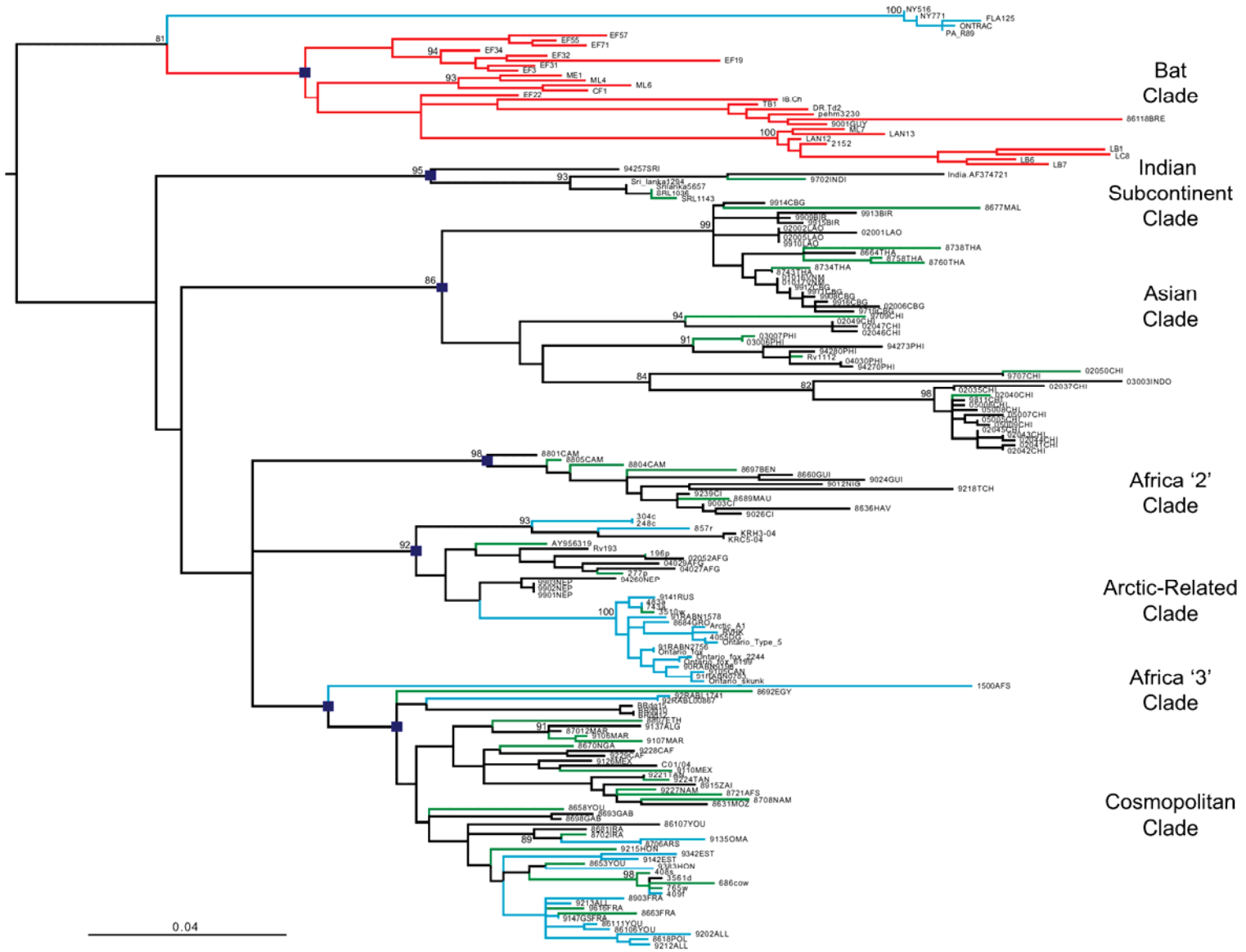

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Supplementary Fig. S1. ML phylogeny of 190 sequences from the partial (400 nt) N-coding region of RABV. The major clades of RABV are also indicated, denoted by blue squares at the relevant nodes. Branches are coloured-coded by species group: black, dogs; red, bats; blue, alternative reservoir hosts (such as the red fox); green, spill-over hosts (such as humans, bovines, wolf). Horizontal branches are drawn to scale, with bootstrap support values (>80%) shown for key nodes. Epidemiological information concerning isolates analysed here that not are described in Supplementary Table S2 is available from the authors on request. Note that although isolates NY516, NY771, FLA125, ONTRAC and PA_R89 were all isolated from raccoons in North America, they are more closely related to RABV from bats than to RABV from non-flying mammals, suggesting that they may represent a secondary cross-species transfer from bats.

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