

## Appendix A

### Species replacement details for cophylogeny analysis

Some host species in the bartonella dataset were only identified to the genus level, but these genera were important to include because their exclusion would have reduced the breadth of the analysis and some represented unique families. Thus, a representative species was chosen based on a) close relatedness with the original host (same genus), b) geographic range overlap with the study capture location, and c) the availability of *cytb* sequences on GenBank with similar length to others in the dataset (~1000 base pairs). For *Micropteropus* sp. and *Epomophorus* sp. from Nigeria, only *Micropteropus pusillus* and *Epomophorus gambianus* had ranges that overlapped with the capture location. *Tylonycteris pachypus* was the only species with a suitable *cytb* sequence for *Tylonycteris* sp. For other representative species, multiple options fulfilled the above criteria:

*Miniopterus* sp. (Kenya) – *M. natalensis*, *M. fraterculus*

*Myotis* sp. (Peru) – *M. nigricans*, *M. keaysi*, *M. riparius*, *M. simus*

*Pipistrellus* sp. (UK) – *P. pipistrellus*, *P. nathusii*, *P. pygmaeus*

*Hipposideros* sp. (Malaysia) – *H. diadema*, *H. armiger*, *H. ater*, *H. bicolor*, *H. cervinus*,

*H. cineraceus*, *H. larvatus*, *H. pomona*

*Rhinolophus* sp. (Nigeria) – *R. landeri*, *R. fumigatus*

From these options, a random choice was drawn from the available set. *Miniopterus natalensis* was chosen to represent *Miniopterus* sp. from Kenya, *Myotis nigricans* for *Myotis* sp. from Peru, *Pipistrellus pipistrellus* for *Pipistrellus* sp. from the UK, *Hipposideros diadema* for *Hipposideros* sp. from Malaysia, and *Rhinolophus landeri* for *Rhinolophus* sp. from Nigeria. These replacements are marked with an asterisk (\*) in Table S3.

For other bat species, no *cytb* sequences could be found or they were too short (much less than 1000 base pairs). Thus, a suitable replacement was found based on a) close relatedness with the original host (same genus), b) geographic range overlap with the study capture location, and c) the availability of *cytb* sequences on GenBank with similar length to others in the dataset (~1000 base pairs). *Phyllostomus discolor* is present in both Guatemala and Peru and only *Phyllostomus hastatus* is present in both locations. *Megaderma lyra* and *Megaerops ecaudatus* were the only other member of their genera in Vietnam to replace *Megaderma spasma* and *Megaerops niphanae*, respectively. For *Hipposideros commersoni*, this species has been split into three additional species previously recognized as subspecies – *H. gigas*, *H. thomensis*, and *H. vittatus*. Only *H. gigas* fulfilled both criteria for overlap with the capture location in Kenya and the availability of a suitable *cytb* sequence. For other replacement species, multiple options fulfilled the above criteria:

*Rhinolophus borneensis* subsp. *chasei* and *R. acuminatus* (Vietnam) – *R. affinis*, *R. malayanus*, *R. pearsonii*, *R. sthenops*

*Hipposideros fulvus* (Thailand) - *H. armiger*, *H. ater*, *H. cineraceus*, *H. diadema*, *H. larvatus*, *H. lylei*, *H. pomona*, *H. pratti*, *H. turpis*

From these options, a random selection was made. *Rhinolophus acuminatus* was replaced with *Rhinolophus malayanus*, *Rhinolophus borneensis* subsp. *chasei* with *Rhinolophus affinis*, and *Hipposideros fulvus* with *Hipposideros cineraceus*. These replacements are marked with a dagger (†) in Table S3. Lei and Olival (2014) made similar replacements for species in their analysis, although without the stipulation that the geographic range of the substitute species should overlap with the capture location. The inclusion of this criterion is important in the present study because of the dual focus on bat phylogeny and sympatry. This stipulation was

only modified for *Chaerephon plicatus*, which has no representative *cytb* sequence in GenBank and no other representatives of the genus present in Thailand.

It would be computationally infeasible to test how each choice of replacement affects our results, however we perform a single sensitivity analysis by using a second set of suitable replacement species in the global fit tests and correlation between bat phylogeny and sympatry. For the sensitivity analysis, we chose *Miniopterus fraterculus* (AJ841975) to represent *Miniopterus* sp. from Kenya, *Chaerephon leucogaster* (GQ489166) for *Chaerephon plicatus* from Thailand, *Myotis riparius* (JX130570) for *Myotis* sp. from Peru, *Pipistrellus pygmaeus* (AJ504442) for *Pipistrellus* sp. from the UK, *Hipposideros pomona* (DQ054810) for *Hipposideros* sp. from Malaysia, *Hipposideros lylei* (JN247043) for *Hipposideros fulvus* from Thailand, *Rhinolophus steno* (FJ185213) for *Rhinolophus acuminatus* from Vietnam, *Rhinolophus pearsonii* (JX502551) for *Rhinolophus borneensis* subsp. *chasei* from Vietnam, *Rhinolophus fumigatus* (FJ457614) for *Rhinolophus* sp. from Nigeria.

Using the maximum likelihood trees of bat species and *Bartonella* genotypes, global fit tests find a strongly significant cophylogenetic signal (ParaFitGlobal = 13.37,  $P = 1E-5$ ;  $m^2$  global value = 8.54,  $P = 1E-4$ ). Using ParaFit, 159/186 of host-parasite links were significant at the  $P \leq 0.05$  level, 129/186 at the  $P \leq 0.005$  level, and 103/186 at the  $P \leq 0.001$  level. Using PACo, 93/186 of host-parasite links were below the median and 9 were above  $Q3+1.5(IQR)$ . The correlation between bat phylogeny and sympatry remains strong with the substitute species (Pearson correlation coefficient = 0.31,  $P = 1E-5$ ). Global fit tests were repeated using bat sympatry and the maximum likelihood tree of *Bartonella* genotypes, finding a significant trend (ParaFitGlobal = 106.3,  $P = 1E-5$ ;  $m^2$  global value = 57.5,  $P = 1E-4$ ). Using ParaFit, 144/186 of host-parasite links were significant at the  $P \leq 0.05$  level, 133/186 at the  $P \leq 0.005$  level, and

126/186 at the  $P \leq 0.001$  level. Using PACo, 93/186 of host-parasite links were below the median and 5 were above  $Q3+1.5(IQR)$ . The optimal linear combination of the bat phylogeny and bat sympatry matrices using ParaFit was  $\omega_{\text{phy}} = 1$  and  $\omega_{\text{geo}} = 0$ , ParaFitGlobal = 13.37; for PACo the optimal combination was  $\omega_{\text{phy}} = 1$  and  $\omega_{\text{geo}} = 0$ ,  $m^2$  global value = 8.54. Our sensitivity analysis indicated that the choice of substitute species does not greatly affect the results of the cophylogeny tests.

## Appendix B

### Analysis of sampling bias

We looked for the presence of bias in the dataset by testing the correlation between the number of host-parasite links and sampling effort. Specifically, we used two measures of sampling effort: the number of published articles on each bat species found on Web of Science and the total sample size of each bat species tested in the individual studies that contribute to the dataset. There was a significant log-log correlation between the number of host-parasite links and Web of Science articles (Fig. S10a; Pearson correlation coefficient,  $r = 0.27$ ,  $P = 0.03$ ). The correlation became only marginally significant when the bat with the highest number of host-parasite links (*Eidolon helvum*, 35 links) was removed (Fig. S10b; Pearson correlation coefficient,  $r = 0.24$ ,  $P = 0.05$ ). There was a significantly positive log-log correlation between the number of links and individual species' sample sizes (Fig. S10c; Pearson correlation coefficient,  $r = 0.71$ ,  $P = 4E-11$ ). This correlation was still significant when the species with the highest number of host-parasite links (*Eidolon helvum*, 35 links) was removed (Fig. S10d; Pearson correlation coefficient,  $r = 0.66$ ,  $P = 4E-09$ ). This suggests that high levels of bartonella diversity found in several bat species are probably due in part to sampling bias, although this does not completely exclude the effects of ecological and evolutionary processes that may increase bartonella diversity in some bats.

## Supplementary Material

**Table S1.** *Bartonella* citrate synthase (*gltA*) genotypes detected in bats included in the analysis dataset with GenBank accession numbers. Host bat genus and species were extracted from GenBank metadata or from published articles (Anh et al., 2015; Bai et al., 2015, 2012, 2011; Brook et al., 2015; Concannon et al., 2005; Judson et al., 2015; Kamani et al., 2014; Kosoy et al., 2010; Lin et al., 2012; Olival et al., 2015; Veikkolainen et al., 2014). Bats from Thailand were included from the CDC database (M. Kosoy, unpublished data).

Genotype	Host species	Location	<i>gltA</i> accession number
M406	<i>Myotis daubentonii</i>	UK	AJ871613
M62	<i>Myotis mystacinus</i>	UK	AJ871612
M207	<i>Pipistrellus</i> sp.	UK	AJ871614
M451	<i>Nyctalus noctula</i>	UK	AJ871615
M409	<i>Pipistrellus</i> sp.	UK	AJ871611
Cul-9	<i>Lophostoma silvicolum</i>	Peru	EF616479
R-191	<i>Rousettus aegyptiacus</i>	Kenya	HM363764
T-837	<i>Triaenops persicus</i>	Kenya	HM545138
H-556	<i>Hipposideros commersoni</i>	Kenya	HM545137
C-583	<i>Coleura afra</i>	Kenya	HM545136
M1-44	<i>Miniopterus</i> sp.	Kenya	HM545139
M2-491	<i>Miniopterus</i> sp.	Kenya	HM545140
M3-373	<i>Miniopterus</i> sp.	Kenya	HM545141
B29042	<i>Desmodus rotundus</i>	Guatemala	HM597187
B29043	<i>Desmodus rotundus</i>	Guatemala	HM597188
B29044	<i>Desmodus rotundus</i>	Guatemala	HM597189
B29107	<i>Desmodus rotundus</i>	Guatemala	HM597190
B29108	<i>Desmodus rotundus, Carollia perspicillata</i>	Guatemala	HM597191
B29114	<i>Desmodus rotundus, Carollia perspicillata</i>	Guatemala	HM597192
B29102	<i>Pteronotus davayi</i>	Guatemala	HM597193
B29109	<i>Pteronotus davayi</i>	Guatemala	HM597194
B29119	<i>Desmodus rotundus</i>	Guatemala	HM597195
B29122	<i>Desmodus rotundus</i>	Guatemala	HM597196
B29116	<i>Phyllostomus discolor</i>	Guatemala	HM597198
B29126	<i>Carollia perspicillata, Sturnira lilium</i>	Guatemala, Costa Rica	HM597199, KJ816674
B29230	<i>Phyllostomus discolor</i>	Guatemala	HM597200
B29115	<i>Phyllostomus discolor</i>	Guatemala	HM597201
B29110	<i>Glossophaga soricina</i>	Guatemala	HM597202
B29105	<i>Pteronotus davayi</i>	Guatemala	HM597203
B29112	<i>Phyllostomus discolor</i>	Guatemala	HM597204
B29134	<i>Pteronotus davayi</i>	Guatemala	HM597205
B29137	<i>Sturnira lilium</i>	Guatemala	HM597206
B29172	<i>Micronycteris microtis</i>	Guatemala	HM597207
B29111	<i>Artibeus toltecus</i>	Guatemala	HM597197
B32945	<i>Desmodus rotundus</i>	Peru	JQ071379
B32947	<i>Phyllostomus discolor</i>	Peru	JQ071387
B32954	<i>Artibeus planirostris</i>	Peru	JQ071382
B32946	<i>Glossophaga soricina</i>	Peru	JQ071383
B32943	<i>Carollia perspicillata</i>	Peru	JQ071384
B32960	<i>Carollia perspicillata</i>	Peru, Costa Rica	JQ071386, KJ816691
B32955	<i>Carollia perspicillata</i>	Peru	JQ071385
B32854	<i>Phyllostomus hastatus</i>	Peru	JQ071388
B32855	<i>Desmodus rotundus</i>	Peru	JQ071378
B32856	<i>Vampyressa bidens</i>	Peru	JQ071389
B32942	<i>Myotis</i> sp.	Peru	JQ071390
B32851	<i>Artibeus obscurus</i>	Peru	JQ071380

Genotype	Host species	Location	gltA accession number
B32953	<i>Artibeus planirostris</i>	Peru	JQ071381
No. 5	<i>Miniopterus schreibersii</i>	Taiwan	JF500511
No. 7	<i>Miniopterus schreibersii</i>	Taiwan	JF500513
AS050	<i>Myotis myotis</i>	Poland	JQ695835
AS071	<i>Myotis myotis</i>	Poland	JQ695834
2574/1	<i>Myotis daubentonii</i>	Finland	KF003129
1160/1	<i>Myotis daubentonii</i>	Finland	KF003122
1157/3	<i>Eptesicus nilssoni</i>	Finland	KF003115
Mr37079	<i>Monophyllus redmani</i> , <i>Phyllonycteris poeyi</i>	Puerto Rico, Dominican Republic	KJ530746, JX416249
Mr37078	<i>Monophyllus redmani</i>	Puerto Rico	KJ530745
Mr37077	<i>Monophyllus redmani</i>	Puerto Rico	KJ530744
Mr37075	<i>Monophyllus redmani</i>	Puerto Rico	KJ530743
Bc37076	<i>Brachyphylla cavernarum</i>	Puerto Rico	KJ530742
Aj37081	<i>Artibeus jamaicensis</i>	Puerto Rico	KJ530741
B23976	<i>Eidolon helvum</i>	Kenya	KM030507
B40005	<i>Eidolon helvum</i>	Cameroon	KM030518
B23979	<i>Eidolon helvum</i>	Kenya	KM030509
B24225	<i>Eidolon helvum</i>	Kenya	KM030511
B40396	<i>Eidolon helvum</i>	Tanzania	KM030522
B40400	<i>Eidolon helvum</i>	Tanzania	KM030523
B23812	<i>Eidolon helvum</i> , <i>Rhinolophus landeri</i>	Kenya, Nigeria	KM030504, KF418810
B24163	<i>Eidolon helvum</i>	Kenya	KM030510
B32120	<i>Eidolon helvum</i>	Nigeria	KM030512
B39301	<i>Eidolon helvum</i>	Ghana	KM030516
B39325	<i>Eidolon helvum</i>	Ghana	KM030517
B23975	<i>Eidolon helvum</i>	Kenya	KM030506
B39286	<i>Eidolon helvum</i>	Ghana	KM030514
B39296	<i>Eidolon helvum</i>	Ghana	KM030515
B40908	<i>Eidolon helvum</i>	Uganda	KM030526
B39249	<i>Eidolon helvum</i>	Ghana	KM030513
B40391	<i>Eidolon helvum</i>	Tanzania	KM030521
B40014	<i>Eidolon helvum</i>	Tanzania	KM030520
B40406	<i>Eidolon helvum</i>	Tanzania	KM030525
B23797	<i>Eidolon helvum</i> , <i>Micropteropus pusillus</i> , <i>Epomophorus gambianus</i>	Kenya, Nigeria	KM030503, KF418812, KF418808
Mi-BA38	<i>Micropteropus</i> sp.	Nigeria	KF418812
Eh-GB64	<i>Eidolon helvum</i>	Nigeria	KF418811
Rh-GB31	<i>Rhinolophus</i> sp.	Nigeria	KF418810
Ep-BA63	<i>Epomophorus</i> sp.	Nigeria	KF418808
Rh-GB59	<i>Rhinolophus</i> sp.	Nigeria	KF418809
Rh-GB1	<i>Rhinolophus</i> sp.	Nigeria	KF418807
Ep-GB65	<i>Epomophorus</i> sp.	Nigeria	KF418806
B110	<i>Hipposideros larvatus</i> , <i>Hipposideros</i> <i>armiger</i>	Vietnam	KP100360, KP100357
B109	<i>Megaderma lyra</i>	Vietnam	KP100359
B102	<i>Rhinolophus chaseni</i>	Vietnam	KP100358
B096	<i>Hipposideros armiger</i>	Vietnam	KP100357
B095	<i>Hipposideros armiger</i>	Vietnam	KP100356
B087	<i>Hipposideros larvatus</i>	Vietnam	KP100355
B081	<i>Hipposideros larvatus</i>	Vietnam	KP100354
B079	<i>Rhinolophus chaseni</i>	Vietnam	KP100353
B072	<i>Megaerops niphanae</i>	Vietnam	KP100352
B068	<i>Rhinolophus acuminatus</i>	Vietnam	KP100351
B064	<i>Rhinolophus acuminatus</i>	Vietnam	KP100350

Genotype	Host species	Location	<i>gltA</i> accession number
B063	<i>Rhinolophus acuminatus</i>	Vietnam	KP100349
B056	<i>Rhinolophus acuminatus</i>	Vietnam	KP100348
B055	<i>Rhinolophus acuminatus</i>	Vietnam	KP100347
B052	<i>Rhinolophus acuminatus</i>	Vietnam	KP100346
B050	<i>Rhinolophus acuminatus</i>	Vietnam	KP100345
B049	<i>Rhinolophus sinicus</i>	Vietnam	KP100344
B047	<i>Rhinolophus sinicus</i>	Vietnam	KP100343
B006	<i>Rhinolophus acuminatus</i>	Vietnam	KP100342
B005	<i>Megaderma spasma</i>	Vietnam	KP100341
B003	<i>Rhinolophus acuminatus</i>	Vietnam	KP100340
SK197	<i>Tadarida plicata</i>	Thailand	-
SK170	<i>Tadarida plicata</i>	Thailand	-
SK157	<i>Tadarida plicata</i>	Thailand	-
CR224	<i>Hipposideros fulvus</i>	Thailand	-
KP270	<i>Hipposideros larvatus</i>	Thailand	-
KP182	<i>Hipposideros armiger, Hipposideros larvatus</i>	Thailand	-
KP283b	<i>Taphozous melanopogon</i>	Thailand	-
SK163	<i>Tadarida plicata</i>	Thailand	-
KP277	<i>Hipposideros larvatus</i>	Thailand	-
KP293b	<i>Hipposideros larvatus</i>	Thailand	-
KEL08	<i>Eidolon dupreanum</i>	Madagascar	KP010191
KEL16	<i>Eidolon dupreanum</i>	Madagascar	KP010192
KEL17	<i>Eidolon dupreanum</i>	Madagascar	KP010193
I	<i>Anoura geoffroyi</i>	Costa Rica	KJ816666
III	<i>Artibeus lituratus, Anoura geoffroyi, Sturnira mordax, Sturnira lilium</i>	Costa Rica	KJ816680
III	<i>Vampyressa thyone</i>	Costa Rica	KJ816672
III	<i>Carollia castanea</i>	Costa Rica	KJ816683
III	<i>Artibeus lituratus</i>	Costa Rica	KJ816675
III	<i>Platyrrhinus vittatus</i>	Costa Rica	KJ816684
VII	<i>Carollia sowelli</i>	Costa Rica	KJ816690
XII	<i>Myotis keaysi</i>	Costa Rica	KJ816676
2308	<i>Brucella melitensis</i>	outgroup	AM040264
OV483	<i>Rhizobium leguminosarum</i>	outgroup	NZ_JQJS01000011
OAB	<i>Ochrobactrum anthropi</i>	outgroup	NZ_CP008820



**Table S2.** *Bartonella* citrate synthase (*gltA*) genotypes detected in ectoparasites included in the analysis dataset with GenBank accession numbers. Ectoparasite and host bat genus and species were extracted from GenBank metadata or from published articles (Billeter et al., 2012; Brook et al., 2015; Judson et al., 2015; Morse et al., 2012; Veikkolainen et al., 2014).

Genotype	Ectoparasite	Host species	Location	<i>gltA</i> accession number
NB-1.2	<i>Siphonaptera</i> sp.	<i>Myotis brandtii</i>	Finland	KF003137
AS025	<i>Spinturnix myoti</i>	<i>Myotis myotis</i>	Poland	JQ695839
AS033	<i>Spinturnix myoti</i>	<i>Myotis myotis</i>	Poland	JQ695838
AS036	<i>Spinturnix myoti</i>	<i>Myotis myotis</i>	Poland	JQ695837
AS048	<i>Spinturnix myoti</i>	<i>Myotis myotis</i>	Poland	JQ695836
AS067	<i>Spinturnix myoti</i>	<i>Myotis myotis</i>	Poland	JQ695840
Cg 462	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172074
Cg 401	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172072
Cg 454	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172071
Cg 414	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172070
Cg 433	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172069
Cg 443	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172068
Cg 465-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172067
Cg 713-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172066
Cg 405	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172065
Cg 424	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172064
Cg 417-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172063
Cg 426-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172062
Cg 436-3	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172061
Cg 418	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172060
Cg 423-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172059
Cg 423-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Bioko	JN172058
Cg 364	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Annobón	JN172049
Cg 374	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Annobón	JN172050
Cg 358-3	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Annobón	JN172051
Cg 366-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Annobón	JN172052
Cg 371	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Annobón	JN172053
Cg 315-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Annobón	JN172054
Cg 303-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Annobón	JN172055
Cg 303-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Annobón	JN172056
Cg 366	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Equatorial Guinea: Annobón	JN172057
Cg K1-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172035
Cg K5-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172036
Cg K8-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172037
Cg Q22-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172038

Genotype	Ectoparasite	Host species	Location	gltA accession number
Cg Q98-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172039
Cg Q100-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172040
Cg Q130	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172041
Cg G35-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172042
Cg G31-1	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172043
Cg G38-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172044
Cg GG236	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172045
Cg GG48	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172046
Cg GG243-2	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172047
Cg GG243-3	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN172048
E-124	<i>Cyclopodia greefi</i>	<i>Eidolon helvum</i>	Ghana	JN190887
E7	<i>Cyclopodia horsfieldii</i>	<i>Pteropus hypomelanus</i>	Malaysia	JX416257
E5	<i>Cyclopodia horsfieldii</i>	<i>Pteropus hypomelanus</i>	Malaysia	JX416256
P2874	<i>Cyclopodia simulans</i>	<i>Ptenochirus jagori</i>	Philippines	JX416255
27_3_4	<i>Paradyschiria lineata</i>	<i>Noctilio leporinus</i>	Panama	JX416254
DR0583	<i>Trichobius adamsi</i>	<i>Macrotus waterhousii</i>	Dominican Republic	JX416253
05_01_07	<i>Phthiridium</i> sp. <i>scissa</i> group	<i>Rhinolophus pearsoni</i>	Laos	JX416252
23_03_04	<i>Strebla diaemi</i>	<i>Diaemus youngi</i>	Panama	JX416251
CWD974	<i>Trichobius johnsonae</i>	<i>Pteronotus personatus</i>	Mexico	JX416248
RCO934	<i>Pseudostrebla ribeiroi</i>	<i>Lophostoma silviculum</i>	Peru	JX416247
Mala11	<i>Basilina</i> ( <i>Tripselia</i> ) <i>coronata</i>	<i>Tylonycteris</i> sp.	Malaysia	JX416246
ZAG03	<i>Basilina</i> <i>nattereri</i>	<i>Myotis nattereri</i>	Slovenia	JX416241
JAE1033	<i>Leptocyclopodia</i> sp. nov.	<i>Harpionycteris whiteheadi</i>	Philippines	JX416239
Mala15	<i>Phthiridium</i> ( <i>Stylidia</i> ) <i>fraterna</i>	<i>Hipposideros</i> sp.	Malaysia	JX416238
DR05241	<i>Trichobius adamsi</i>	<i>Macrotus waterhousii</i>	Dominican Republic	JX416237
ZAG01	<i>Trichobius corynorhinus</i>	<i>Corynorhinus townsendii</i>	USA	JX416236
FG13	<i>Paratrichobius longicrus</i> complex	<i>Artibeus lituratus</i>	French Guyana, Costa Rica	JX416232, KJ816687
FG10	<i>Paratrichobius longicrus</i> complex	<i>Artibeus lituratus</i>	French Guyana	JX416231
KEL02-3	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010152
KEL02-4	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010153
KEL19-1	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010164
KEL09-1	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010159
KEL02-2	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010151
KEL11-1	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010160
KEL07-1	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010158
KEL17-2	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010163
KEL04-1	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010155
ANGB03-1	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010150
KEL04-2	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010156

<b>Genotype</b>	<b>Ectoparasite</b>	<b>Host species</b>	<b>Location</b>	<b>gltA accession number</b>
KEL02-5	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010154
KEL17-1	<i>Cyclopodia dubia</i>	<i>Eidolon dupreanum</i>	Madagascar	KP010162
II	<i>Exastinion clovisi</i>	<i>Anoura geoffroyi</i>	Costa Rica	KJ816688
III	<i>Trichobius dugesii</i>	<i>Glossophaga soricina</i>	Costa Rica	KJ816678
IV	<i>Aspidoptera phyllostomatis</i>	<i>Artibeus jamaicensis</i>	Costa Rica	KJ816682
V	<i>Paratrichobius longicrus</i>	<i>Artibeus lituratus</i>	Costa Rica	KJ816685
VIII	<i>Trichobius joblingi</i>	<i>Carollia castanea</i>	Costa Rica	KJ816686
X	<i>Trichobius costalimai</i>	<i>Phyllostomus discolor</i>	Costa Rica	KJ816665
XI	<i>Trichobius keenani</i>	<i>Micronycteris microtis</i>	Costa Rica	KJ816681
XII	<i>Aspidoptera delatorrei</i>	<i>Sturnira lilium</i>	Costa Rica	KJ816673
XIII	<i>Anatrichobius scorzai</i>	<i>Myotis keaysi</i>	Costa Rica	KJ816669
XIV	<i>Anatrichobius scorzai</i>	<i>Myotis keaysi</i>	Costa Rica	KJ816667
XV	<i>Aspidoptera delatorrei</i>	<i>Sturnira lilium</i>	Costa Rica	KJ816679
XVI	<i>Paratrichobius dunni</i>	<i>Uroderma bilobatum</i>	Costa Rica	KJ816692
XVII	<i>Paratrichobius dunni</i>	<i>Uroderma bilobatum</i>	Costa Rica	KJ816677
XIX	<i>Megistopoda proxima</i>	<i>Sturnira lilium</i>	Costa Rica	KJ816670
XX	<i>Basilia</i> sp.	<i>Myotis keaysi</i>	Costa Rica	KJ816689
2308	<i>Brucella melitensis</i>	-	outgroup	AM040264
OV483	<i>Rhizobium leguminosarum</i>	-	outgroup	NZ_JQJS01000011
OAB	<i>Ochrobactrum anthropi</i>	-	outgroup	NZ_CP008820

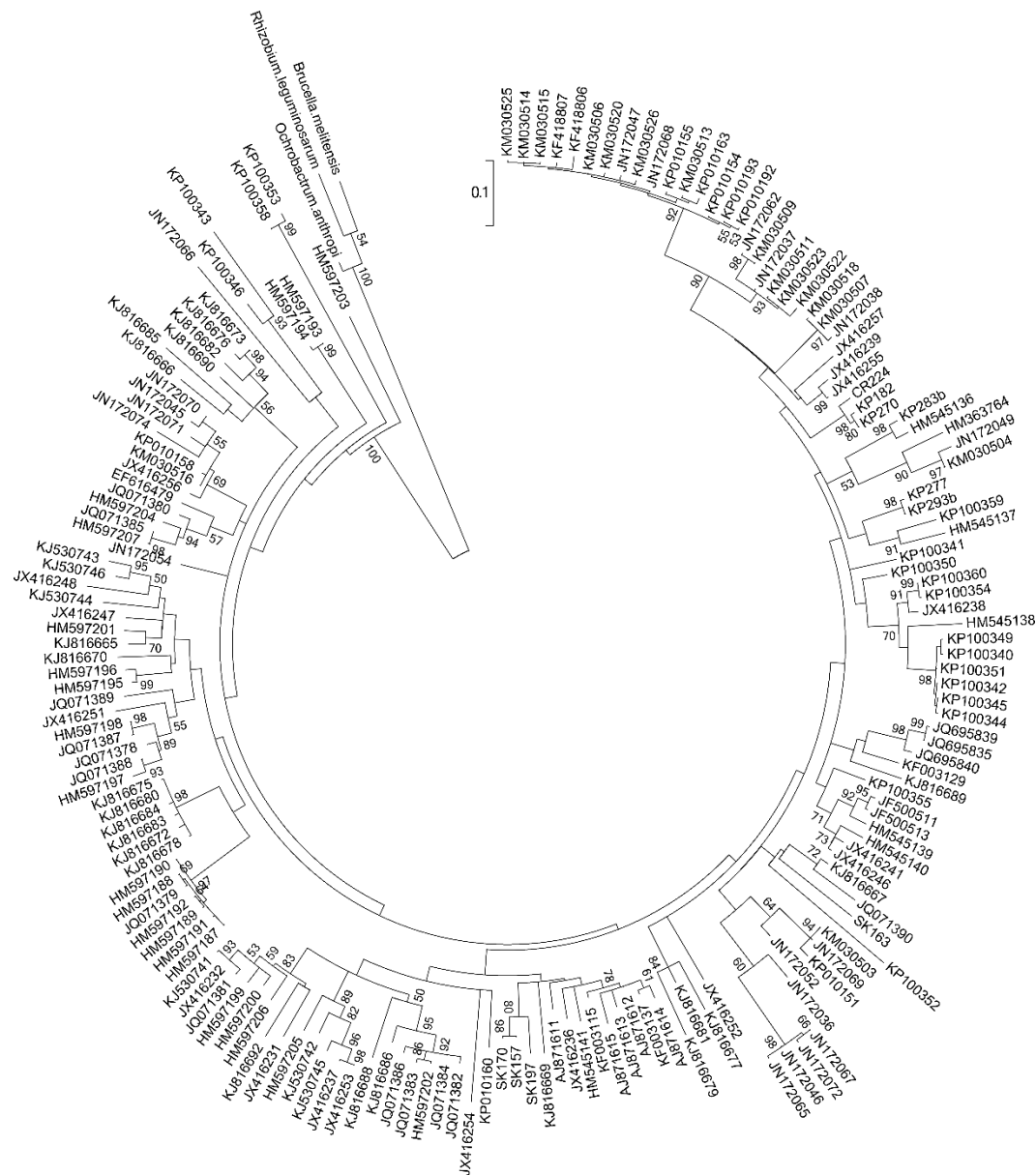
**Table S3.** Cytochrome b (*cytb*) sequences for bat species included in the analysis dataset with GenBank accession numbers. An asterisk (\*) indicates that the species is a representative for sequences attributed only to the bat genus. A dagger (†) indicates that the original host species has no suitable *cytb* sequence in GenBank and was replaced by another species. A double dagger (§) indicates that the host species name listed in the original article has been revised or reclassified. See Appendix A for details on species replacements. Host bat family and suborder were recorded based on the IUCN Red List of Threatened Species (IUCN, 2014), the Mammal Species of the World 3<sup>rd</sup> Edition (Wilson and Reeder, 2005), and published articles (Agnarsson et al., 2011; Teeling et al., 2002). Web of Science citations (as of August 2015) were recorded based on a search of the original host binomial species name. Study sample sizes for each species were quantified from original articles, using the original host species wherever a species-level replacement was made.

Host species	Family	Suborder	Region	<i>cytb</i> accession number	WoS citations	Study sample size	Number of links
<i>Coleura afra</i>	Emballonuridae	Yangochiroptera	Africa	JQ710752	6	9	1
<i>Taphozous melanopogon</i>	Emballonuridae	Yangochiroptera	Asia S/SE/SE	EF584221	28	2	1
<i>Miniopterus natalensis</i> *	Miniopteridae	Yangochiroptera	Africa	AJ841977	28	87	3
<i>Miniopterus schreibersii</i>	Miniopteridae	Yangochiroptera	Europe-Asia-Africa	EF530348	211	14	2
<i>Chaerephon plicatus</i> ( <i>Tadarida plicata</i> )†§	Molossidae	Yangochiroptera	Asia S/SE/SE	GQ489157	5	45	4
<i>Pteronotus davayi</i>	Mormoopidae	Yangochiroptera	America C/S/Carib	AF338672	20	10	5
<i>Pteronotus personatus</i>	Mormoopidae	Yangochiroptera	America C/S/Carib	KC011599	13	1	1
<i>Noctilio leporinus</i>	Noctilionidae	Yangochiroptera	America C/S/Carib	JX257161	64	1	1
<i>Anoura geoffroyi</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	FJ155495	42	6	3
<i>Artibeus toltecus</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	FJ376728	3	1	1
<i>Artibeus jamaicensis</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	GQ861667	235	19	2
<i>Artibeus lituratus</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	KP134571	135	13	5
<i>Artibeus obscurus</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	KP134536	19	10	1
<i>Artibeus planirostris</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	KP134540	40	16	2
<i>Brachyphylla cavernarum</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	AY572383	14	2	1
<i>Carollia castanea</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	AF187022	27	20	2
<i>Carollia perspicillata</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	KF019723	354	49	6
<i>Carollia sowelli</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	AF511973	15	5	1
<i>Desmodus rotundus</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	FJ155477	376	50	10
<i>Diaemus youngi</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	FJ155475	22	1	1
<i>Glossophaga soricina</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	FJ392516	217	18	3
<i>Lophostoma silvicolum</i> ( <i>Tonatia silvicola</i> )†§	Phyllostomidae	Yangochiroptera	America C/S/Carib	JF923862	15	2	2
<i>Macrotus waterhousii</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	AY380745	22	2	2
<i>Micronycteris microtis</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	AY380756	18	3	2
<i>Monophyllus redmani</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	AF382888	17	20	4

Host species	Family	Suborder	Region	cytb accession number	WoS citations	Study sample size	Number of links
<i>Phyllonycteris poeyi</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	GU937240	7	1	1
<i>Phyllostomus hastatus</i> †	Phyllostomidae	Yangochiroptera	America C/S/Carib	FJ155479	94	17	7
<i>Platyrrhinus vittatus</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	FJ154178	1	2	1
<i>Sturnira lilium</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	KC753849	126	20	6
<i>Sturnira mordax</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	KC753824	6	11	1
<i>Uroderma bilobatum</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	AY169955	33	4	2
<i>Vampyressa bidens</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	FJ154181	5	3	1
<i>Vampyressa thylene</i>	Phyllostomidae	Yangochiroptera	America C/S/Carib	DQ312431	4	2	1
<i>Corynorhinus townsendii</i>	Vespertilionidae	Yangochiroptera	America N	KC747680	54	1	1
<i>Eptesicus nilssonii</i>	Vespertilionidae	Yangochiroptera	Europe-Asia C/E	GQ272582	46	1	1
<i>Myotis brandtii</i>	Vespertilionidae	Yangochiroptera	Europe-Asia C/E	AF376844	60	1	1
<i>Myotis daubentonii</i>	Vespertilionidae	Yangochiroptera	Europe-Asia C/E	AB106589	243	6	2
<i>Myotis keaysi</i>	Vespertilionidae	Yangochiroptera	America C/S/Carib	JX130526	5	9	4
<i>Myotis myotis</i>	Vespertilionidae	Yangochiroptera	Europe-Asia C/E	AM261883	2751	7	3
<i>Myotis mystacinus</i>	Vespertilionidae	Yangochiroptera	Europe-Asia C/E	AB106605	81	2	1
<i>Myotis nattereri</i>	Vespertilionidae	Yangochiroptera	Europe-Asia C/E	JF412413	143	2	1
<i>Myotis nigricans</i> *	Vespertilionidae	Yangochiroptera	America C/S/Carib	KP134584	58	6	1
<i>Nyctalus noctula</i>	Vespertilionidae	Yangochiroptera	Europe-Asia C/E	JX570902	195	1	1
<i>Pipistrellus pipistrellus</i> *	Vespertilionidae	Yangochiroptera	Europe-Asia C/E	KF874521	983	36	2
<i>Tylonycteris pachypus</i> *	Vespertilionidae	Yangochiroptera	Asia S/SE/SE	EF517315	15	1	1
<i>Hipposideros armiger</i>	Hipposideridae	Yinpterochiroptera	Asia S/SE/SE	JX849197	42	25	2
<i>Hipposideros diadema</i> *	Hipposideridae	Yinpterochiroptera	Asia S/SE/SE	DQ219421	13	1	1
<i>Hipposideros fulvus</i> †	Hipposideridae	Yinpterochiroptera	Asia S/SE/SE	DQ054809	12	1	1
<i>Hipposideros commersoni</i> ‡	Hipposideridae	Yinpterochiroptera	Africa	EU934469	3	4	1
<i>Hipposideros larvatus</i>	Hipposideridae	Yinpterochiroptera	Asia S/SE/SE	EU434949	19	32	7
<i>Triaenops persicus</i>	Hipposideridae	Yinpterochiroptera	Africa	EU798758	7	8	1
<i>Megaderma lyra</i> †	Megadermatidae	Yinpterochiroptera	Asia S/SE/SE	DQ888678	124	3	2
<i>Eidolon dupreanum</i>	Pteropodidae	Yinpterochiroptera	Africa	KM226003	10	94	8
<i>Eidolon helvum</i>	Pteropodidae	Yinpterochiroptera	Africa	JN398200	101	383	35
<i>Epomophorus gambianus</i> *	Pteropodidae	Yinpterochiroptera	Africa	JF728757	8	53	2
<i>Harpyionycteris whiteheadi</i>	Pteropodidae	Yinpterochiroptera	Asia S/SE/SE	DQ445708	1	1	1
<i>Megaerops niphanae</i> †	Pteropodidae	Yinpterochiroptera	Asia S/SE/SE	GQ410214	1	2	1
<i>Micropteropus pusillus</i> *	Pteropodidae	Yinpterochiroptera	Africa	JF728734	3	11	1
<i>Ptenochirus jagori</i>	Pteropodidae	Yinpterochiroptera	Asia S/SE/SE	AB046325	8	1	1
<i>Pteropus hypomelanus</i>	Pteropodidae	Yinpterochiroptera	Asia S/SE/SE	AB062472	44	2	2
<i>Rousettus aegyptiacus</i>	Pteropodidae	Yinpterochiroptera	Africa	JF728760	254	105	1
<i>Rhinolophus acuminatus</i> †	Rhinolophidae	Yinpterochiroptera	Asia S/SE/SE	FJ185205	2	17	2

Host species	Family	Suborder	Region	<i>cytb</i> accession number	WoS citations	Study sample size	Number of links
<i>Rhinolophus borneensis</i> subsp. <i>chasei</i> †	Rhinolophidae	Yinpterochiroptera	Asia S/SE/SE	DQ987605	2	5	7
<i>Rhinolophus landeri</i> *	Rhinolophidae	Yinpterochiroptera	Africa	EU436668	5	18	2
<i>Rhinolophus pearsonii</i>	Rhinolophidae	Yinpterochiroptera	Asia S/SE/SE	JX502551	2	1	1
<i>Rhinolophus sinicus</i>	Rhinolophidae	Yinpterochiroptera	Asia S/SE/SE	HM134917	18	7	2
<i>Ornithorhynchus anatinus</i>	-	-	outgroup	HQ379928	-	-	-
<i>Rattus rattus</i>	-	-	outgroup	AB033702	-	-	-
<i>Equus caballus</i>	-	-	outgroup	D82932	-	-	-





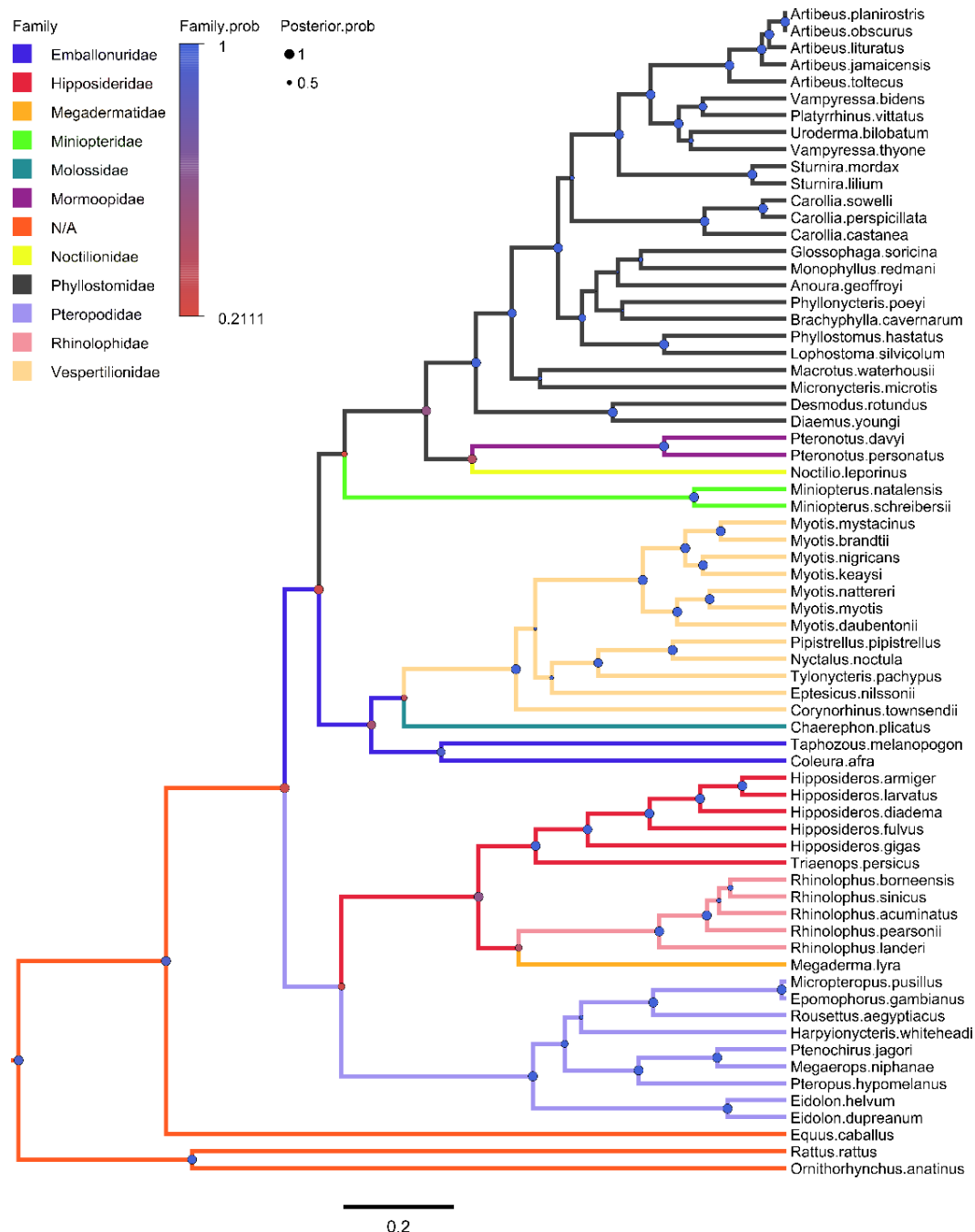
**Fig. S2.** Maximum likelihood (likelihood = -9839.48) phylogenetic tree of *Bartonella* genotypes using 333 base pair sequences of the genomic *gltA* gene aligned using MAFFT (Kato and Standley, 2013). The tree was assembled in MEGA6 (Tamura et al., 2013) using the GTR+ $\Gamma$ +I substitution model with four gamma categories (Nei and Kumar, 2000). Node support values were estimated from 1000 bootstrap replicates; only support values  $\geq 50\%$  are shown.



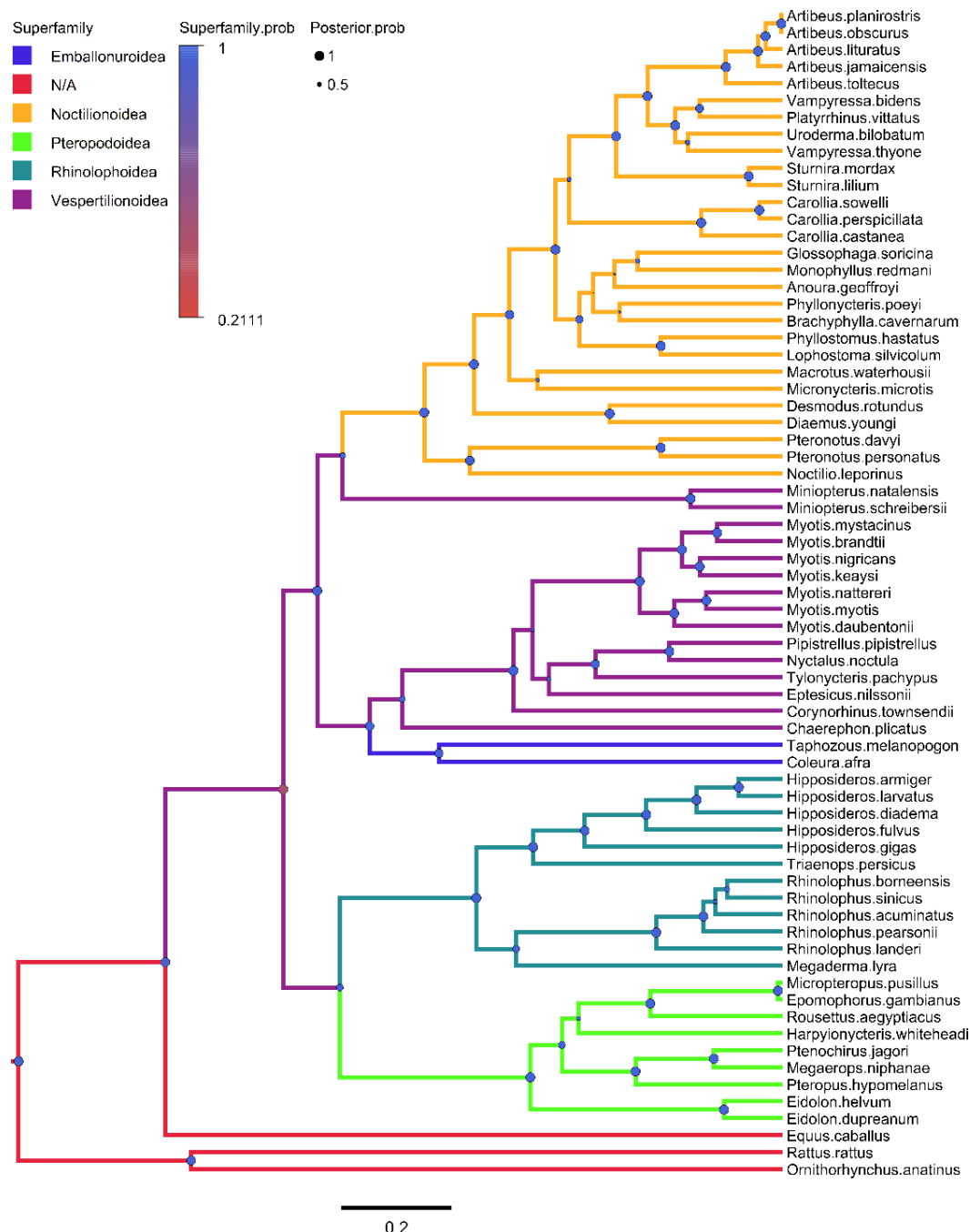
**Table S4.** Global fit test results from ParaFit and PACo analyses. P-values were calculated from global fits (ParaFit and PACo) using 10000 permutations.

Test of cophylogeny (ML trees)		Test of sympatry (ML trees)	
ParaFit		ParaFit	
ParaFitGlobal	12.07	ParaFitGlobal	70.42
p-value	1E-05	p-value	1E-05
F1 statistics with p-value <0.05	157/186	F1 statistics with p-value <0.05	146/186
F1 statistics with p-value <0.005	122/186	F1 statistics with p-value <0.005	135/186
F1 statistics with p-value <0.001	96/186	F1 statistics with p-value <0.001	125/186
PACo		PACo	
m <sup>2</sup> global value	8.11	m <sup>2</sup> global value	56.98
p-value	1E-04	p-value	1E-04
Residuals below overall median	93/186	Residuals below overall median	93/186
Number of outliers (>1.5xIQR)	10	Number of outliers (>1.5xIQR)	5
Test of cophylogeny (Bayesian trees)		Test of sympatry (Bayesian trees)	
ParaFit		ParaFit	
ParaFitGlobal	30.16	ParaFitGlobal	50.20
p-value	1E-05	p-value	1E-05
F1 statistics with p-value <0.05	182/186	F1 statistics with p-value <0.05	159/186
F1 statistics with p-value <0.005	180/186	F1 statistics with p-value <0.005	152/186
F1 statistics with p-value <0.001	180/186	F1 statistics with p-value <0.001	145/186
PACo		PACo	
m <sup>2</sup> global value	17.16	m <sup>2</sup> global value	53.13
p-value	1E-04	p-value	1E-04
Residuals below overall median	93/186	Residuals below overall median	93/186
Number of outliers (>1.5xIQR)	8	Number of outliers (>1.5xIQR)	15

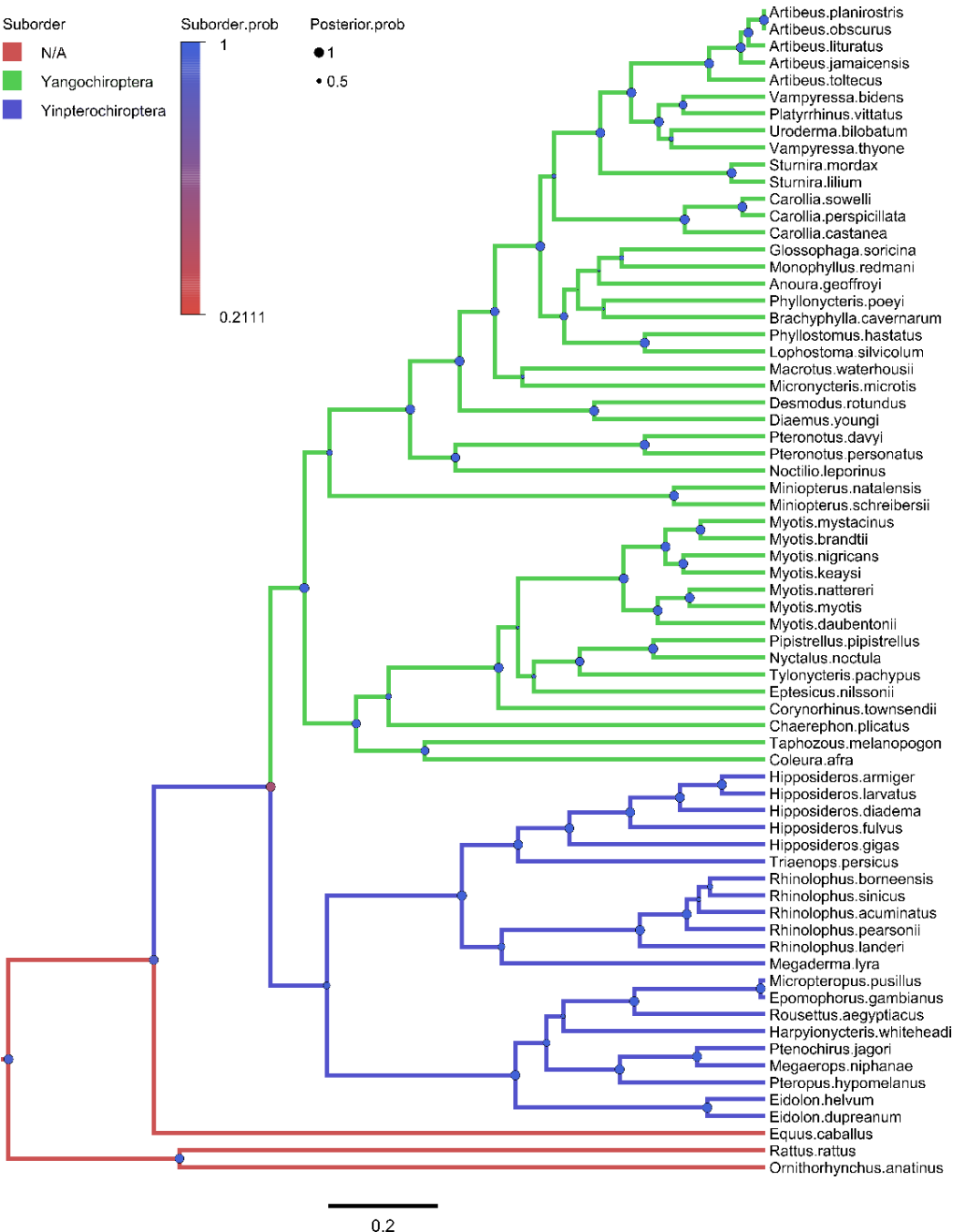
IQR – interquartile range.



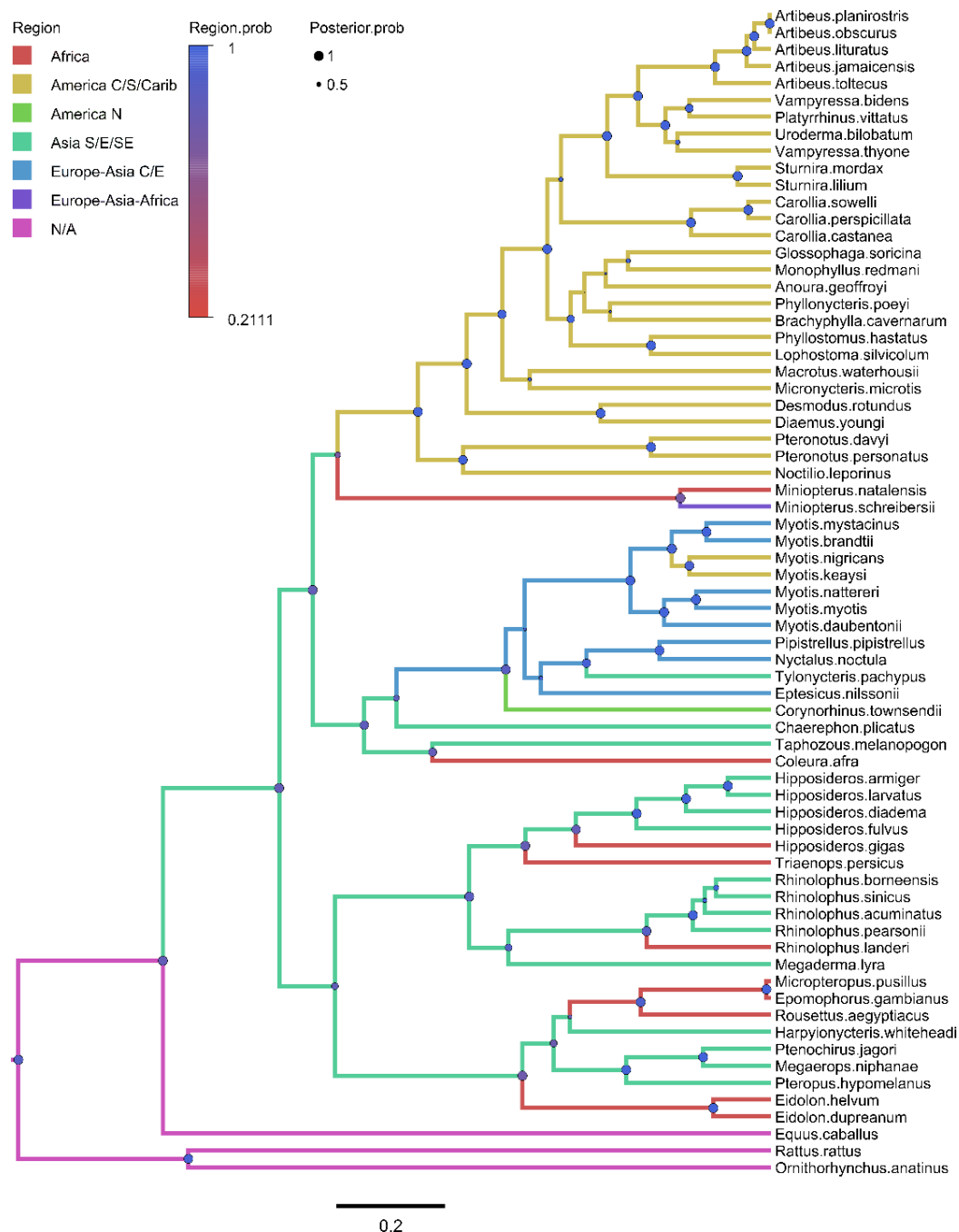
**Fig. S3.** Bayesian phylogeny of bat host species reconstructing bat families, shown by colored branches. Posterior probabilities for nodes are shown as circles (●) scaled by size from 0 to 1 (Posterior.prob) and colored by the support for the family at that node (Family.prob). Mean tree likelihood = -27928.95, ESS = 16066; mean family tree likelihood = -57.93, ESS = 15472.



**Fig. S4.** Bayesian phylogeny of bat host species reconstructing bat superfamilies, shown by colored branches. Posterior probabilities for nodes are shown as circles (●) scaled by size from 0 to 1 (Posterior.prob) and colored by the support for the bat superfamily at that node (Superfamily.prob). Mean tree likelihood = -27928.95, ESS = 16066; mean superfamily tree likelihood = -30.75, ESS = 15199.



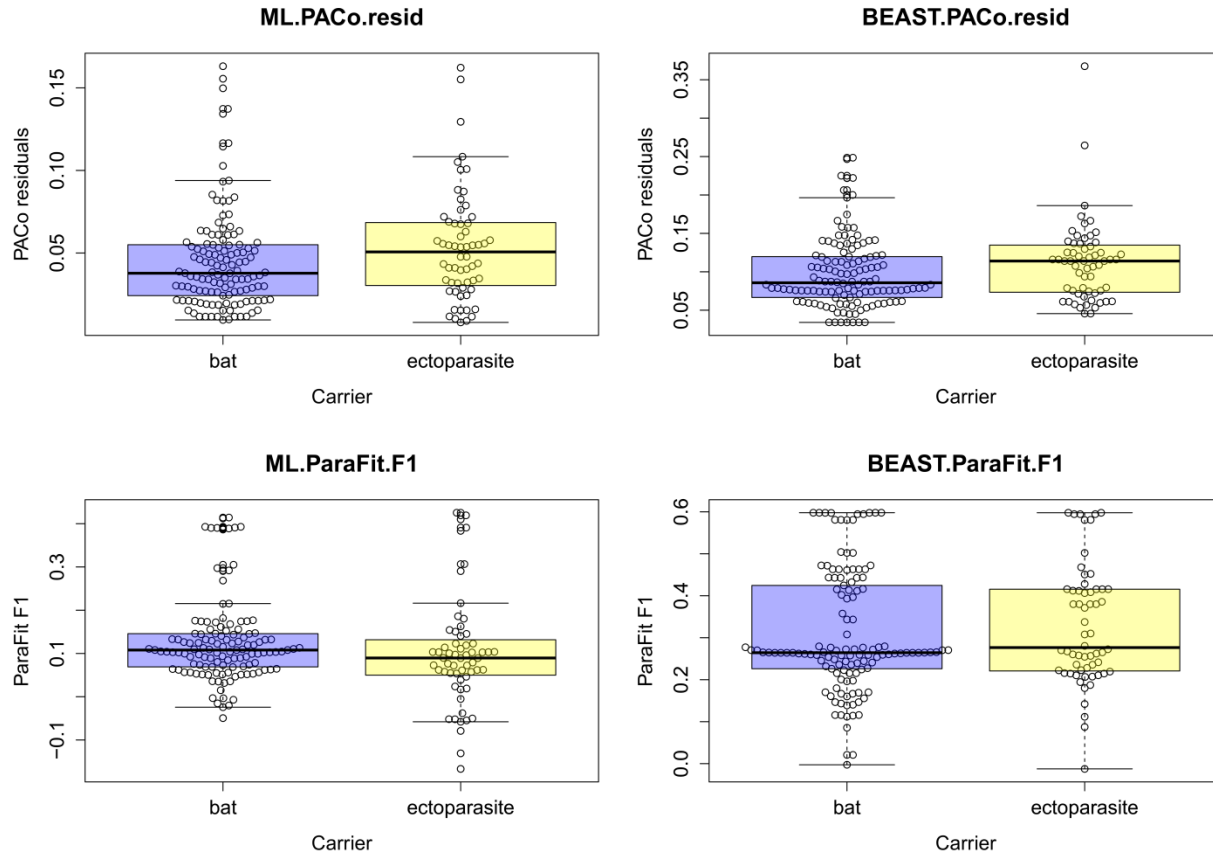
**Fig. S5.** Bayesian phylogeny of bat host species reconstructing bat suborders, shown by colored branches. Posterior probabilities for nodes are shown as circles (●) scaled by size from 0 to 1 (Posterior.prob) and colored by the support for the bat suborder at that node (Suborder.prob). Mean tree likelihood = -27928.95, ESS = 16066; mean suborder tree likelihood = -13.86, ESS = 15871.



**Fig. S6.** Bayesian phylogeny of bat host species reconstructing bat geographic regions, shown by colored branches. Posterior probabilities for nodes are shown as circles (●) scaled by size from 0 to 1 (Posterior.prob) and colored by the support for the geographic region at that node (Region.prob). Note the geographic region represents where the bat host was captured, which may not reflect its total range. Mean tree likelihood = -27928.95, ESS = 16066; mean region tree likelihood = -60.51, ESS = 16166.

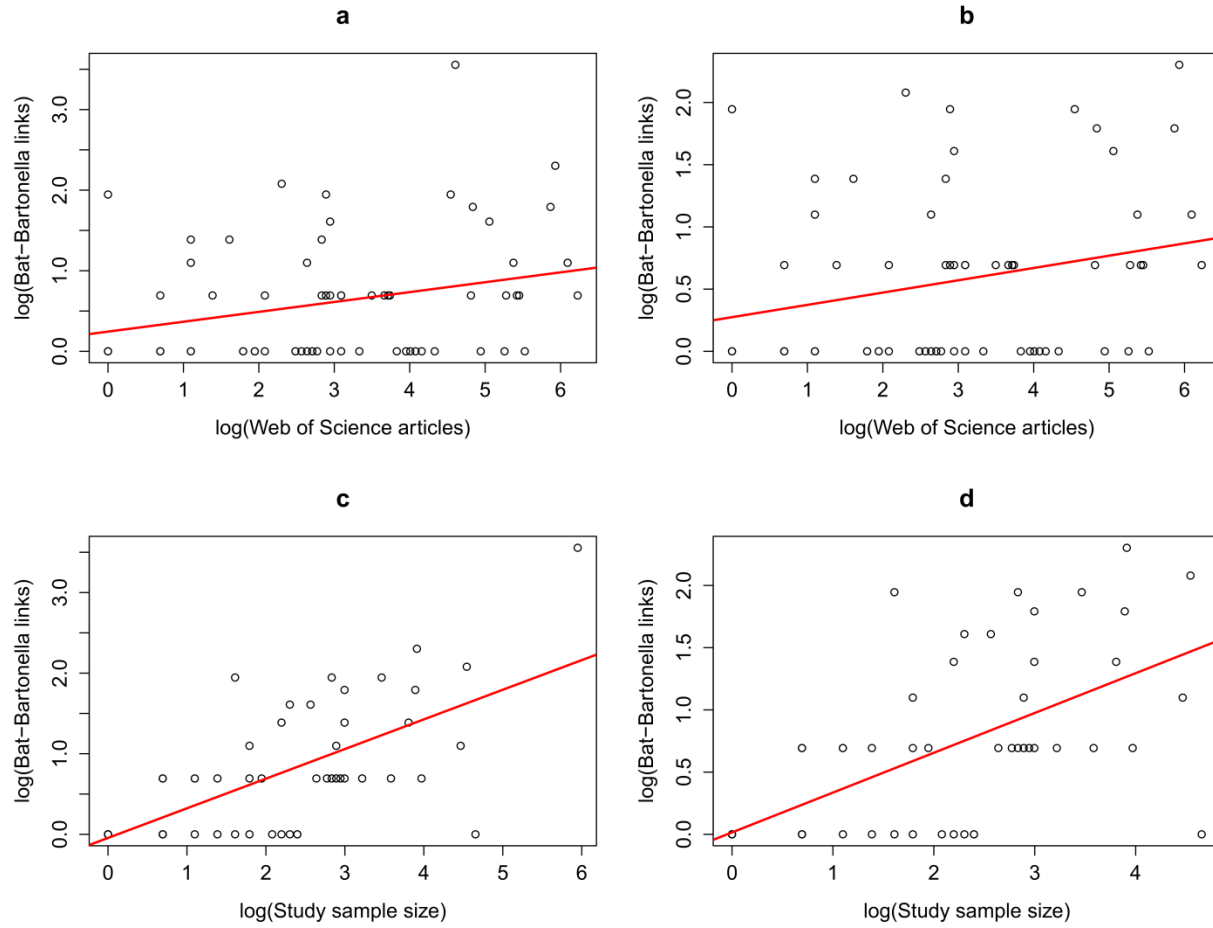






**Fig. S9.** Results of global fit comparisons based on analysis of host phylogeny and *Bartonella* genotypes, divided between genotypes found in bat hosts and ectoparasites. ML.PACo.resid – individual residuals from the PACo global fit using a maximum likelihood tree, BEAST.PACo.resid – individual residuals from the PACo global fit using a Bayesian tree, ML.ParaFit.F1 – F1 fit statistics from the ParaFit global fit using a maximum likelihood tree, BEAST.ParaFit.F1 – F1 fit statistics from the ParaFit global fit using a Bayesian tree.





**Fig. S10.** Results of sampling bias tests for bat species and *Bartonella* genotypes. a) log-log correlation between the number of host-parasite links and Web of Science articles; b) log-log correlation between the number of host-parasite links and Web of Science articles, *Eidolon helvum* removed; c) log-log correlation between the number of links and individual species sample sizes; and d) log-log correlation between the number of links and individual species sample sizes, *Eidolon helvum* removed.

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