

Supplementary data. Phylogenetic analysis of the individual markers.

The COI analyses (both MP and ML) were the ones that best resemble the combined analyses, recovering Clades A and B (Supp. Fig. a, b). The MP analysis of *cytB* failed to recover Clade A (Supp. Fig. c), and although that clade is present in the ML analysis, its support is extremely low (BS 25; Supp. Fig. d). Moreover, in the ML analysis *L. culpaeus* is nested inside Clade B (Supp. Fig. d). Finally, the MP analysis of the CR dataset did not recover Clade B, and most specimens of that clade are in a large polytomy (individually or in small clades) that also include Clade A, and the remaining species of *Lycalopex* (Supp. Fig. e). In the ML analysis of CR, clade B was recovered (but with low support; BS 45), and all the internal nodes that separate the different *Lycalopex* species have almost no support (BS > 30; Supp. Fig. f).

Supp. Fig. Schematic representation of the results of the maximum parsimony (MP) and maximum likelihood (ML) analyses of each marker separately. a, MP analysis of COI; b, ML analysis of COI; c, MP analysis of *cytB*; d, ML analysis of *cytB*; e, MP analysis of CR; f, ML analysis of CR. Numbers above the branches represent jackknife and bootstrap values respectively.

