**Figure S1. Results of hierarchical STRUCTURE analysis in Mesoamerican jaguars**. The optimal number of genetic clusters (*K*) in Mesoamerican jaguars using STRUCTURE, version 2.3.4 [47] was chosen based on posterior probability (mean L(*K*), A) and delta *K* (Δ*K*, mean (|L”(*K*)|)/SD(L(*K*)), D) for each *K* value. Bayesian clustering analysis was conducted for jaguars detected in (a) Guatemala, Belize, and Honduras (*n* = 72), (b) Honduras and Costa Rica (*n* = 43), (c) Guatemala and Belize (*n* = 65), and (d) Costa Rica (*n* = 36). SD, standard deviation; L’(*K*), mean rate of change of the likelihood distribution (B); |L”(*K*)|, absolute value of the 2nd order rate of change of the likelihood distribution (C).

(a)



(b)



(c)



(d)

