SUPPLEMENTARY DATA 3

SUPPLEMENTARY DATA 3.1

Phylogenetic relationships of *Rhinella* and outgroups recovered in one of most parsimonious trees from the total evidence analysis with TNT considering gaps as missing data (length 24,201 steps). Black circles indicate nodes that collapse in the strict consensus. Values around nodes are parsimony jackknife frequencies (frequency differences value [above]/absolute [below]). An asterisk (*) indicates 100% jackknife support. Nodes lacking references have < 25% frequency difference values or < 50% jackknife absolute frequencies. Lower left inset shows the entire cladogram with present view marked in white.

SUPPLEMENTARY DATA 3.2

Phylogenetic relationships of *Rhinella* recovered in one of the most parsimonious trees from the total evidence analysis with TNT considering gaps as missing data (length 24,201 steps). The clades and species groups shown are those recognized in this study.

Part 1 of 4. The *R. marina* Clade (1): the *R. arunco*, *R. spinulosa*, and *R. granulosa*Groups. Black circles indicate nodes that collapse in the strict consensus. Values around nodes are parsimony jackknife frequencies (frequency differences value [above]/absolute [below]). An asterisk (*) indicates 100% jackknife support. Nodes lacking references have < 25% frequency difference values or < 50% jackknife absolute frequencies. Lower left inset shows the entire cladogram with present view marked in white. Abbreviations: MtG, mitochondrial genome; NuG, nuclear genome.

SUPPLEMENTARY DATA 3.3

Phylogenetic relationships of *Rhinella* recovered in one of the most parsimonious trees from the total evidence analysis with TNT considering gaps as missing data (length 24,201 steps). The clades and species groups shown are those recognized in this study. Part 2 of 4. The *R. marina* Clade (2): the ghost introgressed mitochondrion and the *R. crucifer* and *R. marina* Groups. Black circles indicate nodes that collapse in the strict consensus. Values around nodes are parsimony jackknife frequencies (frequency differences value [above]/absolute [below]). An asterisk (*) indicates 100% jackknife support. Nodes lacking references have < 25% frequency difference values or < 50% jackknife absolute frequencies. Lower left inset shows the entire cladogram with present view marked in white. Abbreviations: MtG, mitochondrial genome; NuG, nuclear genome.

SUPPLEMENTARY DATA 3.4

Phylogenetic relationships of *Rhinella* recovered in one of the most parsimonious trees from the total evidence analysis with TNT considering gaps as missing data (length 24,201 steps). The clades and species groups shown are those recognized in this study. Part 3 of 4. The *R. margaritifera* Clade (1): *R. sternosignata* and the *R. veraguensis* and *R. festae* Groups. Black circles indicate nodes that collapse in the strict consensus. Values around nodes are parsimony jackknife frequencies (frequency differences value [above]/absolute [below]). An asterisk (*) indicates 100% jackknife support. Nodes lacking references have < 25% frequency difference values or < 50% jackknife absolute frequencies. Lower left inset shows the entire cladogram with present view marked in white.

SUPPLEMENTARY DATA 3.5

Phylogenetic relationships of *Rhinella* recovered in one of the parsimonious trees from the total evidence analysis with TNT considering gaps as missing data (length 24,201 steps). The clades and species groups shown are those recognized in this study. **Part 4 of 4. The** *R. margaritifera* **Clade (2): the** *R. margaritifera* **Group.** Black circles indicate nodes that collapse in the strict consensus. Values around nodes are parsimony jackknife frequencies (frequency differences value [above]/ absolute [below]). An asterisk (*) indicates 100% jackknife support. Nodes lacking references have < 25% frequency difference values or < 50% jackknife absolute frequencies. Lower left inset shows the entire cladogram with present view marked in white.









