**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. *chaseni* and *R. acuminatus* (Vietnam) – *R. affinis*, *R. malayanus*, *R. pearsonii*, *R. stheno*

*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. *chaseni* 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 stheno* (FJ185213)for *Rhinolophus acuminatus* from Vietnam, *Rhinolophus pearsonii* (JX502551)for *Rhinolophus borneensis* subsp. *chaseni* 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; m2 global value = 8.54, P = 1E-4). Using ParaFit, 159/186 of host-parasite links were significant at the P ≤ 0.05 level, 129/186 at the P ≤ 0.005 level, and 103/186 at the P ≤ 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; m2 global value = 57.5, P = 1E-4). Using ParaFit, 144/186 of host-parasite links were significant at the P ≤ 0.05 level, 133/186 at the P ≤ 0.005 level, and 126/186 at the P ≤ 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 ωphy = 1and ωgeo = 0, ParaFitGlobal = 13.37; for PACo the optimal combination was ωphy = 1and ωgeo = 0, m2 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).

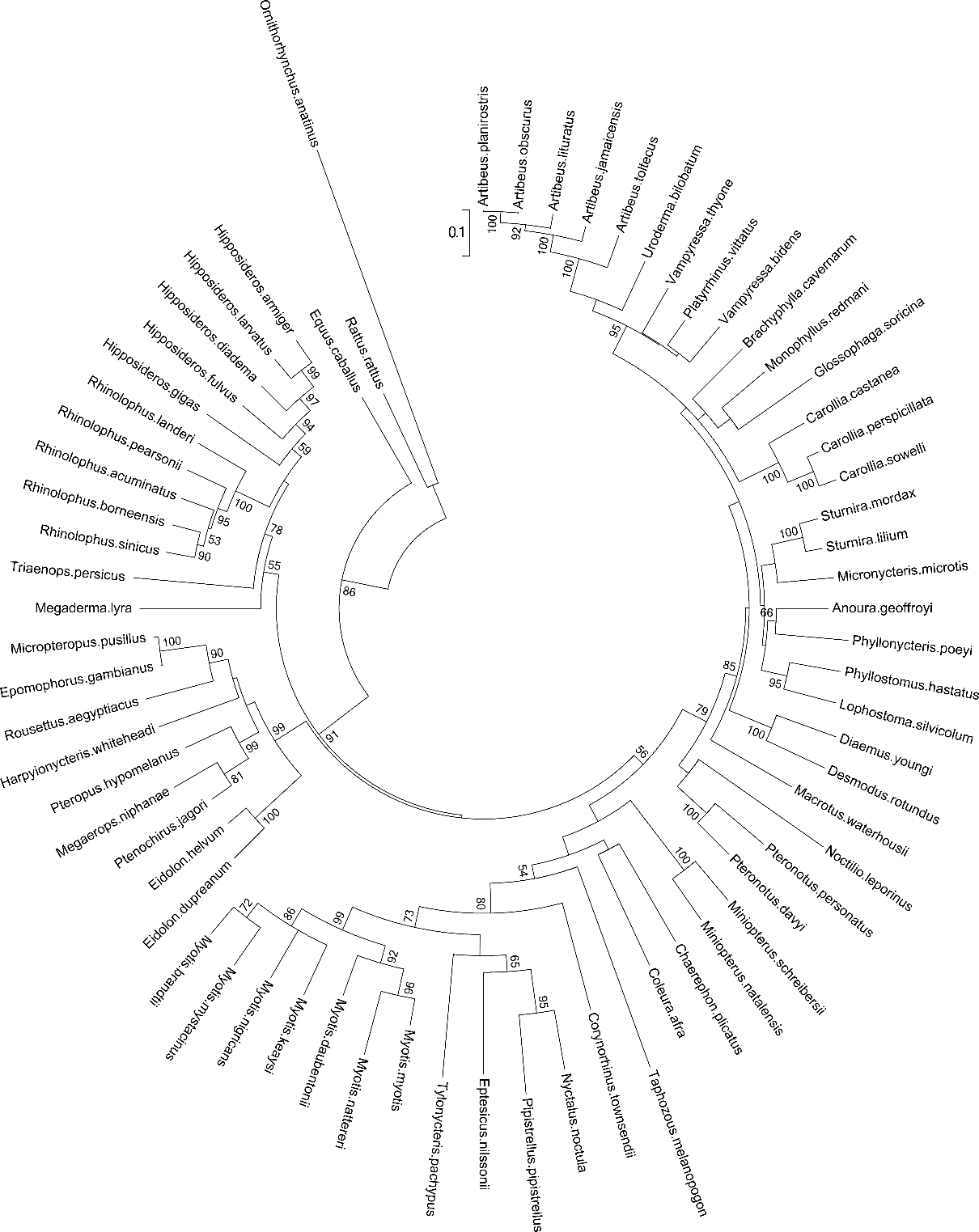
| **Genotype** | **Host species** | **Location** | ***gltA* accession number** |
| --- | --- | --- | --- |
| M406 | *Myotis daubentonii* | UK | AJ871613 |
| M62 | *Myotis mystacinus* | UK | AJ871612 |
| M207 | *Pipistrellus* sp. | UK | AJ871614 |
| M451 | *Nyctalus noctula* | UK | AJ871615 |
| M409 | *Pipistrellus* sp. | UK | AJ871611 |
| Cul-9 | *Lophostoma silvicolum* | Peru | EF616479 |
| R-191 | *Rousettus aegyptiacus* | Kenya | HM363764 |
| T-837 | *Triaenops persicus* | Kenya | HM545138 |
| H-556 | *Hipposideros commersoni* | Kenya | HM545137 |
| C-583 | *Coleura afra* | Kenya | HM545136 |
| M1-44 | *Miniopterus* sp. | Kenya | HM545139 |
| M2-491 | *Miniopterus* sp. | Kenya | HM545140 |
| M3-373 | *Miniopterus* sp. | Kenya | HM545141 |
| B29042 | *Desmodus rotundus* | Guatemala | HM597187 |
| B29043 | *Desmodus rotundus* | Guatemala | HM597188 |
| B29044 | *Desmodus rotundus* | Guatemala | HM597189 |
| B29107 | *Desmodus rotundus* | Guatemala | HM597190 |
| B29108 | *Desmodus rotundus, Carollia perspicillata* | Guatemala | HM597191 |
| B29114 | *Desmodus rotundus, Carollia perspicillata* | Guatemala | HM597192 |
| B29102 | *Pteronotus davyi* | Guatemala | HM597193 |
| B29109 | *Pteronotus davyi* | Guatemala | HM597194 |
| B29119 | *Desmodus rotundus* | Guatemala | HM597195 |
| B29122 | *Desmodus rotundus* | Guatemala | HM597196 |
| B29116 | *Phyllostomus discolor* | Guatemala | HM597198 |
| B29126 | *Carollia perspicillata, Sturnira lilium* | Guatemala, Costa Rica | HM597199, KJ816674 |
| B29230 | *Phyllostomus discolor* | Guatemala | HM597200 |
| B29115 | *Phyllostomus discolor* | Guatemala | HM597201 |
| B29110 | *Glossophaga soricina* | Guatemala | HM597202 |
| B29105 | *Pteronotus davyi* | Guatemala | HM597203 |
| B29112 | *Phyllostomus discolor* | Guatemala | HM597204 |
| B29134 | *Pteronotus davyi* | Guatemala | HM597205 |
| B29137 | *Sturnira lilium* | Guatemala | HM597206 |
| B29172 | *Micronycteris microtis* | Guatemala | HM597207 |
| B29111 | *Artibeus toltecus* | Guatemala | HM597197 |
| B32945 | *Desmodus rotundus* | Peru | JQ071379 |
| B32947 | *Phyllostomus discolor* | Peru | JQ071387 |
| B32954 | *Artibeus planirostris* | Peru | JQ071382 |
| B32946 | *Glossophaga soricina* | Peru | JQ071383 |
| B32943 | *Carollia perspicillata* | Peru | JQ071384 |
| B32960 | *Carollia perspicillata* | Peru, Costa Rica | JQ071386, KJ816691 |
| B32955 | *Carollia perspicillata* | Peru | JQ071385 |
| B32854 | *Phyllostomus hastatus* | Peru | JQ071388 |
| B32855 | *Desmodus rotundus* | Peru | JQ071378 |
| B32856 | *Vampyressa bidens* | Peru | JQ071389 |
| B32942 | *Myotis* sp. | Peru | JQ071390 |
| B32851 | *Artibeus obscurus* | Peru | JQ071380 |
| B32953 | *Artibeus planirostris* | Peru | JQ071381 |
| No. 5 | *Miniopterus schreibersii* | Taiwan | JF500511 |
| No. 7 | *Miniopterus schreibersii* | Taiwan | JF500513 |
| AS050 | *Myotis myotis* | Poland | JQ695835 |
| AS071 | *Myotis myotis* | Poland | JQ695834 |
| 2574/1 | *Myotis daubentonii* | Finland | KF003129 |
| 1160/1 | *Myotis daubentonii* | Finland | KF003122 |
| 1157/3 | *Eptesicus nilssoni* | Finland | KF003115 |
| Mr37079 | *Monophyllus redmani, Phyllonycteris poeyi* | Puerto Rico, Dominican Republic | KJ530746, JX416249 |
| Mr37078 | *Monophyllus redmani* | Puerto Rico | KJ530745 |
| Mr37077 | *Monophyllus redmani* | Puerto Rico | KJ530744 |
| Mr37075 | *Monophyllus redmani* | Puerto Rico | KJ530743 |
| Bc37076 | *Brachyphylla cavernarum* | Puerto Rico | KJ530742 |
| Aj37081 | *Artibeus jamaicensis* | Puerto Rico | KJ530741 |
| B23976 | *Eidolon helvum* | Kenya | KM030507 |
| B40005 | *Eidolon helvum* | Cameroon | KM030518 |
| B23979 | *Eidolon helvum* | Kenya | KM030509 |
| B24225 | *Eidolon helvum* | Kenya | KM030511 |
| B40396 | *Eidolon helvum* | Tanzania | KM030522 |
| B40400 | *Eidolon helvum* | Tanzania | KM030523 |
| B23812 | *Eidolon helvum, Rhinolophus landeri* | Kenya, Nigeria | KM030504, KF418810 |
| B24163 | *Eidolon helvum* | Kenya | KM030510 |
| B32120 | *Eidolon helvum* | Nigeria | KM030512 |
| B39301 | *Eidolon helvum* | Ghana | KM030516 |
| B39325 | *Eidolon helvum* | Ghana | KM030517 |
| B23975 | *Eidolon helvum* | Kenya | KM030506 |
| B39286 | *Eidolon helvum* | Ghana | KM030514 |
| B39296 | *Eidolon helvum* | Ghana | KM030515 |
| B40908 | *Eidolon helvum* | Uganda | KM030526 |
| B39249 | *Eidolon helvum* | Ghana | KM030513 |
| B40391 | *Eidolon helvum* | Tanzania | KM030521 |
| B40014 | *Eidolon helvum* | Tanzania | KM030520 |
| B40406 | *Eidolon helvum* | Tanzania | KM030525 |
| B23797 | *Eidolon helvum,* *Micropteropus pusillus,* *Epomophorus gambianus* | Kenya, Nigeria | KM030503, KF418812, KF418808 |
| Mi-BA38 | *Micropteropus* sp. | Nigeria | KF418812 |
| Eh-GB64 | *Eidolon helvum* | Nigeria | KF418811 |
| Rh-GB31 | *Rhinolophus* sp. | Nigeria | KF418810 |
| Ep-BA63 | *Epomophorus* sp. | Nigeria | KF418808 |
| Rh-GB59 | *Rhinolophus* sp. | Nigeria | KF418809 |
| Rh-GB1 | *Rhinolophus* sp. | Nigeria | KF418807 |
| Ep-GB65 | *Epomophorus* sp. | Nigeria | KF418806 |
| B110 | *Hipposideros larvatus, Hipposideros armiger* | Vietnam | KP100360, KP100357 |
| B109 | *Megaderma lyra* | Vietnam | KP100359 |
| B102 | *Rhinolophus chaseni* | Vietnam | KP100358 |
| B096 | *Hipposideros armiger* | Vietnam | KP100357 |
| B095 | *Hipposideros armiger* | Vietnam | KP100356 |
| B087 | *Hipposideros larvatus* | Vietnam | KP100355 |
| B081 | *Hipposideros larvatus* | Vietnam | KP100354 |
| B079 | *Rhinolophus chaseni* | Vietnam | KP100353 |
| B072 | *Megaerops niphanae* | Vietnam | KP100352 |
| B068 | *Rhinolophus acuminatus* | Vietnam | KP100351 |
| B064 | *Rhinolophus acuminatus* | Vietnam | KP100350 |
| B063 | *Rhinolophus acuminatus* | Vietnam | KP100349 |
| B056 | *Rhinolophus acuminatus* | Vietnam | KP100348 |
| B055 | *Rhinolophus acuminatus* | Vietnam | KP100347 |
| B052 | *Rhinolophus acuminatus* | Vietnam | KP100346 |
| B050 | *Rhinolophus acuminatus* | Vietnam | KP100345 |
| B049 | *Rhinolophus sinicus* | Vietnam | KP100344 |
| B047 | *Rhinolophus sinicus* | Vietnam | KP100343 |
| B006 | *Rhinolophus acuminatus* | Vietnam | KP100342 |
| B005 | *Megaderma spasma* | Vietnam | KP100341 |
| B003 | *Rhinolophus acuminatus* | Vietnam | KP100340 |
| SK197 | *Tadarida plicata* | Thailand | - |
| SK170 | *Tadarida plicata* | Thailand | - |
| SK157 | *Tadarida plicata* | Thailand | - |
| CR224 | *Hipposideros fulvus* | Thailand | - |
| KP270 | *Hipposideros larvatus* | Thailand | - |
| KP182 | *Hipposideros armiger, Hipposideros larvatus* | Thailand | - |
| KP283b | *Taphozous melanopogon* | Thailand | - |
| SK163 | *Tadarida plicata* | Thailand | - |
| KP277 | *Hipposideros larvatus* | Thailand | - |
| KP293b | *Hipposideros larvatus* | Thailand | - |
| KEL08 | *Eidolon dupreanum* | Madagascar | KP010191 |
| KEL16 | *Eidolon dupreanum* | Madagascar | KP010192 |
| KEL17 | *Eidolon dupreanum* | Madagascar | KP010193 |
| I | *Anoura geoffroyi* | Costa Rica | KJ816666 |
| III | *Artibeus lituratus, Anoura geoffroyi, Sturnira mordax, Sturnira lilium* | Costa Rica | KJ816680 |
| III | *Vampyressa thyone* | Costa Rica | KJ816672 |
| III | *Carollia castanea* | Costa Rica | KJ816683 |
| III | *Artibeus lituratus* | Costa Rica | KJ816675 |
| III | *Platyrrhinus vittatus* | Costa Rica | KJ816684 |
| VII | *Carollia sowelli* | Costa Rica | KJ816690 |
| XII | *Myotis keaysi* | Costa Rica | KJ816676 |
| 2308 | *Brucella melitensis* | outgroup | AM040264 |
| OV483 | *Rhizobium leguminosarum* | outgroup | NZ\_JQJS01000011 |
| OAB | *Ochrobactrum anthropi* | 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).

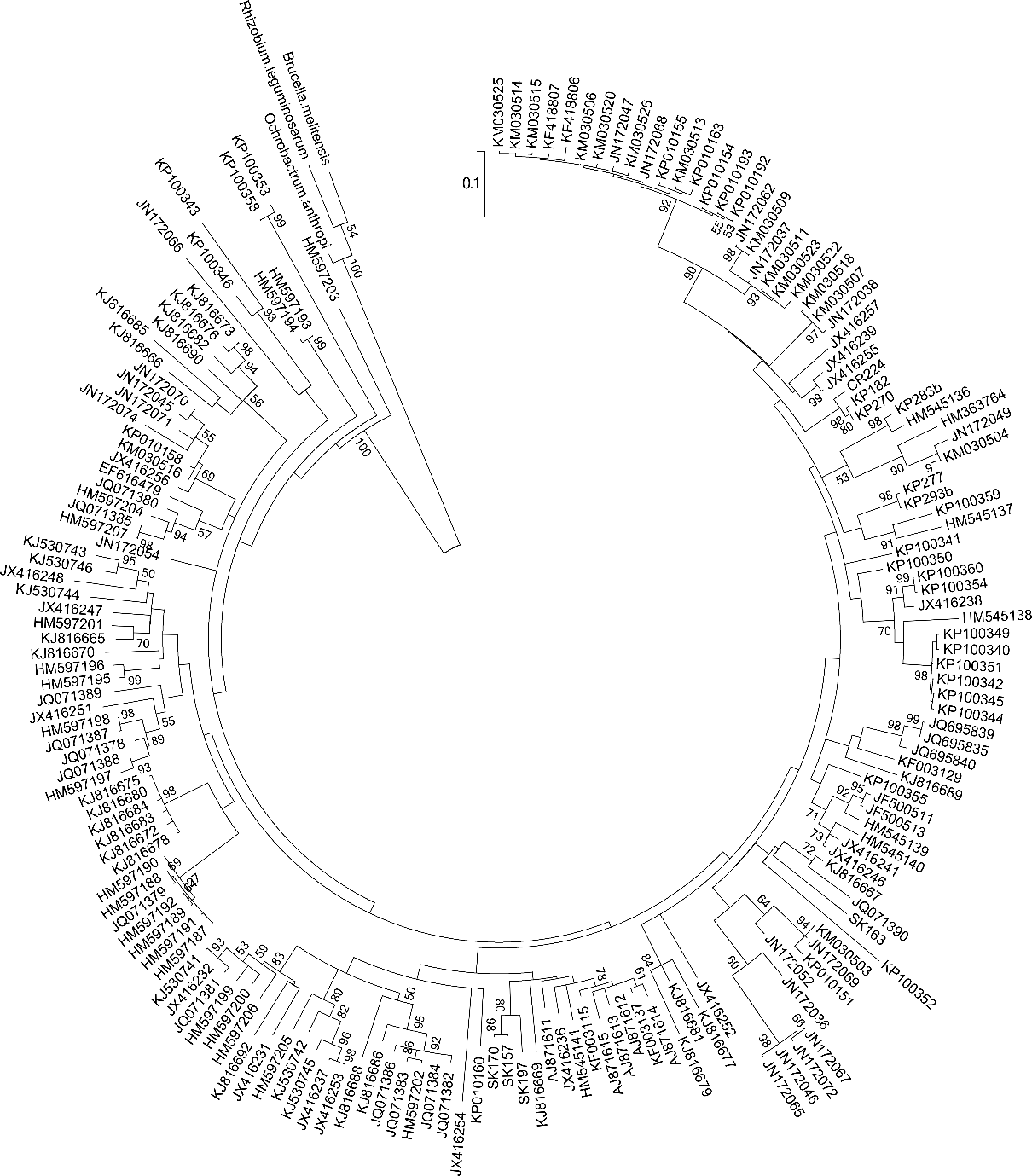
| **Genotype** | **Ectoparasite** | **Host species** | **Location** | **gltA accession number** |
| --- | --- | --- | --- | --- |
| NB-1.2 | *Siphonaptera* sp. | *Myotis brandtii* | Finland | KF003137 |
| AS025 | *Spinturnix myoti* | *Myotis myotis* | Poland | JQ695839 |
| AS033 | *Spinturnix myoti* | *Myotis myotis* | Poland | JQ695838 |
| AS036 | *Spinturnix myoti* | *Myotis myotis* | Poland | JQ695837 |
| AS048 | *Spinturnix myoti* | *Myotis myotis* | Poland | JQ695836 |
| AS067 | *Spinturnix myoti* | *Myotis myotis* | Poland | JQ695840 |
| Cg 462 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172074 |
| Cg 401 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172072 |
| Cg 454 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172071 |
| Cg 414 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172070 |
| Cg 433 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172069 |
| Cg 443 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172068 |
| Cg 465-2 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172067 |
| Cg 713-2 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172066 |
| Cg 405 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172065 |
| Cg 424 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172064 |
| Cg 417-2 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172063 |
| Cg 426-1 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172062 |
| Cg 436-3 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172061 |
| Cg 418 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172060 |
| Cg 423-2 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172059 |
| Cg 423-1 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Bioko | JN172058 |
| Cg 364 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Annobón | JN172049 |
| Cg 374 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Annobón | JN172050 |
| Cg 358-3 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Annobón | JN172051 |
| Cg 366-1 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Annobón | JN172052 |
| Cg 371 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Annobón | JN172053 |
| Cg 315-1 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Annobón | JN172054 |
| Cg 303-1 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Annobón | JN172055 |
| Cg 303-2 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Annobón | JN172056 |
| Cg 366 | *Cyclopodia greefi* | *Eidolon helvum* | Equatorial Guinea: Annobón | JN172057 |
| Cg K1-2 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172035 |
| Cg K5-1 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172036 |
| Cg K8-1 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172037 |
| Cg Q22-1 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172038 |
| Cg Q98-1 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172039 |
| Cg Q100-2 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172040 |
| Cg Q130 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172041 |
| Cg G35-2 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172042 |
| Cg G31-1 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172043 |
| Cg G38-2 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172044 |
| Cg GG236 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172045 |
| Cg GG48 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172046 |
| Cg GG243-2 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172047 |
| Cg GG243-3 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN172048 |
| E-124 | *Cyclopodia greefi* | *Eidolon helvum* | Ghana | JN190887 |
| E7 | *Cyclopodia horsfieldii* | *Pteropus hypomelanus* | Malaysia | JX416257 |
| E5 | *Cyclopodia horsfieldii* | *Pteropus hypomelanus* | Malaysia | JX416256 |
| P2874 | *Cyclopodia simulans* | *Ptenochirus jagori* | Philippines | JX416255 |
| 27\_3\_4 | *Paradyschiria lineata* | *Noctilio leporinus* | Panama | JX416254 |
| DR0583 | *Trichobius adamsi* | *Macrotus waterhousii* | Dominican Republic | JX416253 |
| 05\_01\_07 | *Phthiridium* sp. *scissa* group | *Rhinolophus pearsoni* | Laos | JX416252 |
| 23\_03\_04 | *Strebla diaemi* | *Diaemus youngi* | Panama | JX416251 |
| CWD974 | *Trichobius johnsonae* | *Pteronotus personatus* | Mexico | JX416248 |
| RCO934 | *Pseudostrebla ribeiroi* | *Lophostoma silvicolum* | Peru | JX416247 |
| Mala11 | *Basilia* (*Tripselia*) *coronata* | *Tylonycteris* sp. | Malaysia | JX416246 |
| ZAG03 | *Basilia nattereri* | *Myotis nattererei* | Slovenia | JX416241 |
| JAE1033 | *Leptocyclopodia* sp. *nov.* | *Harpionycteris whiteheadi* | Philippines | JX416239 |
| Mala15 | *Phthiridium* (*Stylidia*) *fraterna* | *Hipposideros* sp. | Malaysia | JX416238 |
| DR05241 | *Trichobius adamsi* | *Macrotus waterhousii* | Dominican Republic | JX416237 |
| ZAG01 | *Trichobius corynorhinus* | *Corynorhinus townsendii* | USA | JX416236 |
| FG13 | *Paratrichobius longicrus* complex | *Artibeus lituratus* | French Guyana, Costa Rica | JX416232, KJ816687 |
| FG10 | *Paratrichobius longicrus* complex | *Artibeus lituratus* | French Guyana | JX416231 |
| KEL02-3 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010152 |
| KEL02-4 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010153 |
| KEL19-1 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010164 |
| KEL09-1 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010159 |
| KEL02-2 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010151 |
| KEL11-1 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010160 |
| KEL07-1 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010158 |
| KEL17-2 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010163 |
| KEL04-1 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010155 |
| ANGB03-1 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010150 |
| KEL04-2 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010156 |
| KEL02-5 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010154 |
| KEL17-1 | *Cyclopodia dubia* | *Eidolon dupreanum* | Madagascar | KP010162 |
| II | *Exastinion clovisi* | *Anoura geoffroyi* | Costa Rica | KJ816688 |
| III | *Trichobius dugesii* | *Glossophaga soricina* | Costa Rica | KJ816678 |
| IV | *Aspidoptera phyllostomatis* | *Artibeus jamaicensis* | Costa Rica | KJ816682 |
| V | *Paratrichobius longicrus* | *Artibeus lituratus* | Costa Rica | KJ816685 |
| VIII | *Trichobius joblingi* | *Carollia castanea* | Costa Rica | KJ816686 |
| X | *Trichobius costalimai* | *Phyllostomus discolor* | Costa Rica | KJ816665 |
| XI | *Trichobius keenani* | *Micronycteris microtis* | Costa Rica | KJ816681 |
| XII | *Aspidoptera delatorrei* | *Sturnira lilium* | Costa Rica | KJ816673 |
| XIII | *Anatrichobius scorzai* | *Myotis keaysi* | Costa Rica | KJ816669 |
| XIV | *Anatrichobius scorzai* | *Myotis keaysi* | Costa Rica | KJ816667 |
| XV | *Aspidoptera delatorrei* | *Sturnira lilium* | Costa Rica | KJ816679 |
| XVI | *Paratrichobius dunni* | *Uroderma bilobatum* | Costa Rica | KJ816692 |
| XVII | *Paratrichobius dunni* | *Uroderma bilobatum* | Costa Rica | KJ816677 |
| XIX | *Megistopoda proxima* | *Sturnira lilium* | Costa Rica | KJ816670 |
| XX | *Basilia* sp. | *Myotis keaysi* | Costa Rica | KJ816689 |
| 2308 | *Brucella melitensis* | - | outgroup | AM040264 |
| OV483 | *Rhizobium leguminosarum* | - | outgroup | NZ\_JQJS01000011 |
| OAB | *Ochrobactrum anthropi* | - | 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 3rd 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** | ***cytb* accession number** | **WoS citations** | **Study sample size** | **Number of links** |
| --- | --- | --- | --- | --- | --- | --- | --- |
| *Coleura afra* | Emballonuridae | Yangochiroptera | Africa | JQ710752 | 6 | 9 | 1 |
| *Taphozous melanopogon* | Emballonuridae | Yangochiroptera | Asia S/SE/SE | EF584221 | 28 | 2 | 1 |
| *Miniopterus natalensis*\* | Miniopteridae | Yangochiroptera | Africa | AJ841977 | 28 | 87 | 3 |
| *Miniopterus schreibersii* | Miniopteridae | Yangochiroptera | Europe-Asia-Africa | EF530348 | 211 | 14 | 2 |
| *Chaerephon plicatus* (*Tadarida plicata*)†‡ | Molossidae | Yangochiroptera | Asia S/SE/SE | GQ489157 | 5 | 45 | 4 |
| *Pteronotus davyi* | Mormoopidae | Yangochiroptera | America C/S/Carib | AF338672 | 20 | 10 | 5 |
| *Pteronotus personatus* | Mormoopidae | Yangochiroptera | America C/S/Carib | KC011599 | 13 | 1 | 1 |
| *Noctilio leporinus* | Noctilionidae | Yangochiroptera | America C/S/Carib | JX257161 | 64 | 1 | 1 |
| *Anoura geoffroyi* | Phyllostomidae | Yangochiroptera | America C/S/Carib | FJ155495 | 42 | 6 | 3 |
| *Artibeus toltecus* | Phyllostomidae | Yangochiroptera | America C/S/Carib | FJ376728 | 3 | 1 | 1 |
| *Artibeus jamaicensis* | Phyllostomidae | Yangochiroptera | America C/S/Carib | GQ861667 | 235 | 19 | 2 |
| *Artibeus lituratus* | Phyllostomidae | Yangochiroptera | America C/S/Carib | KP134571 | 135 | 13 | 5 |
| *Artibeus obscurus* | Phyllostomidae | Yangochiroptera | America C/S/Carib | KP134536 | 19 | 10 | 1 |
| *Artibeus planirostris* | Phyllostomidae | Yangochiroptera | America C/S/Carib | KP134540 | 40 | 16 | 2 |
| *Brachyphylla cavernarum* | Phyllostomidae | Yangochiroptera | America C/S/Carib | AY572383 | 14 | 2 | 1 |
| *Carollia castanea* | Phyllostomidae | Yangochiroptera | America C/S/Carib | AF187022 | 27 | 20 | 2 |
| *Carollia perspicillata* | Phyllostomidae | Yangochiroptera | America C/S/Carib | KF019723 | 354 | 49 | 6 |
| *Carollia sowelli* | Phyllostomidae | Yangochiroptera | America C/S/Carib | AF511973 | 15 | 5 | 1 |
| *Desmodus rotundus* | Phyllostomidae | Yangochiroptera | America C/S/Carib | FJ155477 | 376 | 50 | 10 |
| *Diaemus youngi* | Phyllostomidae | Yangochiroptera | America C/S/Carib | FJ155475 | 22 | 1 | 1 |
| *Glossophaga soricina* | Phyllostomidae | Yangochiroptera | America C/S/Carib | FJ392516 | 217 | 18 | 3 |
| *Lophostoma silvicolum*  (*Tonatia silvicola*)‡ | Phyllostomidae | Yangochiroptera | America C/S/Carib | JF923862 | 15 | 2 | 2 |
| *Macrotus waterhousii* | Phyllostomidae | Yangochiroptera | America C/S/Carib | AY380745 | 22 | 2 | 2 |
| *Micronycteris microtis* | Phyllostomidae | Yangochiroptera | America C/S/Carib | AY380756 | 18 | 3 | 2 |
| *Monophyllus redmani* | Phyllostomidae | Yangochiroptera | America C/S/Carib | AF382888 | 17 | 20 | 4 |
| *Phyllonycteris poeyi* | Phyllostomidae | Yangochiroptera | America C/S/Carib | GU937240 | 7 | 1 | 1 |
| *Phyllostomus hastatus*† | Phyllostomidae | Yangochiroptera | America C/S/Carib | FJ155479 | 94 | 17 | 7 |
| *Platyrrhinus vittatus* | Phyllostomidae | Yangochiroptera | America C/S/Carib | FJ154178 | 1 | 2 | 1 |
| *Sturnira lilium* | Phyllostomidae | Yangochiroptera | America C/S/Carib | KC753849 | 126 | 20 | 6 |
| *Sturnira mordax* | Phyllostomidae | Yangochiroptera | America C/S/Carib | KC753824 | 6 | 11 | 1 |
| *Uroderma bilobatum* | Phyllostomidae | Yangochiroptera | America C/S/Carib | AY169955 | 33 | 4 | 2 |
| *Vampyressa bidens* | Phyllostomidae | Yangochiroptera | America C/S/Carib | FJ154181 | 5 | 3 | 1 |
| *Vampyressa thyone* | Phyllostomidae | Yangochiroptera | America C/S/Carib | DQ312431 | 4 | 2 | 1 |
| *Corynorhinus townsendii* | Vespertilionidae | Yangochiroptera | America N | KC747680 | 54 | 1 | 1 |
| *Eptesicus nilssonii* | Vespertilionidae | Yangochiroptera | Europe-Asia C/E | GQ272582 | 46 | 1 | 1 |
| *Myotis brandtii* | Vespertilionidae | Yangochiroptera | Europe-Asia C/E | AF376844 | 60 | 1 | 1 |
| *Myotis daubentonii* | Vespertilionidae | Yangochiroptera | Europe-Asia C/E | AB106589 | 243 | 6 | 2 |
| *Myotis keaysi* | Vespertilionidae | Yangochiroptera | America C/S/Carib | JX130526 | 5 | 9 | 4 |
| *Myotis myotis* | Vespertilionidae | Yangochiroptera | Europe-Asia C/E | AM261883 | 2751 | 7 | 3 |
| *Myotis mystacinus* | Vespertilionidae | Yangochiroptera | Europe-Asia C/E | AB106605 | 81 | 2 | 1 |
| *Myotis nattereri* | Vespertilionidae | Yangochiroptera | Europe-Asia C/E | JF412413 | 143 | 2 | 1 |
| *Myotis nigricans*\* | Vespertilionidae | Yangochiroptera | America C/S/Carib | KP134584 | 58 | 6 | 1 |
| *Nyctalus noctula* | Vespertilionidae | Yangochiroptera | Europe-Asia C/E | JX570902 | 195 | 1 | 1 |
| *Pipistrellus pipistrellus*\* | Vespertilionidae | Yangochiroptera | Europe-Asia C/E | KF874521 | 983 | 36 | 2 |
| *Tylonycteris pachypus*\* | Vespertilionidae | Yangochiroptera | Asia S/SE/SE | EF517315 | 15 | 1 | 1 |
| *Hipposideros armiger* | Hipposideridae | Yinpterochiroptera | Asia S/SE/SE | JX849197 | 42 | 25 | 2 |
| *Hipposideros diadema*\* | Hipposideridae | Yinpterochiroptera | Asia S/SE/SE | DQ219421 | 13 | 1 | 1 |
| *Hipposideros fulvus*† | Hipposideridae | Yinpterochiroptera | Asia S/SE/SE | DQ054809 | 12 | 1 | 1 |
| *Hipposideros commersoni*‡ | Hipposideridae | Yinpterochiroptera | Africa | EU934469 | 3 | 4 | 1 |
| *Hipposideros larvatus* | Hipposideridae | Yinpterochiroptera | Asia S/SE/SE | EU434949 | 19 | 32 | 7 |
| *Triaenops persicus* | Hipposideridae | Yinpterochiroptera | Africa | EU798758 | 7 | 8 | 1 |
| *Megaderma lyra*† | Megadermatidae | Yinpterochiroptera | Asia S/SE/SE | DQ888678 | 124 | 3 | 2 |
| *Eidolon dupreanum* | Pteropodidae | Yinpterochiroptera | Africa | KM226003 | 10 | 94 | 8 |
| *Eidolon helvum* | Pteropodidae | Yinpterochiroptera | Africa | JN398200 | 101 | 383 | 35 |
| *Epomophorus gambianus*\* | Pteropodidae | Yinpterochiroptera | Africa | JF728757 | 8 | 53 | 2 |
| *Harpyionycteris whiteheadi* | Pteropodidae | Yinpterochiroptera | Asia S/SE/SE | DQ445708 | 1 | 1 | 1 |
| *Megaerops niphanae*† | Pteropodidae | Yinpterochiroptera | Asia S/SE/SE | GQ410214 | 1 | 2 | 1 |
| *Micropteropus pusillus*\* | Pteropodidae | Yinpterochiroptera | Africa | JF728734 | 3 | 11 | 1 |
| *Ptenochirus jagori* | Pteropodidae | Yinpterochiroptera | Asia S/SE/SE | AB046325 | 8 | 1 | 1 |
| *Pteropus hypomelanus* | Pteropodidae | Yinpterochiroptera | Asia S/SE/SE | AB062472 | 44 | 2 | 2 |
| *Rousettus aegyptiacus* | Pteropodidae | Yinpterochiroptera | Africa | JF728760 | 254 | 105 | 1 |
| *Rhinolophus acuminatus*† | Rhinolophidae | Yinpterochiroptera | Asia S/SE/SE | FJ185205 | 2 | 17 | 2 |
| *Rhinolophus borneensis* subsp. *chaseni*† | Rhinolophidae | Yinpterochiroptera | Asia S/SE/SE | DQ987605 | 2 | 5 | 7 |
| *Rhinolophus landeri*\* | Rhinolophidae | Yinpterochiroptera | Africa | EU436668 | 5 | 18 | 2 |
| *Rhinolophus pearsonii* | Rhinolophidae | Yinpterochiroptera | Asia S/SE/SE | JX502551 | 2 | 1 | 1 |
| *Rhinolophus sinicus* | Rhinolophidae | Yinpterochiroptera | Asia S/SE/SE | HM134917 | 18 | 7 | 2 |
| *Ornithorhynchus anatinus* | - | - | outgroup | HQ379928 | - | - | - |
| *Rattus rattus* | - | - | outgroup | AB033702 | - | - | - |
| *Equus caballus* | - | - | outgroup | D82932 | - | - | - |



**Fig. S1.** Maximum likelihood (likelihood = -28954.11) phylogenetic tree of bat species using 1140 base pair sequences of the mitochondrial *cytb* gene aligned using MAFFT (Katoh and Standley, 2013). The tree was assembled in MEGA6 (Tamura et al., 2013) using the GTR+Γ+I substitution model with four gamma categories (Nei and Kumar, 2000). Node support values were estimated from 1000 bootstrap replicates; only support values ≥50% are shown.

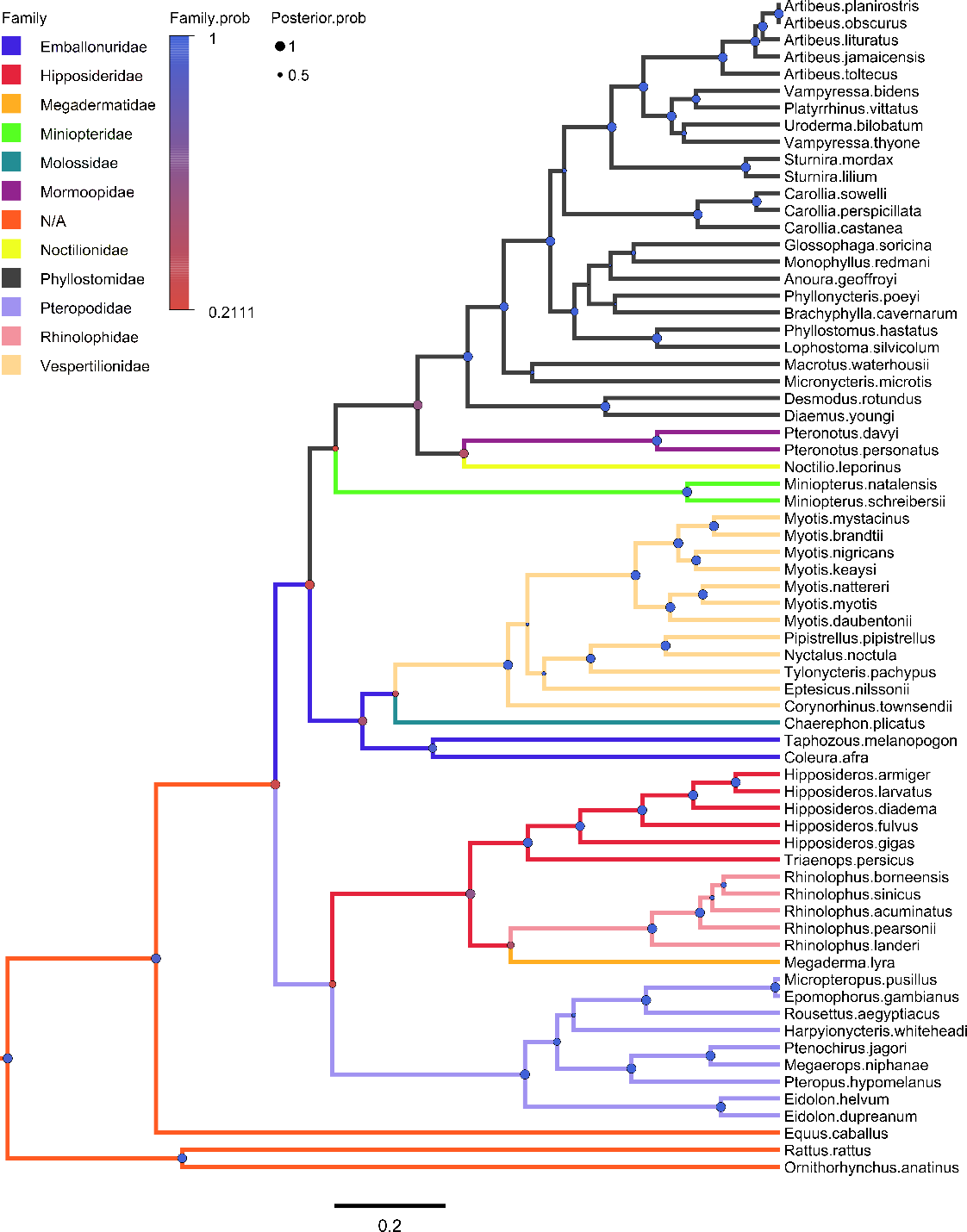


**Fig. S2.** Maximum likelihood (likelihood = -9839.48) phylogenetic tree of *Bartonella* genotypes using 333 base pair sequences of the genomic *gltA* gene aligned using MAFFT (Katoh and Standley, 2013). The tree was assembled in MEGA6 (Tamura et al., 2013) using the GTR+Γ+I substitution model with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

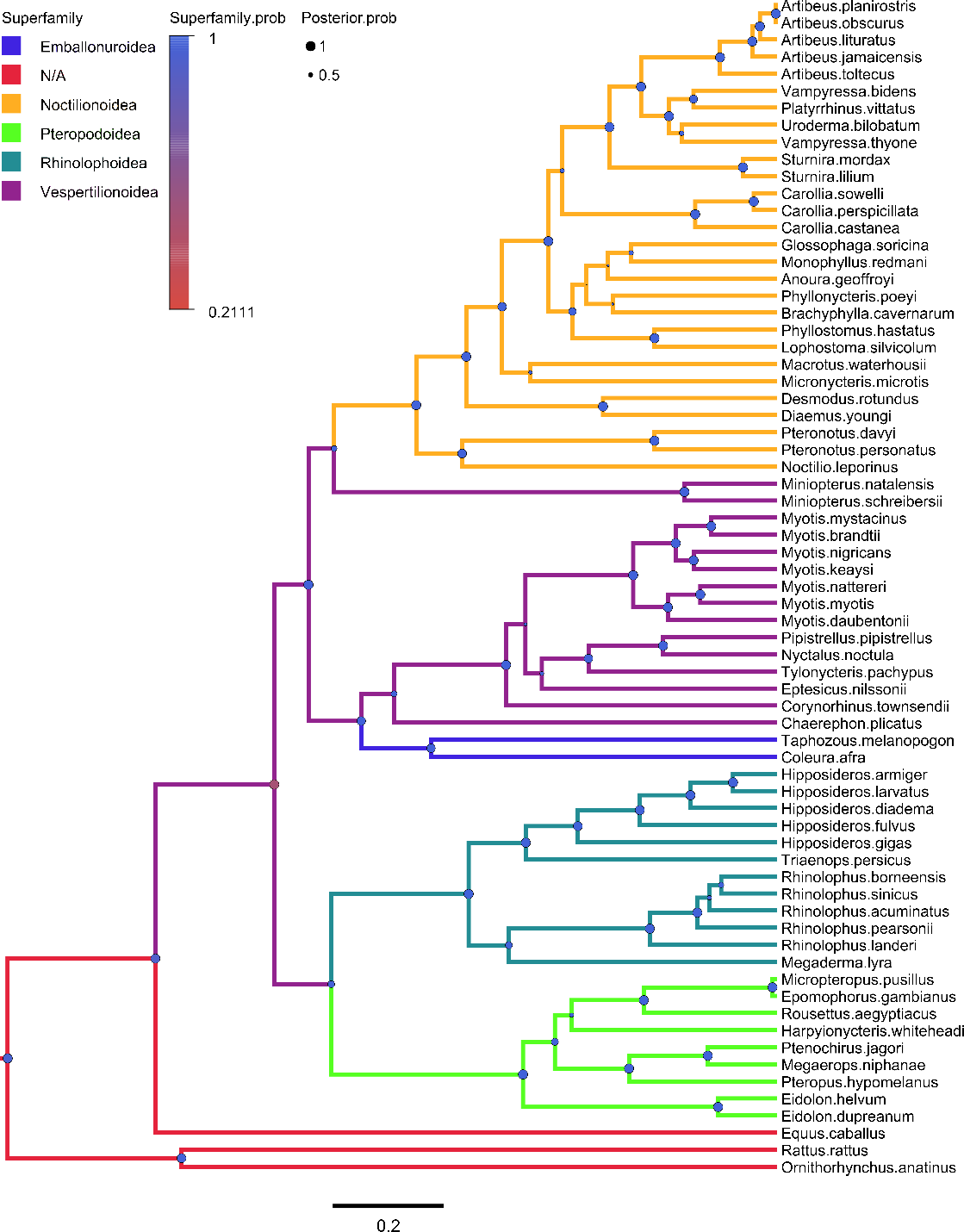
**Table S4.** Global fit test results from ParaFit and PACo analyses. P-values were calculated from global fits (ParaFit and PACo) using 10000 permutations.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **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** |  |
| m2 global value | 8.11 |  | m2 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** |  |
| m2 global value | 17.16 |  | m2 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 |

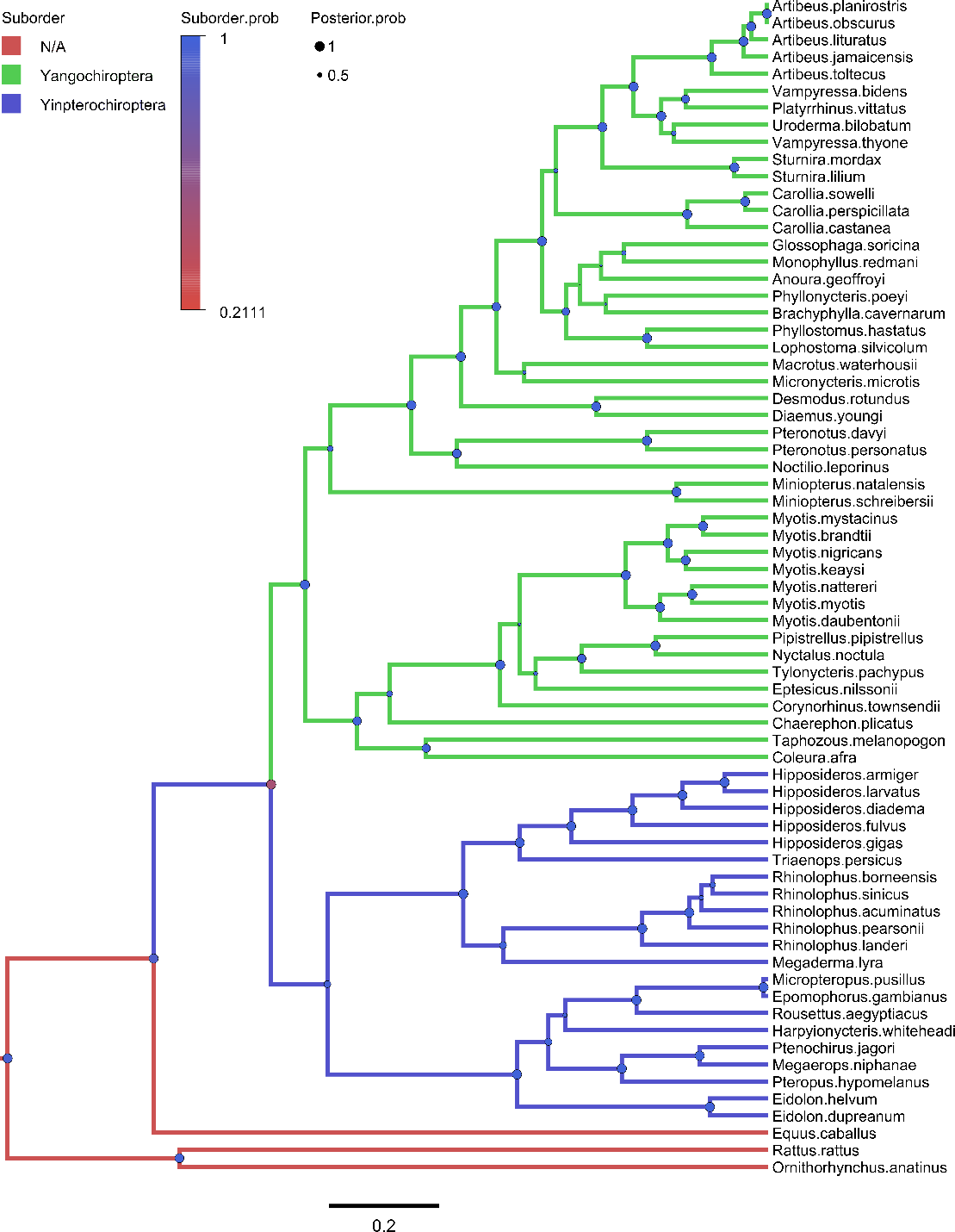
IQR – interquartile range.



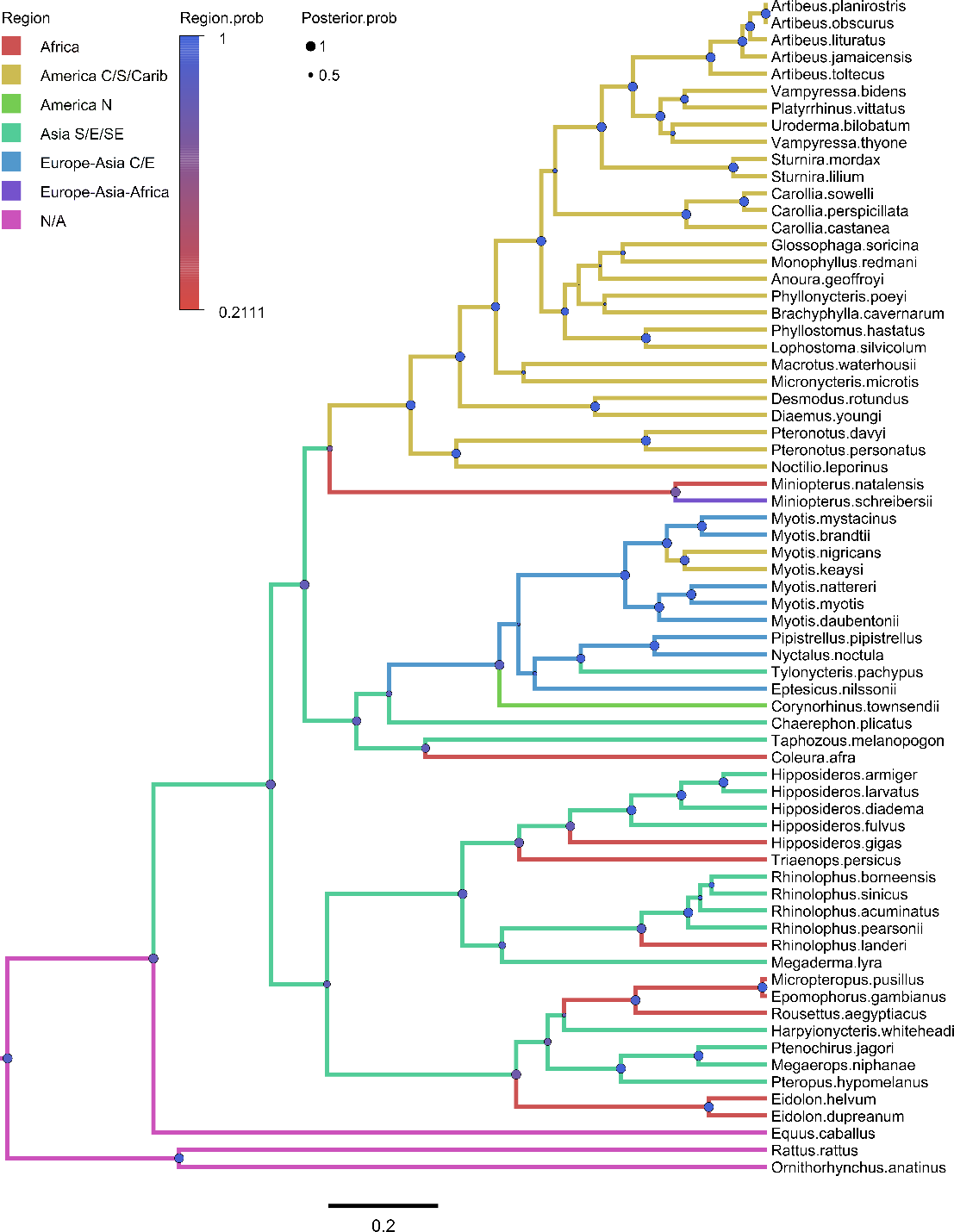
**Fig. S3.** Bayesian phylogeny of bat host species reconstructing bat families, shown by colored branches. Posterior probabilities for nodes are shown as circles (●) scaled by size from 0 to 1 (Posterior.prob) and colored by the support for the family at that node (Family.prob). Mean tree likelihood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



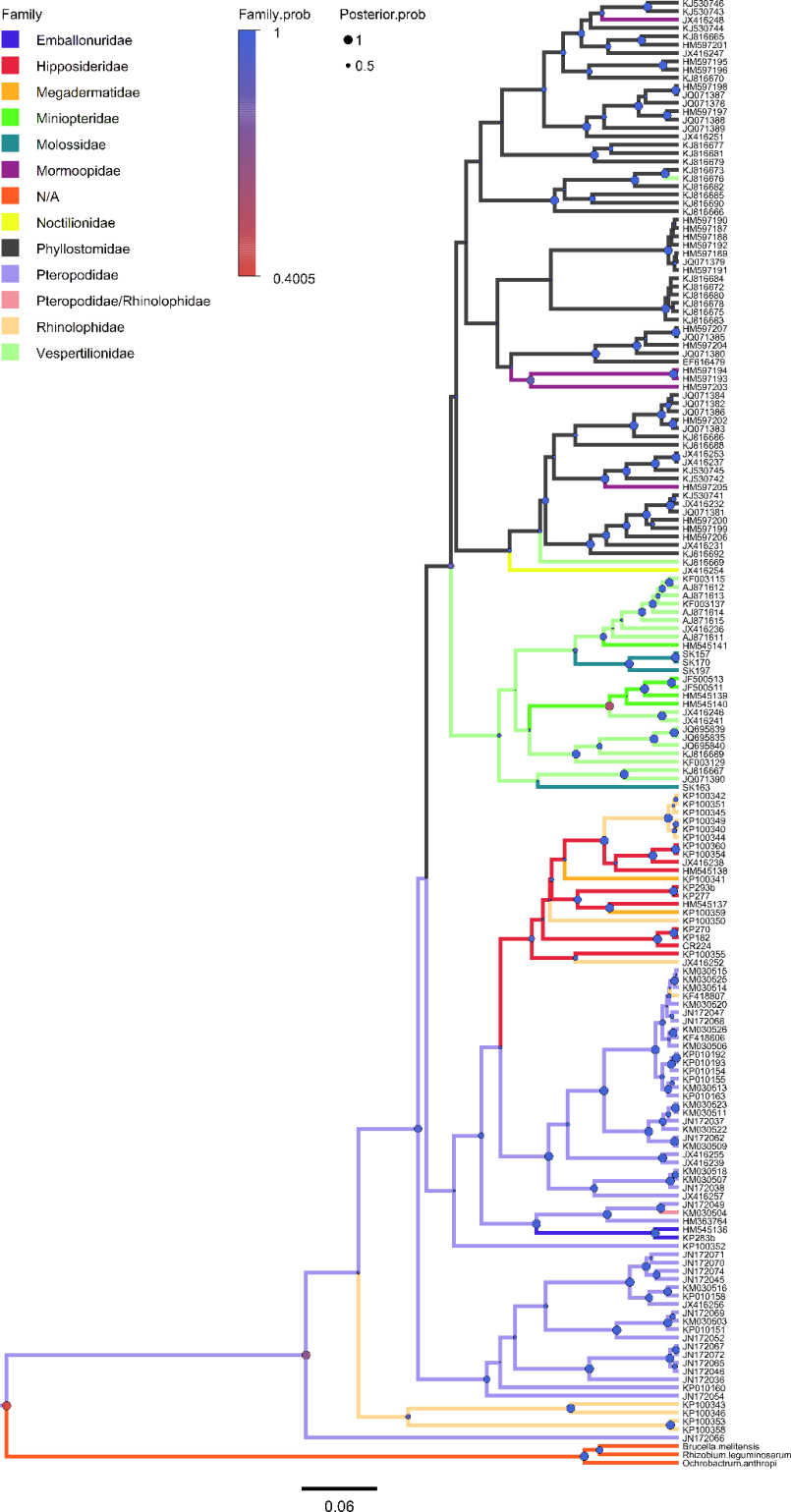
**Fig. S4.** Bayesian phylogeny of bat host species reconstructing bat superfamilies, shown by colored branches. Posterior probabilities for nodes are shown as circles (●) scaled by size from 0 to 1 (Posterior.prob) and colored by the support for the bat superfamily at that node (Superfamily.prob). Mean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



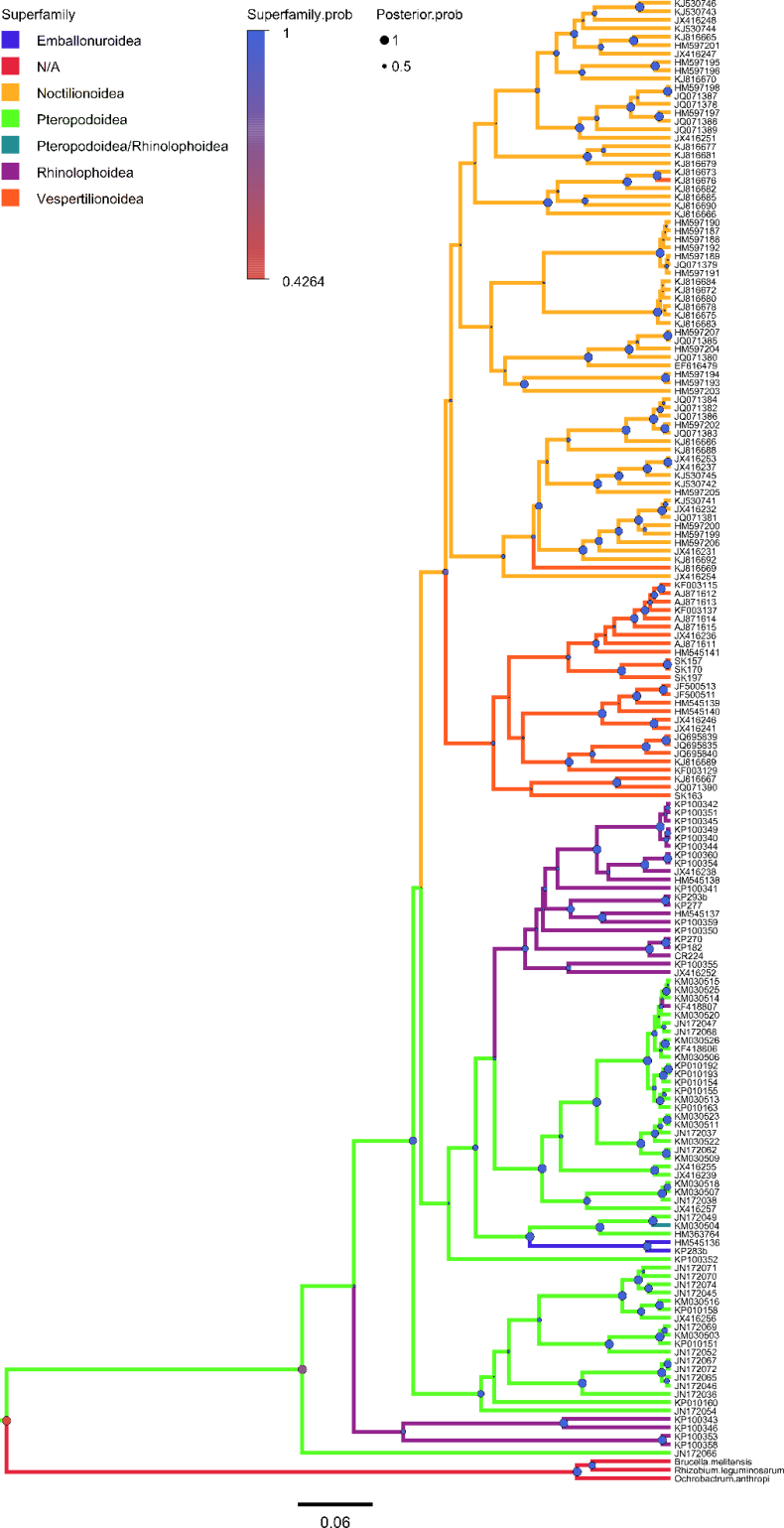
**Fig. S5.** Bayesian phylogeny of bat host species reconstructing bat suborders, shown by colored branches. Posterior probabilities for nodes are shown as circles (●) scaled by size from 0 to 1 (Posterior.prob) and colored by the support for the bat suborder at that node (Suborder.prob). Mean tree likelihood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



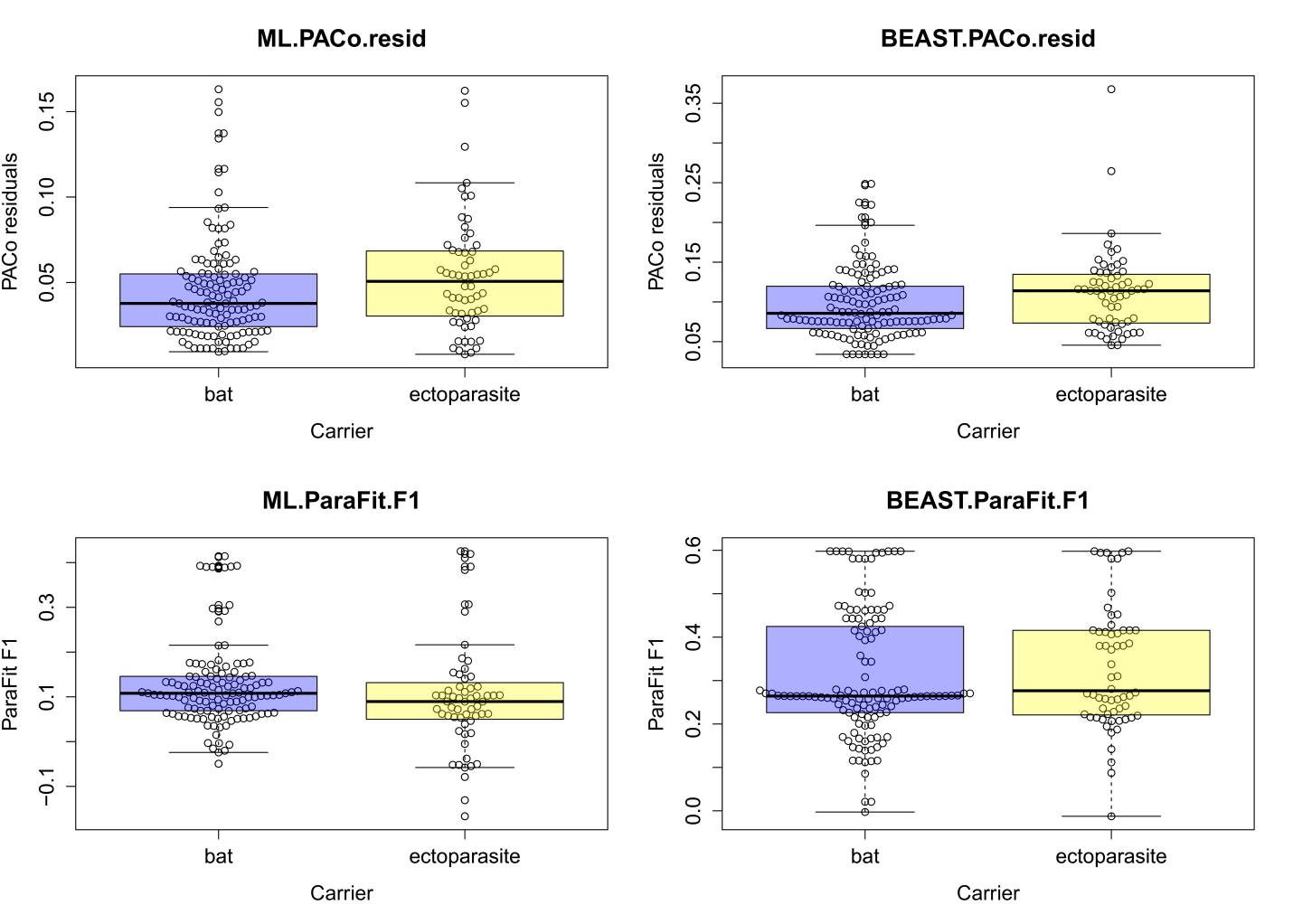
**Fig. S6.** Bayesian phylogeny of bat host species reconstructing bat geographic regions, shown by colored branches. Posterior probabilities for nodes are shown as circles (●) scaled by size from 0 to 1 (Posterior.prob) and colored by the support for the geographic region at that node (Region.prob). 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.



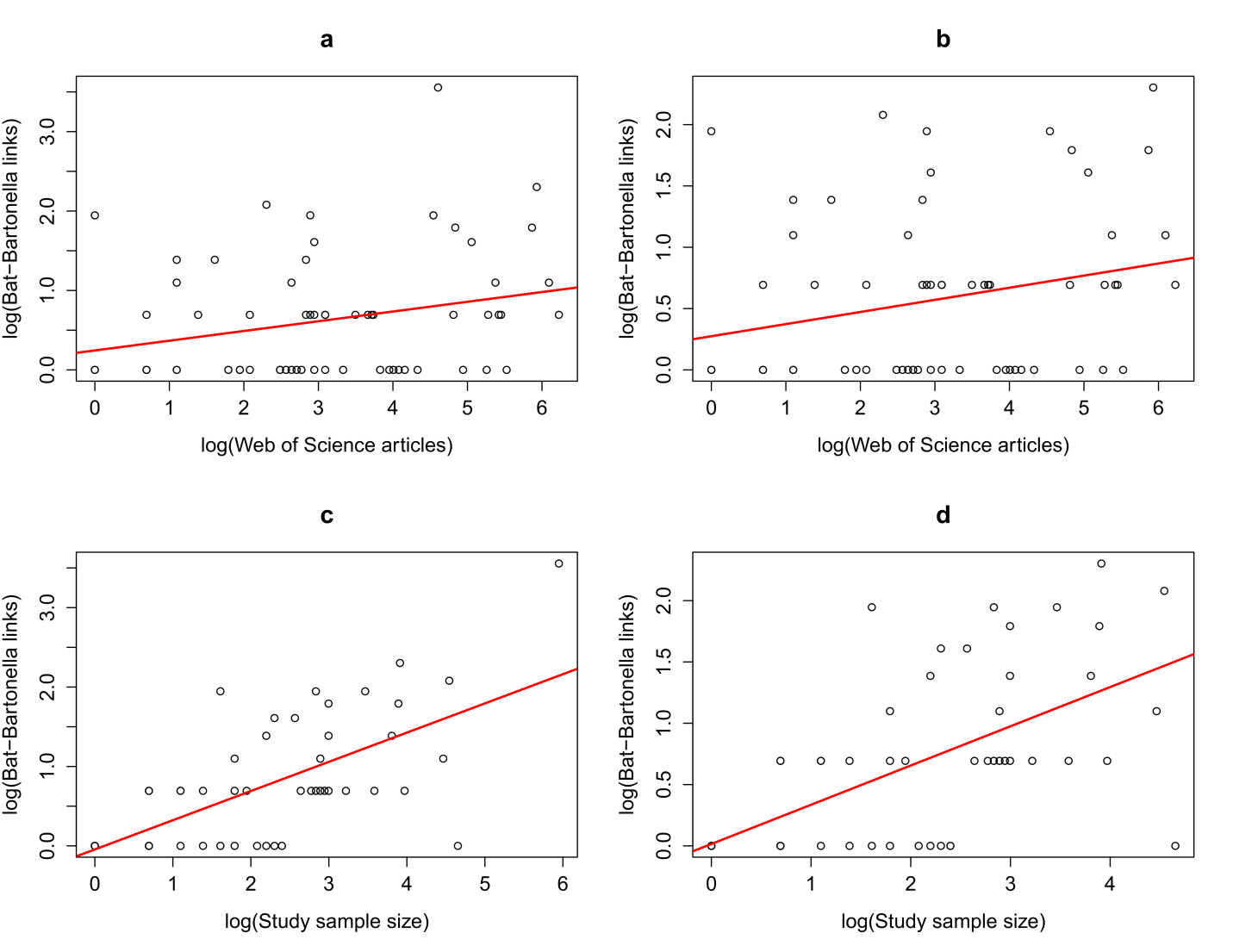
**Fig. S7.** Bayesian phylogeny of *Bartonella* genotypes reconstructing bat host families, shown by colored branches. Posterior probabilities for nodes are shown as circles (●) scaled by size from 0 to 1 (Posterior.prob) and colored by the support for the bat host family at that node (Family.prob). Mean tree likelihood = -9981.92, ESS = 2713; mean family tree likelihood = -125.52, ESS = 1028. Details on tip labels for *Bartonella* genotypes and associated host species are listed in Table S1 and S2.



**Fig. S8.** Bayesian phylogeny of *Bartonella* genotypes reconstructing bat host 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 host suborder at that node (Superfamily.prob). Mean tree likelihood = -9981.92, ESS = 2713; mean superfamily tree likelihood = -60.36, ESS = 525. Details on tip labels for *Bartonella* genotypes and associated host species are listed in Table S1 and S2.



**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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