Appendix S4

Figure S1. Strict consensus tree of 260 most parsimonious trees (MPTs; 3,279 steps) found in round one of successive outgroup expansion. Numbers around nodes are Goodman-Bremer support values / jackknife absolute frequencies (asterisks indicate 100% values; <50% values are not shown).

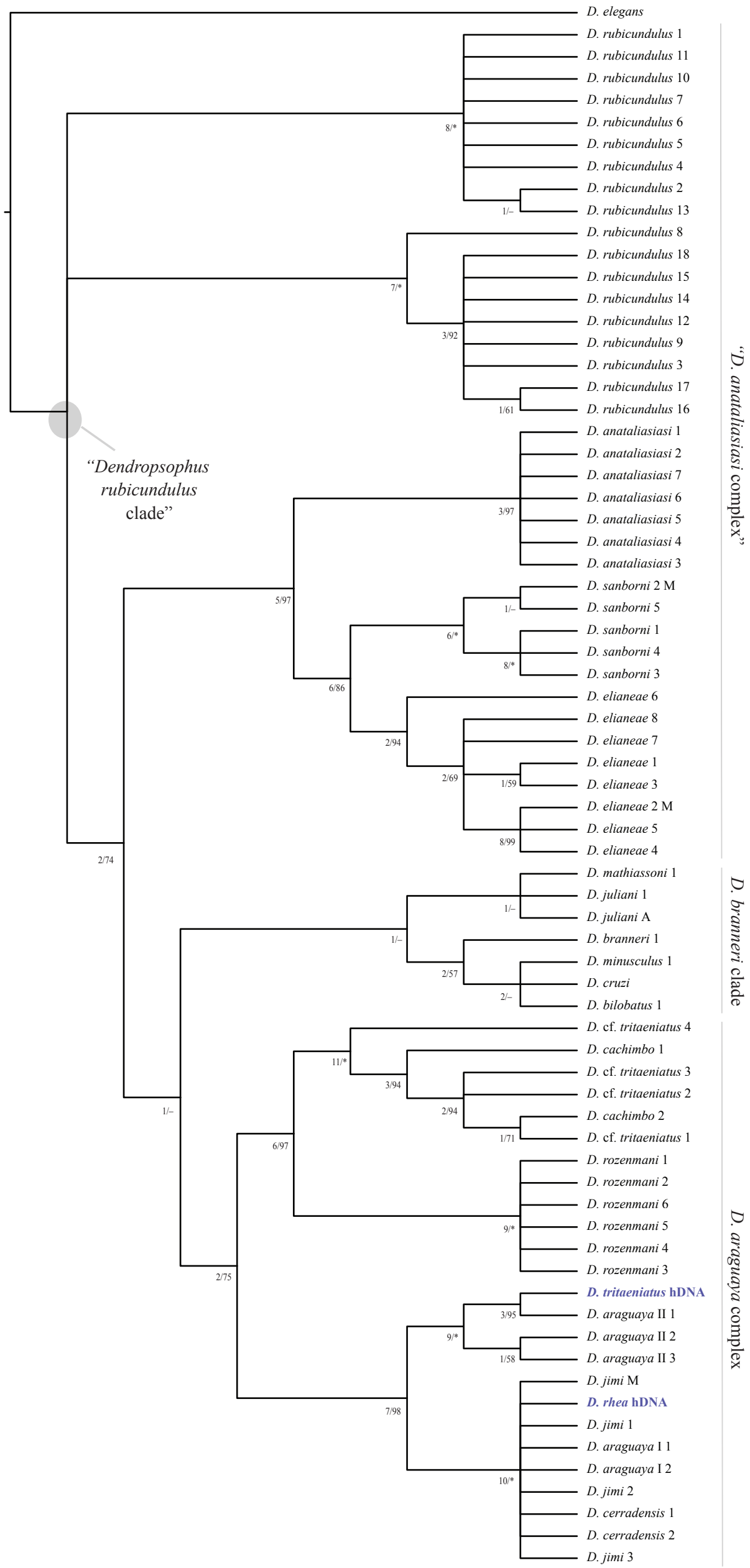

Figure S2. Strict consensus tree of 63 most parsimonious trees (MPTs; 5,443 steps) found in round two of successive outgroup expansion. Numbers around nodes are Goodman-Bremer support values / jackknife absolute frequencies (asterisks indicate 100% values; <50% values are not shown).

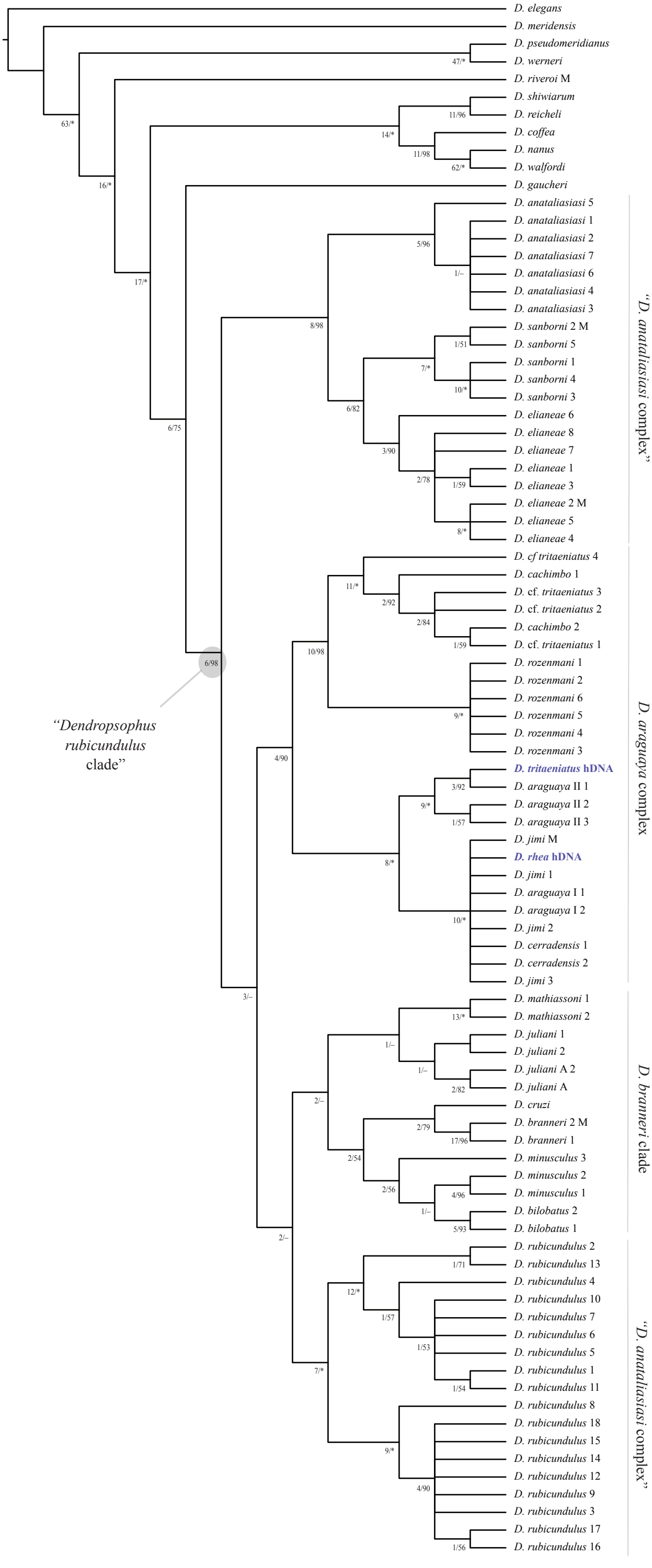

Figure S3. Strict consensus tree of 120 most parsimonious trees (MPTs; 7,203 steps) found in round three of successive outgroup expansion. Numbers around nodes are Goodman-Bremer support values / jackknife absolute frequencies (asterisks indicate 100% values; <50% values are not shown).

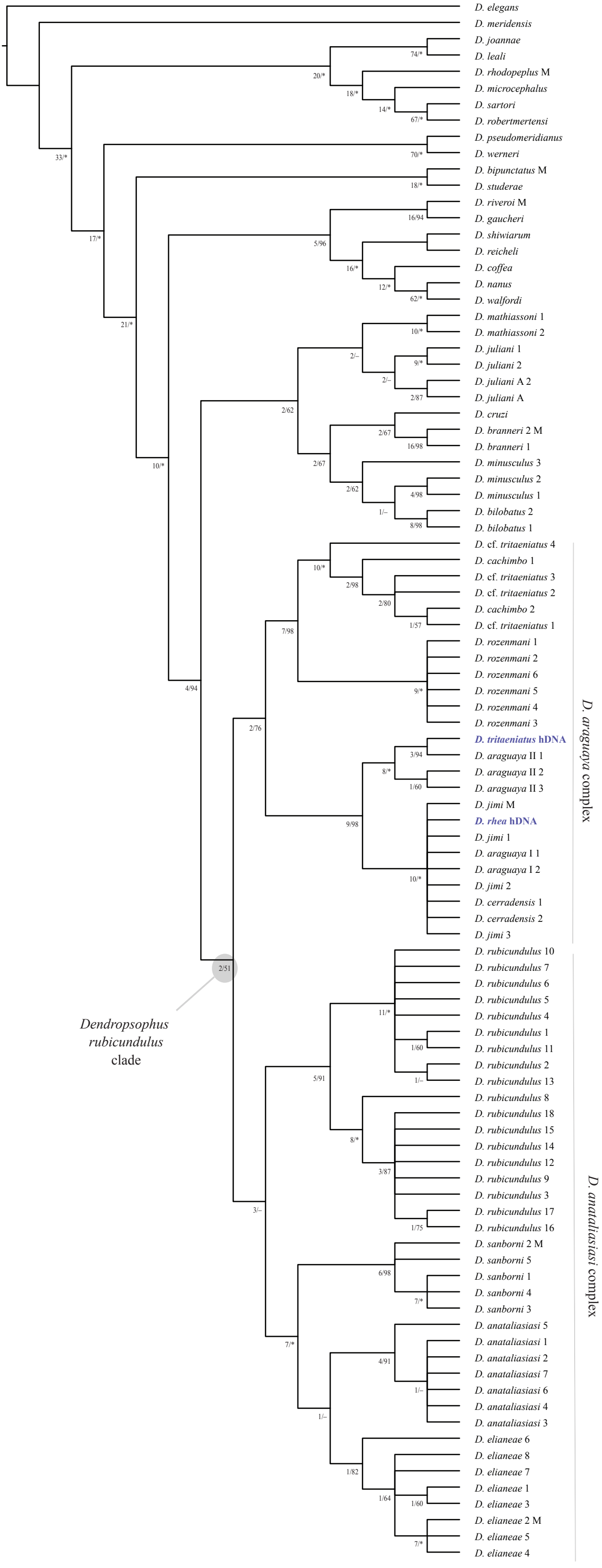

Figure S4. Strict consensus tree of 176 most parsimonious trees (MPTs; 10,303 steps) found in round four of successive outgroup expansion. Numbers around nodes are Goodman-Bremer support values / jackknife absolute frequencies (asterisks indicate 100% values; <50% values are not shown).

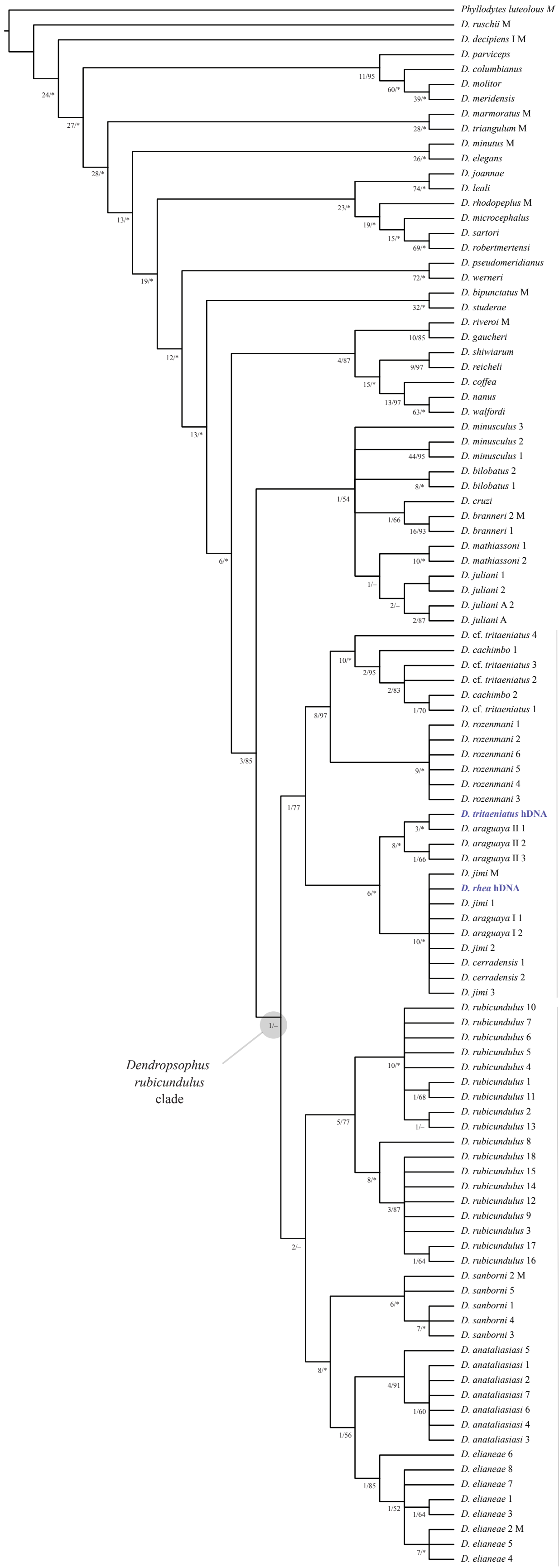

Figure S5. Strict consensus tree of 184 most parsimonious trees (MPTs; 13,653 steps) found in round five of successive outgroup expansion. Numbers around nodes are Goodman-Bremer support values / jackknife absolute frequencies (asterisks indicate 100% values; <50% values are not shown).

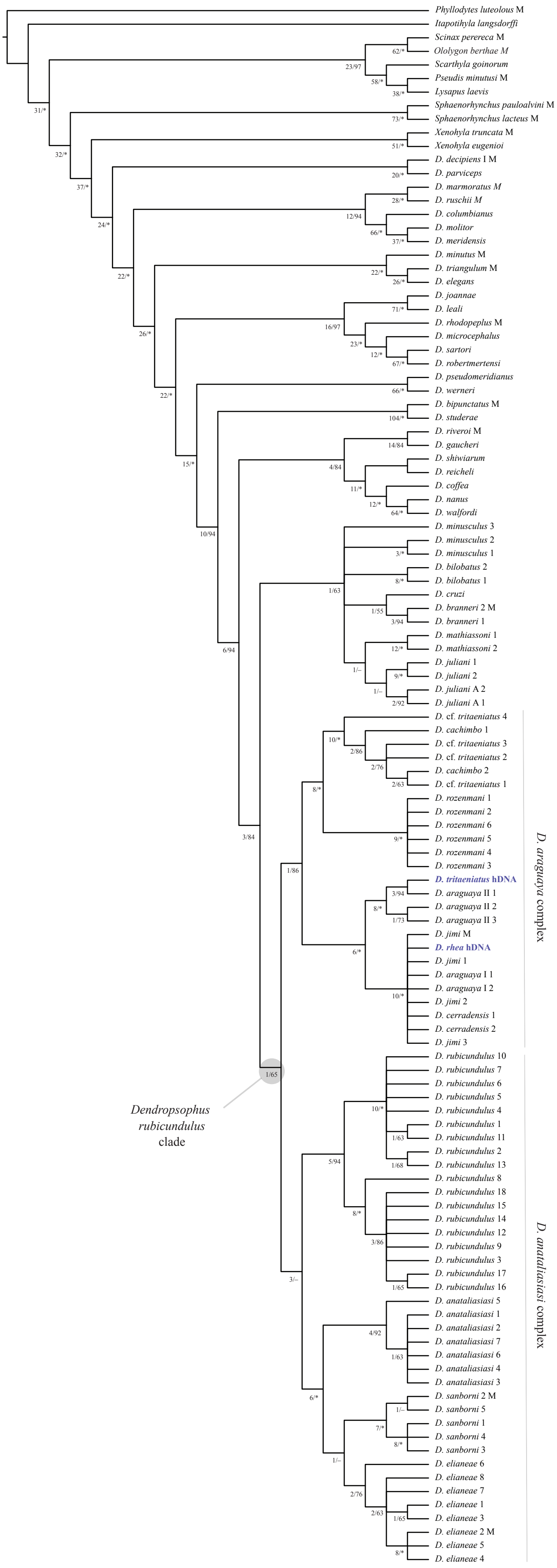

Figure S6. Maximum likelihood tree. Numbers above nodes are approximate likelihood ratio test (aLRT) values, whereas numbers below are bootstrap absolute frequencies (asterisks indicate 100% values; <50% values are not shown).

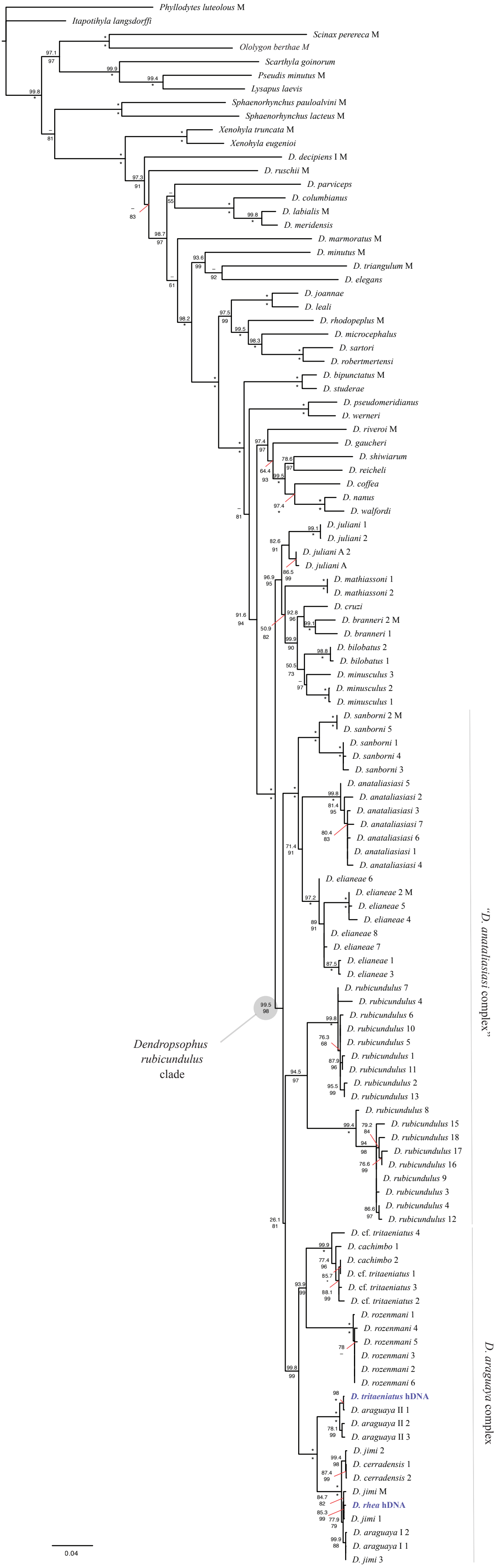

Figure S7. Strict consensus from unweighted parsimony trees analysed in TNT, including Sanger + phenomic + AHE characters using the same taxon sample as Figs. S5–6 (round five). Numbers around nodes are Goodman-Bremer support values / jackknife absolute frequencies (asterisks indicate 100% values; <50% values are not shown).

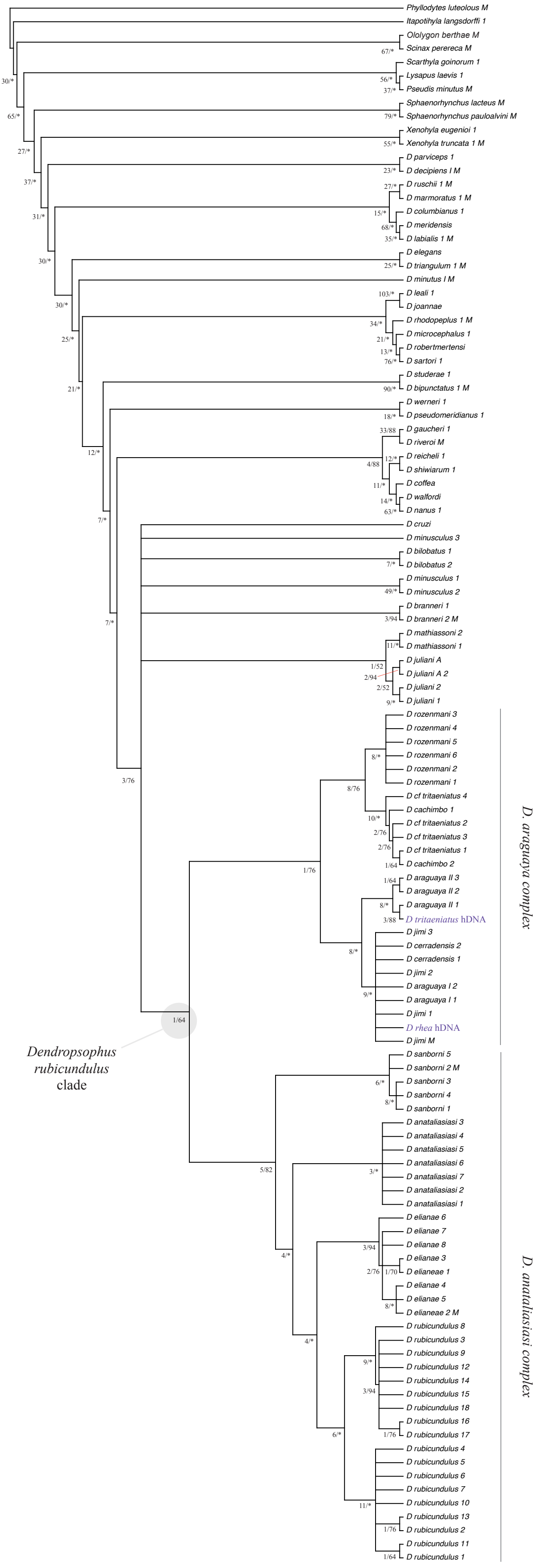

Table S1. Best fitting models employed in molecular partitions of maximum likelihood analyses. Abbreviations: AICc = corrected Akaike Information Criterion; BIC = Bayesian Information Criterion; logL = log likelihood estimation.

Partition	Model	logL	AICc	BIC
COI	TPM2u+F+I+G4	-7341.5	14699.2	14734.8
CYTB	TIM2+F+I+I+R4	-9732.3	19493.1	19560.0
H1	GTR+F+I+I+R4	-34447.1	68926.4	69021.9
POMC	TN+F+I+I+R2	-1868.3	3755.1	3791.5
RAG1	K2P+I+I+R2	-1828.8	3667.8	3687.9
RHOD	TPM3+I+I+R2	-1091.1	2194.5	2216.7
SIA	K2P+R2	-1176.4	2360.9	2376.9
TYR	TNe+I+G4	-2881.5	5773.0	5794.4