

Appendix S2 Phylogeny of *Cyanoramphus* parakeets based on 1605 bp mtDNA *CR* alignment. Branch lengths are proportional to the number of substitutions/site. The maximum likelihood tree was generated in PhyML using the GTR + I + G model of nucleotide substitution. For clarity, only Bayesian posterior probability (PP) and bootstrap support (BS; **bold**: maximum likelihood; *italics*: maximum parsimony) values for major clades are shown. The asterisks indicate strong support from all of these measures i.e. Bayesian posterior probability of 0.95 and above, and bootstrap values of 80% and above. Coloured bars represent the dominant crown colouration of each species.

