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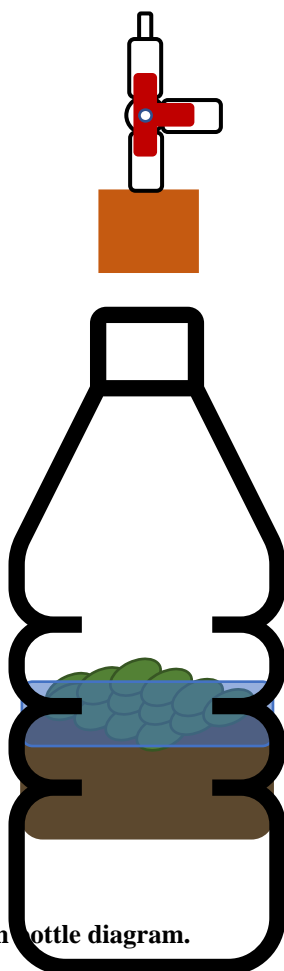
**Table S1. Comparison of the flux of emission of CO<sub>2</sub> and CH<sub>4</sub> in microcosms of mangrove sediments during leaf litter during 45 days of degradation. Incubated under different pHs and temperature.**

Incubation condition	Average emission flow of CO <sub>2</sub> (µg C cm <sup>-2</sup> day <sup>-1</sup> )			
	<i>R. mangle</i>	<i>L. racemosa</i>	<i>A. schaueriana</i>	Control
29.5°C	580.46 <sup>a</sup>	489.92 <sup>a</sup>	551.37 <sup>A</sup>	-177.10 <sup>a'</sup>
27.5°C	823.18 <sup>a</sup>	275.37 <sup>a</sup>	248.09 <sup>B</sup>	156.16 <sup>b'</sup>
pH 7.05	582.29 <sup>a</sup>	380.75 <sup>A</sup>	381.16 <sup>A</sup>	-2.57 <sup>a'</sup>
pH 6.74	821.35 <sup>a</sup>	384.53 <sup>A</sup>	418.3 <sup>A</sup>	-18.56 <sup>a'</sup>

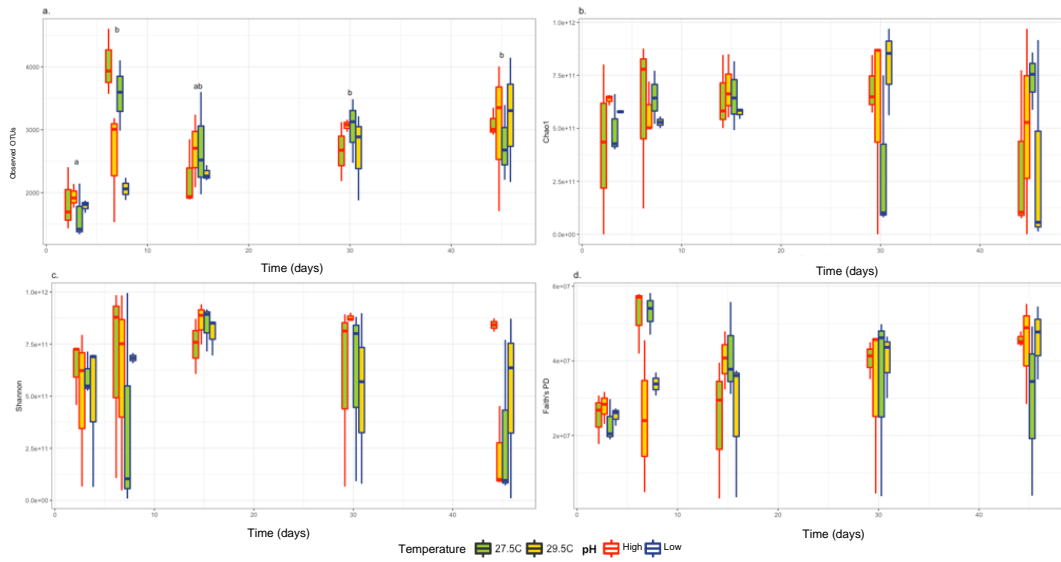
Incubation condition	Average emission flow of CH <sub>4</sub> (µg CO <sub>2eq</sub> .cm <sup>-2</sup> day <sup>-1</sup> )			
	<i>R. mangle</i>	<i>L. racemosa</i>	<i>A. schaueriana</i>	Control
29.5°C	183.86 <sup>a</sup>	59.13 <sup>A</sup>	345.16 <sup>a</sup>	-46.75 <sup>a'</sup>
27.5°C	203.89 <sup>a</sup>	9.94 <sup>B</sup>	126.33 <sup>b</sup>	-13.94 <sup>b'</sup>
pH 6.74	195.81 <sup>A</sup>	38.40 <sup>A</sup>	282.75 <sup>a</sup>	-26.52 <sup>a'</sup>
pH 7.05	191.81 <sup>A</sup>	30.67 <sup>A</sup>	188.74 <sup>a</sup>	-34.17 <sup>a'</sup>

\*different letters over each value indicate significant differences in Tukey's HSD test with  $\alpha$  0.05. capital letters indicate differences between different pH treatment and regular letters indicate differences between temperature treatments.

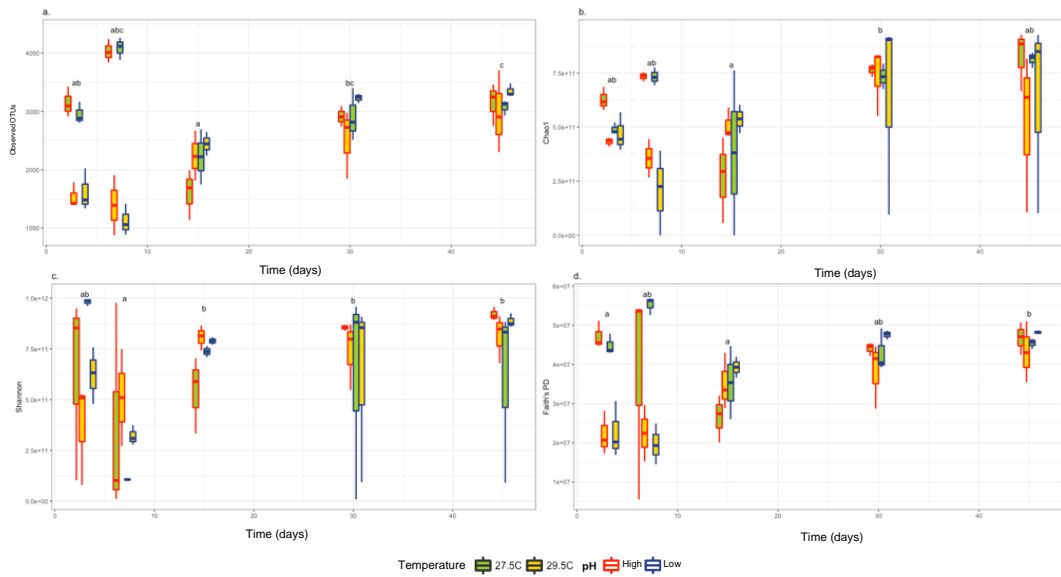


**Figure S1: Microcosm bottle diagram.**

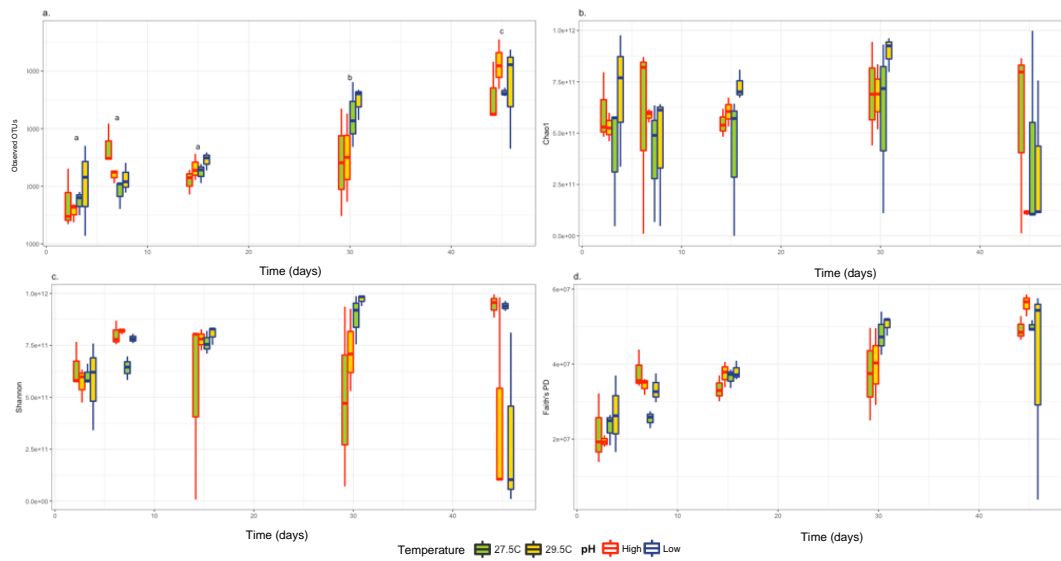
*Rhizophora mangle*



*Laguncularia racemosa*

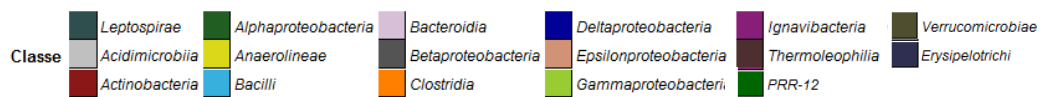
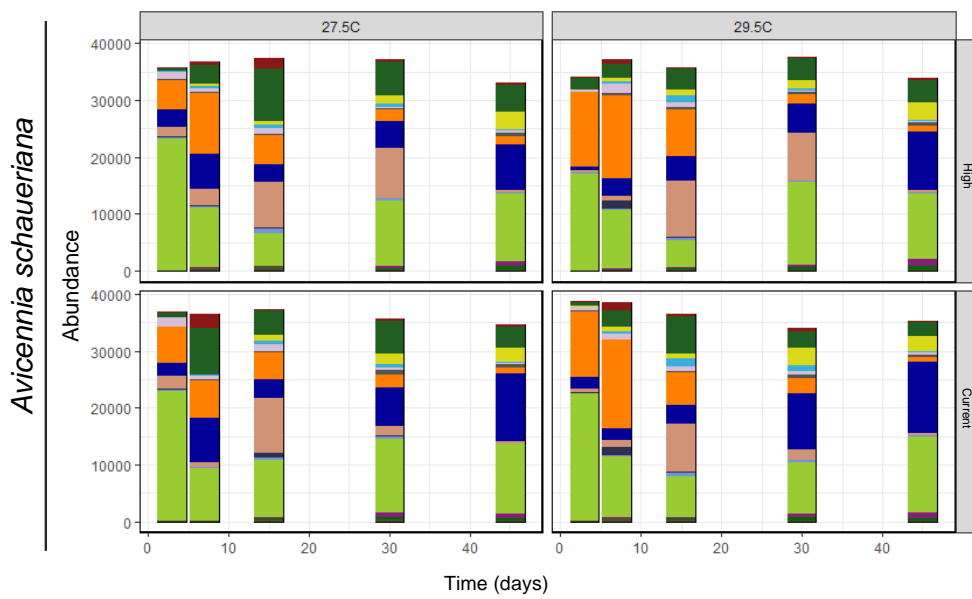
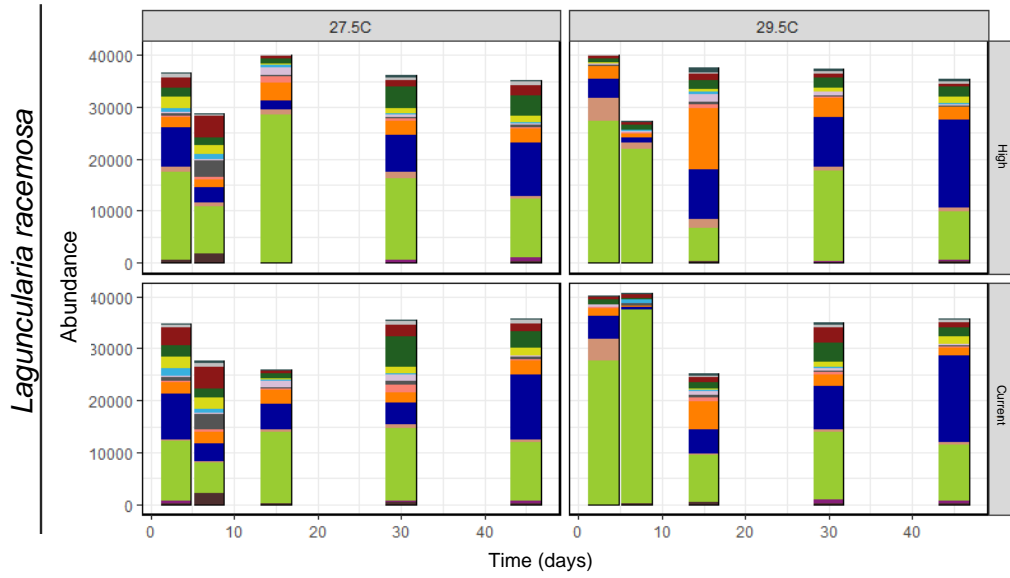
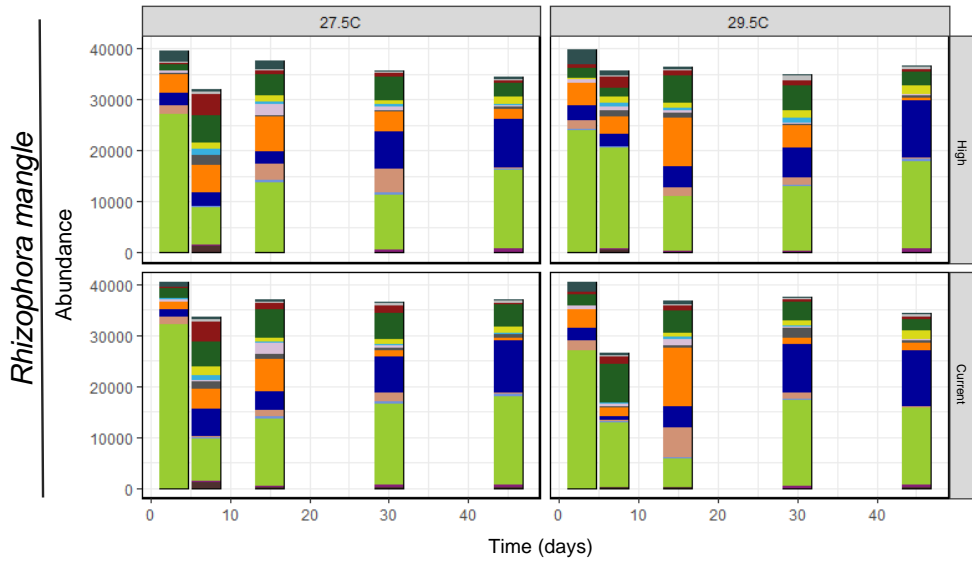


*Avicennia schaueriana*

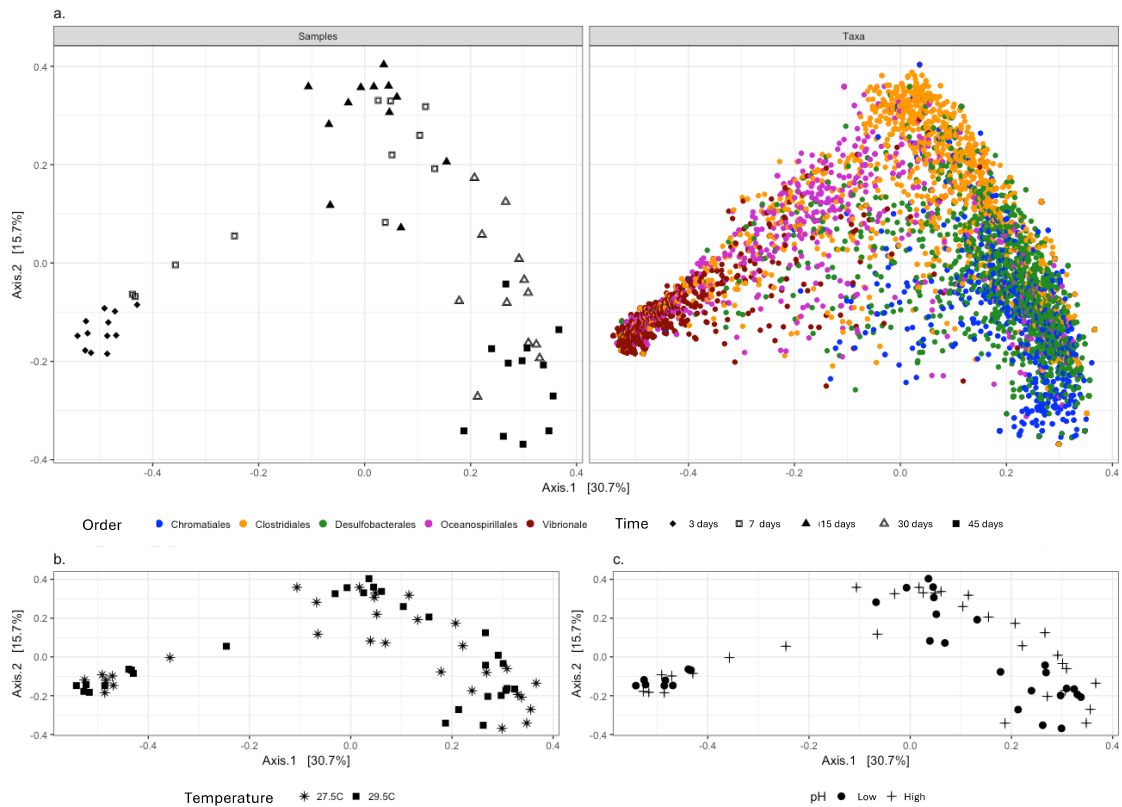


**Figure S2. Comparison of the results of diversity indexes obtained** from the bacterial community 16S rRNA gene sequencing obtained from in microcosms of mangrove sediments during leaf litter decomposition. Samples are color coded according to the legend (a.) **Observed OTUs**; (b.) **Richness**

estimator Chao1; **(c.)** Shannon's H' diversity index e **(d.)** Faith's phylogenetic diversity (PD). Letters on top of samples indicate a significant difference in Tukey's HSD with an  $\alpha$  of 0.05



**Figure S3.** Composition of the bacterial community 16S rRNA gene sequencing obtained from in microcosms of mangrove sediments during leaf litter decomposition. The Y-axis represents the number of reads after rarefaction to 40,000 reads per sample.



**Figure S4.** Principal coordinate analysis (PCoA) based on a distance matrix of Bray-Curtis of the bacterial community of decaying leaves of *Rhizophora mangle*. Samples are coded according to (a.) Time and order (OTU plot); (b.) temperature e (c.) pH.