Figure S1: Maximum likelihood (ML) phylogenetic tree of 154 Columbiformes based on 8950 bp of concatenated sequences of six mitochondrial (12S, cytb, ND2, ATPase8/6, CO3, and CO1) and three nuclear (FIB7, RAG-1 and IRBP) genes. Eight specimens of the genera *Anhima*, *Caprimulgus*, *Chaetura*, *Crax*, *Gallus*, *Hirundapus*, *Podargus* and *Struthio* were used to root the tree and have not been included in the figure (see Table S2). Tree topology and branch lengths are for the sampled tree with the highest likelihood by RaxML (100 searches, log likelihood = -126492.974854). Maximum-likelihood bootstrap support value above 70% and posterior probability values ≥ 0.95 of the Bayesian analysis using BEAST are indicated above branches. Clades A, B and C, correspond to Pereira et al. 2007.