

Supplementary Material

A phylogenetic investigation of the taxonomically problematic *Eucalyptus odorata* complex (*E.* section *Adnataria* series *Subbuxaeales*): evidence for extensive interspecific gene flow and reticulate evolution

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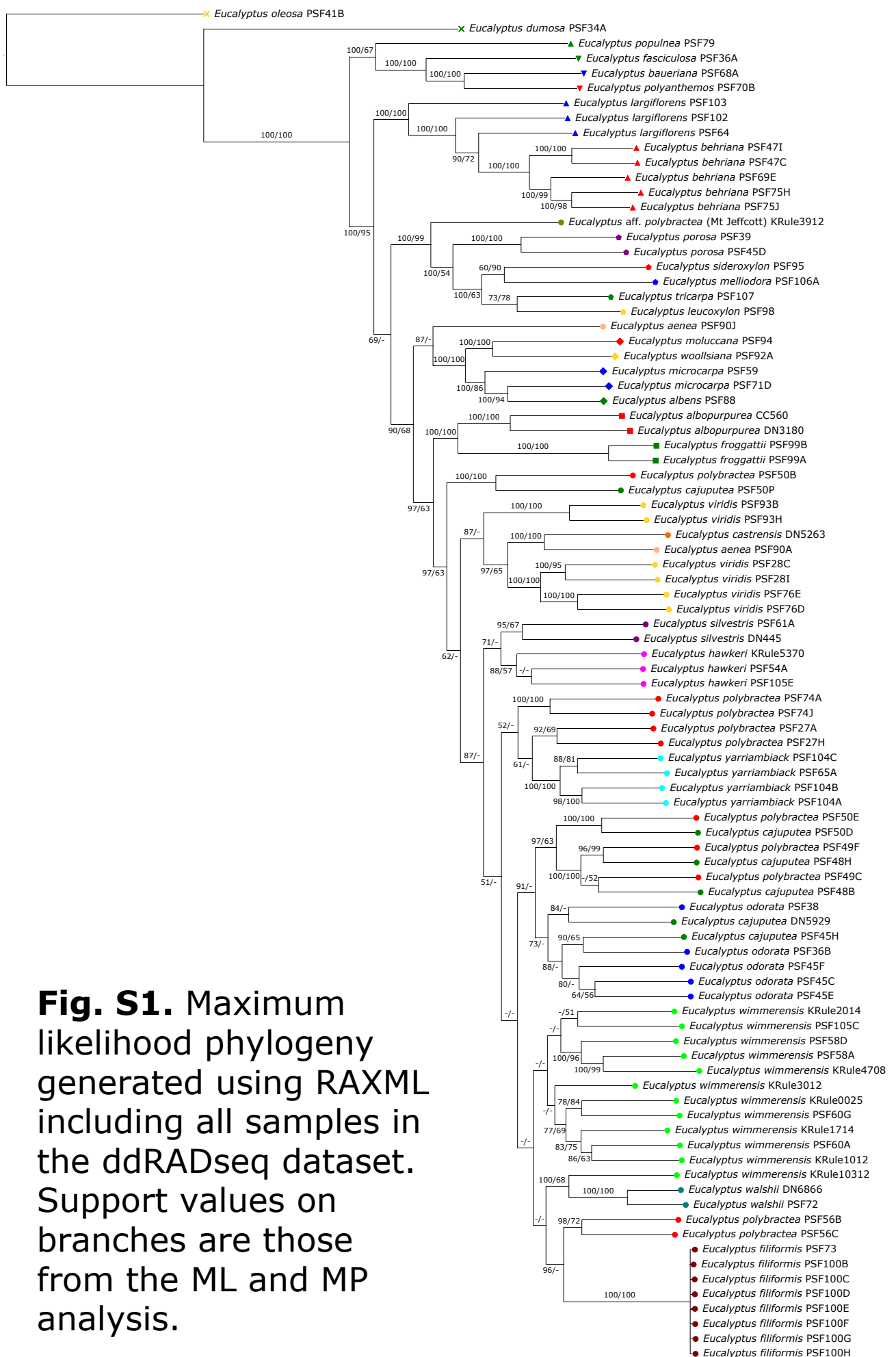
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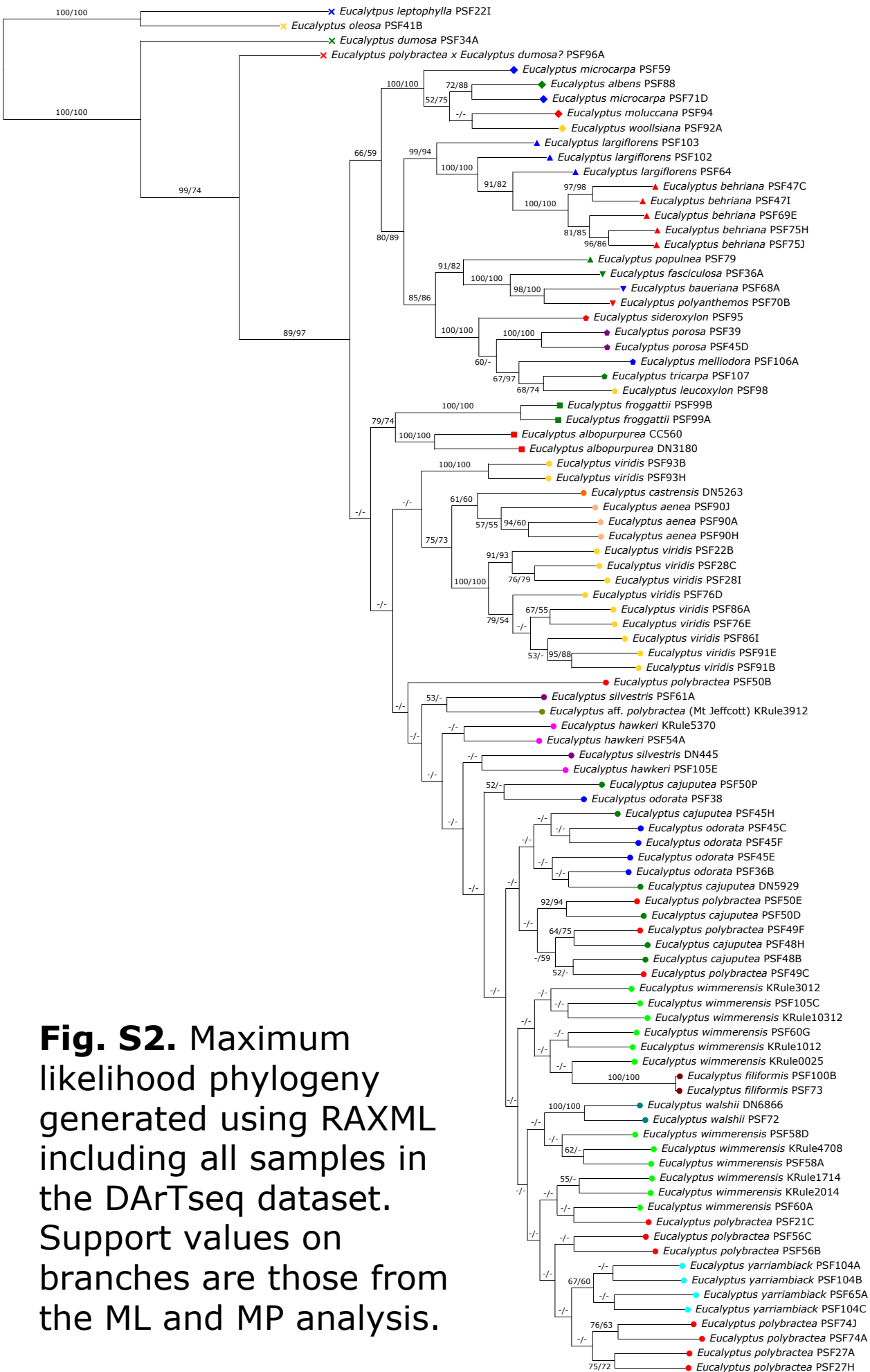
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Table S1. Key statistics of loci recovered using various reconstruction parameters in *ipyrad* on the ddRADseq dataset, showing minimal differences between datasets using differing clustering thresholds and coverage depths.

Clustering threshold	Coverage depth for call (number of reads)	Samples coverage needed for inclusion	Loci recovered	Percentage missing sites in sequence matrix	Average heterozygosity
0.85	20	4	21670	79.11	0.0160
		6	42387	79.93	0.0138
	6	25%	11697	57.11	0.0138
		50%	6021	43.15	0.0138
		75%	3298	32.09	0.0138
0.9	6	25%	11697	57.11	0.0138
		50%	6021	43.15	0.0138
		75%	3298	32.09	0.0138
0.95	6	25%	11697	57.11	0.0138
		50%	6021	43.15	0.0138
		75%	3298	32.09	0.0138





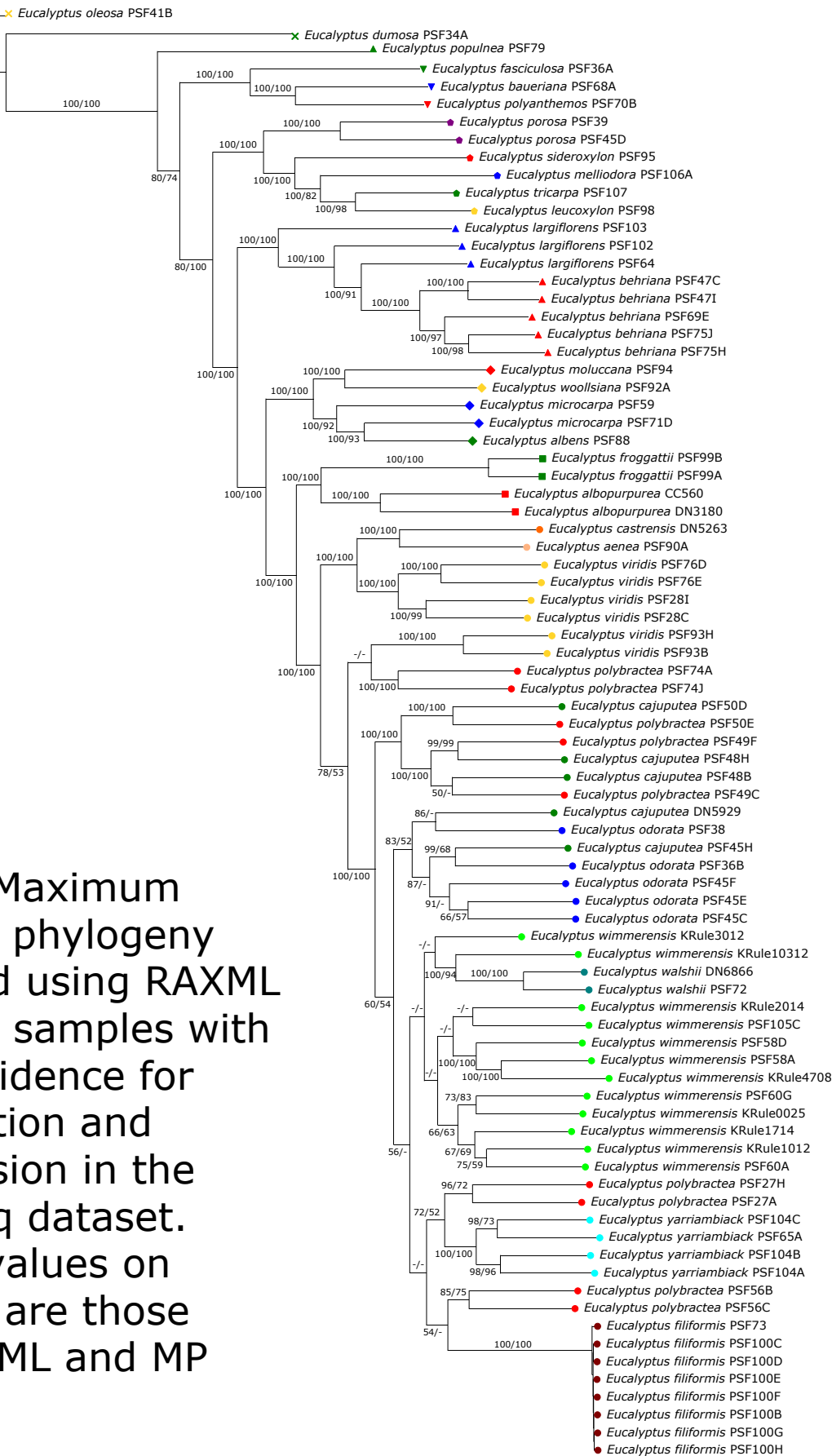


Fig. S3. Maximum likelihood phylogeny generated using RAXML excluding samples with strong evidence for hybridisation and introgression in the ddRADseq dataset. Support values on branches are those from the ML and MP analysis.

