

## Supplementary Files

**Supplementary Table S1.** Statistics of raw data of Miombo soil samples collected from the rhizosphere of *Brachystegia spiciformis* (SBSP) and *Brachystegia boehmii* (SBBP).

Samples	Total Bases	Read Count	GC (%)	Q20 (%)	Q30 (%)
SBBP001	99.655.142	219.839	57.58	97.38	90.62
SBBP002	107.734.810	236.512	57.64	97.25	90.25
SBBP003	99.443.763	218.438	57.78	97.35	90.42
SBBP006	99.102.894	217.796	57.43	97.33	90.49
SBBP007	89.702.471	197.247	57.16	97.53	90.83
SBBP008	87.016.503	191.400	57.54	97.48	90.80
SBBP011	95.090.206	208.870	56.93	97.54	91.15
SBBP012	92.241.797	205.388	57.56	97.57	91.10
SBBP013	100.966.144	222.433	57.36	97.5	90.91
SBBP016	89.591.127	197.165	57.17	97.39	90.60
SBBP017	97.890.593	215.237	57.54	97.52	90.93
SBBP018	97.160.430	213.993	57.9	97.43	90.61
SBSP001	91.306.056	200.782	57.24	97.55	91.02
SBSP002	94.859.771	208.460	56.95	97.45	90.76
SBSP003	97.966.413	215.555	57.83	97.47	90.77
SBSP006	103.437.817	227.661	57.33	97.49	90.91
SBSP007	96.179.736	211.279	57.68	97.36	90.56
SBSP008	93.502.194	206.270	57.32	97.22	90.13
SBSP011	100.986.457	223.419	57.26	97.63	91.13
SBSP012	90.737.076	200.357	57.19	97.39	90.65
SBSP013	90.806.816	200.893	55.26	97.65	91.40
SBSP016	90.748.702	200.082	57.42	97.48	90.83
SBSP017	97.147.660	216.018	56.96	97.61	91.33
SBSP018	104.186.032	229.401	57.75	97.47	90.89

**Supplementary Table S2.** ANOVA results showing bacterial differences at the phylum level between the two plant species, the type of soil type and the fire frequency (SS: Sum of Squares; df: degrees of freedom). Significant values are indicated in bold.

<b>Phylum</b>	<b>Factor</b>	<b>df</b>	<b>SS</b>	<b>F value</b>	<b>P</b>
<i>Acidobacteria</i>	Species	1	3953628	4.16	0.0536
	Soil Type	1	6370	0.01	0.9410
	Fire Frequency	1	27540	0.02	0.8770
<i>Actinobacteria</i>	Species	1	4105228	1.73	0.2020
	Soil Type	1	6692928	2.97	0.0989
	Fire Frequency	1	214326	0.08	0.7750
<i>Bacteroidetes</i>	Species	1	477	0.01	0.9130
	Soil Type	1	457332	25.02	<b>0.0001</b>
	Fire Frequency	1	9243	0.24	0.6300
<i>Chloroflexi</i>	Species	1	26600	1.04	0.3180
	Soil Type	1	158275	8.10	<b>0.0094</b>
	Fire Frequency	1	72051	3.07	0.0936
<i>Firmicutes</i>	Species	1	196928	0.01	0.9170
	Soil Type	1	58693793	3.91	<b>0.0307</b>
	Fire Frequency	1	49749122	3.23	0.0862
<i>Proteobacteria</i>	Species	1	1992384	4.85	<b>0.0384</b>
	Soil Type	1	11660	0.02	0.8800
	Fire Frequency	1	1920438	4.64	<b>0.0424</b>
<i>Verrucomicrobia</i>	Species	1	1034180	1.24	0.2780
	Soil Type	1	94753	0.11	0.7460
	Fire Frequency	1	4072208	5.83	<b>0.0245</b>

**Supplementary Table S3.** Relative abundance of bacterial classes in the rhizosphere of *Brachystegia spiciformis* and *Brachystegia boehmii* sampled in cambic arenosol and ferric lixisol soils with low and high fire frequencies.

Phylum	Class	<i>B. spiciformis</i>		<i>B. boehmii</i>						Average
		Cambic arenosol soils		Ferric lixisol soils		Cambic arenosol soils		Ferric lixisol soils		
		High Fire	Low Fire	High Fire	Low Fire	High Fire	Low Fire	High Fire	Low Fire	
Acidobacteria	<i>Blastocatellia</i>	8.92%	8.37%	7.27%	3.97%	11.23%	10.26%	6.86%	3.54%	7.55 ± 0.03%
Acidobacteria	<i>Vicinamibacteria</i>	5.22%	4.13%	3.86%	2.03%	5.01%	4.25%	3.61%	1.46%	3.70 ± 0.16%
Actinobacteria	<i>Acidimicrobiia</i>	3.10%	1.96%	2.29%	1.43%	2.46%	2.25%	2.34%	1.57%	2.18 ± 0.01%
Actinobacteria	<i>Actinobacteria</i>	19.64%	18.44%	18.13%	22.28%	16.29%	18.94%	17.11%	18.58%	18.68 ± 0.06%
Actinobacteria	<i>Rubrobacteria</i>	11.19%	11.01%	9.27%	6.28%	9.42%	10.19%	7.40%	4.52%	8.66 ± 0.03%
Actinobacteria	<i>Thermoleophilia</i>	8.77%	6.12%	7.13%	4.47%	6.56%	5.68%	6.06%	2.39%	5.90 ± 0.03%
Bacteroidetes	<i>Chitinophagia</i>	1.92%	1.94%	0.89%	0.78%	2.32%	1.93%	1.25%	0.63%	1.46 ± 0.01%
Bacteroidetes	<i>Cytophagia</i>	0.54%	0.06%	0.05%	0.03%	0.17%	0.09%	0.09%	0.03%	0.13 ± 0.01%
Chloroflexi	<i>Dehalococcoidia</i>	1.76%	1.00%	1.62%	0.60%	1.28%	1.23%	1.26%	0.40%	1.14 ± 0.01%
Firmicutes	<i>Bacilli</i>	1.42%	8.96%	12.39%	22.93%	2.21%	4.53%	5.25%	25.73%	10.43 ± 0.14%
Firmicutes	<i>Clostridia</i>	0.82%	0.34%	0.44%	0.26%	0.61%	0.33%	0.47%	0.25%	0.44 ± 0.01%
Nitrospirae	<i>Nitrospira</i>	0.28%	0.17%	0.15%	0.08%	0.51%	0.29%	0.14%	0.06%	0.21 ± 0.01%
Proteobacteria	<i>Alphaproteobacteria</i>	11.43%	10.42%	13.40%	9.39%	13.85%	12.22%	17.18%	10.48%	12.30 ± 0.03%
Proteobacteria	<i>Betaproteobacteria</i>	2.55%	2.10%	1.91%	1.87%	2.49%	2.12%	2.37%	2.39%	2.23 ± 0.01%
Proteobacteria	<i>Deltaproteobacteria</i>	3.26%	1.73%	2.54%	1.18%	2.13%	1.97%	1.81%	1.29%	1.99 ± 0.01%
Proteobacteria	<i>Gammaproteobacteria</i>	1.28%	0.74%	0.78%	0.28%	1.63%	1.10%	0.86%	0.45%	0.89 ± 0.01%
Verrucomicrobia	<i>Verrucomicrobiae</i>	1.57%	1.33%	1.50%	1.18%	1.51%	1.24%	1.65%	1.40%	1.42 ± 0.01%
Others	Others	16.34%	21.19%	16.36%	20.97%	20.32%	21.39%	24.29%	24.81%	20.71 ± 0.07%

**Supplementary Table S4.** Relative abundance of the most frequent bacterial genus (>1% across all samples) in the rhizosphere of *Brachystegia spiciformis* and *Brachystegia boehmii* sampled in cambic arenosol and ferric lixisol soils with low and high fire frequencies.

Phylum	Genus	<i>B. spiciformis</i>		<i>B. boehmii</i>		Average				
		Cambic arenosol soils		Ferric lixisol soils		Cambic arenosol soils		Ferric lixisol soils		
		High Fire	Low Fire	High Fire	Low Fire	High Fire	Low Fire	High Fire	Low Fire	
Actinobacteria	<i>Streptomyces</i>	3.25%	6.80%	5.90%	15.23%	5.86%	6.67%	4.93%	11.92%	7.57 ± 0.06%
Actinobacteria	<i>Gaiella</i>	8.79%	9.68%	8.55%	6.02%	7.41%	8.21%	6.86%	4.28%	7.48 ± 0.03%
Verrucomicrobia	<i>Chthoniobacter</i>	3.52%	9.66%	5.75%	5.33%	6.95%	8.83%	3.69%	9.28%	6.63 ± 0.04%
Firmicutes	<i>Bacillus</i>	1.08%	8.23%	12.28%	10.93%	2.10%	3.62%	3.77%	8.74%	6.34 ± 0.07%
Acidobacteria	<i>Brevitalea</i>	6.68%	6.21%	5.63%	2.87%	8.36%	7.17%	5.29%	2.52%	5.59 ± 0.03%
Proteobacteria	<i>Rhodoplanes</i>	4.11%	4.63%	6.38%	4.05%	5.16%	4.98%	6.97%	4.00%	5.04 ± 0.02%
Actinobacteria	<i>Solirubrobacter</i>	7.12%	4.03%	4.13%	2.55%	4.92%	4.01%	3.35%	1.37%	3.93 ± 0.02%
Firmicutes	<i>Lactobacillus</i>	0.00%	0.64%	0.00%	11.76%	0.00%	0.80%	1.23%	16.92%	3.92 ± 0.12%
Acidobacteria	<i>Vicinamibacter</i>	4.70%	3.99%	3.65%	1.97%	4.44%	3.85%	3.39%	1.40%	3.42 ± 0.01%
Acidobacteria	<i>Acidobacterium</i>	0.19%	0.71%	1.01%	6.58%	0.59%	1.11%	6.83%	7.21%	3.03 ± 0.05%
Actinobacteria	<i>Aciditerrimonas</i>	2.02%	1.47%	1.65%	1.05%	1.61%	1.50%	1.44%	1.26%	1.50 ± 0.01%
Verrucomicrobia	<i>Limisphaera</i>	1.56%	1.33%	1.49%	1.17%	1.50%	1.24%	1.64%	1.40%	1.42 ± 0.01%
Actinobacteria	<i>Saccharopolyspora</i>	1.52%	1.51%	4.26%	0.34%	0.15%	1.84%	1.52%	0.16%	1.41 ± 0.03%
Proteobacteria	<i>Bradyrhizobium</i>	0.82%	1.17%	1.64%	1.03%	0.98%	1.15%	2.49%	1.85%	1.39 ± 0.01%
Acidobacteria	<i>Paludibaculum</i>	0.82%	1.14%	1.02%	1.48%	1.30%	1.24%	2.37%	1.63%	1.38 ± 0.01%
Acidobacteria	<i>Arenimicrobium</i>	1.33%	1.23%	0.90%	0.66%	1.86%	2.18%	0.90%	0.57%	1.20 ± 0.01%
Actinobacteria	<i>Rubrobacter</i>	2.39%	1.34%	0.72%	0.26%	2.00%	1.98%	0.54%	0.25%	1.18 ± 0.02%
Planctomycetes	<i>Tepidisphaera</i>	0.91%	1.10%	1.13%	1.13%	1.22%	1.13%	1.63%	0.96%	1.15 ± 0.01%
Chloroflexi	<i>Dehalogenimonas</i>	1.76%	1.00%	1.62%	0.60%	1.28%	1.23%	1.26%	0.40%	1.14 ± 0.01%
Actinobacteria	<i>Micromonospora</i>	2.73%	1.15%	0.50%	0.48%	1.23%	1.41%	0.77%	0.30%	1.07 ± 0.01%

**Supplementary Table S5.** Topological properties of the empirical networks and their 100 corresponding random networks.

Network Indexes		High fire frequency			Low fire frequency		
		Empirical Network	100 Networks	Random	Empirical Network	100 Networks	Random
1.	Average clustering coefficient (avgCC)	0.167	0.027 +/- 0.008		0.378	0.259 +/- 0.016	
2.	Average path distance (GD)	6.042	3.927 +/- 0.084		3.033	2.509 +/- 0.027	
3.	Geodesic efficiency (E)	0.241	0.294 +/- 0.005		0.407	0.447 +/- 0.003	
4.	Harmonic geodesic distance (HD)	4.149	3.408 +/- 0.056		2.456	2.239 +/- 0.016	
5.	Centralization of degree (CD)	0.073	0.073 +/- 0.000		0.222	0.222 +/- 0.000	
6.	Centralization of betweenness (CB)	0.174	0.125 +/- 0.021		0.057	0.063 +/- 0.010	
7.	Centralization of stress centrality (CS)	0.775	0.331 +/- 0.055		1.383	0.404 +/- 0.044	
8.	Centralization of eigenvector centrality (CE)	0.319	0.262 +/- 0.034		0.172	0.156 +/- 0.007	
9.	Density (D)	0.021	0.021 +/- 0.000		0.07	0.070 +/- 0.000	
10.	Reciprocity	1	1.000 +/- 0.000		1	1.000 +/- 0.000	
11.	Transitivity (Trans)	0.249	0.046 +/- 0.009		0.481	0.296 +/- 0.007	
12.	Connectedness (Con)	0.559	0.879 +/- 0.044		0.787	0.978 +/- 0.019	
13.	Efficiency	0.972	0.983 +/- 0.001		0.917	0.934 +/- 0.001	
14.	Hierarchy	0	0.000 +/- 0.000		0	0.000 +/- 0.000	
15.	Lubness	1	1.000 +/- 0.000		1	1.000 +/- 0.000	
16.	Modularity (fast_greedy)	0.701	0.533 +/- 0.010		0.312	0.186 +/- 0.005	

**Supplementary Table S6.** Top pathways detected by Picrust in samples.

Pathways	Description	<i>B. spiciformis</i>				<i>B. boehmii</i>			
		Cambic arenosol soils		Ferric lixisol soils		Cambic arenosol soils		Ferric lixisol soils	
		High Fire	Low Fire	High Fire	Low Fire	High Fire	Low Fire	High Fire	Low Fire
PWY-3781	aerobic respiration I (cytochrome c)	58602.15	64611.06	56699.90	53909.96	59113.76	60482.69	59567.91	60546.25
PWY-7111	pyruvate fermentation to isobutanol (engineered)	32710.61	36439.80	33030.12	29908.47	32758.97	34490.05	36597.58	37522.41
PWY-5101	L-isoleucine biosynthesis II	32555.50	35190.35	31132.74	28234.22	32439.40	33301.03	34087.91	33764.92
ILEUSYN-PWY	L-isoleucine biosynthesis I (from threonine)	31790.04	34252.84	30601.62	27728.31	31737.33	32579.77	33655.77	33424.84
VALSYN-PWY	L-valine biosynthesis	31790.04	34252.84	30601.62	27728.31	31737.33	32579.77	33655.77	33424.84
BRANCHED-CHAIN-AA-SYN-PWY	superpathway of branched amino acid biosynthesis	28378.56	30661.49	26561.04	24508.79	27993.13	28712.49	28646.35	28234.90
PWY-7094	fatty acid salvage	26958.94	28244.93	25796.09	22907.30	25202.69	26340.63	25911.64	23527.52
PWY-5103	L-isoleucine biosynthesis III	24845.76	27060.88	23408.65	21481.84	24551.31	25254.78	25246.44	24520.10
FAO-PWY	fatty acid & beta;-oxidation I	24698.92	25695.89	22947.81	20779.39	23066.12	23874.31	23342.87	21062.27
NONOXIPENT-PWY	pentose phosphate pathway (non-oxidative branch)	24206.93	28166.22	24729.15	23730.95	23539.17	25621.48	25428.78	35541.26
PWY-5659	GDP-mannose biosynthesis	24185.10	25443.23	20752.9	19683.13	23198.65	23988.39	22224.85	23536.73
PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)	23792.52	26465.20	22889.71	21685.75	23499.39	24389.29	23696.58	24556.61
PHOSLIPSYN-PWY	superpathway of phospholipid biosynthesis I (bacteria)	23544.00	26394.53	22312.38	24499.81	23465.79	24564.79	23814.10	29312.41
TCA	TCA cycle I (prokaryotic)	23226.82	25959.17	22286.46	21043.14	23197.26	24040.80	23398.31	24227.29
PWY-5667	CDP-diacylglycerol biosynthesis I	22617.98	25542.52	22021.82	24687.28	22553.45	23673.38	23076.87	29538.37
PWY0-1319	CDP-diacylglycerol biosynthesis II	22617.98	25542.52	22021.82	24687.28	22553.45	23673.38	23076.87	29538.37
PWY-5973	cis-vaccenate biosynthesis	22465.22	26724.38	23365.76	22062.35	23982.11	25185.5	27007.31	35597.42
PWY-3001	superpathway of L-isoleucine biosynthesis I	22296.69	24791.85	21428.10	20633.58	22099.68	23012.00	22762.92	25642.24
PWY4FS-7	phosphatidylglycerol biosynthesis I (plastidic)	22252.02	24998.96	21126.66	23228.22	22212.53	23249.64	22612.1	27893.92
PWY4FS-8	phosphatidylglycerol biosynthesis II (non-plastidic)	22252.02	24998.96	21126.66	23228.22	22212.53	23249.64	22612.1	27893.92
PWY-7229	superpathway of adenosine nucleotides de novo biosynthesis I	22134.79	24281.99	20826.73	22928.53	21681.83	22537.95	22183.68	27978.90
P108-PWY	pyruvate fermentation to propanoate I	22056.68	23320.47	20906.46	19388.80	21097.45	21630.76	21317.90	20454.15
PWY-7208	superpathway of pyrimidine nucleobases salvage	21965.95	24562.50	20587.70	23142.17	21658.05	22666.09	21838.74	28840.44

PWY-7219	adenosine ribonucleotides de novo biosynthesis	21893.84	23851.91	20165.14	22160.19	21377.88	22230.63	21837.58	26947.98
PWY-6126	superpathway of adenosine nucleotides de novo biosynthesis II	21343.28	23274.7	20029.46	22050.70	20846.94	21594.37	21354.12	26892.63
FASYN-ELONG-PWY	fatty acid elongation -- saturated	21274.89	25490.21	22585.78	21216.20	22422.71	23783.31	25547.81	33766.38
PWY-7663	gondoate biosynthesis (anaerobic)	21274.89	25705.11	22585.78	21233.71	22823.29	24039.18	26288.48	37512.10
PWY-5686	UMP biosynthesis	21184.50	23437.28	19922.45	21679.00	20905.74	21828.79	21561.96	26931.00
PWY0-162	superpathway of pyrimidine ribonucleotides de novo biosynthesis	21168.30	23147.11	19818.04	21651.00	20749.02	21521.31	21365.61	26708.33
PWY-2942	L-lysine biosynthesis III	20985.95	23959.73	20664.38	22889.49	20975.74	22050.49	22113.63	30436.84

---

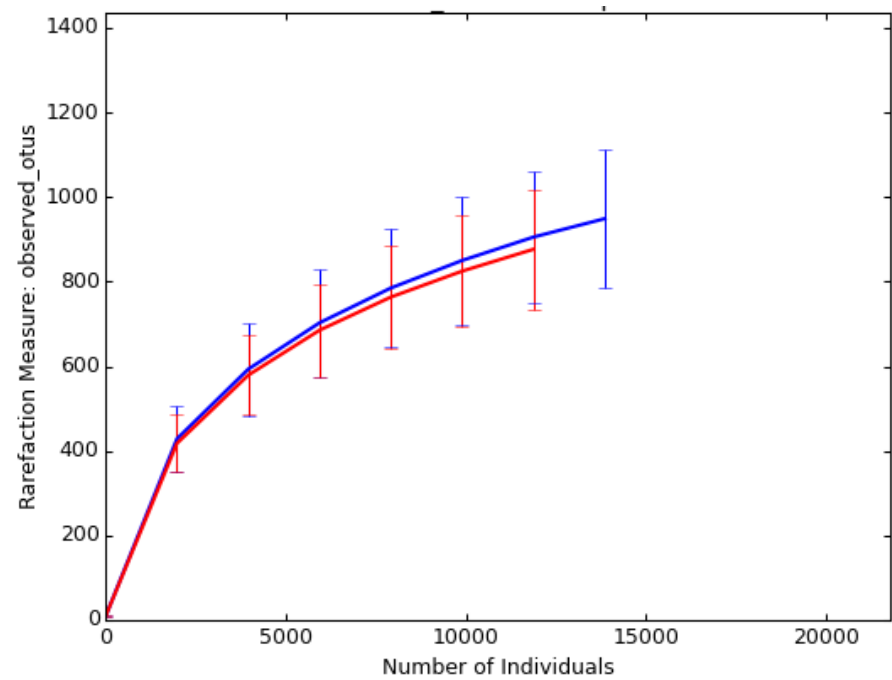
**Supplementary Table S7.** Two-way ANOVA of effects of species, soil type and fire frequency on  $\delta^{13}\text{C}$ ,  $\delta^{15}\text{N}$  and CN ratio. SS: Sum of Squares; df: degrees of freedom.

	Factor	df	SS	F value	P
$\delta^{15}\text{N}$	Species	1	2.824	10.220	<b>0.003</b>
	Soil Type	1	0.443	1.272	0.268
	Fire Frequency	1	1.258	3.886	0.057
	Fire Frequency*Species	1	0.797	3.453	0.073
	Fire Frequency*Soil Type	1	0.287	0.890	0.353
	Soil Type*Species	1	0.012	0.043	0.838
$\delta^{13}\text{C}$	Species	1	0.073	0.123	0.728
	Soil Type	1	0.456	0.788	0.381
	Fire Frequency	1	0.605	1.052	0.312
	Fire Frequency*Species	1	0.900	1.472	0.234
	Fire Frequency*Soil Type	1	0.400	0.619	0.437
	Soil Type*Species	1	0.200	0.280	0.601
C/N	Species	1	240.400	18.230	<b>&lt; 0.001</b>
	Soil Type	1	36.900	1.906	0.177
	Fire Frequency	1	25.800	1.311	0.260
	Fire Frequency*Species	1	41.100	3.424	0.074
	Fire Frequency*Soil Type	1	18.000	0.941	0.340
	Soil Type*Species	1	29.900	2.483	0.125

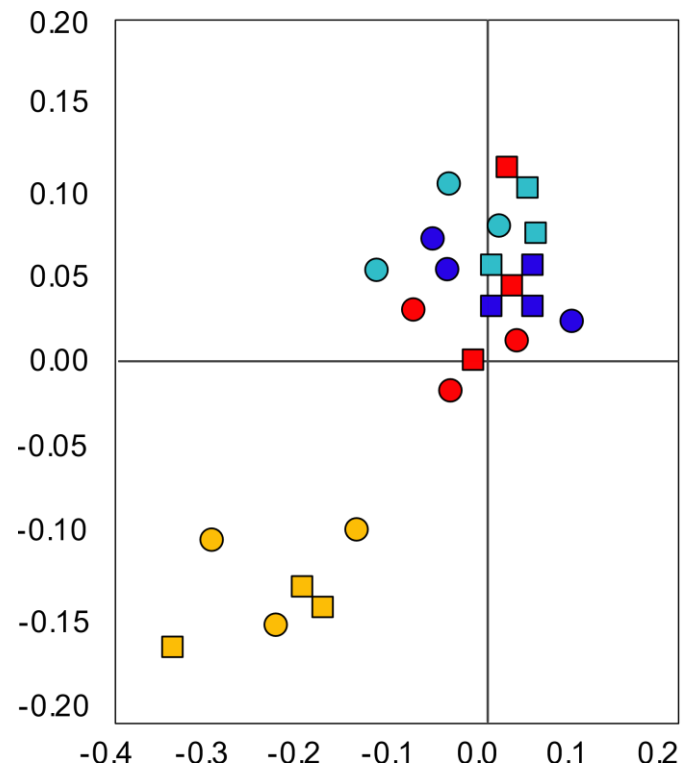


Supplementary Figures

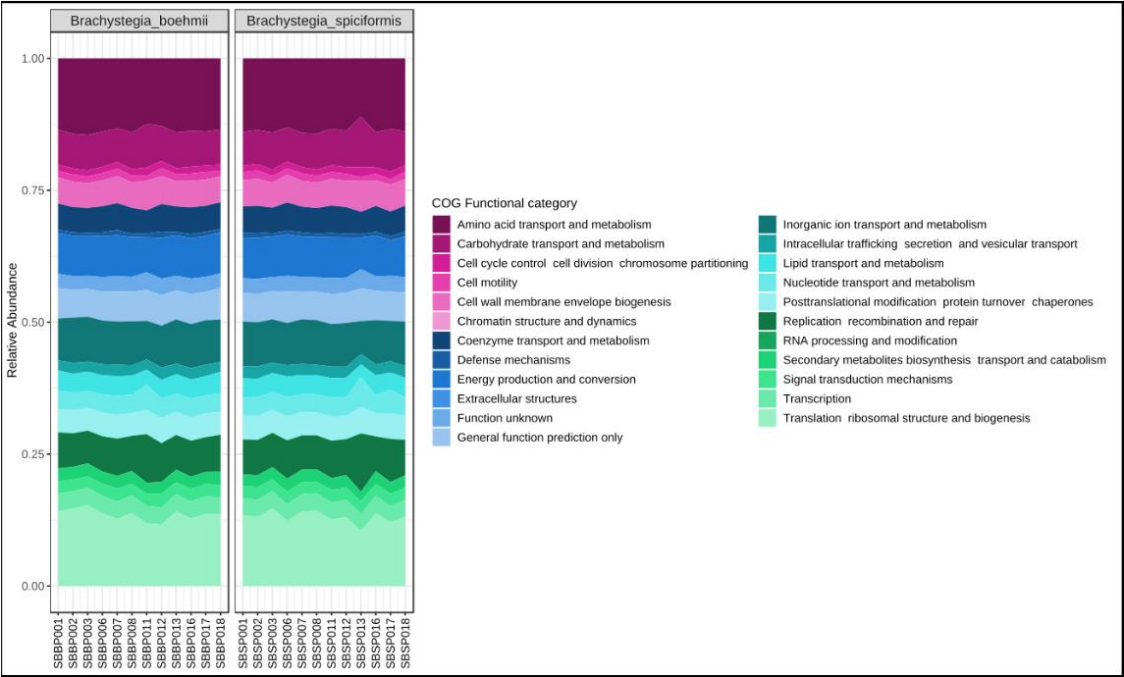
Supplementary Figure S1. Rarefaction curves of rhizobacteria from *B. spiciformis* (blue) and *B. boehmii* (red).



**Supplementary Figure S2.** Principal coordinates analysis of the weighted UniFrac distance matrix. Each point corresponds to a sample and indicates the effect of fire, soil, and species: circles: *B. spiciformis*; *B. boehmii*: squares. LFF in ferric lixisol soils: yellow. HFF in ferric lixisol soils: red. LFF in cambic arenosol soils: light blue. HFF in cambic arenosol soils: dark blue.



Supplementary Figure S3. Functional categories predicted by Tax4Fun in the rhizosphere of *B. spiciformis* and *B. boehmii*.



**Supplementary Figure S4.** Scatter plot showing the correlation between the functional profiles across samples of the two groups of species, *Brachystegia spiciformis* (red) and *Brachystegia boehmii* (blue).

