

Supplementary Table S1 : Number of samples collected (N) at the different geographic locations in each country. The location of the different sites is visualized in **Figure 1**.

Guinea	N
Boffa	21
Boke	49
Conakry	175
Faranah	48
Forecariah	15
Gueckedou	71
Kankan	110
Kindia	224
Kissidougou	25
Koundara	249
Lola	16
Macenta	154
Mali	119
Maman/Mamou	164
Nzerekore	11
Siguri	58
Cameroon	N
Bipindi	1138
Campo	1
Doumo Pierre	41
Mambele	268
Mbankomo	56
Nkolbisson	62
Obala	131
Tibati	52
Yaoundé	462
DRC	
Beni	245
Bikoro	136
Butembo	33
Iboko	76
Ingende	44
Mangina	79
Mbandaka	284

Supplementary Table S2 : Number (n) and percentages (%) of bat genus/species positive for coronaviruses per country and per species.

	DRC		Cameroon		Guinea		Total	
	n tested	n pos (%)	n tested	n pos (%)	n tested	n pos (%)	n tested	n (%)
Frugivorous bats								
<i>Pteropodidae</i>								
<i>Casinycteris arginnis</i>	22	0 (0)	2	0 (0)	nt ^d	nt	24	0 (0)
<i>Eidolon helvum</i>	56	12 (21.4)	500	211 (42.2)	177	70 (39.5)	733	293 (39.9)
<i>Epomophorus</i> sp. ^a	258	9 (3.5)	nt	nt	479	63 (13.2)	737	72 (9.8)
<i>Epomops</i> sp. ^b	210	3 (1.4)	28	2 (7.1)	20	3 (15.0)	258	8 (3.1)
<i>Hypsignathus monstrosus</i>	8	0 (0)	76	9 (11.8)	19	3 (15.8)	103	12 (11.7)
<i>Lissonycteris angolensis</i>	10	0 (0)	9	0 (0)	46	2 (4.3)	65	2 (3.1)
<i>Megaloglossus woermanni</i>	12	2 (6.7)	3	0 (0)	nt	nt	15	2 (13.3)
<i>Micropteropus pusillus</i>	147	4 (2.7)	2	0 (0)	16	1 (6.3)	165	5 (3.0)
<i>Myonycteris torquata</i>	86	6 (7.1)	4	0 (0)	1	0 (0)	91	6 (6.6)
<i>Nanonycteris</i> sp. ^c	nt	nt	nt	nt	3	1 (33.3)	3	1 (33.3)
<i>Rousettus aegyptiacus</i>	nt	nt	226	49 (21.7)	565	65 (11.5)	791	114 (14.4)
<i>Scotonycteris bergmansi</i>	1	0 (0)	nt	nt	nt	nt	1	0 (0)
subtotal	810	36 (4.4)	850	271 (31.9)	1326	208 (15.7)	2986	515 (17.2)
Insectivorous bats								
<i>Emballonuridae</i>								
<i>Coleura afra</i>	nt	nt	1	1 (100)	nt	nt	1	1 (100)
<i>Hipposideridae</i>								
<i>Hipposideros</i> sp. ^c	47	0 (0)	206	51 (24.8)	38	10 (26.3)	291	61 (20.9)
<i>Miniopteridae</i>								
<i>Miniopterus</i> sp. ^c	nt	nt	9	9 (100)	nt	nt	9	9 (100)
<i>Molossidae</i>								
<i>Chaerephon</i> sp. ^c	3	0 (0)	nt	nt	9	0 (0)	12	0 (0)
<i>Mops</i> sp. ^c	21	0 (0)	235	6 (2.6)	nt	nt	256	6 (2.3)
<i>Mops/Chaerephon</i> sp. ^c	13	0 (0)	104	0 (0)	14	4 (28.6)	131	4 (3.1)
<i>Nycteridae</i>								
<i>Nycteris</i> sp. ^c	nt	nt	nt	nt	5	1 (20.0)	5	1 (20)
<i>Rhinolophidae</i>								
<i>Rhinolophus</i> sp.	nt	nt	786	289 (36.8)	113	17 (15.0)	899	306 (34.1)
<i>Vespertilionidae</i>								
<i>Myotis</i> sp. ^c	3	0 (0)	nt	nt	1	0 (0)	4	0 (0)
<i>Scotophilus</i> sp. ^c	nt	nt	nt	nt	3	0 (0)	3	0 (0)
subtotal	87	0 (0)	1341	356 (26.5)	183	32 (17.5)	1611	388 (24.1)
Total	897	36 (4.0)	2191	627 (28.6)	1509	240 (15.9)	4597	903 (19.6)

^a Two *Epomophorus* species were observed, *E. gambianus* in Guinea, Cameroon and Western DRC and *E. labiatus* in Eastern DRC.

^b Two *Epomops* species were observed, *E. franqueti* in Cameroon and DRC and *E. buettikoferi* in Guinea.

^c Identification at species level was not possible for a significant proportion of samples tested and were therefore grouped at the genus level.

^d nt: not tested

Supplementary Table S3: Number (n) and proportion (%) of alpha and beta coronaviruses per bat genus/species, and p-values resulting from comparison of the proportions between alpha and betacoronavirus per genus/species, when applicable (χ^2 test).

	Sequences n	alpha coronavirus n pos (%)	beta coronavirus n pos (%)	p-value χ^2 test
Frugivorous bats				
<i>Pteropodidae</i>				
<i>Eidolon helvum</i>	238	2 (0.8)	236 (99.2)	<10 ⁻⁴ *
<i>Epomophorus</i> sp. ^a	55	2 (3.6)	53 (96.4)	<10 ⁻⁴ *
<i>Epomops</i> sp. ^b	5	0 (0.0)	5 (100)	na ^d
<i>Hypsignathus monstrosus</i>	10	0 (0.0)	10 (100)	na
<i>Lissonycteris angolensis</i>	2	1 (50.0)	1 (50.0)	na
<i>Megaloglossus woermanni</i>	2	0 (0.0)	2 (100)	na
<i>Micropteropus pusillus</i>	5	0 (0.0)	5 (100)	na
<i>Myonycteris torquata</i>	6	0 (0.0)	6 (100)	na
<i>Nanonycteris</i> sp. ^c	1	0 (0.0)	1 (100)	na
<i>Rousettus aegyptiacus</i>	97	21 (21.6)	76 (78.4)	<10 ⁻⁴ *
subtotal frugivorous bats	421	26 (6.2%)	395 (93.8%)	0.0029*
Insectivorous bats				
<i>Emballonuridae</i>				
<i>Coleura afra</i>	1	1 (100)	0 (0.0)	na
<i>Hipposideridae</i>				
<i>Hipposideros</i> sp. ^c	53	16 (30.2)	37 (69.8)	na
<i>Miniopteridae</i>				
<i>Miniopterus</i> sp. ^c	7	7 (100)	0 (0.0)	na
<i>Molossidae</i>				
<i>Mops</i> sp. ^c	6	3 (50.0)	3 (50.0)	na
<i>Mops/Chaerephon</i> sp. ^c	4	0 (0.0)	4 (100)	na
<i>Nycteridae</i>				
<i>Nycteris</i> sp. ^c	1	0 (0.0)	1 (100)	
<i>Rhinolophidae</i>				
<i>Rhinolophus</i> sp. ^c	275	122 (44.4)	153 (55.6)	0.0545, ns ^e
subtotal insectivorous bats	347	149 (42.9%)	198 (57.1%)	0.44, ns
Total	768	175 (22.8)	593 (77.2)	<10⁻⁴ *

^a Two *Epomophorus* species were observed, *E. gambianus* in Guinea, Cameroon and Western DRC and *E. labiatus* in Eastern DRC

^b Two *Epomops* species were observed, *E. franqueti* in Cameroon and DRC and *E. buettikoferi*

^c Identification at species level was not possible for a significant proportion of samples tested and were therefore grouped at the genus level.

^d na: non applicable χ^2 test (numbers too low, or do not exist)

^e ns : non significant χ^2 test (p-value>0.05)

* significant χ^2 test (p-value<0.05)

Supplementary Table S4: Number of bats positive for coronaviruses (n pos) on total number tested (N) and percentages (%) of samples per bat genus/species in Cameroon per age category (adults (A), immature adults (imm) and juveniles (J) and per species). The p-values result from comparison of the proportions of positive per genus/species, when applicable (χ^2 test).

	A n pos/N	A % pos	imm n pos/N	imm % pos	J n pos/N	J %pos	p-value
Frugivorous bats							
Pteropodidae							
<i>Casinycteris arginnis</i>	0/1	0.0	0/1	0.0	-	-	na ^d
<i>Eidolon helvum</i>	41/146	28.1	89/200	44.5	80/153	52.3	ns
<i>Epomops franqueti</i>	2/19	10.5	0/3	0.0	0/4	0.0	ns
<i>Hypsignathus monstrosus</i>	10/58	17.2	1/10	10	2/8	25.0	
<i>Lissonycteris angolensis</i>	0/6	0.0	0/2	0.0	0/1	0.0	na
<i>Megaloglossus woermanni</i>	0/2	0.0	0/1	0.0	-	-	na
<i>Micropteropus pusillus</i>	0/1	0.0	0/1	0.0	-	-	na
<i>Myonycteris torquata</i>	0/2	0.0	0/1	0.0	-	-	na
<i>Rousettus aegyptiacus</i>	5/109	4.6	18/38	47.4	26/79	32.9	ns
Subtotal frugivorous bats	58/344	16.9	108/257	42	108/245	44.1	<10⁻⁴ *
Insectivorous bats							
Emballonuridae							
<i>Coleura</i> sp.	1/1	100	-	-	-	-	na
Hipposideridae							
<i>Hipposideros</i> sp.	27/108	25.0	23/97	23.7	1/1	100	na
Miniopteridae							
<i>Miniopterus</i>	3/3	100	5/5	100	-	-	na
Molossidae							
<i>Chaerephon</i> sp.	0/77	0.0	-	-	0/25	0.0	na
<i>Mops</i> sp.							
Rhinolophidae							
<i>Rhinolophus</i> sp.	117/411	28.5	150/347	43.2	21/26	80.7	ns
Subtotal insectivorous bats	151/759	19.9	179/450	39.8	22/83	26.5	<10⁻⁴ *
Total	209/1103	18.9	287/707	40.6	130/328	39.6	10⁻⁴ *

^a Two *Epomophorus* species were observed, *E. gambianus* in Guinea, Cameroon and Western DRC and *E. labiatus* in Eastern DRC

^b Two *Epomops* species were observed, *E. franqueti* in Cameroon and DRC and *E. buettikoferi*

^c Identification at species level was not possible for a significant proportion of samples tested and were therefore grouped at the genus level.

^d na non applicable (numbers too low or do not exist)

^e ns : non significant χ^2 test (p-value>0.05)

* significant χ^2 test (p-value<0.05)