Supporting Figures

Article title: Reticulate evolution, ancient chloroplast haplotypes, and rapid radiation of an Australian plant genus – *Adenanthos* (Proteaceae)

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Fig. S1 Calibrated BEAST chronogram of *Adenanthos* inferred from combined ITS, and plastid (*matK, rbcL*), with branch lengths scaled according to time (Ma). Divergence times (Ma) are given at each node, with 95% confidence intervals indicated as blue bars.

Fig. S2 Calibrated BEAST chronogram of *Adenanthos* inferred from ITS only under the birth death model, with branch lengths scaled according to time (Ma). Divergence times (Ma) are given at each node, with 95% confidence intervals indicated as blue bars.

Fig. S3 TSC network of *Adenanthos* chloroplast haplotypes coloured according to species. Circle size represents number of taxa (1–3) sharing chloroplast haplotypes. Black dots represent missing unsampled or extinct intermediate lineages. Subspecies were abbreviated by the first two letters of the epithet.

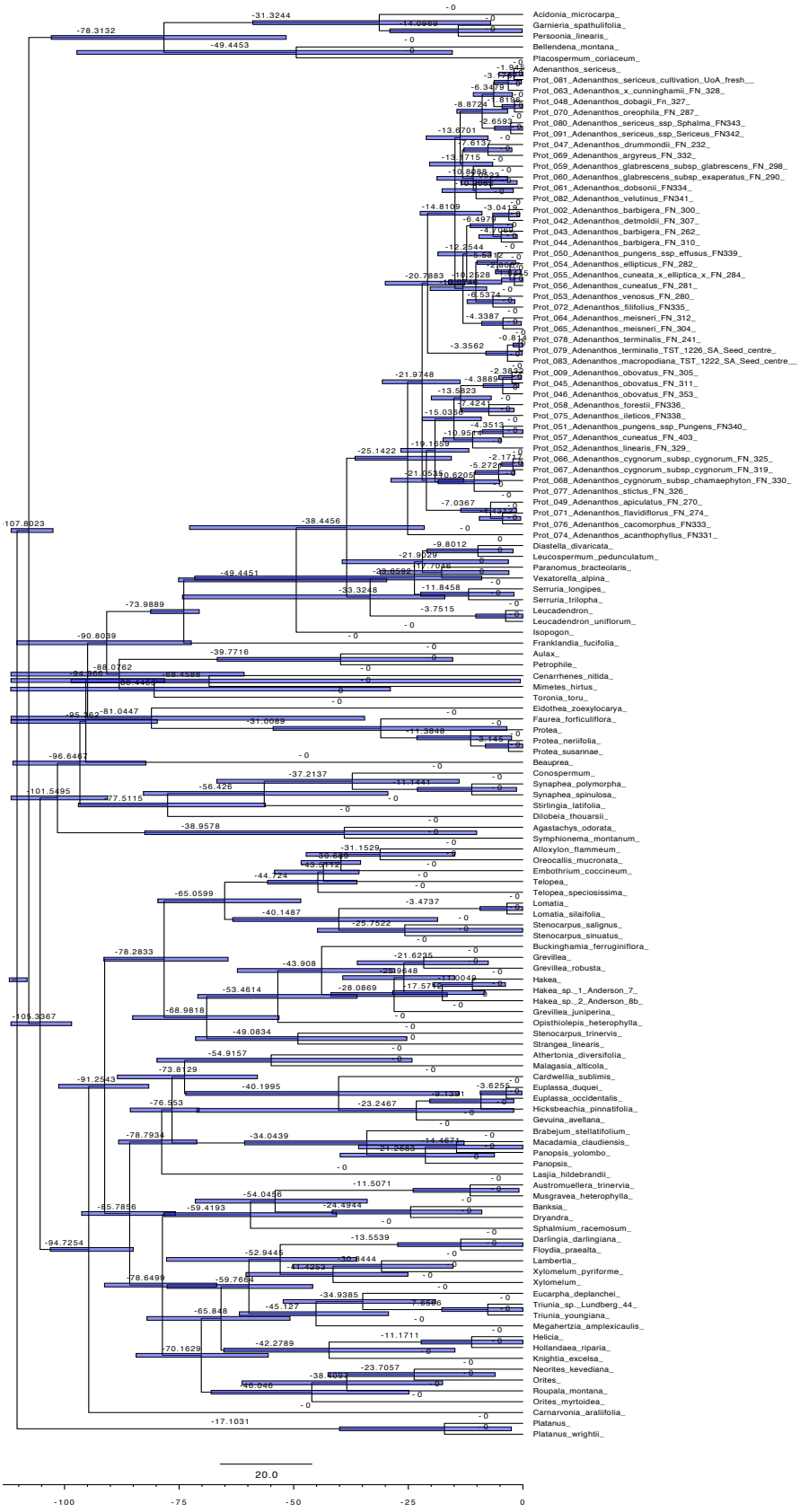
Fig. S4 Splitstree neighbour-nets of *Adenanthos* derived from concatenated NGS nuclear markers.

Fig. S5 Splitstree neighbour-nets of *Adenanthos* derived from concatenated NGS chloroplast markers.

Fig. S6 Splitstree neighbour-nets of *Adenanthos* derived from combined concatenated NGS nuclear and chloroplast markers.

Fig. S7 Maximum-likelihood concatenated RaxML tree from phased nuclear loci. Support values indicated on each node represents bootstrap values.

Fig. S8 Calibrated BEAST chronogram of *Adenanthos* inferred from 35 nuclear markers, with branch lengths scaled according to time (Ma). Divergence times (Ma) are given at each node, with 95% confidence intervals indicated as blue bars.



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Ad.PROT.combine.its.matk.rbcl.100mil.SUM.NODE.AGE.tree.pdf

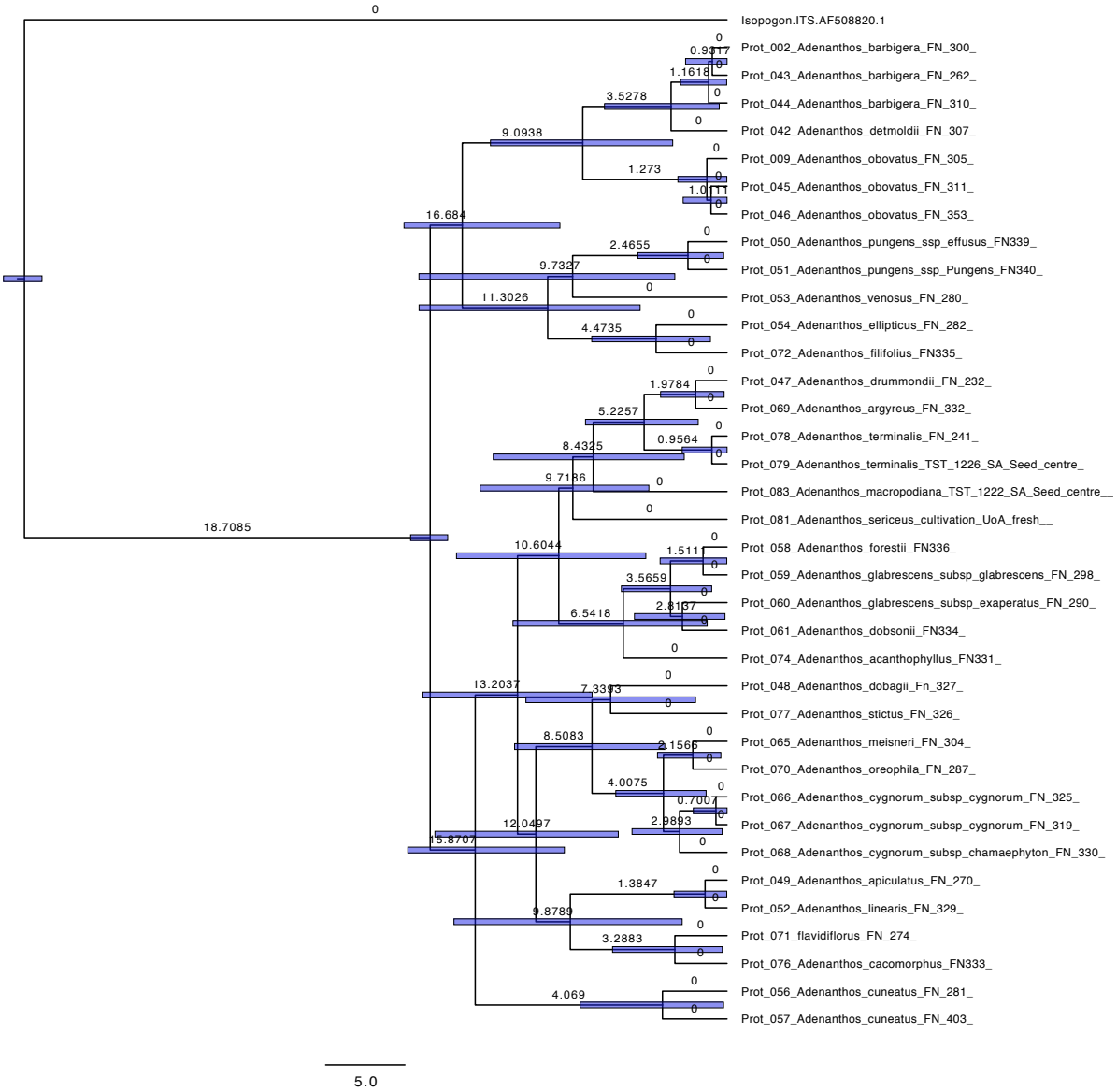

Fig. S2 Calibrated BEAST chronogram of *Adenanthos* inferred from ITS only, with branch lengths scaled according to time (Ma). Divergence times (Ma) are given at each node, with 95% confidence intervals indicated as blue bars.

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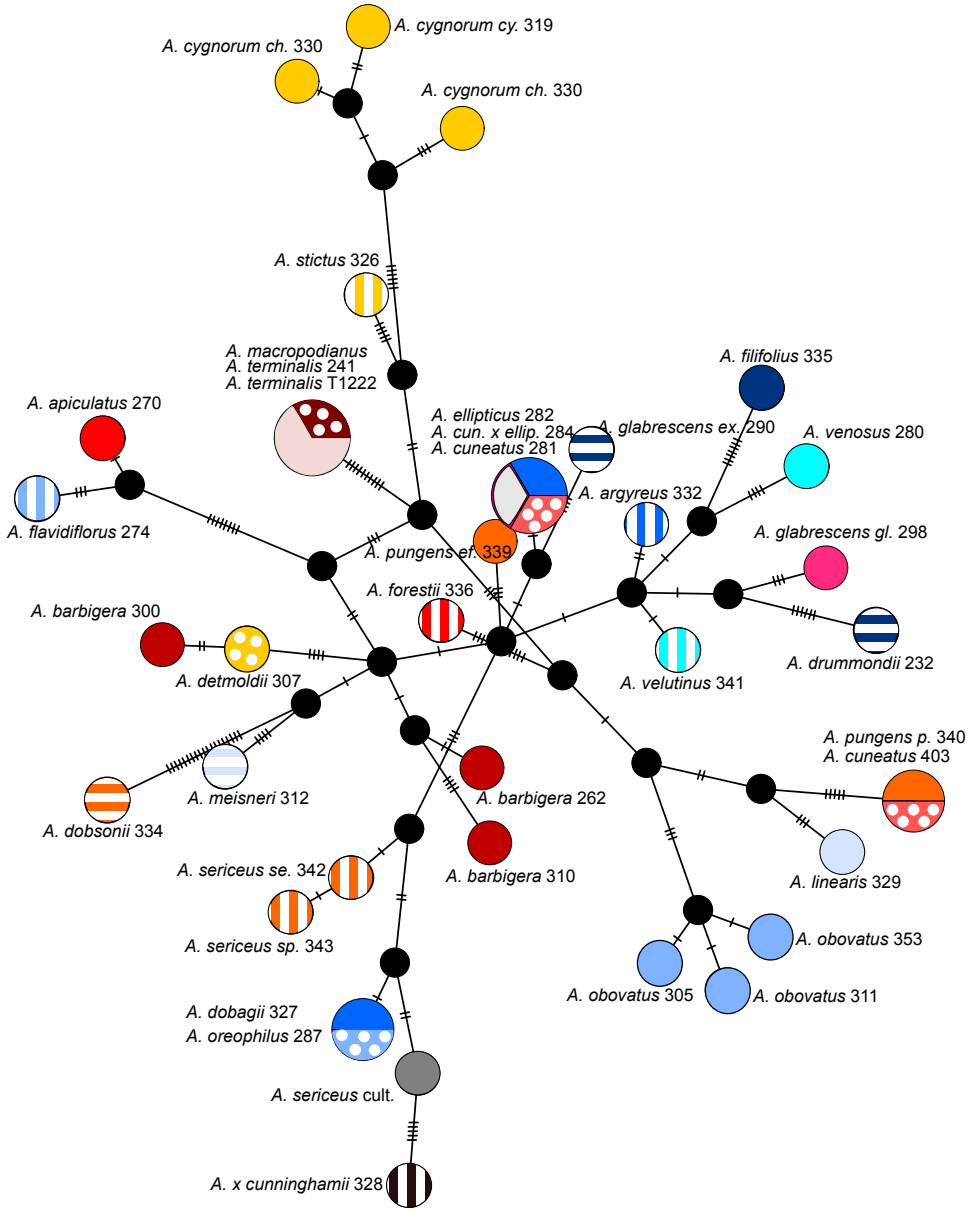

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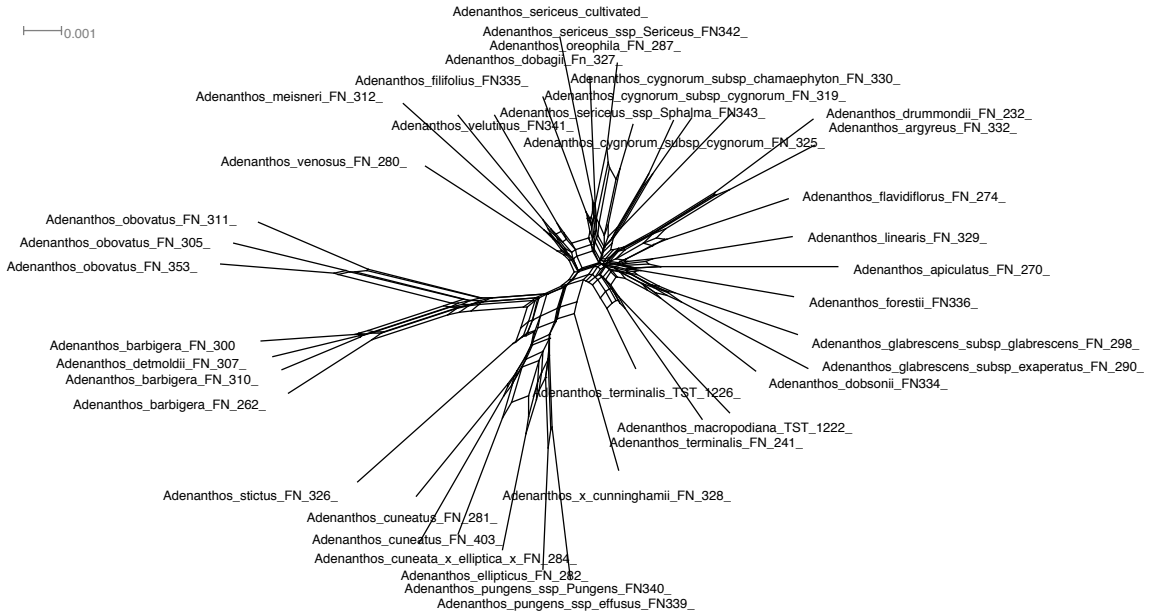


Fig. S4 Splitstree neighbour-nets of *Adenanthos* derived from concatenated NGS nuclear markers.

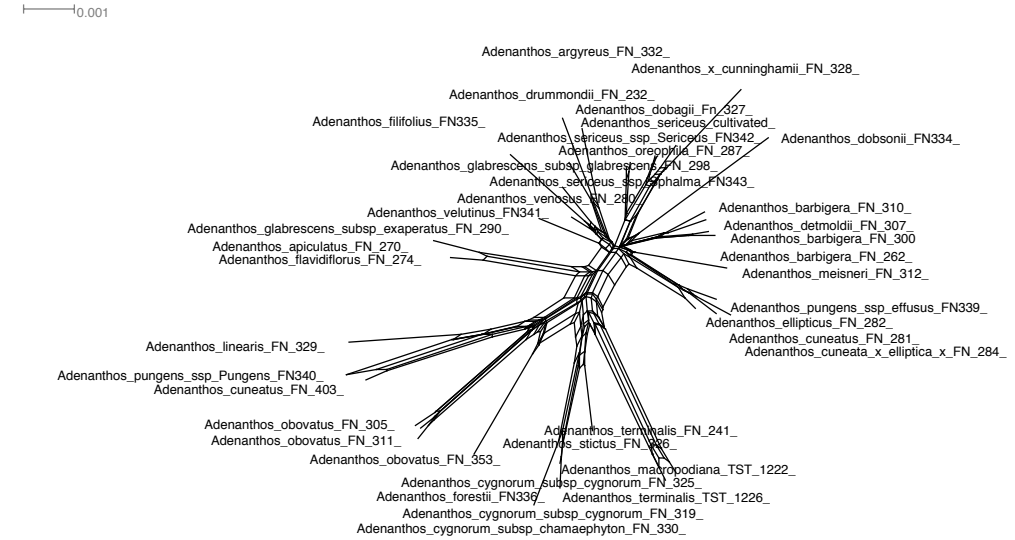


Fig. S5 Splitstree neighbour-nets of *Adenanthos* derived from concatenated NGS chloroplast markers.

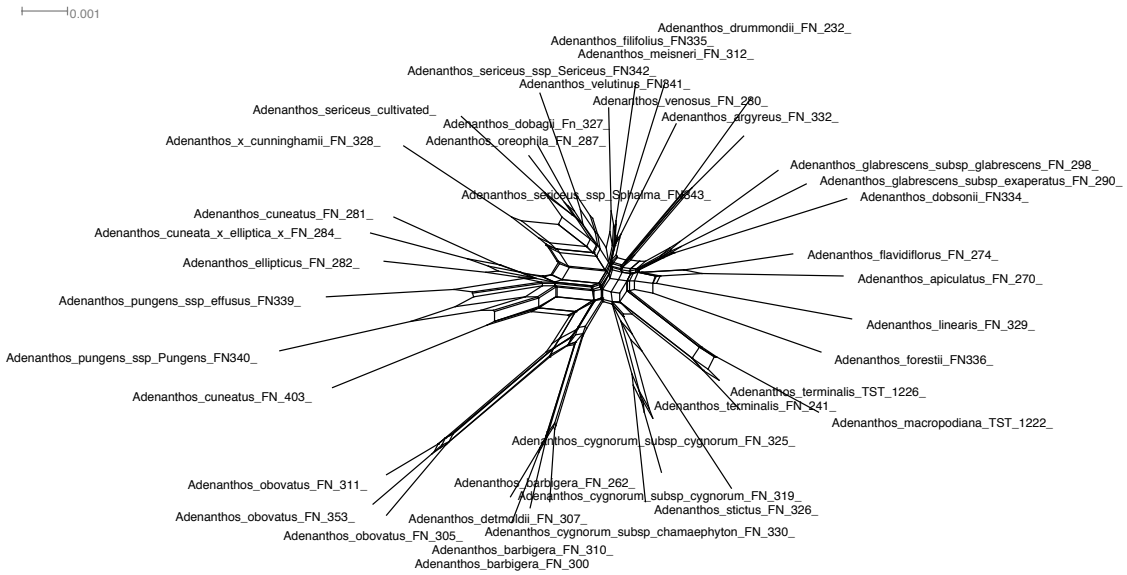


Fig. S6 Splitstree neighbour-nets of *Adenanthos* derived from combined concatenated NGS nuclear and chloroplast markers.

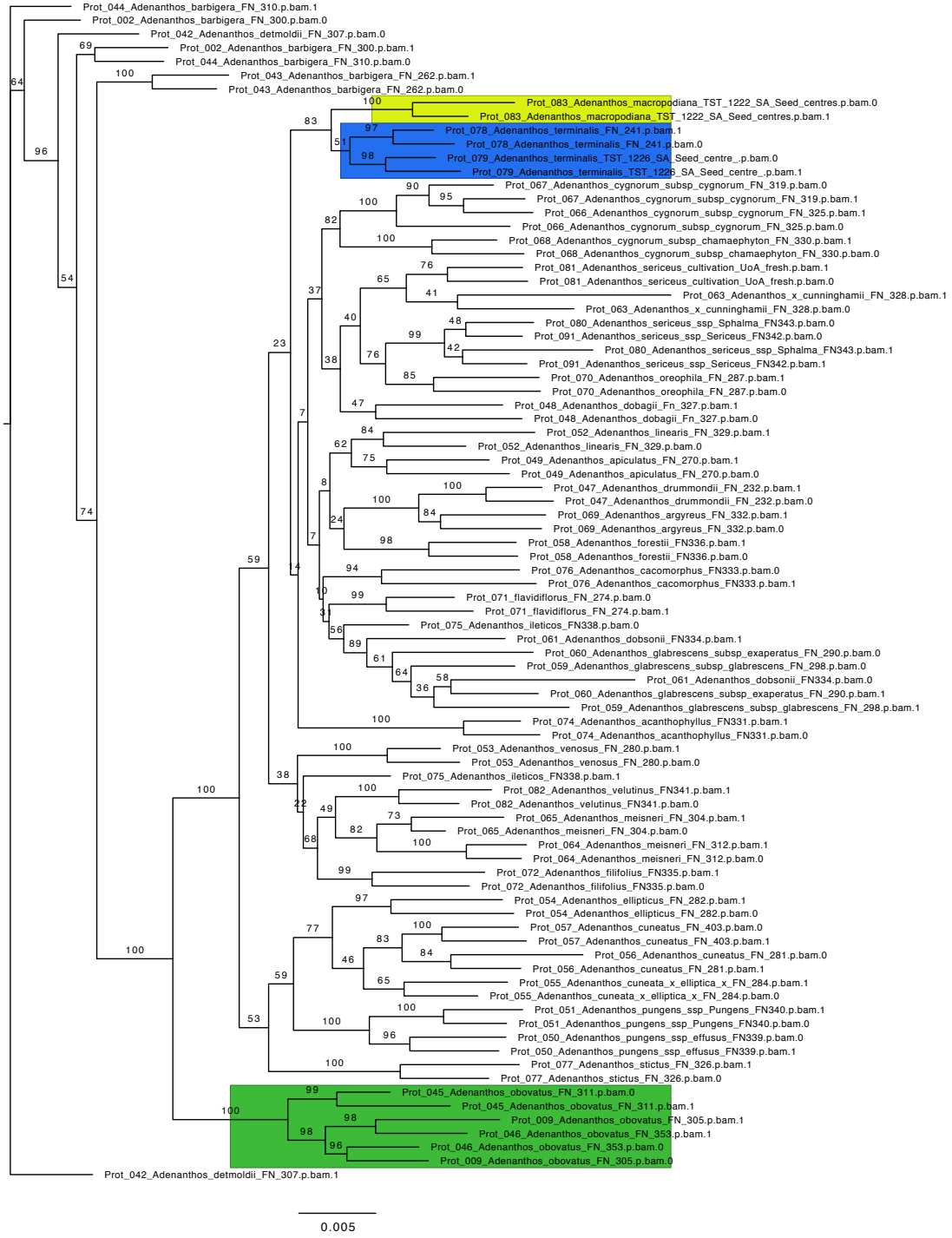
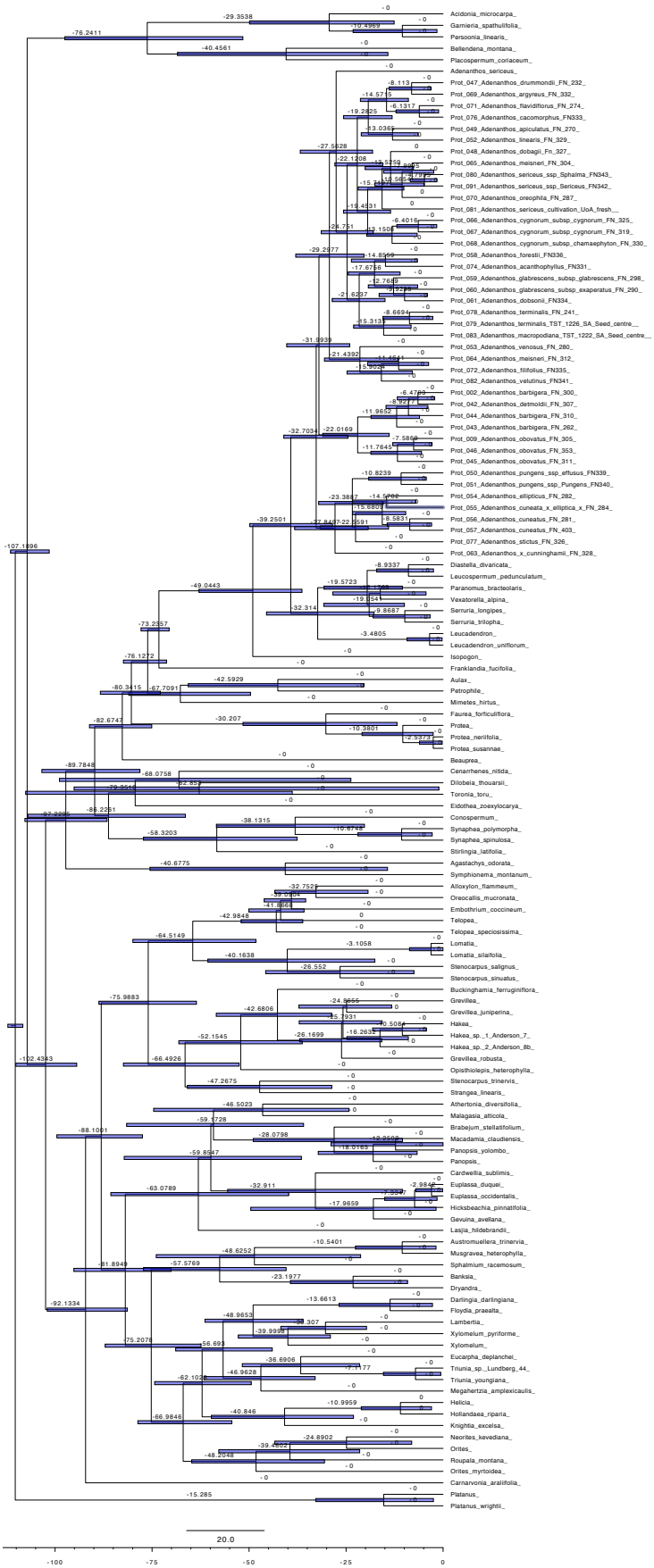


Fig. S7 Maximum-likelihood concatenated RaxML tree from phased nuclear loci. Support values indicated on each node represents bootstrap values.



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