

Additional file 1 Figure S1: Bayesian estimate of Mirbelieae and Bossiaeeae phylogeny using combined cpDNA sequence data showing clades that include both bird (red) and bee (black) pollinator syndromes. Full tree is shown on left with partial tree (bold in full tree) on right of a: *Gastrolobium*, b: *Bossiaea* and *Platylobium*, c: *Daviesia* and d: *Gompholobium*, *Urodon*, *Aotus*, *Euchilopsis*, *Phyllota*, *Dillwynia*, *Jacksonia*, *Leatrobea*, *Pultenaea* and *Leptosema*. Posterior probabilities ($PP > 0.95$) from Bayesian analysis and bootstrap support of bipartitions ($BS > 0.70$) from maximum likelihood analysis are shown on branches. Scale bar represents substitutions per site.

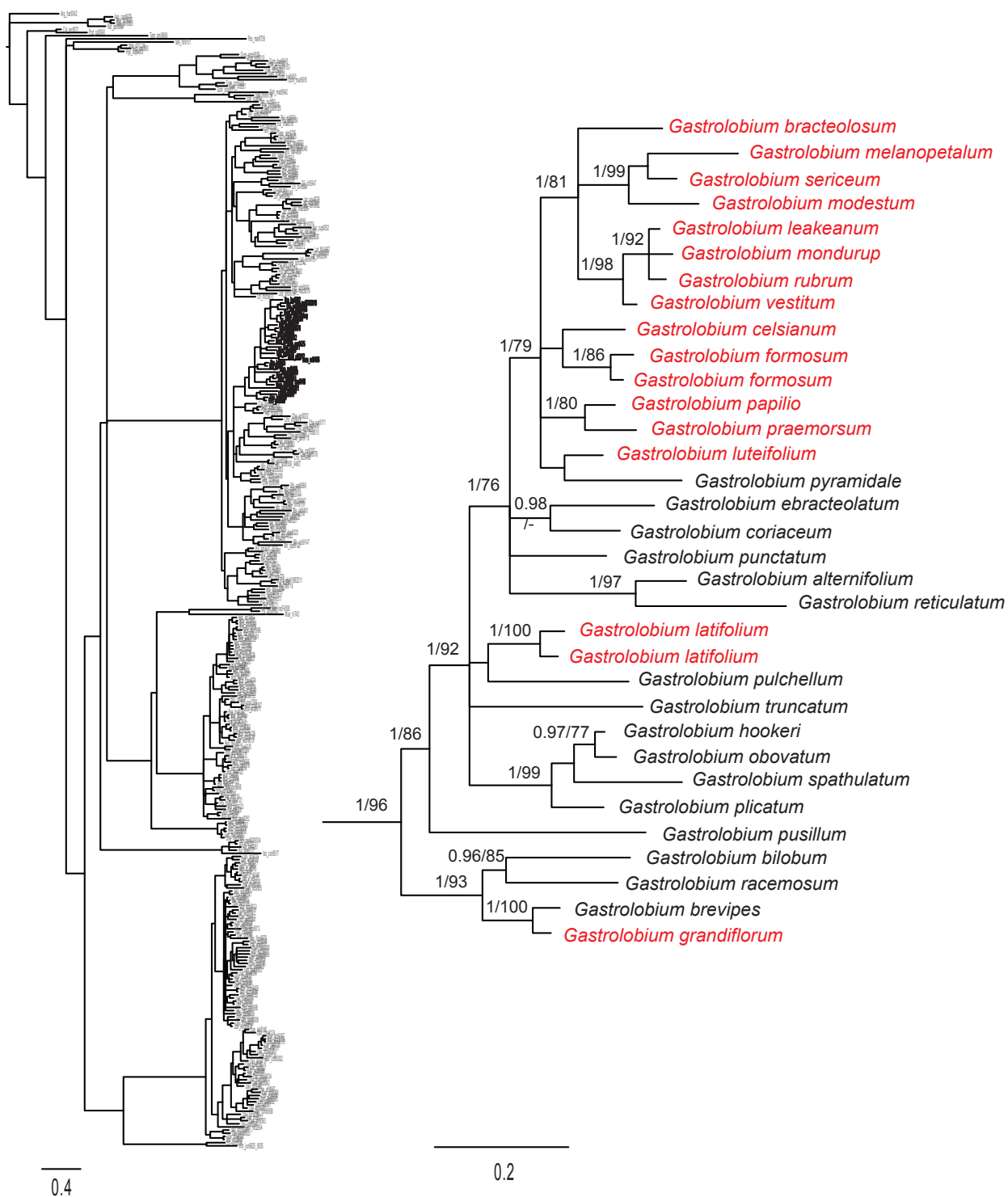


Figure S1a

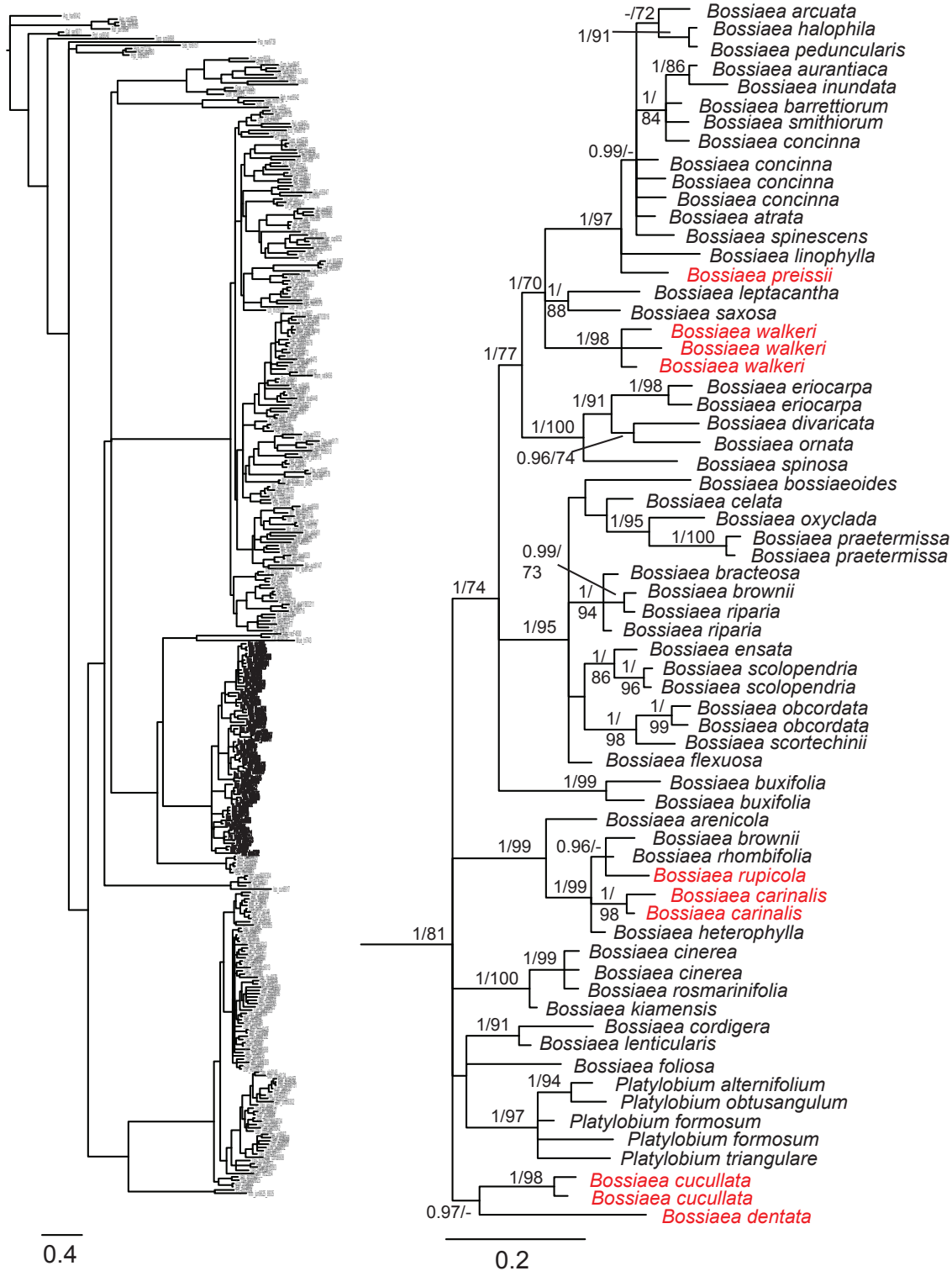


Figure S1b

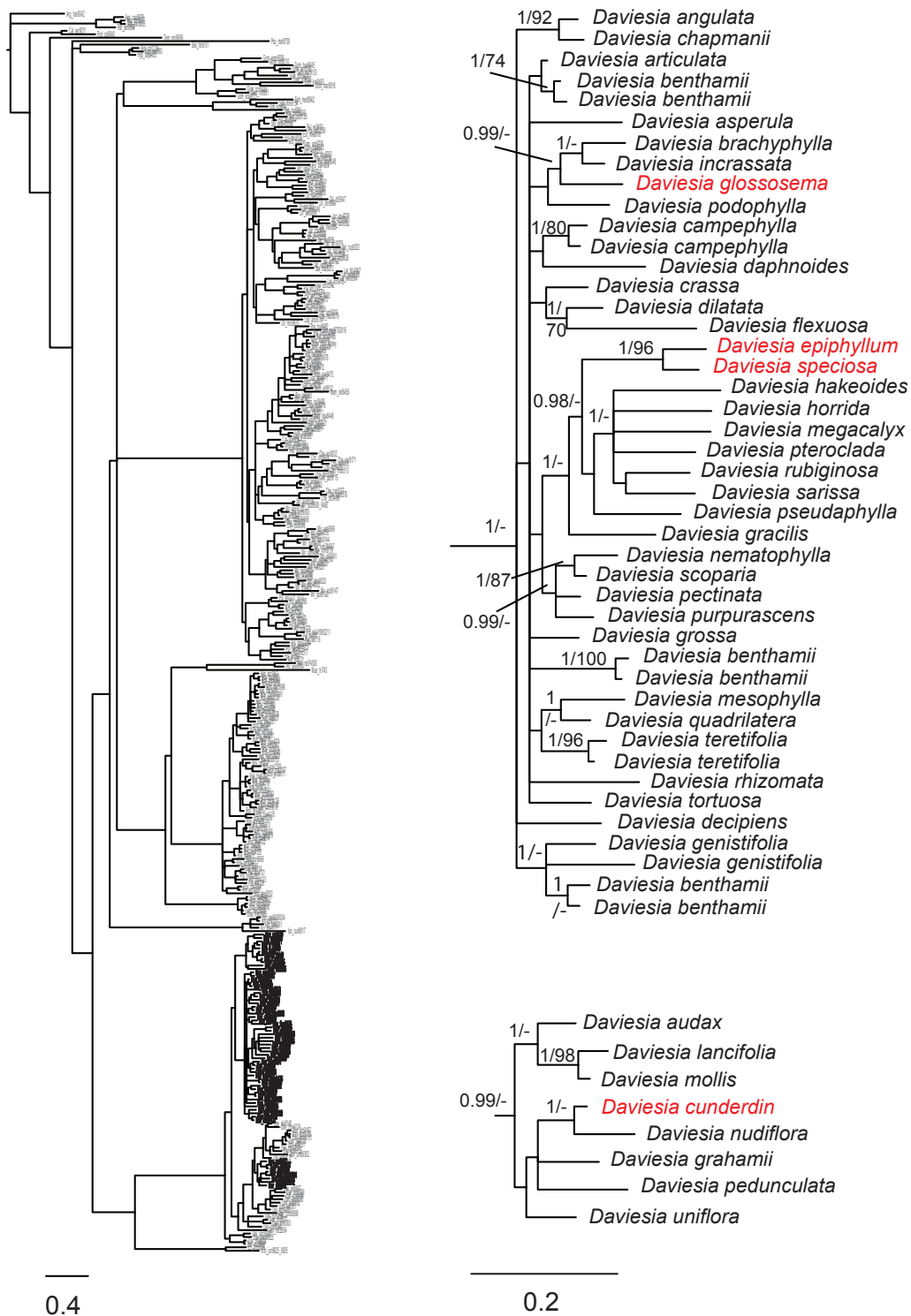


Figure S1c

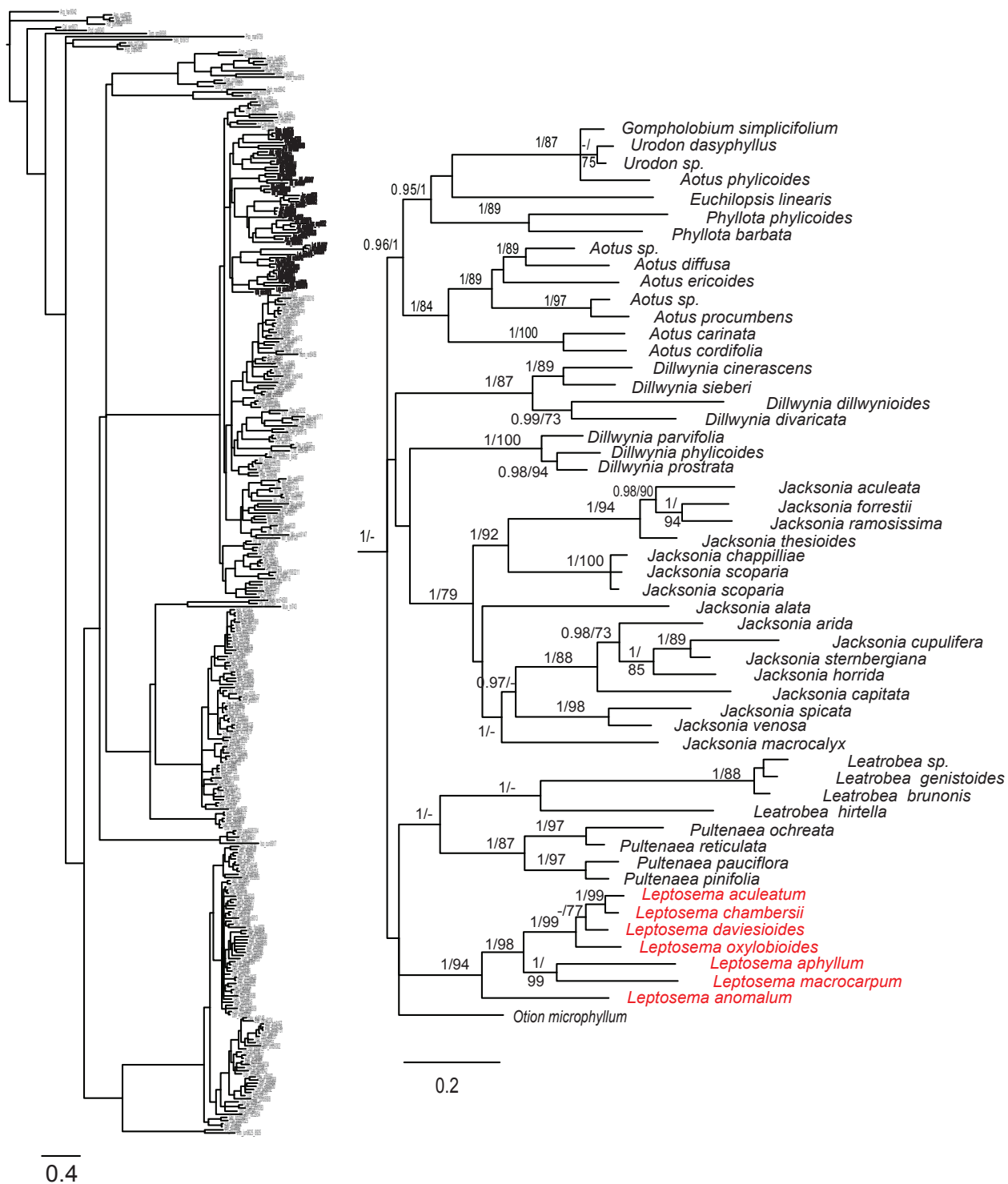


Figure S1d