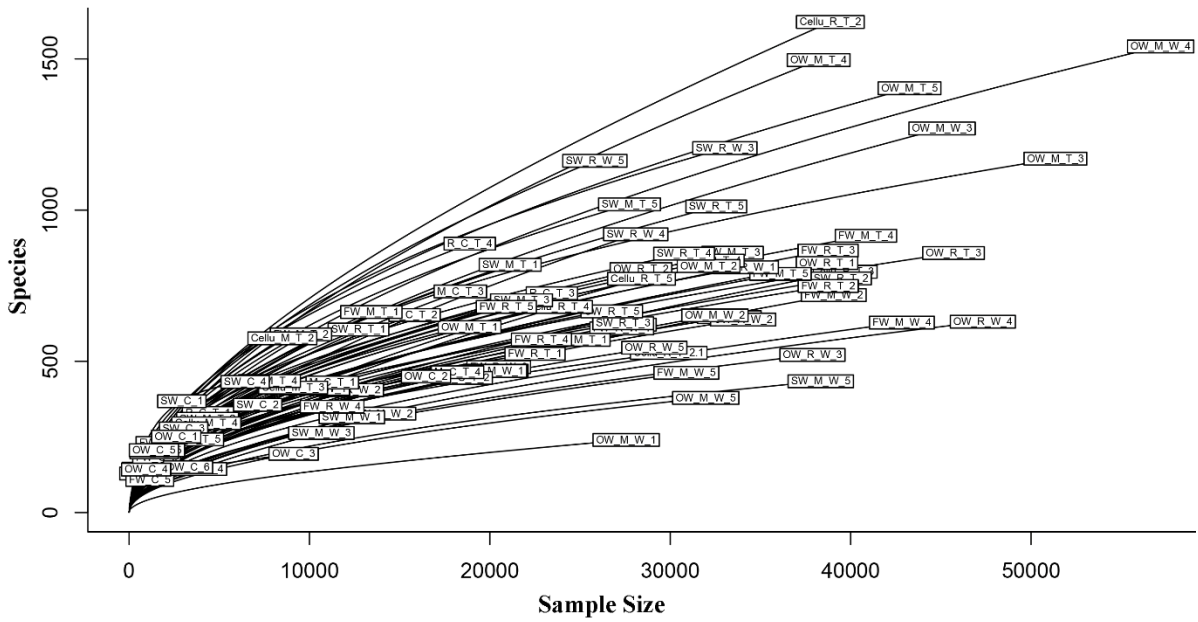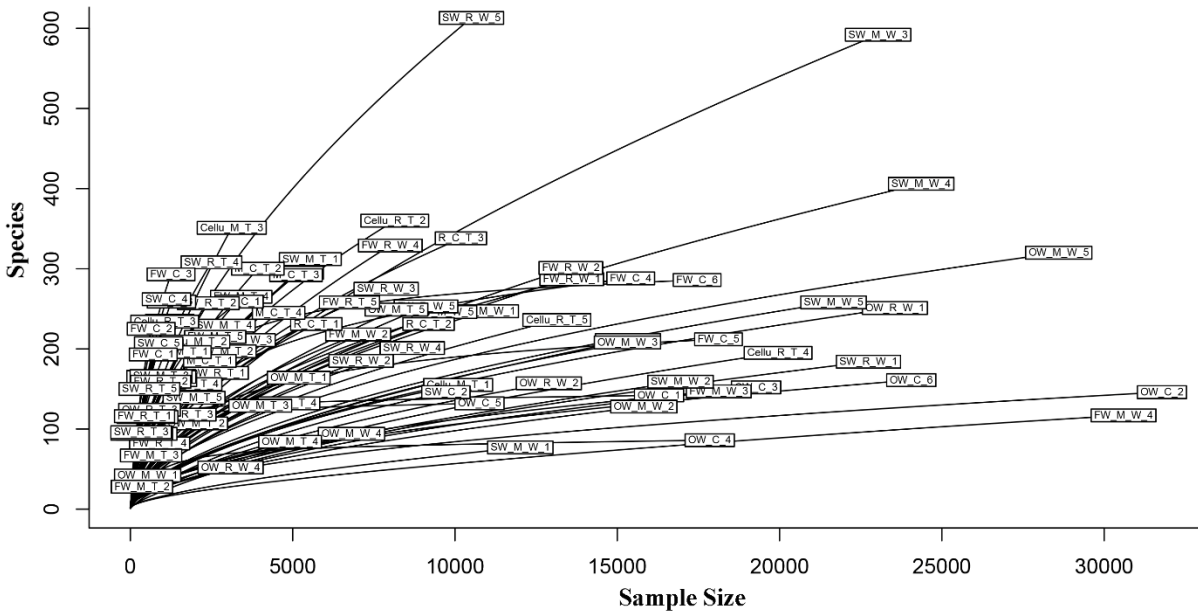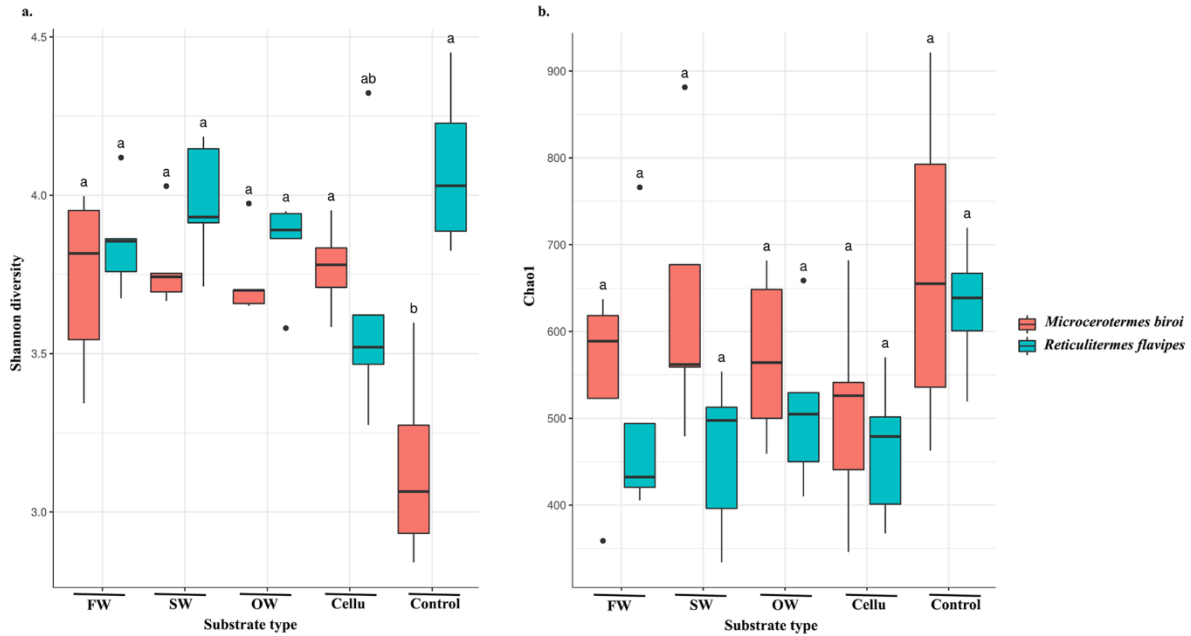# Supplementary Figures

### a. Rarefaction curve for bacteria

b. Rarefaction curve for fungi

Supplementary Figure 1 (a) Rarefaction curve for bacterial 16S sequences. **(b)** Rarefaction curve for fungal ITS sequences.

5

Supplementary Figure 2. Box plot illustrating the Alpha diversity Indices in termites.

(**a**) The bacterial diversity estimated by Shannon index and (**b**) the community richness determined by Chao1 analysis within the two termite species feeding on different substrates. The different alphabets denote significant differences estimated by Tukey HSD *post hoc* test, p<0.05. FW- fresh wood, SW-standard wood, OW- old wood, Cellu- Cellulose, Control- unfed termites.

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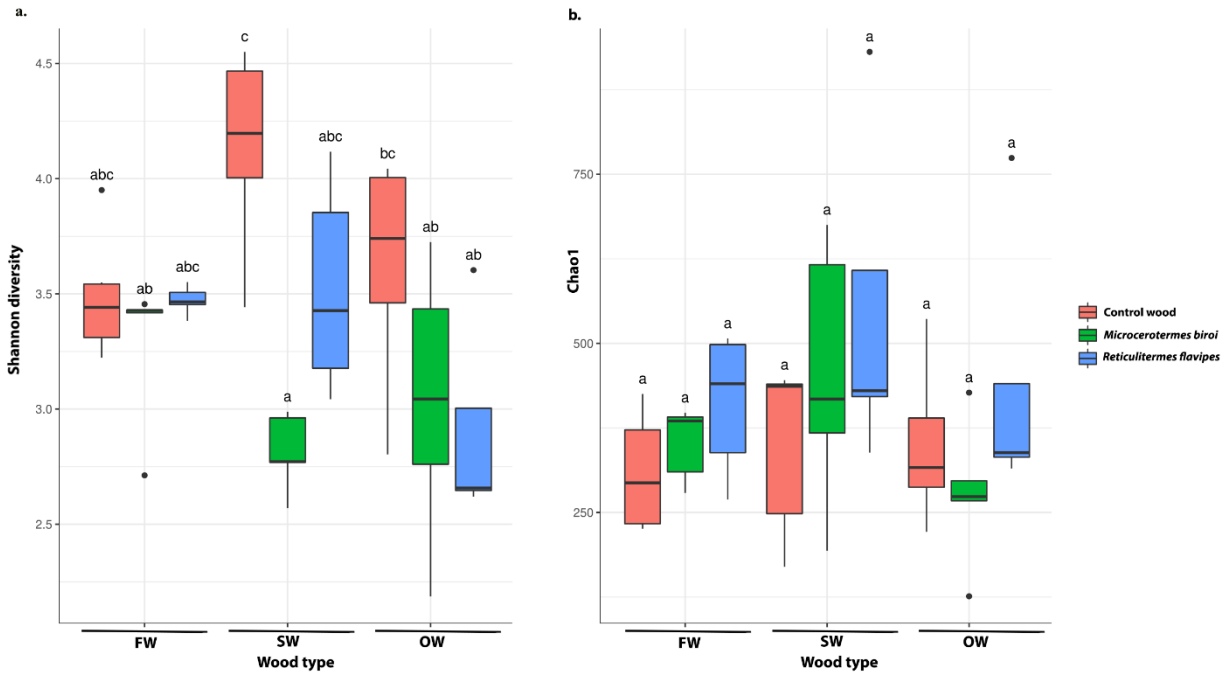
Supplementary Figure 3. Box plot illustrating the Alpha diversity Indices in wood.

(a) The bacterial diversity estimated by Shannon index and **(b)** the community richness determined by Chao1 analysis within the different wood either infested by termites or uninfested control. The different alphabets denote significant differences estimated by Tukey HSD *post hoc* test, p<0.05. FW- fresh wood, SW-standard wood, OW- old wood.

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Supplementary Figure 4. Box plot illustrating the Alpha diversity Indices in termites.

(a) The fungal diversity estimated by Shannon index and **(b)** the community richness determined by Chao1 analysis within the different termite species feeding on different substrates. The different alphabets denote significant differences estimated by Tukey HSD *post hoc* test, p<0.05. FW- fresh wood, SW-standard wood, OW- old wood, Cellu- Cellulose, Control- unfed termites.
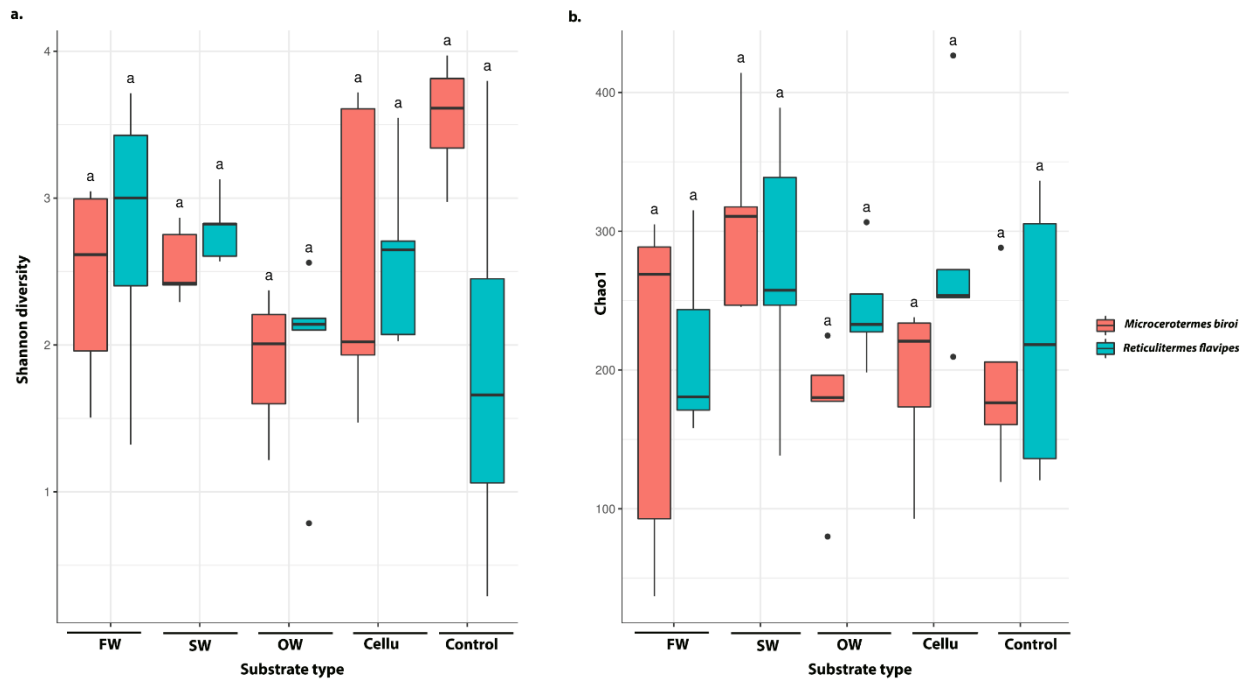
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Supplementary Figure 5. Box plot illustrating the Alpha diversity Indices in wood.

(a) The fungal diversity estimated by Shannon index and (b) the community richness determined
by Chao1 analysis within the different wood either infested by termites or uninfested control. The
different alphabets denote significant differences estimated by Tukey HSD *post hoc* test, p<0.05.
FW- fresh wood, SW-standard wood, OW- old wood.

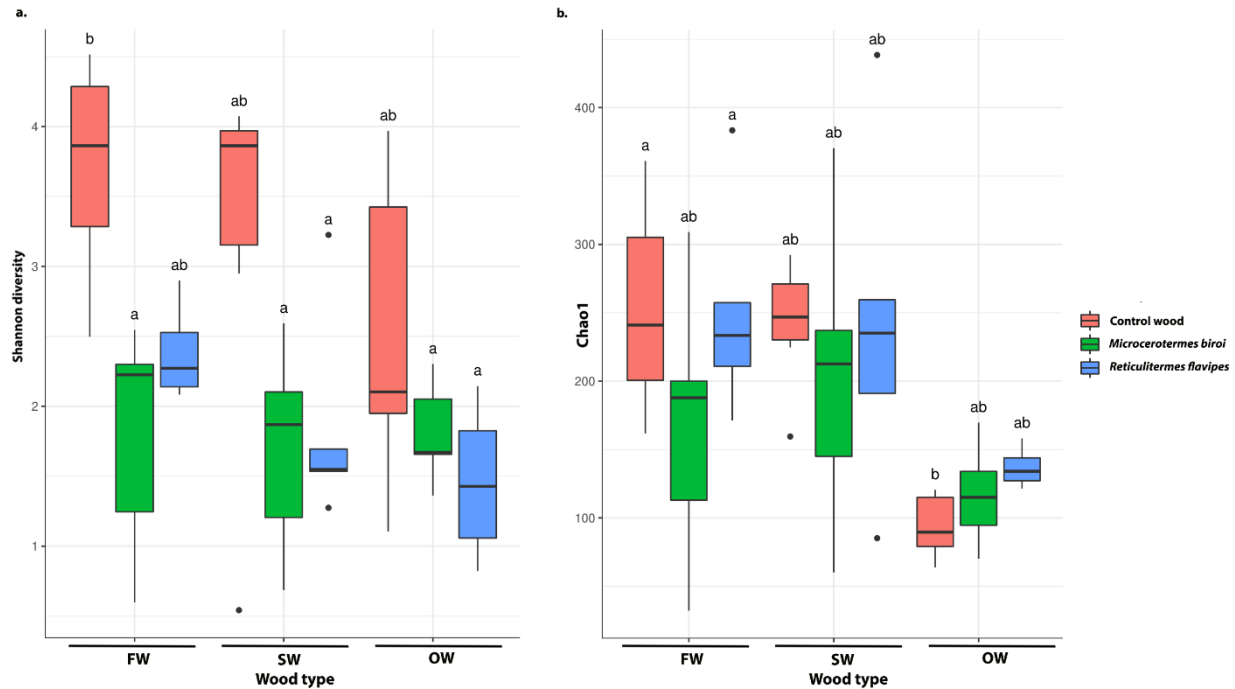## Supplementary Tables

Supplementary Table 1. Pairwise PERMANOVA results of bacterial community composition in termite bodies. All possible pairwise comparisons were included in the analysis but only comparisons between substrate types within species are represented in the table. M: *Microcerotermes biroi*; R: *Reticulitermes flavipes*; FW: fresh wood; SW: standard wood; OW: old wood; Cellu: Cellulose; C: Control.; T- termite

Comparisons	*F*-value	*P*-value	Adjusted *P*-value
FW_M_T vs. SW_M_T	1.12	0.249	0.255
FW_M_T vs. OW_M_T	1.35	0.14	0.15
SW_M_T vs. OW_M_T	1.44	0.11	0.12
FW_M_T vs. M_C_T	2.69	0.005	0.015
FW_M_T vs. Cellu_M_T	3.07	0.008	0.015
SW_M_T vs. M_C_T	2.48	0.01	0.015
SW_M_T vs. Cellu_M_T	2.15	0.016	0.019
OW_M_T vs. M_C_T	3.13	0.007	0.015
OW_M_T vs. Cellu_M_T	3.71	0.004	0.015
M_C_T vs. Cellu_M_T	2.43	0.012	0.017
FW_R_T vs. SW_R_T	1.09	0.26	0.26
FW_R_T vs. OW_R_T	1.39	0.017	0.02
SW_R_T vs. OW_R_T	1.31	0.066	0.072
FW_R_T vs. R_C_T	3.11	0.007	0.015
FW_R_T vs. Cellu_R_T	4.55	0.009	0.015
SW_R_T vs. R_C_T	2.77	0.01	0.015
SW_R_T vs. Cellu_R_T	4.23	0.007	0.015
OW_R_T vs. R_C_T	3.33	0.007	0.015
OW_R_T vs. Cellu_R_T	4.69	0.01	0.015
R_C_T vs. Cellu_R_T	4.4	0.008	0.015

41 **Supplementary Table 2**. Pairwise PERMANOVA results of bacterial community composition in wood
42 pieces. All possible pairwise comparisons were included in the analysis but only comparisons between wood
43 types within species are represented in the table. M: *Microcerotermes biroi*; R: *Reticulitermes flavipes*; FW:
44 fresh wood; SW: standard wood; OW: old wood; C: Control; W: wood

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Comparisons	*F*-value	*P*-value	Adjusted *P*-value
FW_C vs. SW_C	3.77	0.003	0.008
FW_C vs. OW_C	3.89	0.003	0.008
SW_C vs. OW_C	2.05	0.047	0.047
FW_M_W vs. SW_M_W	2.61	0.006	0.009
FW_M_W vs. OW_M_W	3.8	0.008	0.01
SW_M_W vs. OW_M_W	2.72	0.012	0.014
FW_R_W vs. SW_R_W	1.76	0.021	0.023
FW_R_W vs. OW_R_W	3.09	0.008	0.01
SW_R_W vs. OW_R_W	1.7	0.022	0.023

Supplementary Table 3. Pairwise PERMANOVA results of fungal community composition in termite bodies. All possible pairwise comparisons were included in the analysis but only comparisons between substrate types within species are mentioned in the table. M: *Microcerotermes biroi*; R: *Reticulitermes flavipes*; FW: fresh wood; SW: standard wood; OW: old wood; Cel: Cellulose; C: Control; T:termite

Comparisons	*F*-value	*P*-value	Adjusted *P*-value
FW_M_T vs. SW_M_T	0.96	0.486	0.486
FW_M_T vs. OW_M_T	1.35	0.141	0.167
SW_M_T vs. OW_M_T	2.03	0.02	0.033
FW_M_T vs. M_C_T	1.79	0.05	0.066
FW_M_T vs. Cellu_M_T	1.09	0.275	0.302
SW_M_T vs. M_C_T	2.2	0.026	0.039
SW_M_T vs. Cellu_M_T	1.03	0.356	0.381
OW_M_T vs. M_C_T	2.33	0.008	0.024
OW_M_T vs. Cellu_M_T	2.0	0.007	0.024
M_C_T vs. Cellu_M_T	2.34	0.006	0.024
FW_R_T vs. SW_R_T	1.16	0.215	0.248
FW_R_T vs. OW_R_T	0.97	0.481	0.486
SW_R_T vs. OW_R_T	1.06	0.383	0.4
FW_R_T vs. R_C_T	7.99	0.01	0.024
FW_R_T vs. Cellu_R_T	2.2	0.022	0.035
SW_R_T vs. R_C_T	7.6	0.011	0.024
SW_R_T vs. Cellu_R_T	2.27	0.055	0.069
OW_R_T vs. R_C_T	5.48	0.007	0.024
OW_R_T vs. Cellu_R_T	1.51	0.115	0.14
R_C_T vs. Cellu_R_T	5.31	0.006	0.024

54 **Supplementary Table 4**. Pairwise PERMANOVA results of fungal community composition in wood
55 pieces. All possible pairwise comparisons were included in the analysis but only comparisons between wood
56 types within species are represented in the table. M: *Microcerotermes biroi*; R: *Reticulitermes flavipes*; FW:
57 fresh wood; SW: standard wood; OW: old wood; C: Control; W: wood

Comparisons	*F*-value	*P*-value	Adjusted *P*-value
FW_C vs. SW_C	4.69	0.016	0.019
FW_C vs. OW_C	5.5	0.003	0.007
SW_C vs. OW_C	8.41	0.003	0.007
FW_M_W vs. SW_M_W	1.13	0.309	0.309
FW_M_W vs. OW_M_W	1.28	0.145	0.155
SW_M_W vs. OW_M_W	1.31	0.166	0.171
FW_R_W vs. SW_R_W	1.42	0.146	0.155
FW_R_W vs. OW_R_W	2.79	0.021	0.024
SW_R_W vs. OW_R_W	1.57	0.019	0.022

69 **Supplementary Table 5.** The overall Bacterial beta diversity associated with termites and wood samples
70 based on weighted and unweighted UniFrac distances. Termite species (factor with two levels:
71 *Microcerotermes biroi* (M) and *Reticulitermes flavipes* (R)), wood type (factor with five levels: fresh wood,
72 standard wood, old wood, cellulose, and controls), and their interaction (Termite species: wood type). Df
73 represents degree of freedom, SumsOfSqs denotes sums of squares of deviations, MeanSqs stands for SS/Df.
74 F. Model represents F-test value. The R2 value illustrates the ratio of grouping variance and total variance.
75 Pr value determines the significant variation.

Bacterial communities in termite bodies (weighted UniFrac)						
	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
Termite species	1	1.91673	1.91673	413.78	0.85002	0.001 ***
Wood type	4	0.11114	0.02778	6.00	0.04929	0.001 ***
Termite species: wood type	4	0.05102	0.01276	2.75	0.02263	0.028 *
Residuals	38	0.17602	0.00463		0.07806	
Total	47	2.25491			1.00000	
Bacterial communities in termite bodies (unweighted UniFrac)						
Termite species	1	3.8909	3.8909	50.192	0.47729	0.001 ***
Wood type	4	0.7140	0.1785	2.303	0.08759	0.017 *
Termite species: wood type	4	0.6013	0.1503	1.939	0.07377	0.048 *
Residuals	38	2.9458	0.0775		0.36136	
Total	47	8.1521			1.00000	
Bacterial communities in wood (weighted UniFrac)						

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
Termite species	2	1.5906	0.79528	33.430	0.48554	0.001 ***
Wood type	2	0.2720	0.13600	5.717	0.08303	0.001 ***
Termite species: wood type	4	0.4855	0.12137	5.102	0.14820	0.001 ***
Residuals	39	0.9278	0.02379		0.28322	
Total	47	3.2758			1.00000	
Bacterial communities in wood (unweighted UniFrac)						
Termite species	2	3.1090	1.55451	9.7020	0.26739	0.001 ***
Wood type	2	0.8743	0.43713	2.7282	0.07519	0.001 ***
Termite species: wood type	4	1.3954	0.34885	2.1772	0.12001	0.001 ***
Residuals	39	6.2488	0.16023		0.53742	
Total	47	11.6275			1.00000	

Supplementary Table 6: Bacterial and Fungal beta diversities associated with termites and wood samples based on Bray-Curtis distances using Hellinger-transformed relative abundance table. Termite species (factor with two levels: *Microcerotermes biroi* (M) and *Reticulitermes flavipes* (R)), wood type (factor with five levels: fresh wood, standard wood, old wood, cellulose, and controls), and their interaction (Termite species: wood type). Df represents degree of freedom, SumsOfSqs denotes sums of squares of deviations, MeanSqs stands for SS/Df. F. Model represents F-test value. The R2 value illustrates the ratio of grouping variance and total variance. Pr value determines the significant variation.

Bacterial communities in termite bodies						
	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
Termite species	1	8.8634	8.8634	176.317	0.73644	0.001 ***
Wood type	4	0.6747	0.1687	3.355	0.05606	0.007 **
Termite species: wood type	4	0.5871	0.1468	2.920	0.04878	0.016 *
Residuals	38	1.9103	0.0503		0.15872	
Total	47	12.0355			1.00000	
Bacterial communities in wood						
Termite species	2	4.9888	2.49438	16.2029	0.35866	0.001 ***
Wood type	2	1.2801	0.64005	4.1576	0.09203	0.001 ***
Termite species: wood type	4	1.6368	0.40920	2.6580	0.11767	0.001 ***
Residuals	39	6.0039	0.15395		0.43164	
Total	47	13.9095			1.00000	
Fungal communities in termite bodies						
Termite species	1	1.3235	1.32349	8.1006	0.12201	0.001 ***
Wood type	4	1.7391	0.43477	2.6611	0.16033	0.001 ***
Termite species: wood type	4	1.5761	0.39403	2.4117	0.14530	0.001 ***
Residuals	38	6.2085	0.16338		0.57236	
Total	47	10.8472			1.00000	
Fungal communities in wood						
Termite species	2	5.4221	2.71103	13.0706	0.32005	0.001 ***
Wood type	2	1.4944	0.74718	3.6023	0.08821	0.001 ***
Termite species: wood type	4	2.1434	0.53584	2.5834	0.12652	0.001 ***

Residuals	38	7.8818	0.20741		0.46523	
Total	46	16.9415			1.00000	

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87 **Supplementary Excel files**

88 Supplementary Excel 1 – Table S1. Normalized bacterial OTU table.

89 Supplementary Excel 2 – Table S2. Differential abundant bacterial communities in wood.

90 Supplementary Excel 3 – Table S3. Differential abundant bacterial communities in termites.

91 Supplementary Excel 4 – Table S4. Normalized fungal OTU table.

92 Supplementary Excel 5 – Table S5. Differential abundant fungal communities in wood.

93 Supplementary Excel 6 – Table S6. Differential abundant fungal communities in termites.

94 Supplementary Excel 7 – Table S7. Common and unique bacterial communities associated with
95 *Reticulitermes flavipes* upon feeding on different substrates.

96 Supplementary Excel 8 – Table S8. Core and unique fungal communities associated with
97 *Reticulitermes flavipes* upon feeding on different substrates.

98 Supplementary Excel 9 – Table S9. Common and unique bacterial communities associated with
99 *Microcerotermes biroi* upon feeding on different substrates.

100 Supplementary Excel 10 – Table S10. Core and unique fungal communities associated with
101 *Microcerotermes biroi* upon feeding on different substrates.