

1 **Supplementary information**

2 **Assembly and maintenance of phyllosphere microbial diversity during**
3 **rubber tree leaf senescence**

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6 The following supporting information is available for this article:

7 **Supplementary figures**

8 **Supplementary Figure 1** Study sites and sampling design on Hainan Island and in
9 Xishuangbanna. (A) There are 6 study sites. Red solid circles indicate study sites on
10 the maps. (B and C) Each site was further divided into 3 plots, totaling 18 sampling
11 plots. Blue solid squares indicate study plots on the maps. (D) For each plot, we
12 selected three trees and sampled green and yellow leaves from all four cardinal
13 directions. The red solid stars indicate sampling locations of a tree.

14 **Supplementary Figure 2** Polymerase chain reaction (PCR) amplification gel
15 electrophoresis image for rubber tree leaf bacteria and fungi

16 **Supplementary Figure 3** Principal coordinates analysis (PCoA) of taxonomical
17 similarity based on Bray-Curtis distances for different season (A) and different site (B)
18 of rubber tree leaves. Significant level: * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

19 **Supplementary Figure 4** Rarefaction curves for bacterial (A) and fungal (B)
20 community in green and yellow rubber tree leaves.

21 **Supplementary Figure 5** Number of accumulated ASVs for green and yellow rubber
22 tree leaves (γ diversity).

23 **Supplementary Figure 6** Principal coordinates analysis (PCoA) of functional
24 similarity based on Bray-Curtis distances for green and yellow rubber tree leaves. (A)
25 Bacterial functional gene composition at KEGG level2 as inferred from PICRUSt2 (B)
26 Fungal functional gene composition as inferred from FUNguild. Significant level: * $p <$
27 0.05 ; ** $p < 0.01$; *** $p < 0.001$.

28 **Supplementary Figure 7** Relative abundance of fungal functional genes as inferred
29 from FUNguild for green and yellow rubber tree leaves

30 **Supplementary Figure 8** The elbow approach and last 2% increase in beta-diversity
31 method were used to quantifying the contribution of the core membership to beta
32 diversity. (A) 68 core ASVs were identified for bacterial community. (B) 79 core ASVs
33 were identified for fungal community.

Supplementary tables

Supplementary Table1 Physicochemical properties of green and yellow leaves of rubber tree. The letters (a, b) indicate whether the properties are significantly different or not between green and yellow leaves at p -value < 0.05 level.

Supplementary Table2 Permutational multivariate analysis of variance (PERMANOVA) tables for differences in bacterial and fungal community compositions at genera level for rubber tree leaves

Supplementary Table3 PERMDISP2 analysis tables for bacterial and fungal community compositions (at genera level) and gene functional compositions for green and yellow rubber tree leaves

Supplementary Table4 Permutational multivariate analysis of variance (PERMANOVA) tables for differences in bacterial functions (KEEG at level2) and fungal functions for rubber tree leaves

Supplementary Data

Supplementary Data1: Changes in core bacterial ASVs abundance for endophytic and epiphytic during leaf senescence and their ecological process. Enriched: Fold change (FC) > 1.0 & $p < 0.05$; Depleted: Fold change (FC) < 1.0 & $p < 0.05$; ns: not significant in abundance between yellow and green leaves. The ecological process was derived from Shade & Stopnisek methods (2018). (FC and p value were not shown in this table)

Supplementary Data2: Changes in core fungal ASVs abundance for endophytic and epiphytic during leaf senescence and their ecological process. Enriched: Fold change (FC) > 1.0 & $p < 0.05$; Depleted: Fold change (FC) < 1.0 & $p < 0.05$; ns: not significant in abundance between yellow and green leaves. The ecological process was derived from Shade & Stopnisek methods (2018). (FC and p value were not shown in this table)

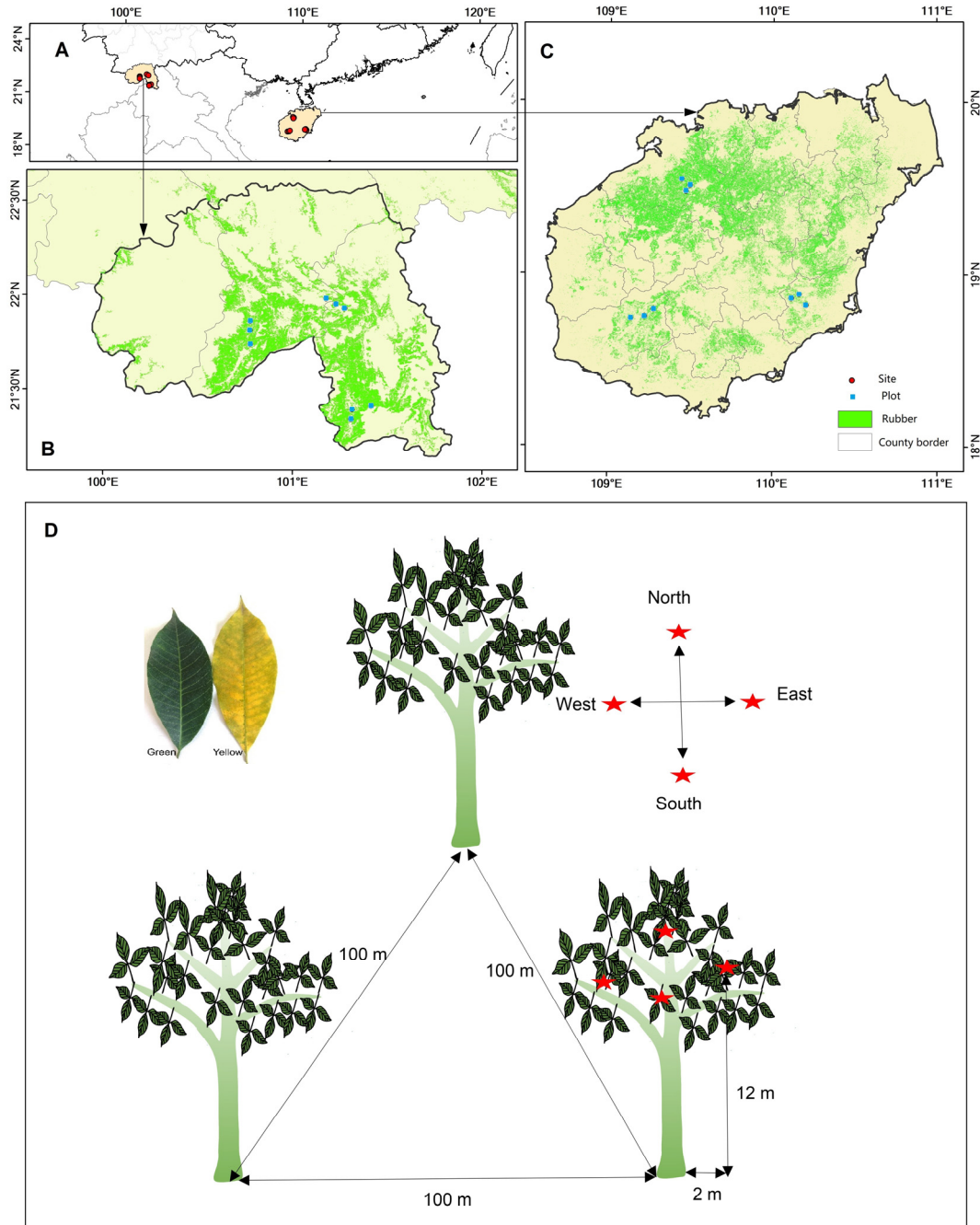
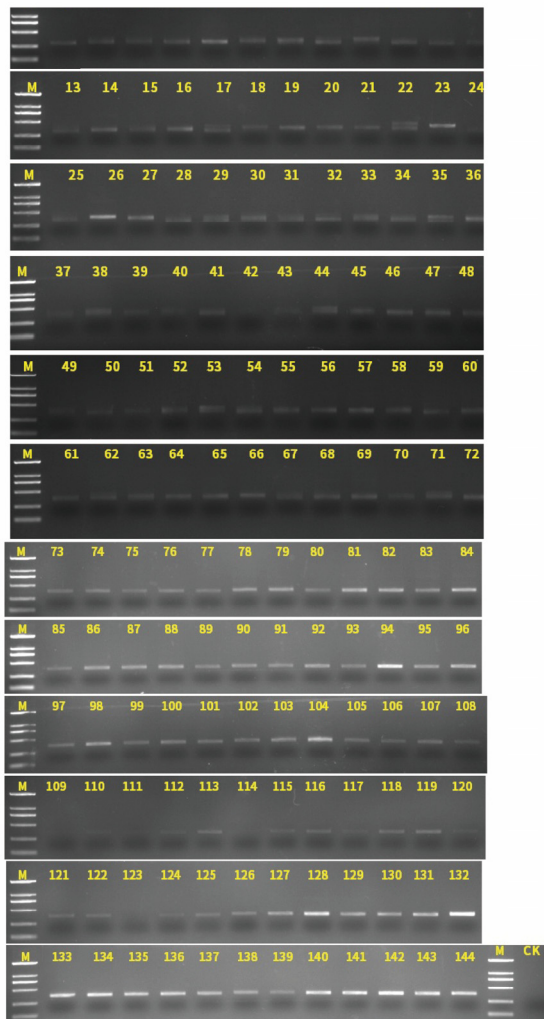
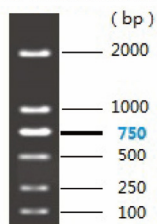


Figure S1 Study sites and sampling design on Hainan Island and in Xishuangbanna. (A) There are 6 study sites. Red solid circles indicate study sites on the maps. (B and C) Each site was further divided into 3 plots, totally 18 sampling plots. Blue solid squares indicate study plots on the maps. (D) For each plot, we selected three trees and sampled green and yellow leaves from all four cardinal directions. The red solid stars indicate sampling locations of a tree.



The distribution of the bands in DL2000.



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70 **Figure S2** Polymerase chain reaction (PCR) amplification gel electrophoresis image

71 for rubber tree leaf bacteria and fungi

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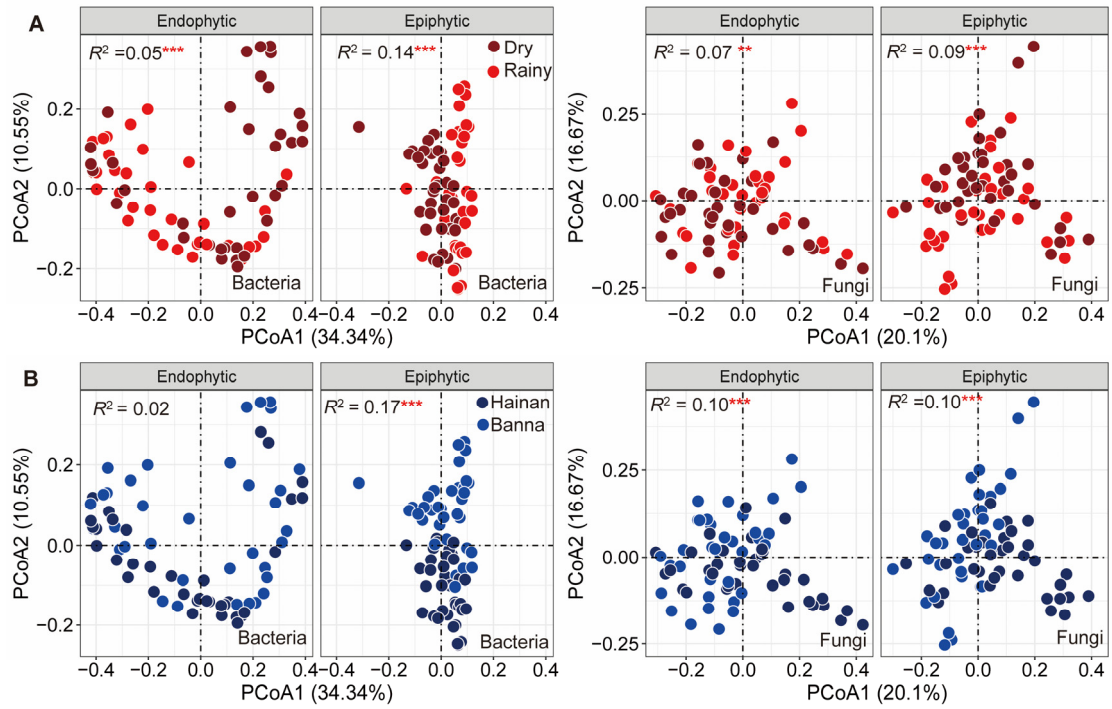


Figure S3: Principal coordinates analysis (PCoA) of taxonomical similarity based on Bray-Curtis distances for different season (A) and different site (B) of rubber tree leaves. Significant level: * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

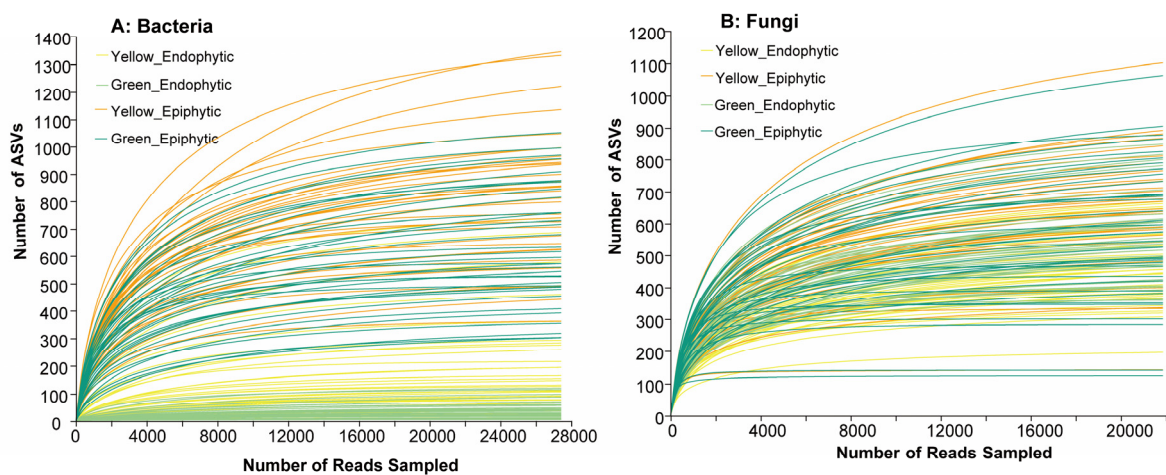
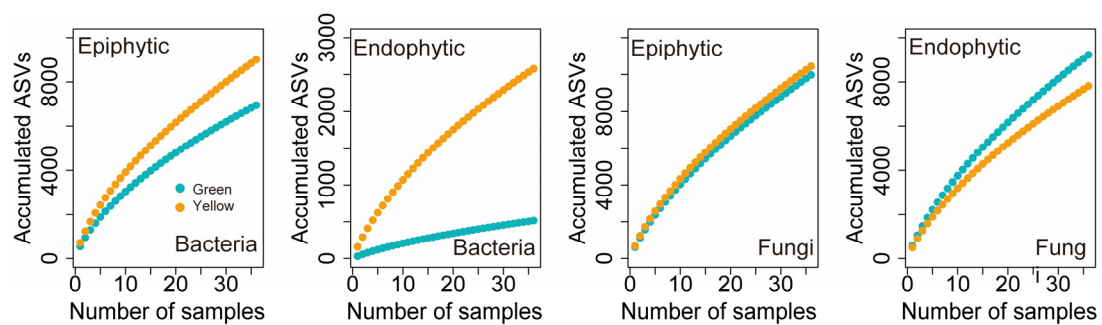
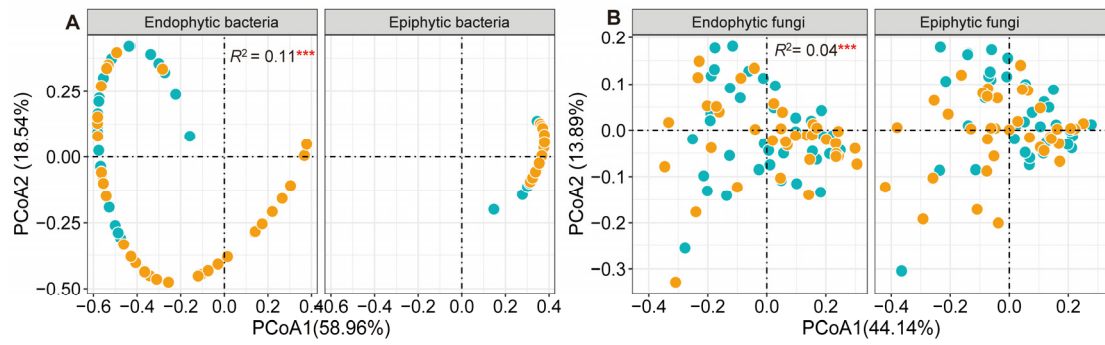


Figure S4 Rarefaction curves for bacterial (A) and fungal (B) community in green and yellow rubber tree leaves.

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83 **Figure S5** Number of accumulated ASVs for green (green solid circles) and yellow
 84 (yellow solid circles) rubber tree leaves (γ diversity).
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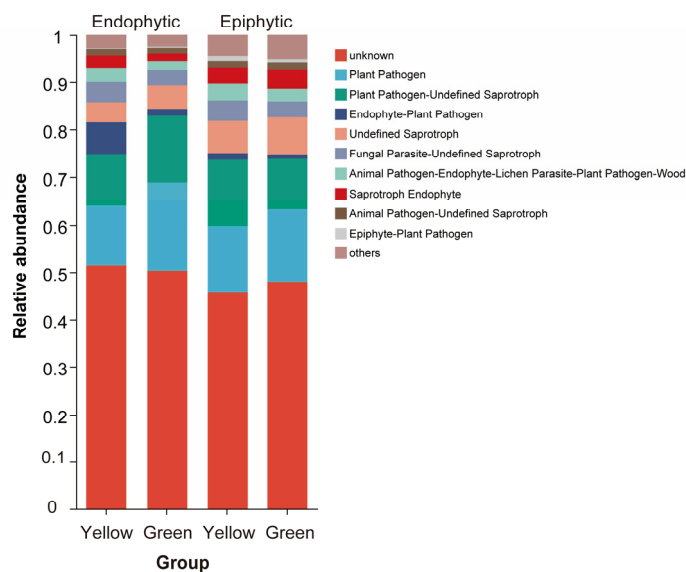


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88 **Figure S6:** Principal coordinates analysis (PCoA) of functional similarity based on
 89 Bray-Curtis distances for green (green solid circles) and yellow (yellow solid circles)
 90 rubber tree leaves. (A) Bacterial functional gene composition at KEGG level2 as
 91 inferred from PICRUSt2 (B) Fungal functional gene composition as inferred from
 92 FUNguild. Significant level: * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.

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95 **Figure S7:** Relative abundance of fungal functional genes as inferred from FUNguild
 96 for green and yellow rubber tree leaves

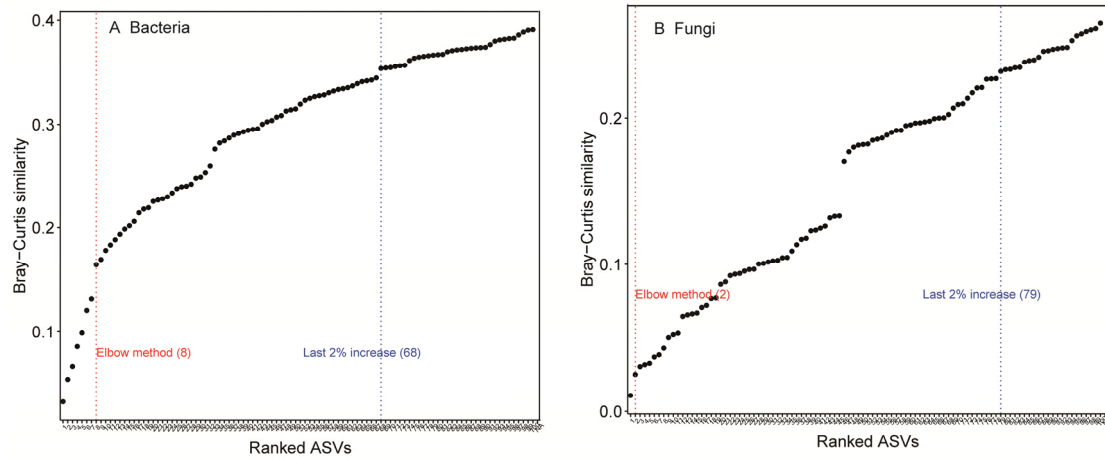


Figure S8: The elbow approach and last 2% increase in beta-diversity method were used to quantifying the contribution of the core membership to beta diversity. (A) 68 core ASVs were identified for bacterial community. (B) 79 core ASVs were identified for fungal community.

Supplementary tables

Table S1 Physicochemical properties of green and yellow leaves of rubber tree. The letters (a, b) indicate whether the properties are significantly different or not between green and yellow leaves at p -value < 0.05 level.

	pH	WC (%)	OM (%)	TN (g/kg)	TP (g/kg)	TK (g/kg)
Green	5.63±0.15a	61.45±3.74a	7.96±0.64a	1.87±0.34a	0.18±0.07a	0.99±0.22a
Yellow	5.53±0.29a	60.47±6.62a	7.59±0.60b	1.29±0.40b	0.17±0.08a	0.60±0.29b

Table S2 Permutational multivariate analysis of variance (PERMANOVA) tables for differences in bacterial and fungal community compositions at genera level for rubber tree leaves

Taxa	Compartments	Variables	Df	PseudoF	R^2	p -value
Bacteria	Endophytic	Season	1	4.17	0.05	0.001
		Site	1	1.56	0.02	0.081
		Stage	1	5.81	0.07	0.001
		Season:	1	1.72	0.02	0.061
		Site: Stage	1	1.78	0.02	0.065
		Residual	66		0.81	
		Total	71		1.00	
	Epiphytic	Season	1	14.18	0.14	0.001
		Site	1	17.35	0.17	0.001
		Stage	1	3.31	0.03	0.001
		Season:	1	1.01	0.01	0.409
		Site: Stage	1	2.88	0.03	0.005
		Residual	66		0.63	
		Total	71		1.00	
Fungi	Endophytic	Season	1	5.87	0.07	0.001
		site	1	8.86	0.10	0.001
		Stage	1	3.62	0.04	0.001
		Season:	1	0.66	0.01	0.761
		Site: Stage	1	1.53	0.02	0.120
		Residual	66		0.76	
		Total	71		1.00	
	Epiphytic	Season	1	7.50	0.09	0.001
		Site	1	8.80	0.10	0.001
		Stage	1	2.34	0.03	0.011
		Season:	1	0.31	0.00	0.998
		Site: Stage	1	1.06	0.01	0.350
		Residual	66		0.77	
		Total	71		1.00	

Table S3 PERMDISP2 analysis tables for bacterial and fungal community compositions (at genera level) and gene functional compositions for green and yellow rubber tree leaves

Contents	Taxa	Compartment	Sample size	F-value	number of permutations	<i>p</i> -value
Composition	Bacteria	Endophytic	72	0.373	999	0.535
		Epiphytic	72	0.411	999	0.531
	Fungi	Endophytic	72	17.80	999	0.001
		Epiphytic	72	1.00	999	0.325
Function	Bacteria	Endophytic	72	0.922	999	0.340
		Epiphytic	72	0.246	999	0.621
	Fungi	Endophytic	72	5.075	999	0.027
		Epiphytic	72	0.768	999	0.384

Table S4 Permutational multivariate analysis of variance (PERMANOVA) tables for differences in bacterial functions (KEEG at level2) and fungal functions for rubber tree leaves

Taxa	Compartments	Variables	Df	PseudoF	R^2	p -value
Bacteria	Endophytic	Season	1	4.32	0.05	0.003
		Site	1	1.42	0.01	0.211
		Stage	1	9.65	0.11	0.001
		Season:	1	1.90	0.02	0.125
		Site: Stage	1	2.22	0.02	0.075
		Residual	66		0.77	
		Total	71		1.00	
	Epiphytic	Season	1	4.76	0.06	0.025
		Site	1	2.52	0.03	0.078
		Stage	1	1.70	0.02	0.182
		Season:	1	1.08	0.01	0.325
		Site: Stage	1	0.25	0.00	0.766
		Residual	66		0.86	
		Total	71		1.00	
Fungi	Endophytic	Season	1	2.78	0.03	0.001
		site	1	1.72	0.02	0.007
		Stage	1	3.18	0.04	0.001
		Season:	1	2.82	0.04	0.001
		Site: Stage	1	3.48	0.04	0.000
		Residual	66		0.83	
		Total	71		1.00	
	Epiphytic	Season	1	3.66	0.05	0.004
		Site	1	6.79	0.08	0.001
		Stage	1	1.28	0.02	0.250
		Season:	1	0.27	0.00	0.948
		Site: Stage	1	1.91	0.03	0.101
		Residual	66		0.83	
		Total	71		1.00	