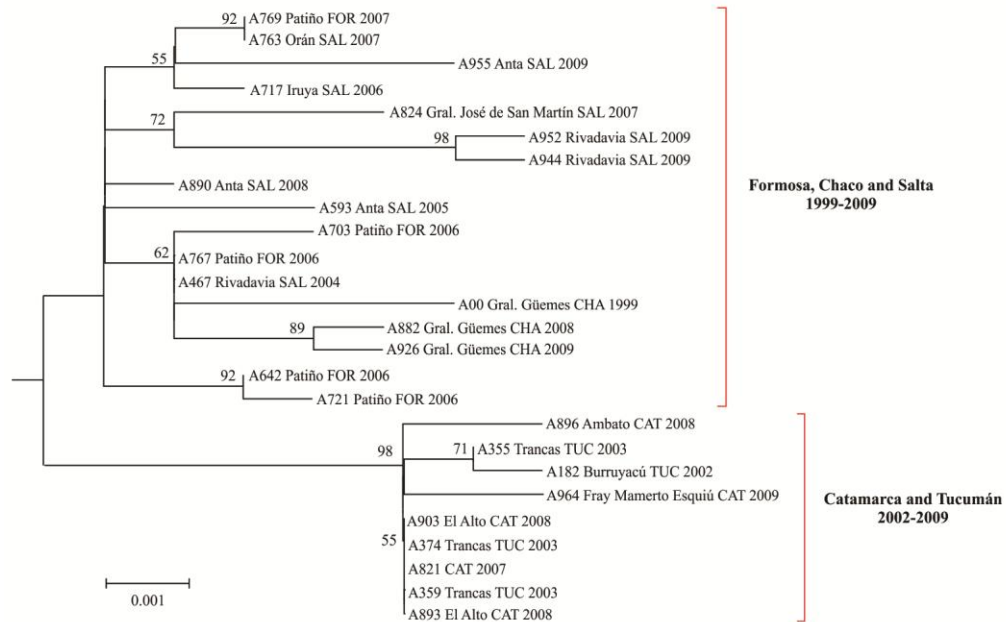


## Supplementary Figures

**Figure S1.** Partial ML tree (complete N sequences) - Group NWA.



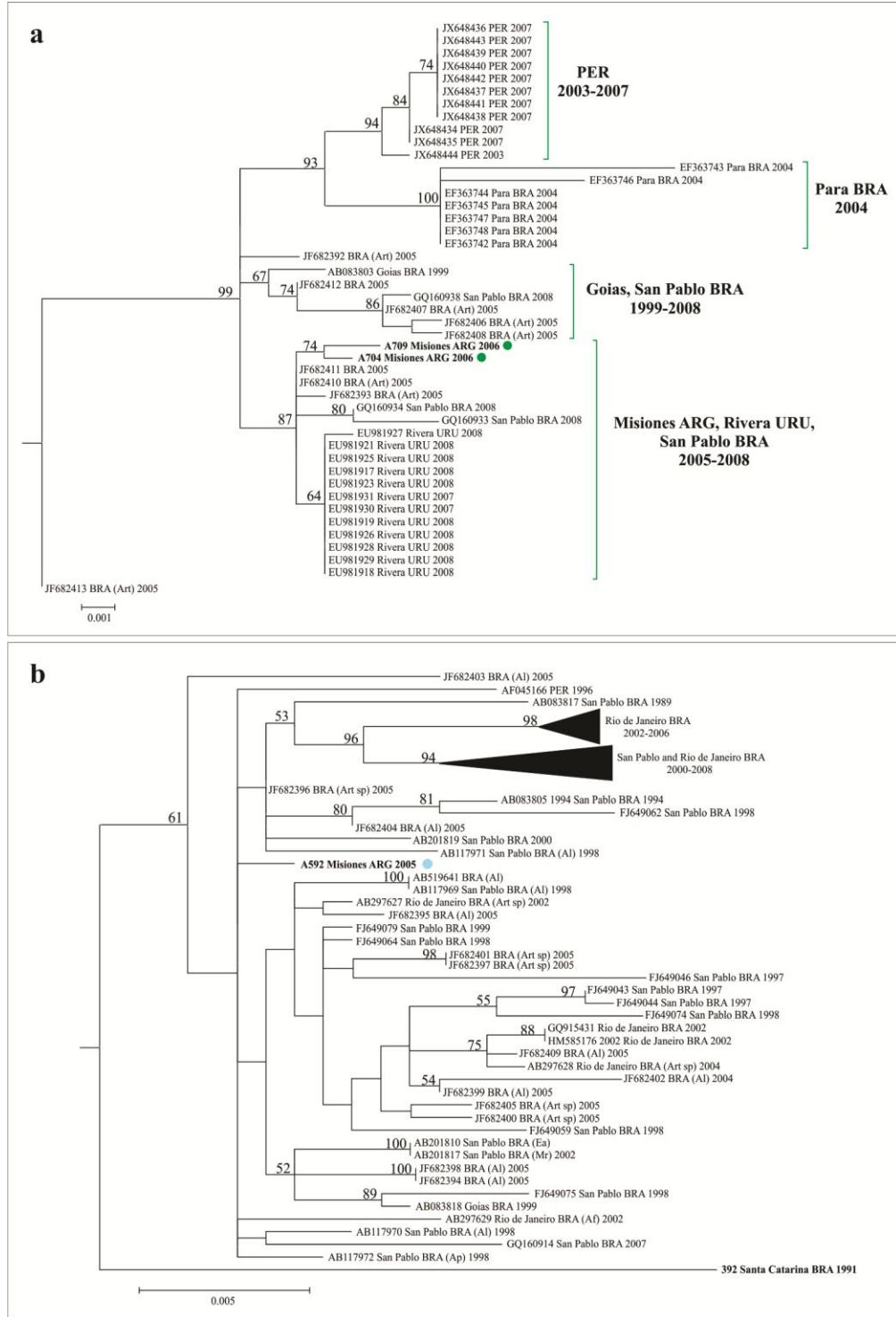
**Figure S1.** Partial ML phylogenetic tree of complete N sequences showing the group of sequences from Northwestern Argentina (NWA) (group V). Department, province (abbreviated in uppercase) and year of isolation are indicated when available. CAT: Catamarca, CHA: Chaco, FOR: Formosa, SAL: Salta, TUC: Tucumán. Note that samples from the same department may be originated in different cities (information available in Table S1).

**Figure S2. Partial ML tree (complete N sequences) - Group NEA.**



**Figure S2.** Partial ML phylogenetic tree of complete N sequences showing the group of sequences from Northeastern Argentina (NEA) (group VIb). Department, province (abbreviated in uppercase) and year of isolation are indicated when available. Red dots indicate sequences belonging to samples from NWA. CHA: Chaco, CORR: Corrientes, FOR: Formosa, MIS: Misiones, SAL: Salta, STA FE: Santa Fé. Note that samples from the same department may be originated in different cities (information available in Table S1).

**Figure S3.** Partial ML tree (complete N sequences) - Other Argentinean groups (a) y (b).



**Figure S3.** Partial ML phylogenetic tree of complete N sequences showing the groups with sequences from Argentina intermingled with sequences from Brazil, Uruguay and Peru (a) (group Ia) and from Brazil and Peru (b) (group II). State or province, country (abbreviated in uppercase) and year of isolation are indicated when available. Sequences introduced in this work are shown in bold and sequences from Argentina are indicated with a green or a sky-blue dot. BRA: Brazil, PER: Peru, URU: Uruguay. The host is indicated in parentheses when samples were labeled as originated from non hematophagous bats, Af: *Artibeus fimbriatus*, Al: *Artibeus lituratus*, Ap: *Artibeus planirostris*, Art sp: *Artibeus* spp, Ea: *Eumops auripendulus*, Mr: *Molossus rufus*.

Figure S4. ML tree (partial N sequences).

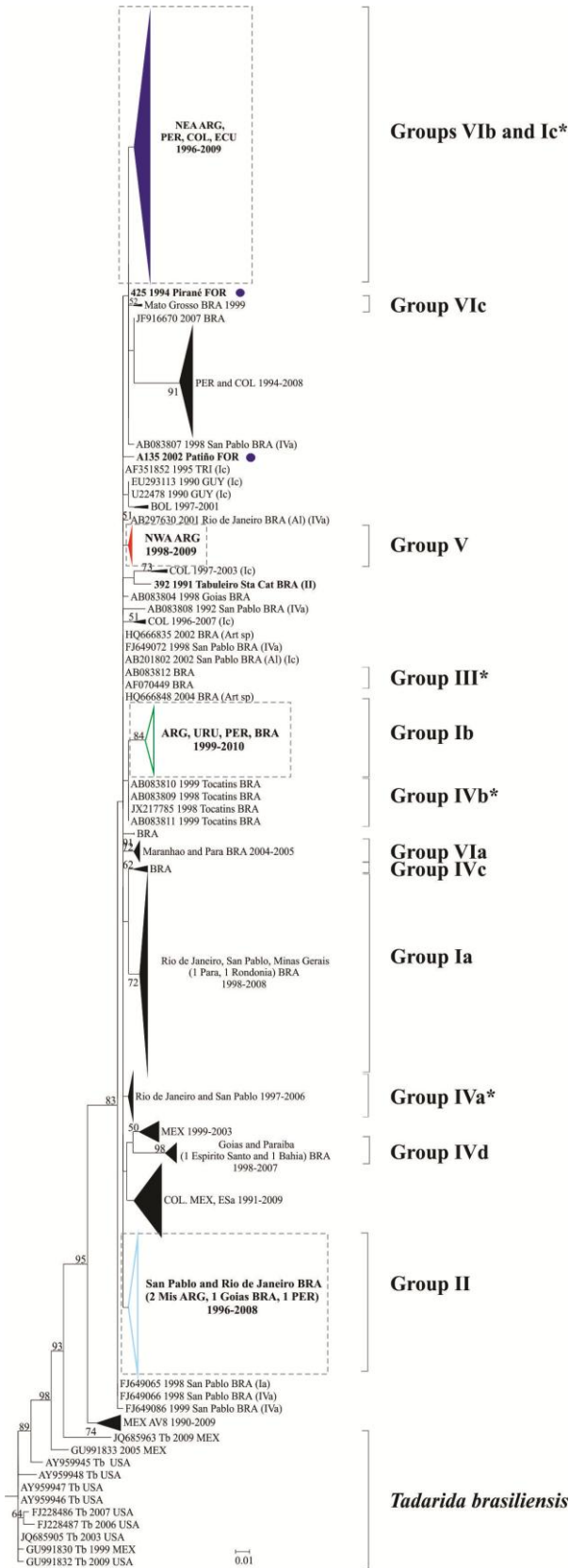
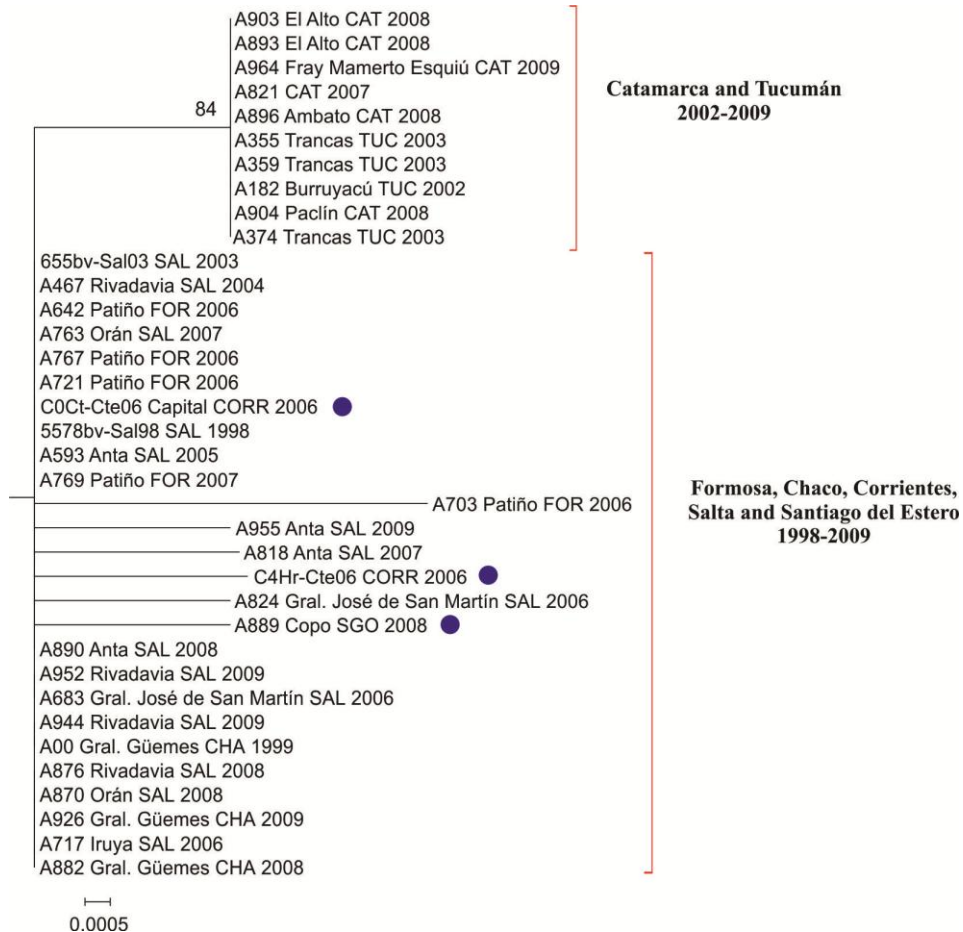


Figure S4. Maximum Likelihood (ML) phylogenetic tree of partial N sequences related to vampire bats. Bootstrap values higher than 50 % are shown at nodes for relevant groups. Individual sequences or groups of sequences containing isolates introduced in this work are shown in bold. Sequences or groups containing isolates from Argentina are indicated with a colored dot or a colored triangle. In dotted lines are groups shown in Figures S5, S6 and S7. State or province, country (abbreviated in uppercase) and year of isolation are indicated when available. BRA: Brazil, COL: Colombia, ECU; Ecuador, ESa: El Salvador, GUY: French Guyana, MEX: Mexico, PER: Peru, URU: Uruguay. Clusters and subclusters denomination according to the phylogenetic analysis of complete N gene is indicated in parentheses (individual sequences) or in the squares brackets (group of sequences).

**Figure S5.** ML tree (partial N sequences) - Group NWA.



**Figure S5.** Partial ML phylogenetic tree of partial N sequences showing the group of sequences from Northwestern Argentina (NWA) (group V). Department, province (abbreviated in uppercase) and year of isolation are indicated when available. Blue dots indicate sequences belonging to samples from NEA. CAT: Catamarca, CHA: Chaco, FOR: Formosa, SAL: Salta, TUC: Tucumán. Note that samples from the same department may be originated in different cities (information available in Table S2).

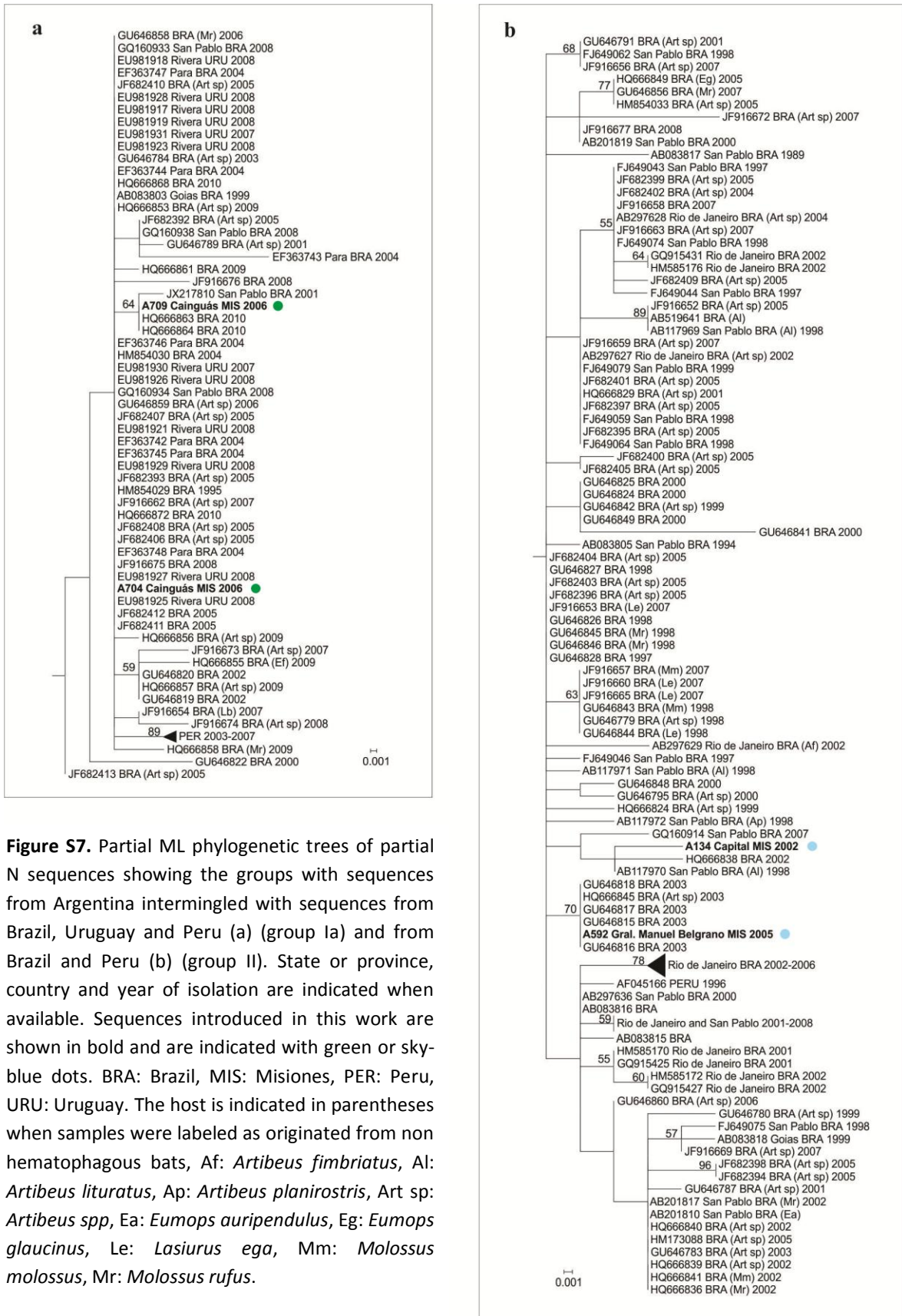


Figure S6. ML tree (partial N sequences) - Group NEA.



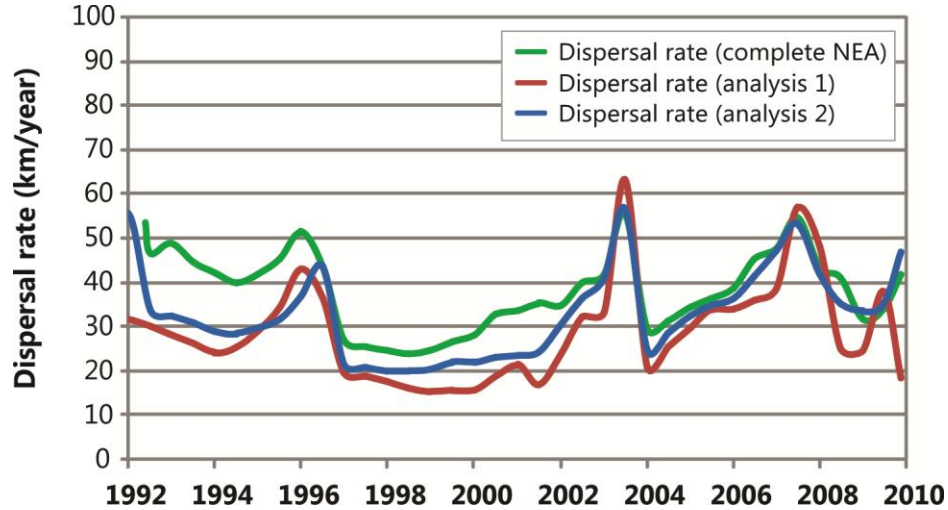
Figure S6. Partial ML phylogenetic tree of partial N sequences showing the group of sequences from Northeastern Argentina (NEA) (group VIb). Department, province (abbreviated in uppercase) and year of isolation are indicated when available. Red dots indicate sequences belonging to samples from NWA. CHA: Chaco, CORR: Corrientes, FOR: Formosa, MIS: Misiones, SAL: Salta, STA FE: Santa Fé. Note that samples from the same department may be originated in different cities (information available in Table S2).

**Figure S7.** ML tree (partial N sequences) - Other Argentinean groups (a) y (b).



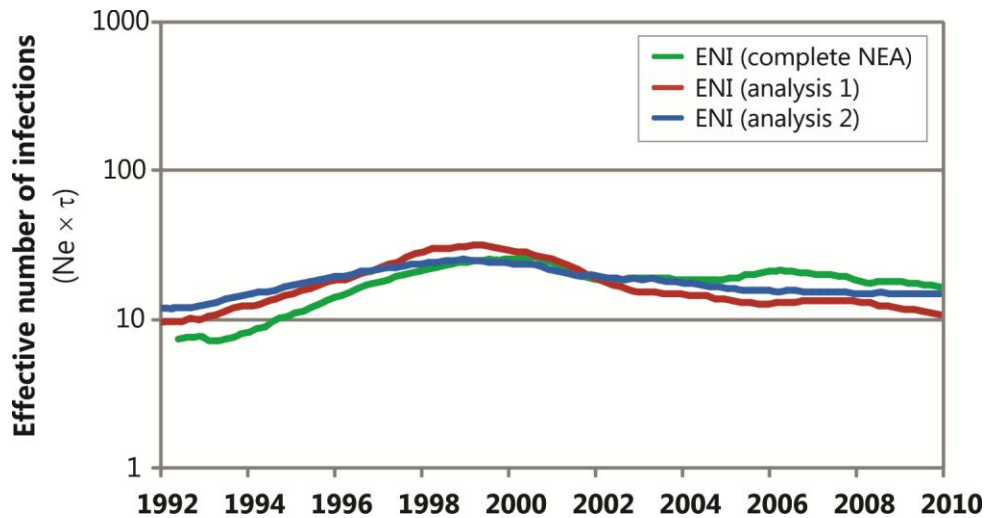
**Figure S7.** Partial ML phylogenetic trees of partial N sequences showing the groups with sequences from Argentina intermingled with sequences from Brazil, Uruguay and Peru (a) (group Ia) and from Brazil and Peru (b) (group II). State or province, country and year of isolation are indicated when available. Sequences introduced in this work are shown in bold and are indicated with green or sky-blue dots. BRA: Brazil, MIS: Misiones, PER: Peru, URU: Uruguay. The host is indicated in parentheses when samples were labeled as originated from non hematophagous bats, Af: *Artibeus fimbriatus*, Al: *Artibeus lituratus*, Ap: *Artibeus planirostris*, Art sp: *Artibeus spp*, Ea: *Eumops auripendulus*, Eg: *Eumops glaucinus*, Le: *Lasiurus ega*, Mm: *Molossus molossus*, Mr: *Molossus rufus*.

**Figure S8.** Dispersal rate for the complete NEA dataset and for the sensitivity analyses<sup>a</sup>.



<sup>a</sup> Results correspond to those obtained with the model selected by Bayes Factor test (Table S5). Analysis 1: Dataset NEA subsampled to obtain a uniform distribution of samples per year. Analysis 2: Dataset NEA subsampled to obtain a uniform distribution of samples per department.

**Figure S9.** Effective number of infections for the complete NEA dataset and for the sensitivity analyses.



<sup>a</sup> Results correspond to those obtained with the model selected by Bayes Factor test (Table S5). Analysis 1: Dataset NEA subsampled to obtain a uniform distribution of samples per year. Analysis 2: Dataset NEA subsampled to obtain a uniform distribution of samples per department.