

**Table S3.** Genovariants of *Babesia*, *Theileria*, *Hemolivia* and *Hepatozoon* detected in French Guiana and best nucleotide identities with 18S rRNA gene sequences obtained in this study and sequences available in GenBank identified through Basic Local Alignment Search Tool (BLAST; <https://blast.ncbi.nlm.nih.gov/Blast.cgi>) searches (Last update: 01/04/2024).

Genovariant	Host species	Number of infected specimens	Best match in Genbank [% nucleotide identity; length of the 18S rRNA gene sequence; query cover; E-value; accession number]	Best match in the present study (% nucleotide identity)
<i>Hemolivia</i> #1	<i>Amblyomma dissimile</i> (iguana tick)	11	<i>Hemolivia stellata</i> , hosted by the tick <i>Amblyomma rotundatum</i> , Brazil [100%; 462 bp; 100%; E=0.0; KP881349]	<i>Hepatozoon</i> genovariant #3 of <i>Felis wiedii</i> (97.40%)
<i>Hepatozoon</i> #2	<i>Didelphis marsupialis</i> (common opossum)	7	<i>Hepatozoon</i> sp. DG1, hosted by the colocolo opossum <i>Dromiciops gliroides</i> , Chile [97.63%; 462 bp; 100%; E=0.0; FJ719813]	<i>Hepatozoon</i> genovariant #3 of <i>Felis wiedii</i> (98.05%)
	<i>Philander opossum</i> (gray four-eyed opossum)	1		
	<i>Coendou</i> sp. (prehensile-tailed porcupine)	1		
	<i>Ixodes luciae</i> (opossum tick)	1		
<i>Hepatozoon</i> #3	<i>Felis wiedii</i> (margay)	1	<i>Hepatozoon luiperdjie</i> , hosted by the African leopard <i>Panthera pardus pardus</i> , South Africa [100%; 462 bp; 100%; E=0.0; MN793004]	<i>Hepatozoon</i> genovariant #2 of opossums (98.05%)
	<i>Amblyomma oblongoguttatum</i> (tick)	1		
<i>Hepatozoon</i> #4	<i>Galictis vittata</i> (greater grison)	1	<i>Hepatozoon felis</i> , hosted by the domestic cat <i>Felis silvestris</i> , Hungary [98.05%; 462 bp; 100%; E=0.0; OM422756]	<i>Hepatozoon</i> genovariant #3 of <i>Felis wiedii</i> (97.83%)
<i>Hepatozoon</i> #5	<i>Amblyomma dissimile</i> (iguana tick)	2	<i>Hepatozoon cuorae</i> , hosted by the Indochinese box turtle <i>Cuora galbinifrons</i> , Viet Nam [100%; 462 bp; 100%; E=0.0; MW514214]	<i>Hepatozoon</i> genovariant #2 of opossums (97.41%)
<i>Theileria</i> #6	<i>Dasyus novemcinctus</i> (nine-banded armadillo)	3	<i>Theileria luwenshun</i> , hosted by domestic ruminants, China [90.41%; 462 bp; 100%; E=3e-155; KC769997]	<i>Babesia</i> genovariant #8 of <i>Amblyomma cajennense</i> (87.97%)
<i>Babesia</i> #7	<i>Choloepus didactylus</i> (two-toed sloth)	7	<i>Babesia</i> sp. isolate ID21ND, hosted by the tick <i>Amblyomma dubitatum</i> , Brazil [92.97%; 462 bp; 100%; E=1e-180; OQ194053]	<i>Babesia</i> genovariant #8 of <i>Amblyomma cajennense</i> (91.73%)
<i>Babesia</i> #8	<i>Amblyomma cajennense</i> (Cayenne tick)	14	<i>Babesia vogeli</i> , hosted by the brown dog tick <i>Rhipicephalus sanguineus</i> , Trinidad and Tobago [97.98%; 462 bp; 99%; E=1e-180; OR077270]	<i>Babesia</i> genovariant #7 of <i>Choloepus didactylus</i> (91.73%)