A PROLEGOMENON TO THE SYSTEMATICS OF SOUTH AMERICAN COTTONTAIL RABBITS (MAMMALIA, LAGOMORPHA, LEPORIDAE: *SYLVILAGUS*): DESIGNATION OF A NEOTYPE FOR *S. BRASILIENSIS* (LINNAEUS, 1758), AND RESTORATION OF *S. ANDINUS* (THOMAS, 1897) AND *S. TAPETILLUS* THOMAS, 1913

SUPPLEMENTARY FIGURES

Figure S1— Results of the cladistics analysis of dental morphological characters, with taxa reduced to *Sylvilagus floridanus*, *S. dicei*, and the focal *Sylvilagus* species of this work. A and B: two most parsimonious trees resulting from a heuristic search using PAUP* (v. 4.0b10 for Unix). Tree length: 28; consistency index: 0.678; retention index: 0.470. Tree calculated based on characters i–xviii of Ruedas (1998) with an additional character: lacunar remnant of anterointernal reentrant present (0) or absent (1). Thirteen of the characters were parsimony informative. Nodes labelled a–e (tree A), and f–j (tree B) are defined based on these characters; details are provided in the text. C: consensus tree derived from 10,000 bootstrap and jackknife replicates. Numbers above the node correspond to the percent support based on the bootstrap analysis, those below to the percent based on the jackknife analysis.
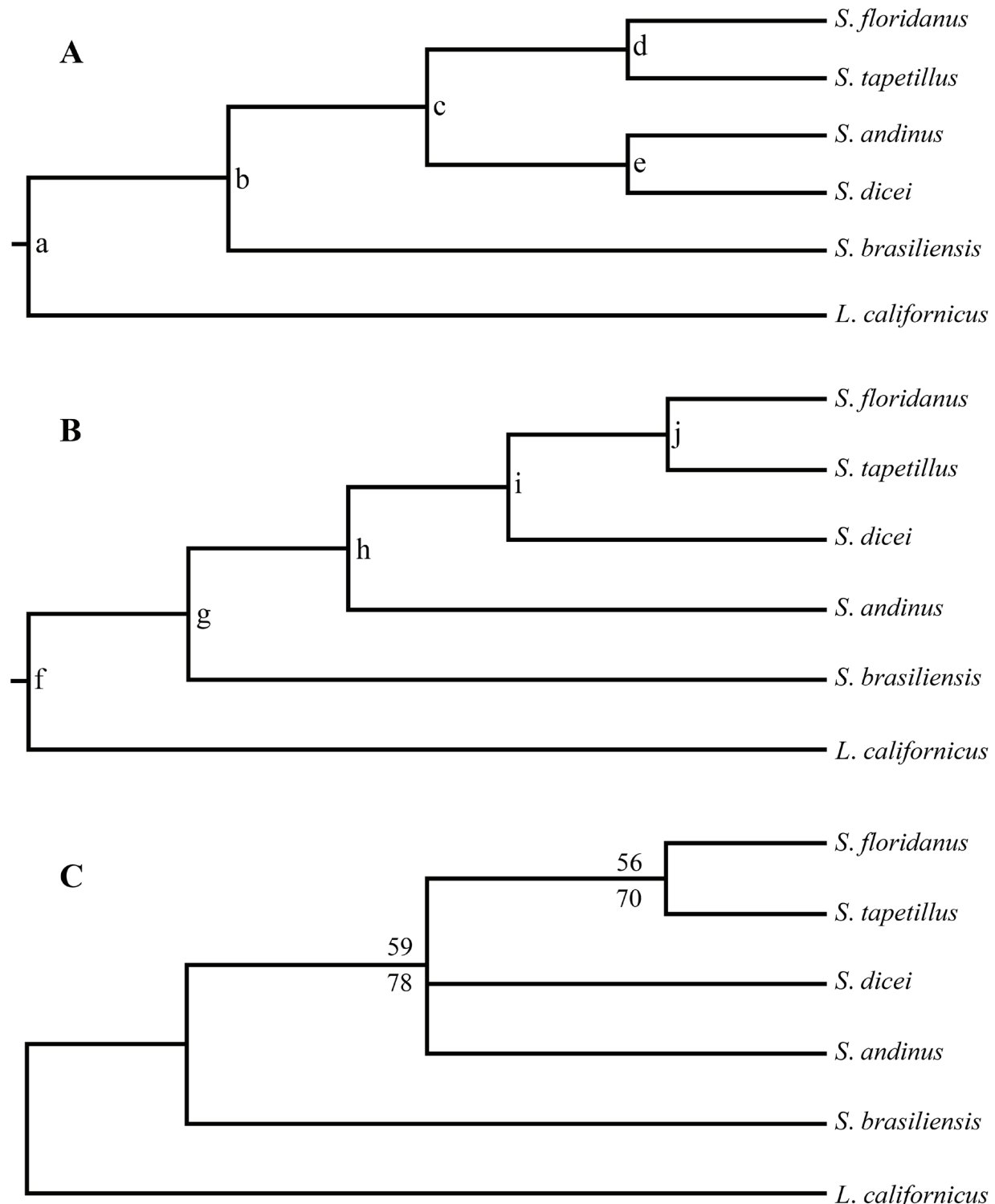
Figure S2— Results of the cladistics analysis of combined dental and morphological morphological characters, with the following taxa added to the analysis of dental characters only: *Sylvilagus cunicularius*, *S. nuttallii*, and *S. palustris*. Top six: all the equally most parsimonious trees resulting from a heuristic search using PAUP* (v. 4.0b10 for Unix). Tree length: 56 steps; consistency index: 0.518; retention index: 0.449. Tree calculated based on dental characters as outlined in Fig. 30, and the ten cranial morphological characters outlined in the body of the text used in the diagnoses of *S. andinus*, *S. brasiliensis*, and *S. tapetillus*. Twenty–four of the 34 characters were parsimony informative. Bottom: consensus tree derived from 10,000 bootstrap and jackknife replicates. Numbers above the node correspond to the percent support based on the bootstrap analysis, those below to the percent based on the jackknife analysis.
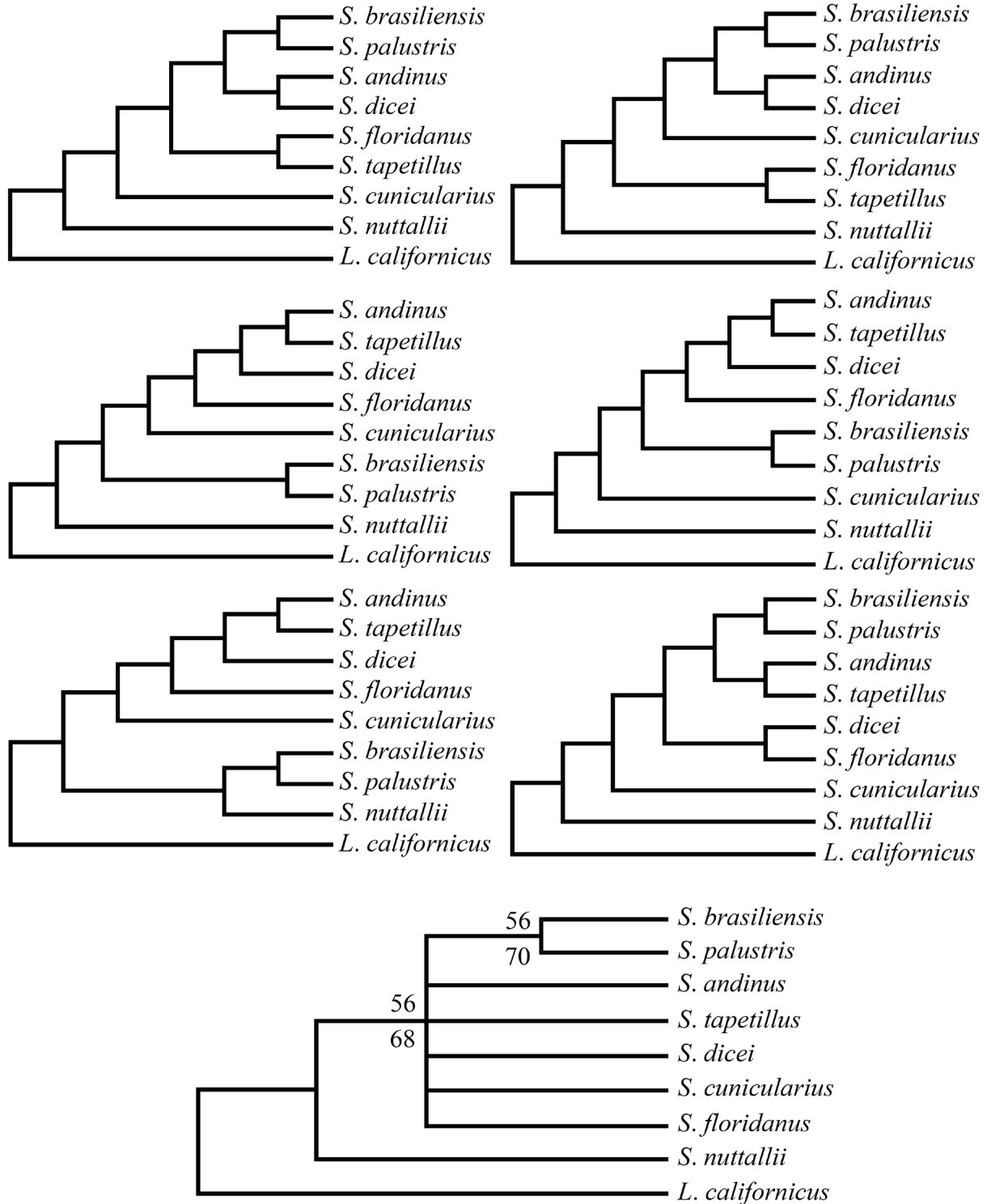
Figure S3— Phylogenies derived from the analysis of mitochondrial sequences data using Maximum Likelihood (ML) as implemented in PAUP* (Swofford 2003). Top, ML analysis of 12S rRNA gene for the sample including *Sylvilagus* for which cyt–*b* data were available and could be replicated with the latter gene, below. Bottom, ML analysis of Cytochrome b gene. Inset in both figures: alternative topologies obtained using Bayesian analysis as implemented in MrBayes 3.2.5 (Ronquist *et al*. 2011). Numbers above the branches indicate bootstrap support based on 1000 bootstrap replicates carried out in PAUP*. Numbers below the branches indicate the percent of 5×10^7 trees supporting the topology in the Bayesian analysis (initial 5X107 trees discarded as burnin). The taxonomic identification of the specimens marked as *S. gabbi* should be regarded as tentative at best: the identification is based on geographic location of capture (Tabasco, 17.74315833N, 91.30466944W), and the specimens consist of tissue only obtained from automobile fatalities, with no cranioskeletal material available for morphological corroboration. Distribution maps based on specimens as depicted in Hall (1981) would indicate that there are no *S. floridanus* present in that area, but that "*S. brasiliensis gabbi*" are in contrast present.
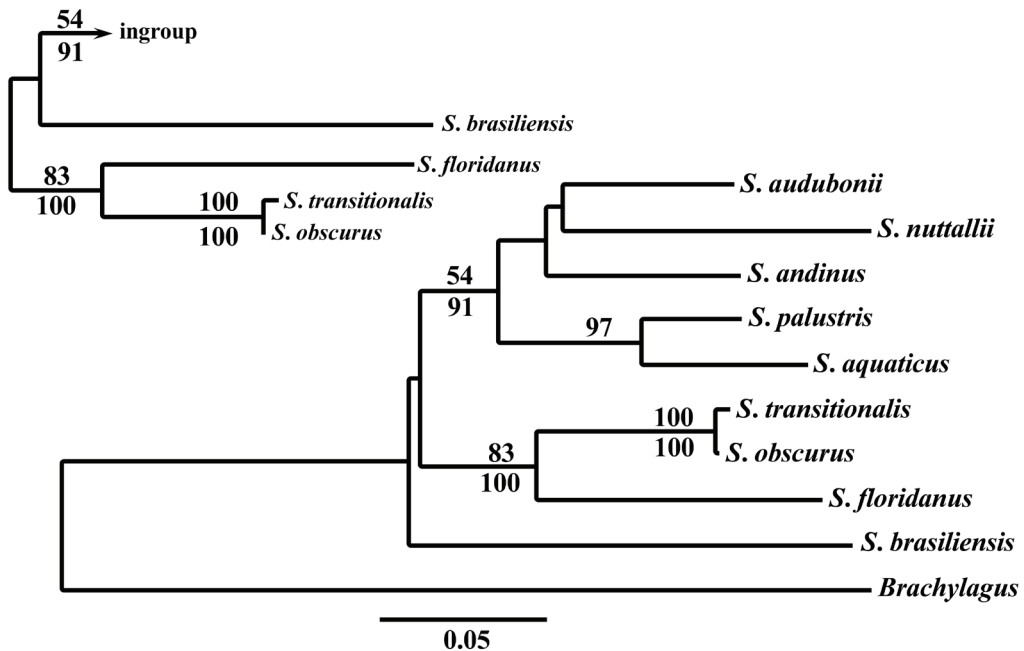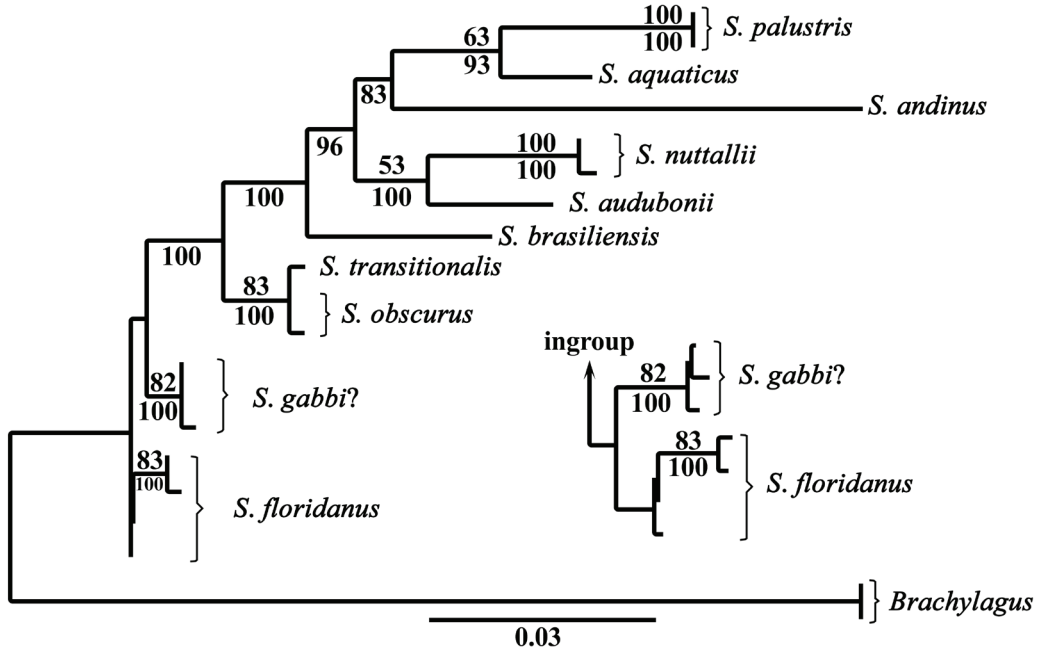
Figure S4— Phylogenies derived from the analysis of the combined 12S rRNA and Cytochrome b mitochondrial gene sequences. Top, Maximum Likelihood (ML) as implemented in PAUP* (Swofford 2003). Numbers above the branches indicate bootstrap support based on 1000 bootstrap replicates. Bottom, Bayesian analysis as implemented in MrBayes 3.2.5 (Ronquist *et al*. 2011). Numbers above the branches indicate the percent of 5×10^7 trees supporting the topology in the Bayesian analysis (initial 5×10^7 trees discarded as burnin). The analysis in this instance is based on species for which chimeric sequences could be created.
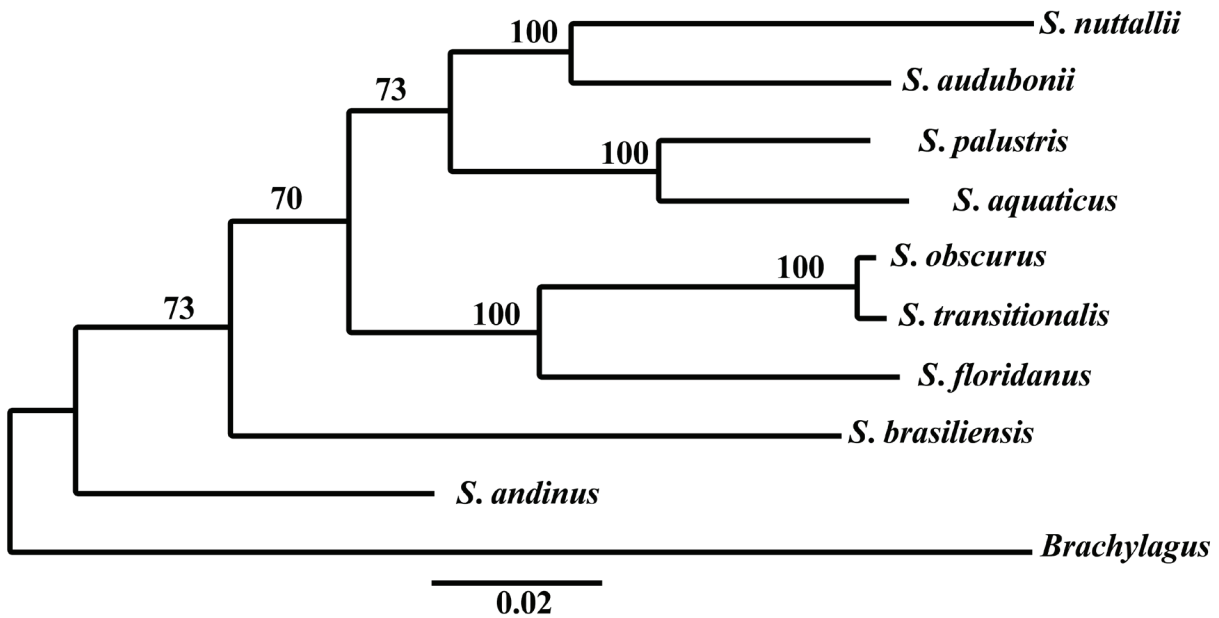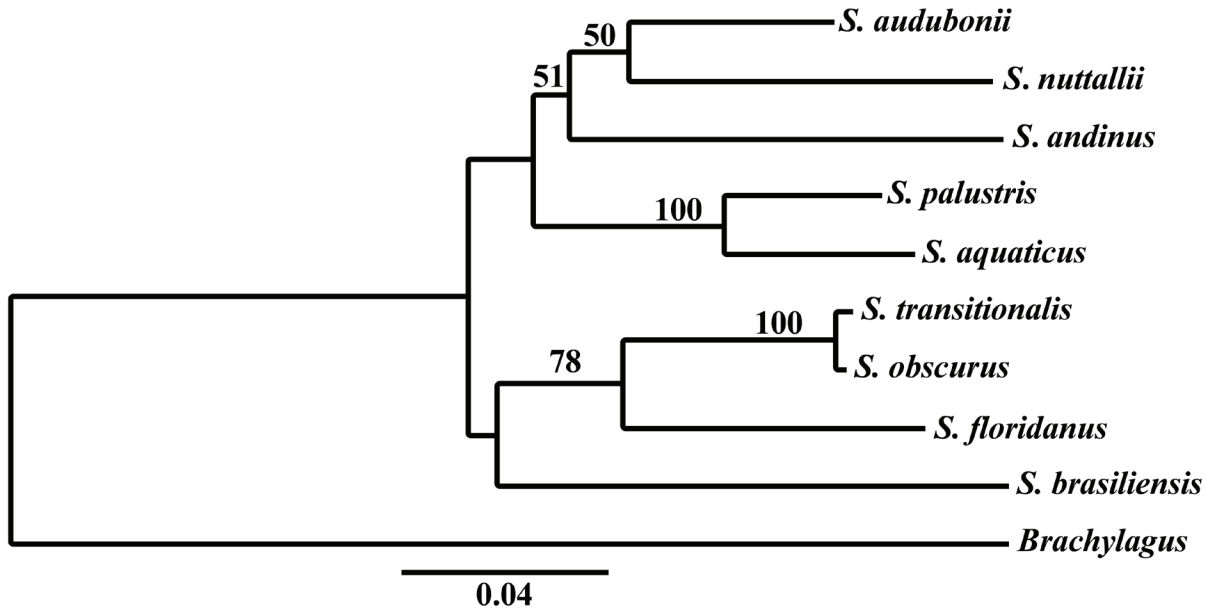
Figure S5— Divergence dates and 95% credibility intervals (grey bars) resulting from the analysis of a combined 12S rRNA + Cytochrome b dataset using the uncorrelated lognormal relaxed clock method implemented in BEAST (v. 1.8.2, Drummond *et al*. 2012).
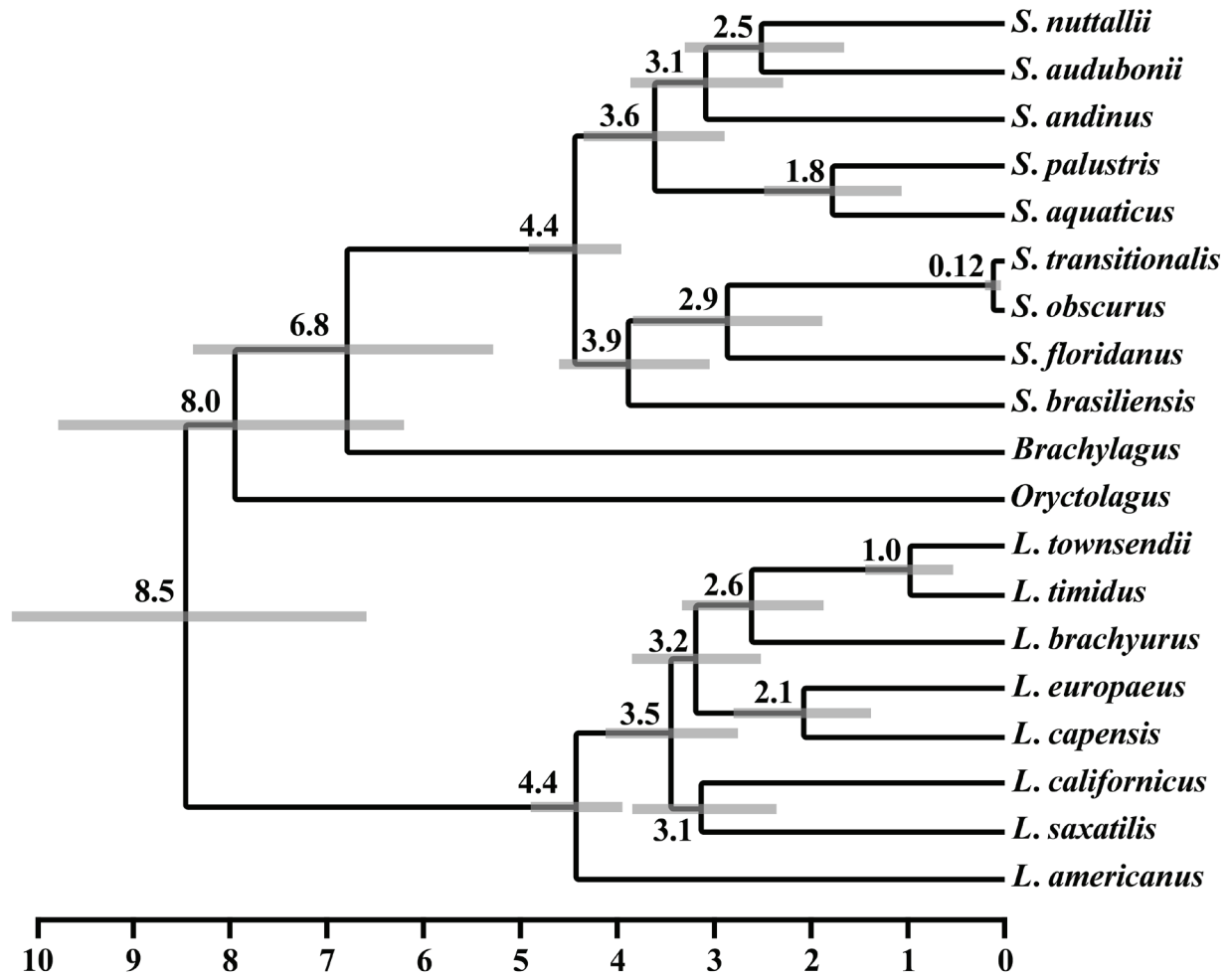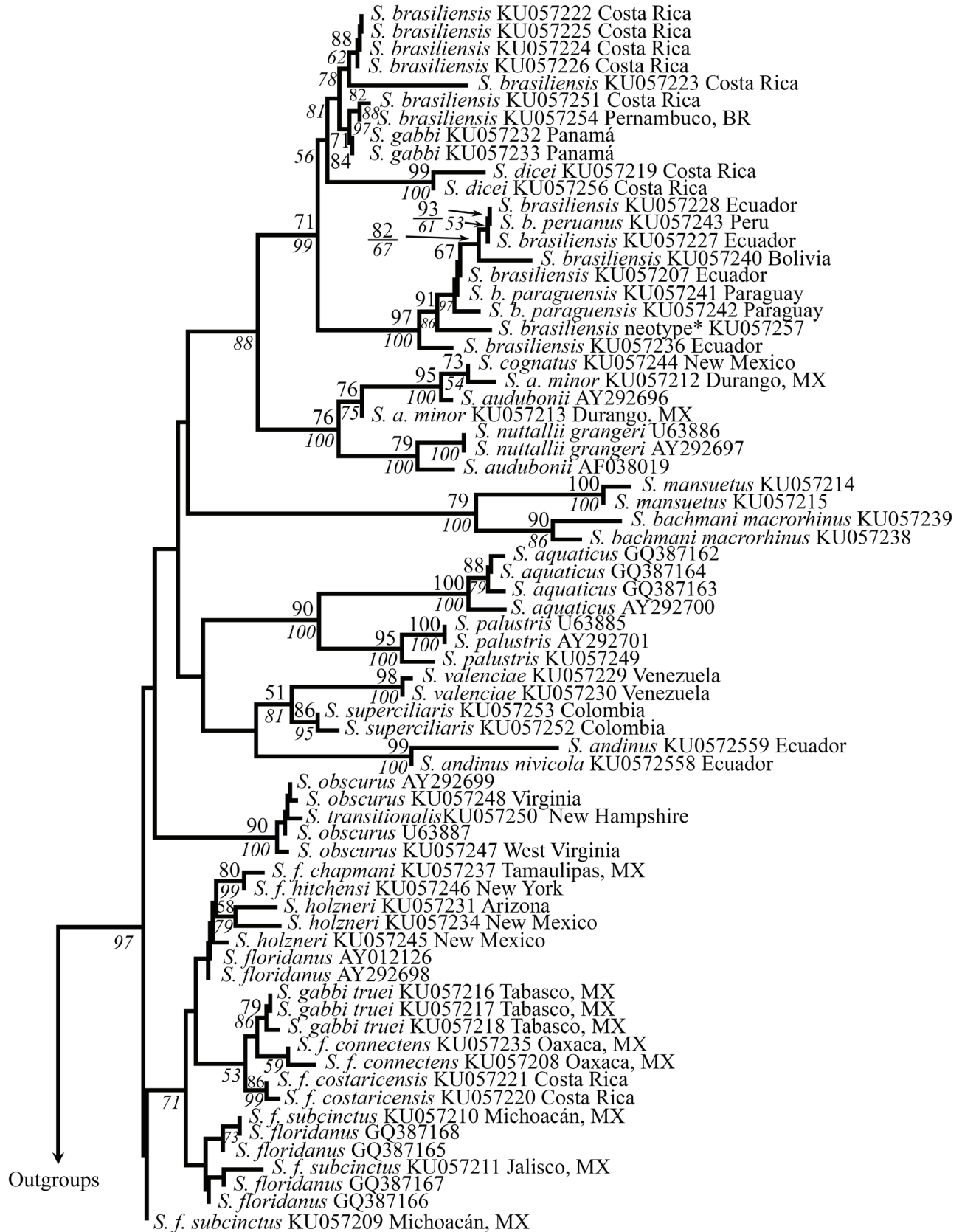
Figure S6 (Figure 30 full version)— Maximum Likelihood phylogeny derived from the analysis of the expanded 12S rRNA dataset, as implemented in RAxML (HPC–2 v. 8.2.4, Stamatakis 2014). Numbers above the branches indicate bootstrap support based on 1000 bootstrap replicates. Numbers below the branches indicate the percent of 5X107 trees supporting the topology in the Bayesian analysis (initial 2.8X107 trees discarded as burnin) implemented in MrBayes 3.2.5 (Ronquist *et al*. 2012). The neotype of *S. brasiliensis* is denoted by an asterisk.

0.05