Appendix J. Comparative phylogeography between *Casinycteris* and *Scotonycteris* in eastern Democratic Republic of the Congo based on complete Cytb sequences.

Median joining networks of *Casinycteris* and *Scotonycteris* are based respectively on 37 and 15 sequences of the complete *Cytb* gene. Haplotypes shared by several individuals are designated CA1 (n = 24), CA2 (n = 7), and CA3 (n = 4) for *Casinycteris*, and SZ8 (n = 4), SZ9 (n = 3), and SZ10 (n = 2) for *Scotonycteris* (see list in Appendix C). The circle size is proportional to the number of identical haplotypes observed in the dataset. The number of mutations between haplotypes are indicated on the branches.
Black small circles indicate median vectors representing missing or not sampled haplotypes.
The central map shows the collecting localities (see Appendix A for more details). The image was extracted from Google Earth (US Dept of State Geographer; ©2014 Google; Image Landsat; Data SIO, NOAA, U.S. Navy, NGA, GEBCO). Orange highlights animals obtained on the right bank of the Congo River and blue the left bank of the Congo River.