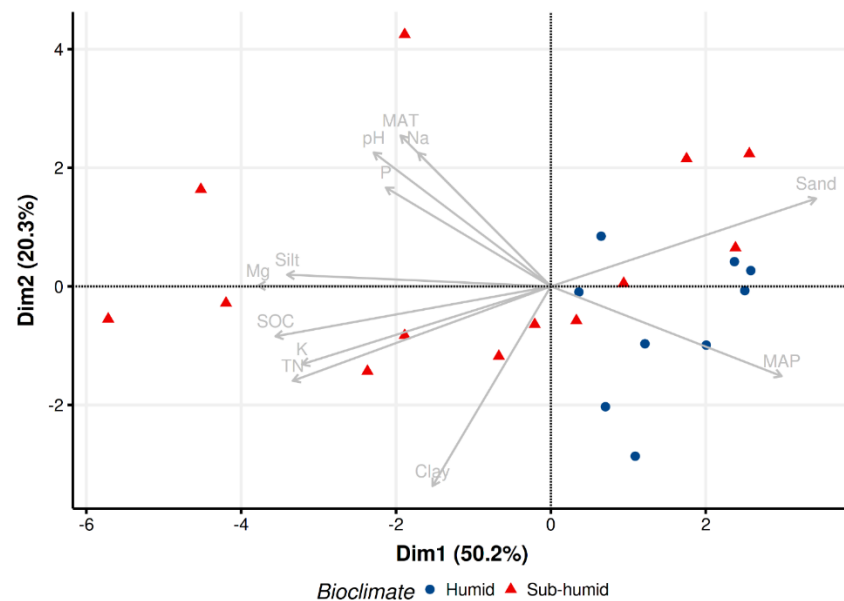


Figure S2. Principal component analysis of the environmental data. Sampled sites are colored according to bioclimates.

Table S1. Average ASV abundance and occurrence per phylum.

Phylum	Average ASV Percentage (%)	Occurrence (%)
Proteobacteria	29.76	100
Acidobacteria	15.45	100
Actinobacteria	14.18	100
Bacteroidetes	9.29	100
Planctomycetes	8.42	100
Chloroflexi	6.47	100
Verrucomicrobia	5.11	100
candidate division WPS-1	2.59	100
Firmicutes	2.52	100
Thaumarchaeota	1.93	100
Gemmatimonadetes	1.05	100
Armatimonadetes	0.6	100
Cyanobacteria/Chloroplast	0.45	95.45
Latescibacteria	0.43	100
Pacearchaeota	0.34	50
candidate division WPS-2	0.31	77.27
Nitrospirae	0.29	100
Chlamydiae	0.19	63.63
Ignavibacteriae	0.18	72.72
Euryarchaeota	0.16	63.63
Crenarchaeota	0.14	4.54
Diapherotrites	0.14	4.54
Elusimicrobia	0.13	72.72
Synergistetes	0.13	86.36
Parcubacteria	0.12	22.72
Thermodesulfobacteria	0.12	63.63
Aquificae	0.11	54.54
Woesearchaeota	0.11	31.81
Deinococcus-Thermus	0.1	72.72
Acetothermia	0.09	27.27
BRC1	0.09	31.81
Candidatus Saccharibacteria	0.09	13.63
Chlorobi	0.08	9.09
Microgenomates	0.08	31.81
Omnitrophica	0.08	54.54
Aenigmarchaeota	0.07	9.09
Chrysiogenetes	0.07	50
Deferribacteres	0.07	4.54
Hydrogenedentes	0.07	18.18
Spirochaetes	0.07	18.18
Thermotogae	0.07	9.09
candidate division ZB3	0.07	9.09
Cloacimonetes	0.06	4.54

Table S2. Total variation of microbial phylum explained by physicochemical properties and climatic variables.

Phylum	SOC	TN	Mg	Clay	MAT	pH	K	Na	MAP	Silt	P	Residuals
Actinobacteria	0.066	0.268	0.032	0.183	0.0008	1.87E-05	0.011	0.00074	0.005	0.00033	0.053	0.378
Acidobacteria	0.082	0.057	0.294	0.00027	0.0015	0.029	0.004	0.00073	0.002	0.016	0.0061	0.505
Proteobacteria	0.0001	0.126	0.271	0.01	0.01	0.02	0.016	0.0071	0.023	0.0017	0.0137	0.497
Bacteroidetes	0.122	0.080	0.0179	0.047	0.078	0.00016	0.136	0.00089	0.0017	0.0023	0.0014	0.510
Firmicutes	0.038	0.001	0.062	0.090	0.002	0.0215	0.102	0.062	0.00018	0.017	0.00021	0.599
Planctomycetes	0.143	0.213	0.063	0.0033	0.109	0.0234	0.0015	0.0068	0.014	0.0016	0.0012	0.417
candidate division WPS-1	0.270	0.268	0.0083	0.057	0.034	3.59E-05	0.0012	0.00059	0.0042	0.00019	0.023	0.331
Nitrospirae	0.156	0.025	0.129	0.034	0.013	0.053	0.019	0.042	0.005	0.035	7.04E-05	0.483
Chloroflexi	0.154	0.133	0.021	0.0034	0.111	0.0014	0.0016	0.0047	2.27E-05	0.014	0.0019	0.55
Verrucomicrobia	0.051	0.329	0.165	0.062	0.006	0.011	0.0019	0.0015	0.0093	0.002	0.00074	0.357
Thaumarchaeota	0.012	0.030	0.049	0.067	0.095	0.056	0.022	0.010	0.00033	0.107	0.043	0.503
Cyanobacteria/Chloroplast	0.156	0.111	0.010	0.039	0.112	0.019	0.0015	0.024	0.023	0.005	0.0163	0.478
candidate division WPS-2	0.118	0.042	0.007	0.129	0.092	0.055	0.098	0.04	0.015	0.003	0.001	0.394

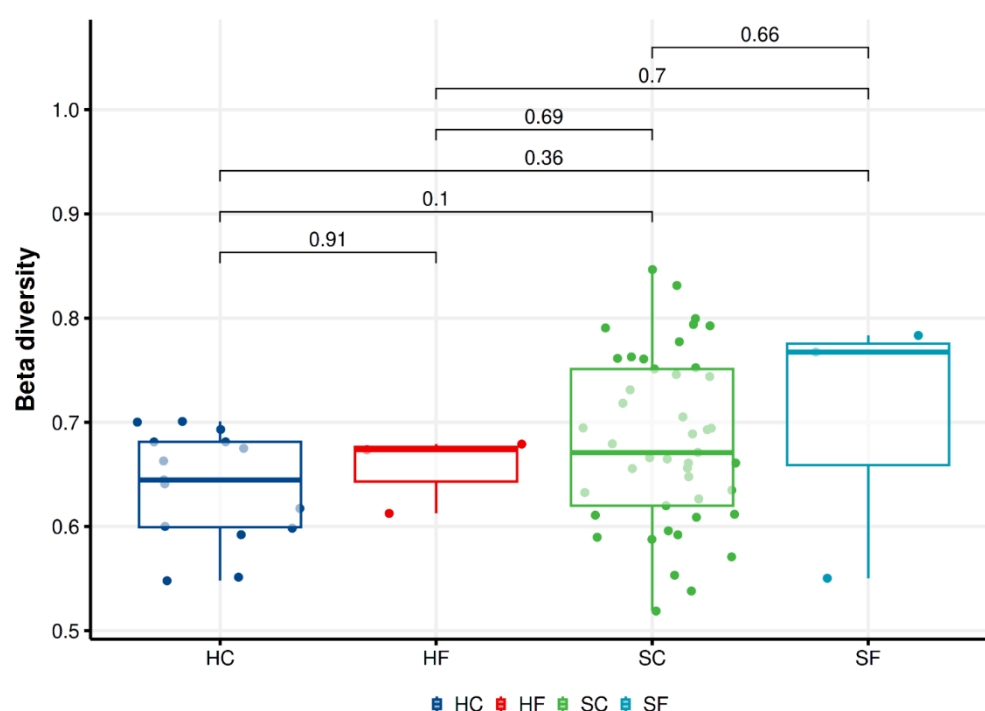


Figure S3. Beta diversity per soil type with multiple pairwise comparisons. Soil types are HC: Humid and cropland, HF: Humid and forest land, SC: Sub-humid and cropland and SF: sub-humid and forest land.

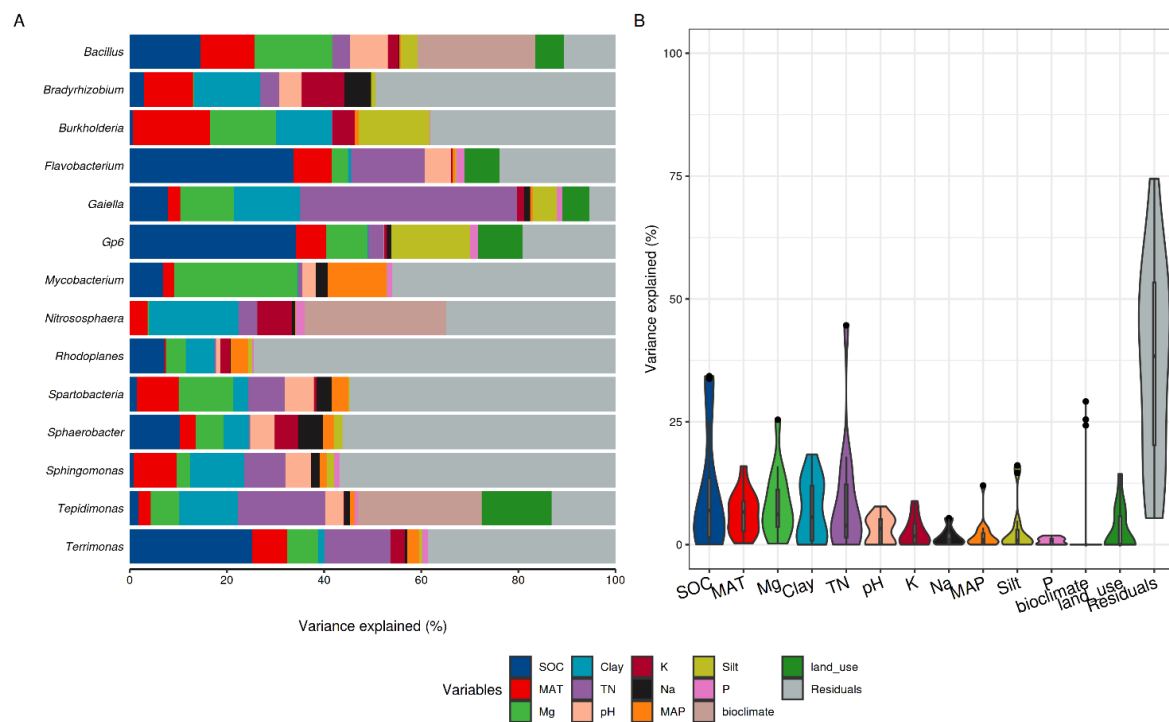


Figure S4. Variance partitioning of core genus across forest soil ecosystem. **(A)** Total variance for each genus is partitioned into the fraction due to environmental properties. **(B)** Violin and box plot of percent variation in genus diversity explained by each variable.

References

1. Gnangui, S.L.E.; Fossou, R.K.; Ebou, A.; Amon, C.E.R.; Koua, D.K.; Kouadjo, C.G.Z.; Cowan, D.A.; Zézé, A. The Rhizobial Microbiome from the Tropical Savannah Zones in Northern Côte d'Ivoire. *Microorganisms* **2021**, *9*, 1842. <https://doi.org/10.3390/microorganisms9091842>.