

Table S1. Primers used for the molecular identification of ticks and Rickettsia.

Biological group	Gene	Amplicon (pb)	Primer	Primer sequence (5'-3')	Temperature (°C)	Reference
Ticks	COI	710	LCO1490	GGT CAA CAA ATC ATA AAG ATA TTG G	45	(Folmer et al., 1994)
			HCO2198	TAA ACT TCA GGG TGA CCA AAA AAT CA		
Rickettsia	16SrRNA	460	16S+1 16s-1	CCG GTC TGA ACT CAG ATC AAG T GCT CAA TGA TTT TTT AAA TTG CTG T	48	(Mangold et al., 1998)
	GltA	401	CS-78 CS-323	GCAAGTATCGGTGAGGATGTAAT GCTTCCTTAAAATTCAATAAATCAG GAT	54	(Labruna et al., 2004a)
	ompA	444	OMPA-F OMPA-R	CAC YAC CTC AAC CGC AGC AAA GTT ATATTCCT AAA CCY GTA TAA KTA TCR GC	52	(Phan et al., 2011)
	Sca1	488	SCA1-F2 SCA1-R2	GGTGATGAAGAAGAGTCTC CTCTTTAAAATTATGTTCTAC	49	(Anstead and Chilton, 2013)

Table S2. Blood samples from birds and ticks from vegetation processed by 16S metataxonomy amplicon sequencing.

Biological group	Species	month	Sample code
Birds	<i>Campylorhynchus griseus</i>	-	DLM1
	<i>Crotophaga ani</i>	-	DL151
	<i>Furnarius leucopus</i>	-	DLM2
	<i>Cyclarhis gujanensis</i>	-	DLM3
	<i>Glaucidium brasilianum</i>	-	DL241
	<i>Hypnelus ruficollis</i>	-	DLM4
	<i>Melanerpes rubricapillus</i>	-	DL88
	<i>Leptotila verreauxi</i>	-	DLM5
	<i>Parkesia noveborasensis</i>	-	DLM6
	<i>Quiscalus lugubris</i>	-	DLM7
	<i>Saltator coerulescens</i>	-	DLM8
Ticks	<i>Amblyomma dissimile</i>	Feb	ES2N
	<i>Amblyomma dissimile</i>	Feb	ES2L
	<i>Amblyomma dissimile</i>	Mar	ES3N
	<i>Amblyomma dissimile</i>	Mar	ES3L
	<i>Amblyomma dissimile</i>	Mar	ES3A
	<i>Amblyomma dissimile</i>	Abr	ES4N

<i>Amblyomma dissimile</i>	Abr	ES4L
<i>Amblyomma dissimile</i>	May	ES5N
<i>Amblyomma dissimile</i>	May	ES5L
<i>Amblyomma dissimile</i>	Jun	ES6N
<i>Amblyomma dissimile</i>	Jun	ES6L
<i>Amblyomma dissimile</i>	Jul	ES7N
<i>Amblyomma dissimile</i>	Jul	ES7L
<i>Amblyomma dissimile</i>	Ago	ES8N
<i>Amblyomma dissimile</i>	Ago	ES8L
<i>Amblyomma dissimile</i>	Oct	ES10L
<i>Amblyomma dissimile</i>	Oct	ES10N
<i>Amblyomma dissimile</i>	Nov	ES11L
<i>Amblyomma dissimile</i>	Nov	ES11N
<i>Amblyomma dissimile</i>	Dic	ES12N
<i>Amblyomma dissimile</i>	Dic	ES12L
<i>Amblyomma dissimile</i>	Ene	ES1N
<i>Amblyomma dissimile</i>	Ene	ES1L
<i>Amblyomma dissimile</i>	Ene	ES1A
<i>Amblyomma dissimile</i>	Feb	2ES2N
<i>Amblyomma dissimile</i>	Feb	2ES2L
<i>Amblyomma dissimile</i>	Feb	2ES2A

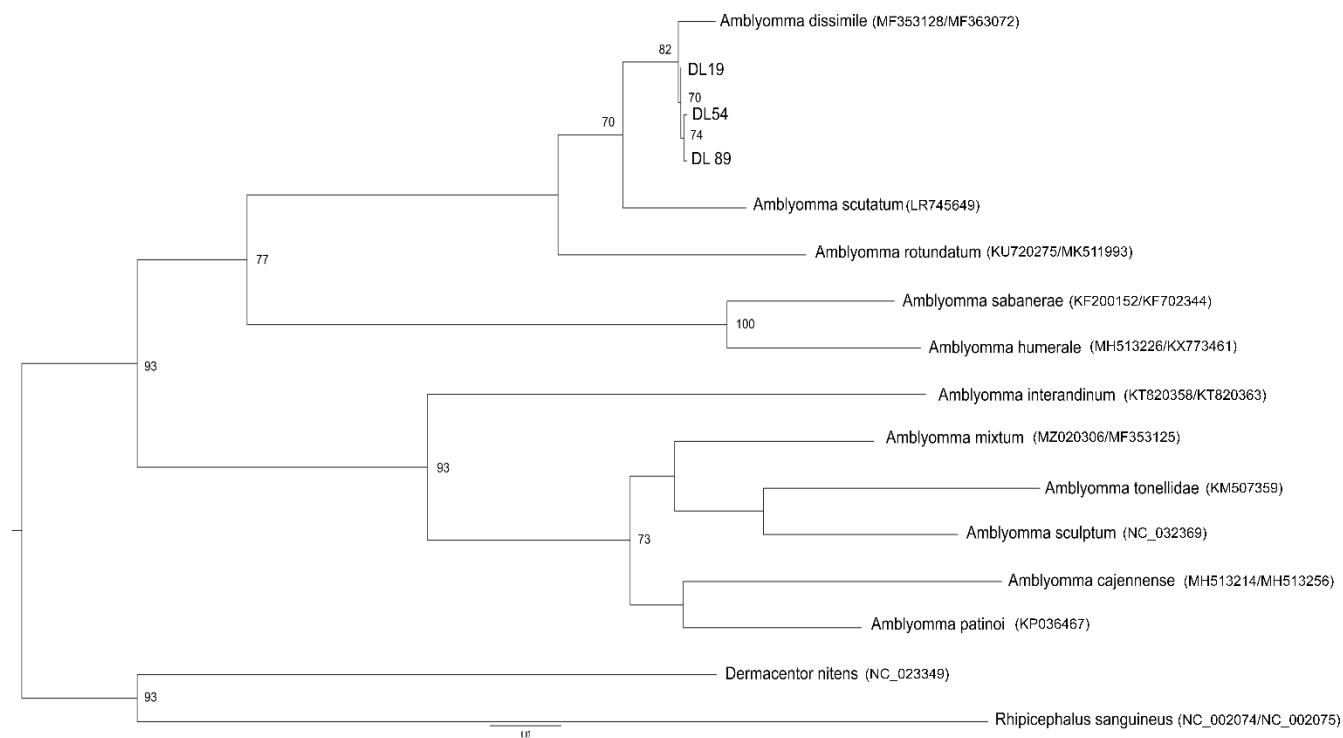


Figure S1. Phylogenetic reconstruction using maximum likelihood of the concatenated COI and 16S rDNA *Amblyomma* sequences obtained in this study and others downloaded from genbank with accession numbers included COI/16S. Numbers on the nodes correspond to bootstrap values.

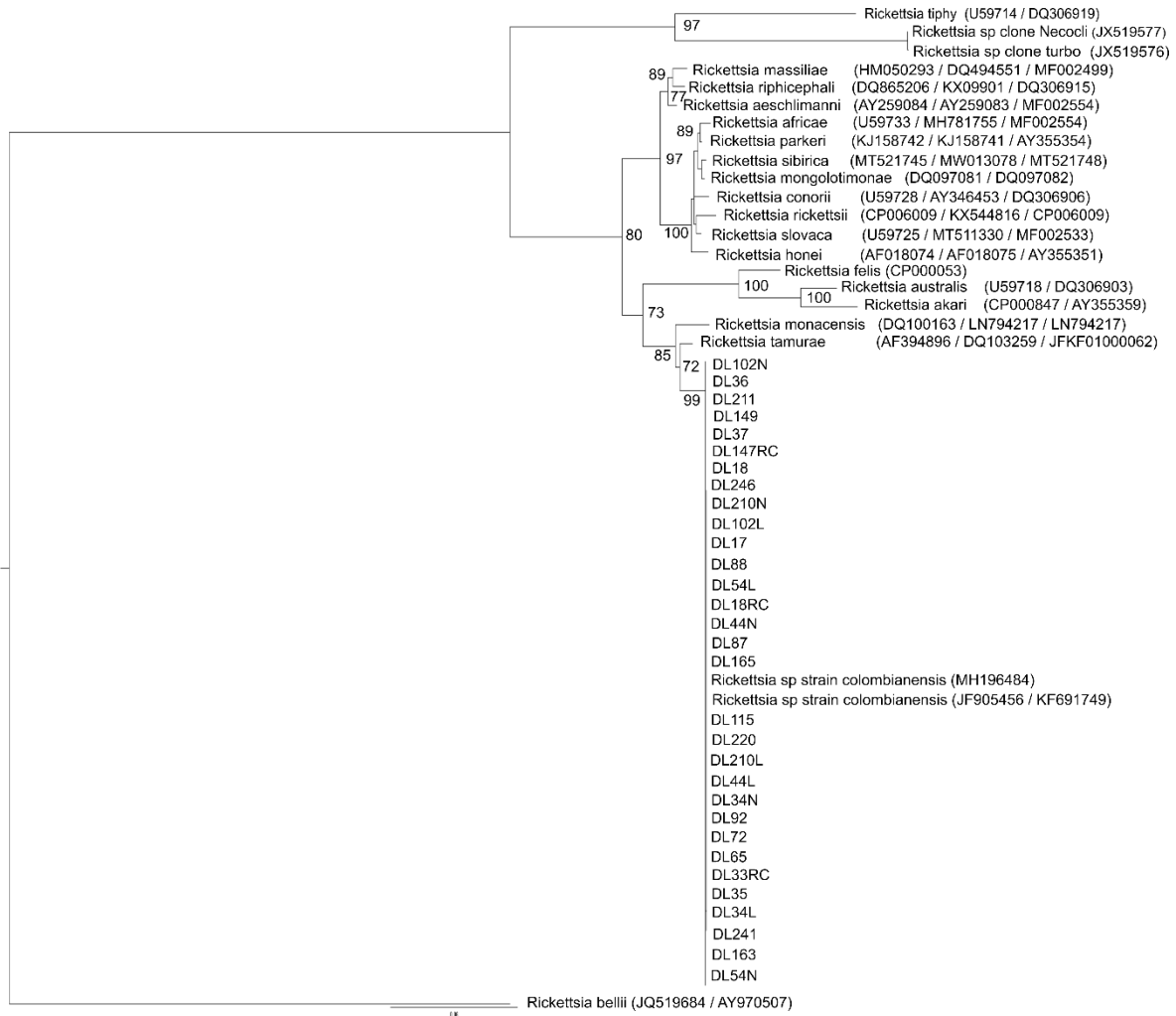


Figure S2. Phylogenetic reconstruction using maximum likelihood of concatenated GltA, OmpA and Sca1 genes for *Rickettsia*, including our sequences and sequences downloaded from genbank (with accession numbers included GltA/OmpA/Sca1). Numbers on nodes correspond to bootstrap values.

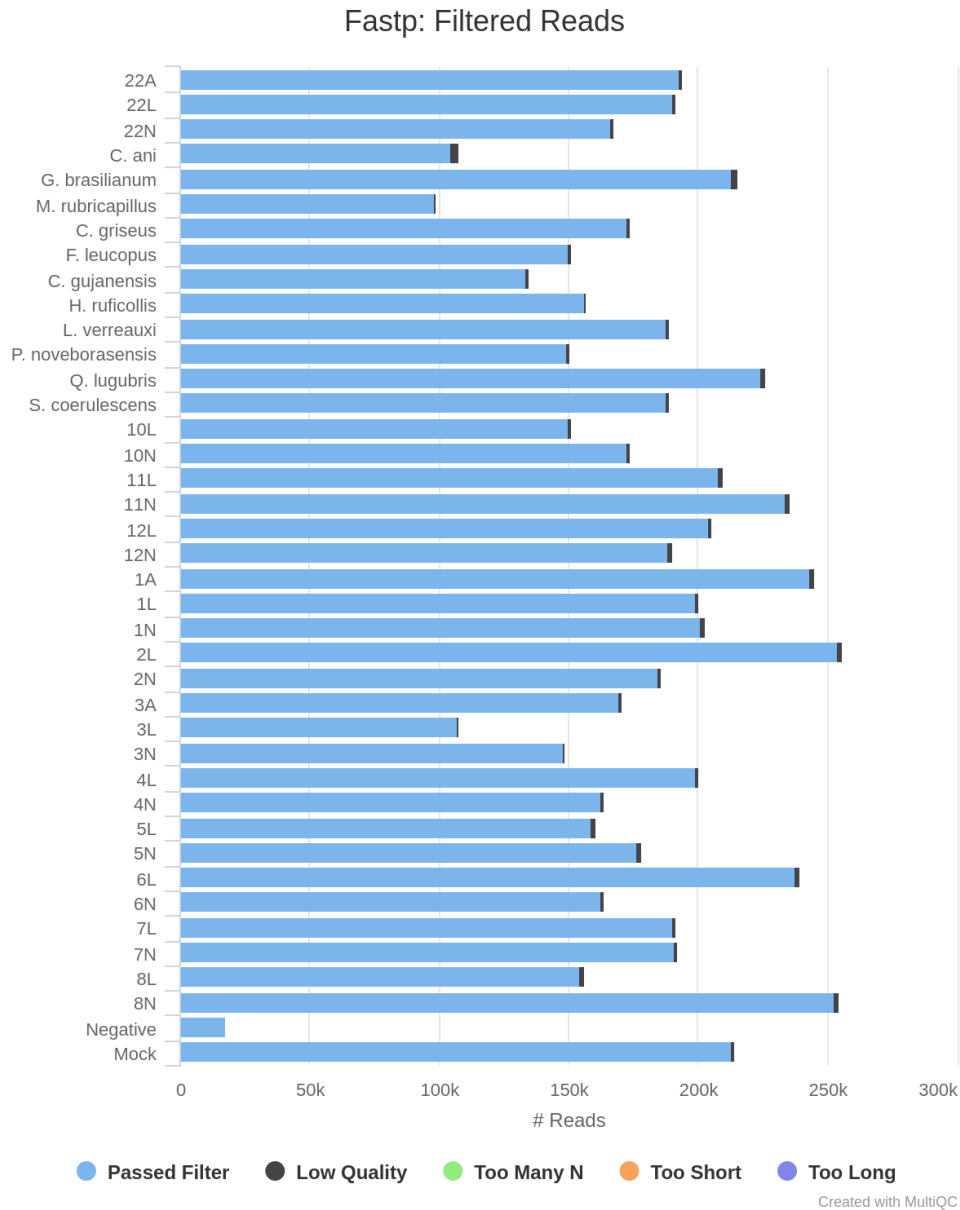
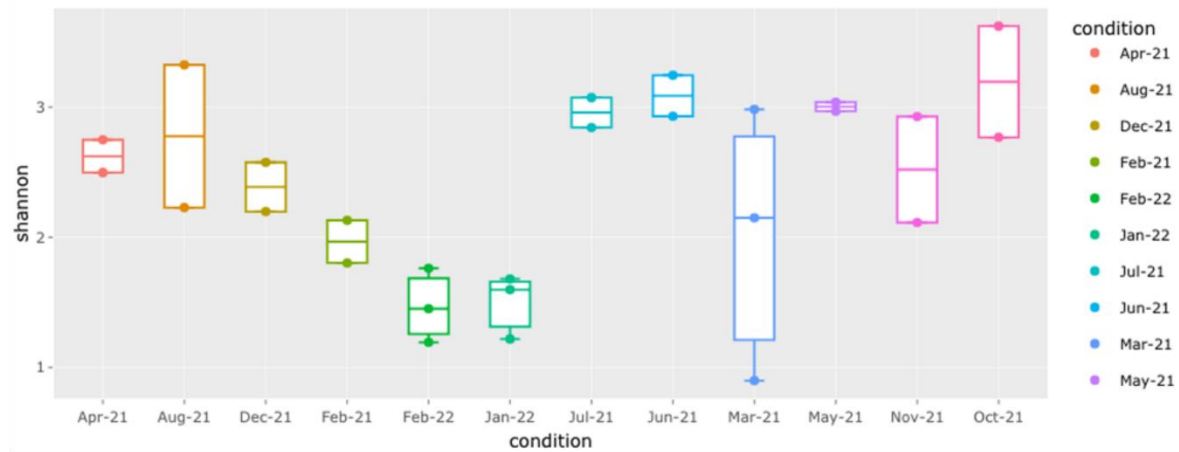
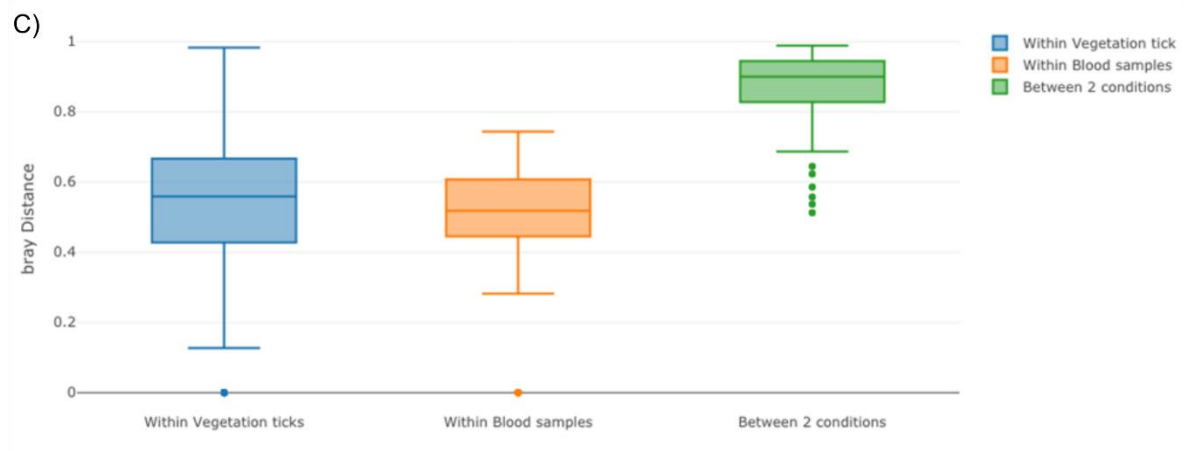
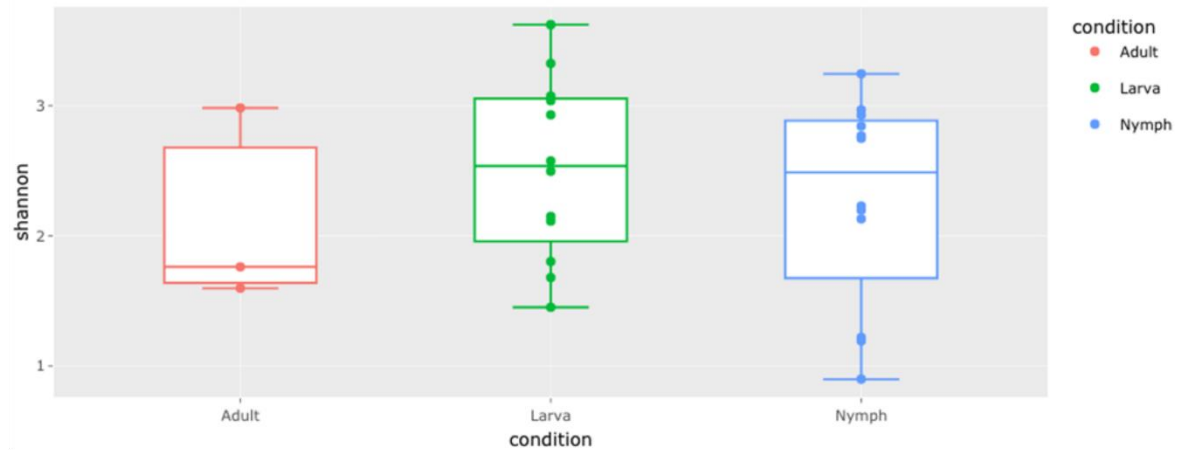


Figure S3. Number of reads for all samples. For the blood of birds' samples, the scientific name of the host where it was isolated is used. For the vegetation ticks' samples, the number represents the month of collection (1-12 for all samples taken in 2021, 22 for the February 2022 samples), and the letter represents the ticks' life stage: (L)arva, (N)ymp, (A)dult.

A) Alpha diversity between Mes_a (shannon)



B) Alpha diversity between Estado (shannon)



Supplementary Figure S4. Alpha diversity analysis based on Shannon index showed no significant differences (Kruskal-Wallis's rank sum test, $P < 0.05$) between A) Ticks life stage and B) vegetation ticks and blood samples. PERMANOVA test using Bray distance did showed significant beta diversity difference existing between vegetation ticks and blood samples ($P < 0.05$).