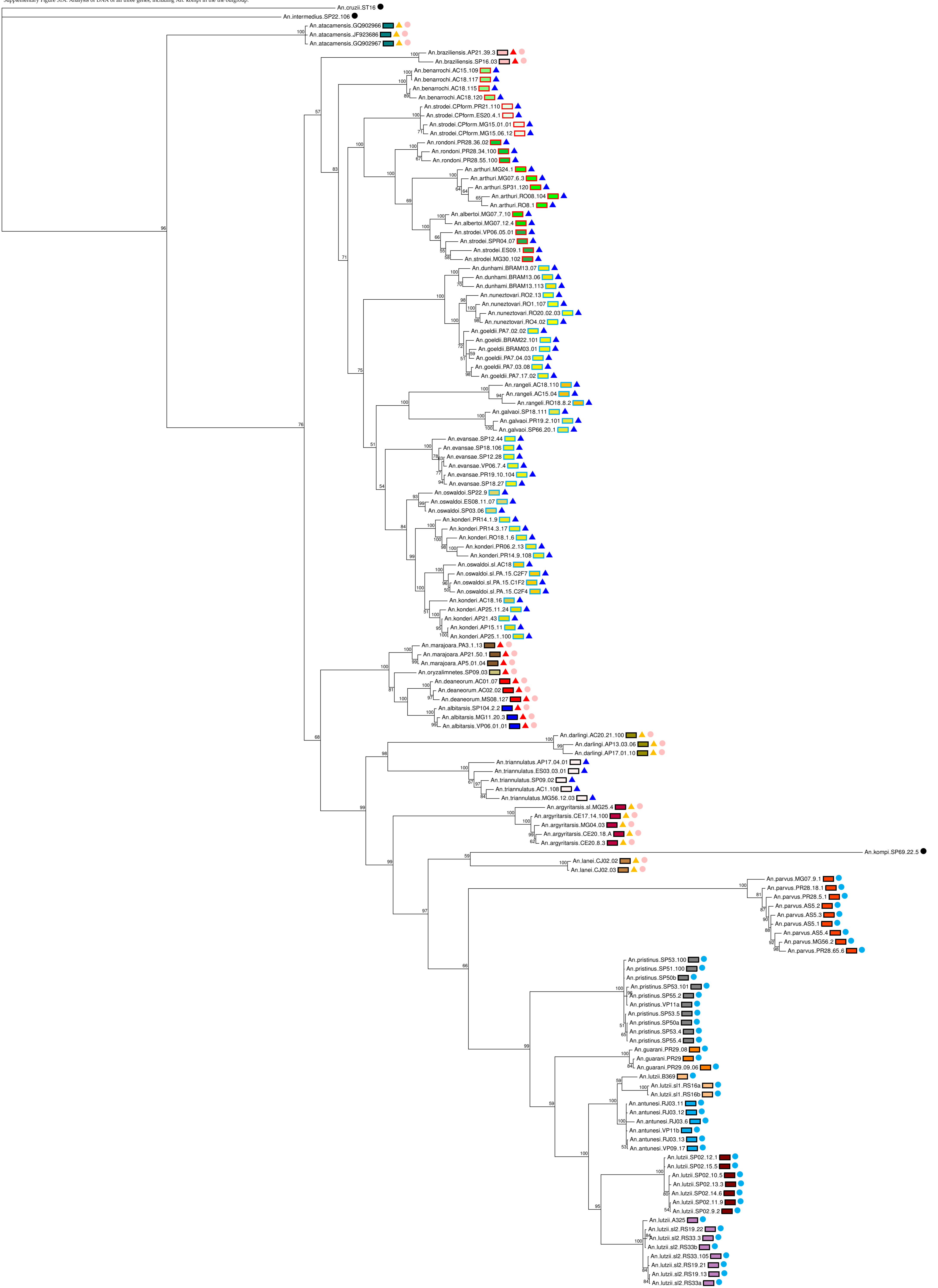
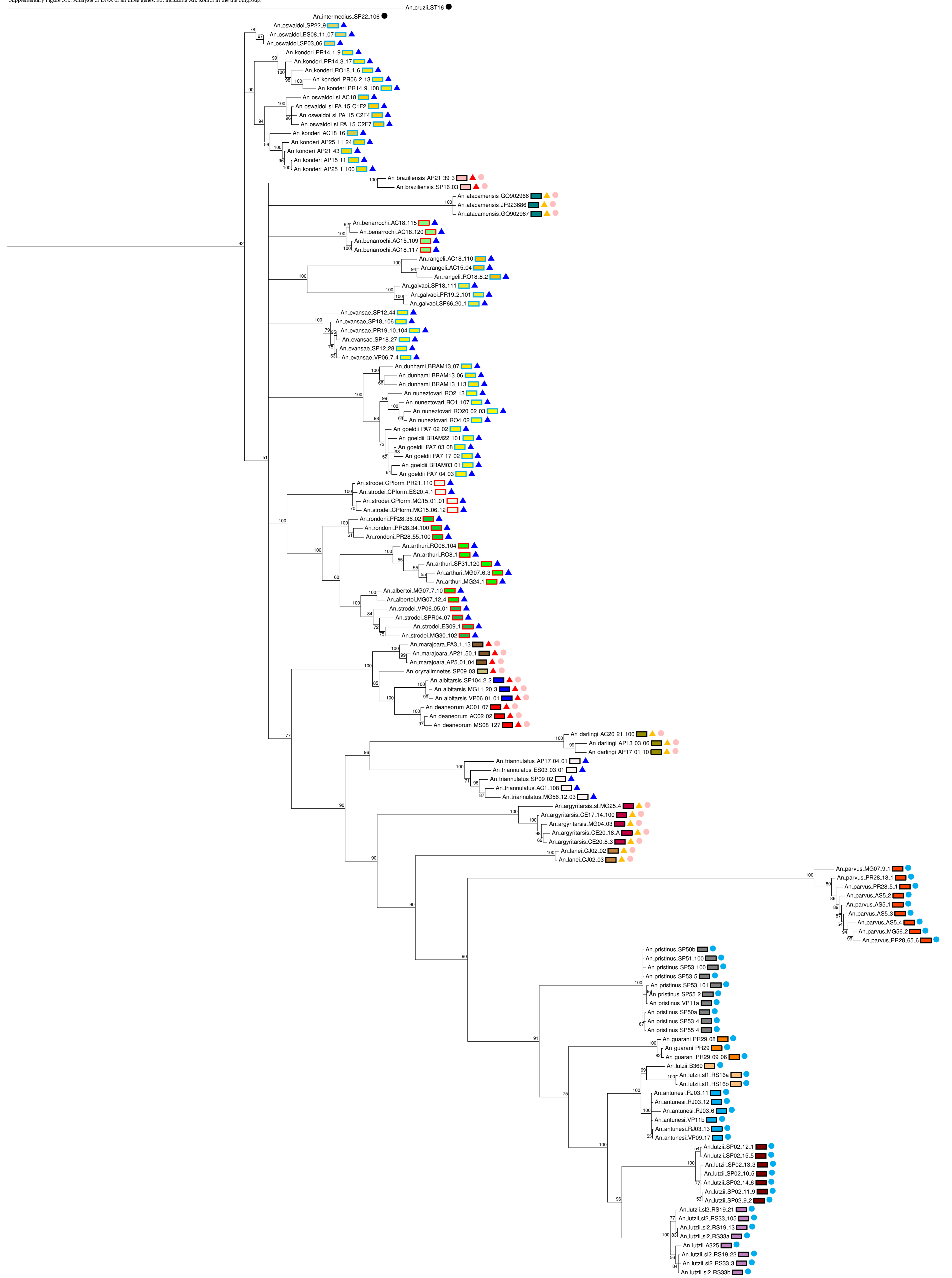


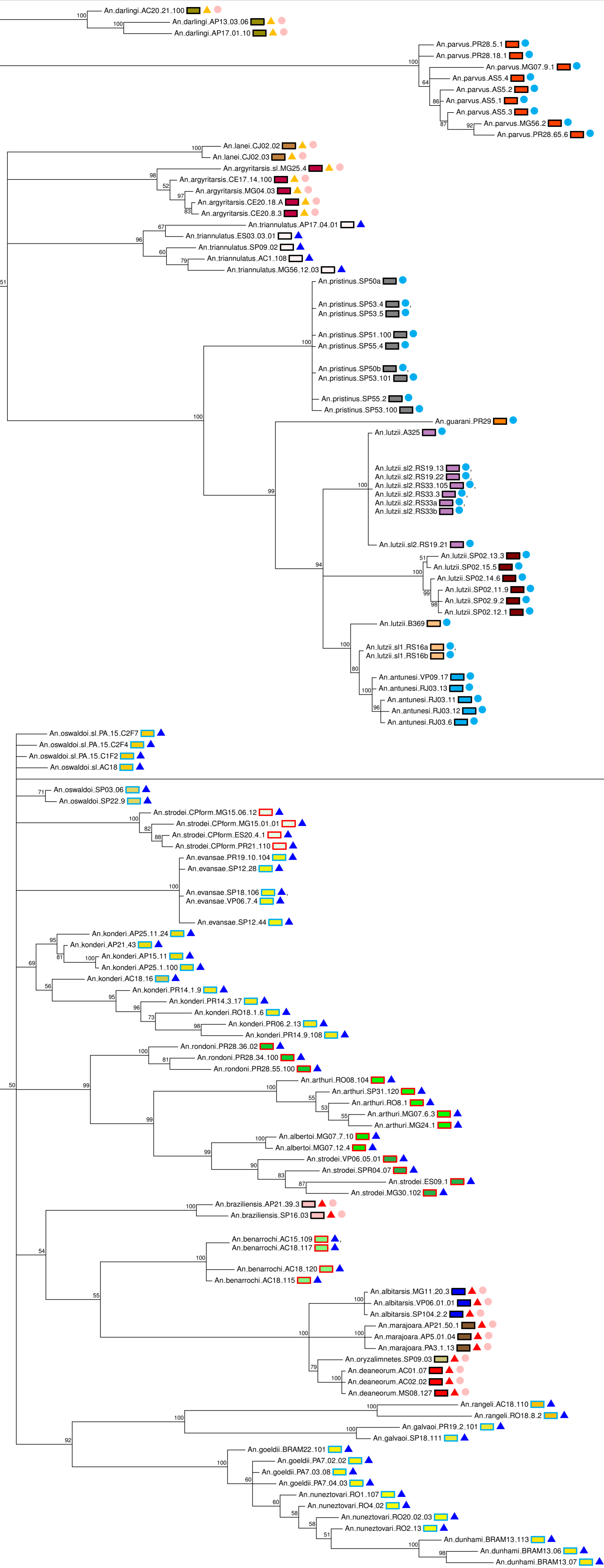
Figure S1A-E. Bayesian analyses using both MrBayes and p4 were run for 10 million generations, with each codon position of each gene given its own model characteristics in a multi-partition model as described in Supplemental Tables S2A and S2B (although the COI second codon position 2 had no informative sites and so was not used). MrBayes used an MCMCMC with 4 chains; p4 used a single chain (i.e. no MCMCMC). MrBayes runs collected 1001 samples, and used a burnin of 751 samples. The p4 analysis collected 2000 samples and used a burnin of 1500 samples. Two runs were made using MrBayes, and 5 runs with p4; separate results can be seen in Supplemental Tables S4 and S6. The figures here (S1A-E) are consensus trees made from pooled samples. Internal nodes are decorated with posterior probabilities, expressed as percent.

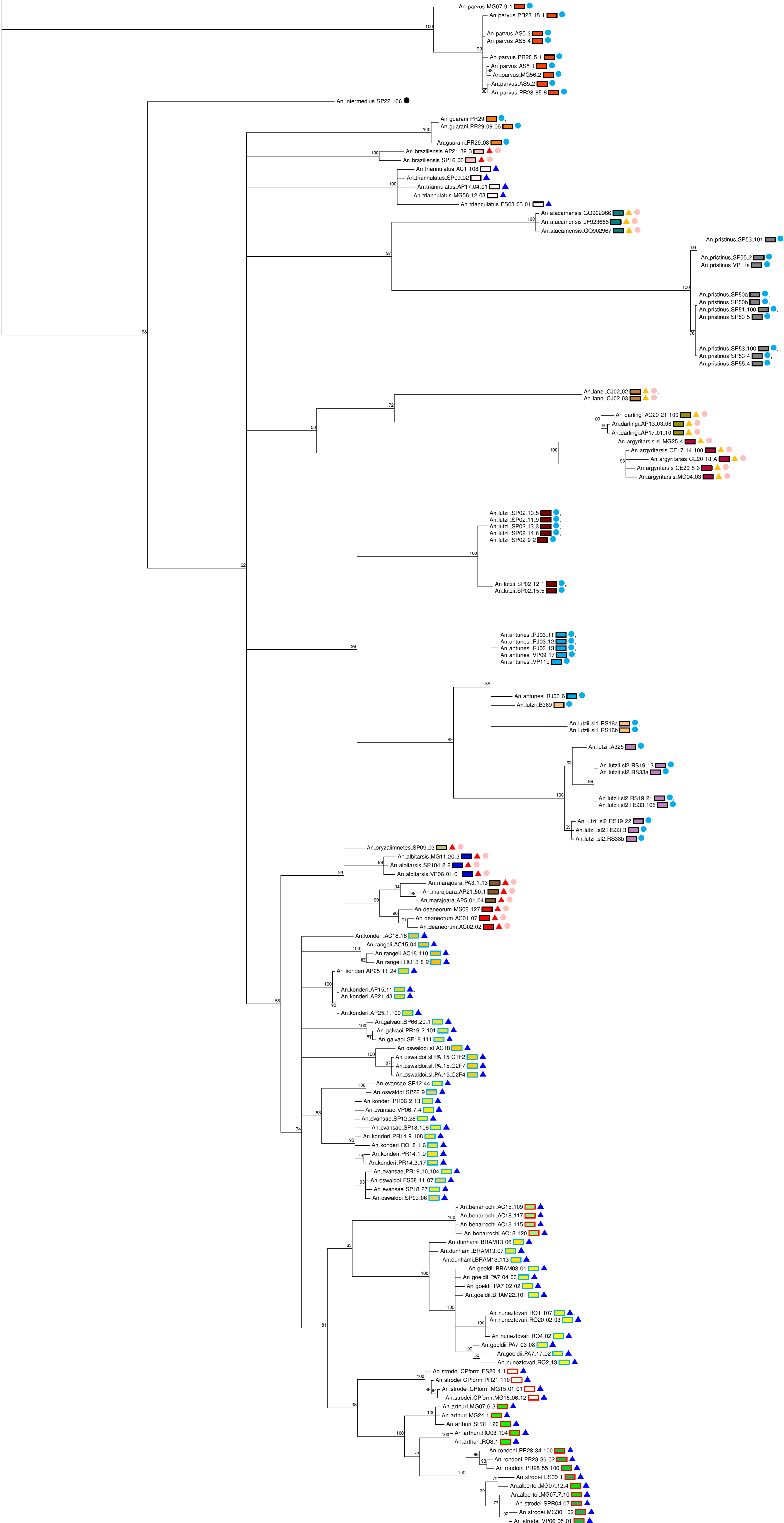
Figure S1F-S1G. K_{2P}/NJ trees. Pairwise K_{2P} distances were used to make a neighbor-joining tree, as shown. Negative branch lengths were collapsed to zero length.

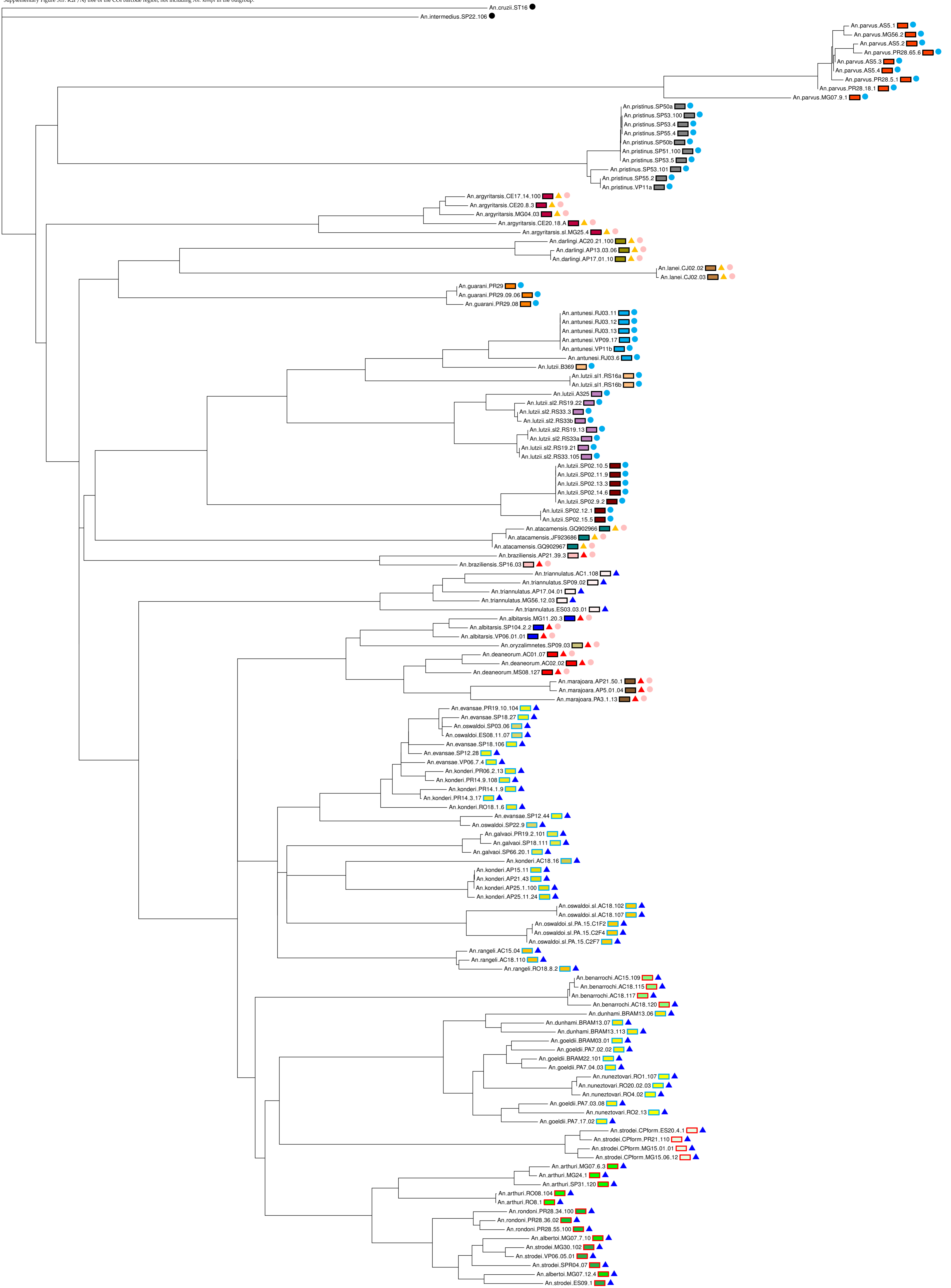












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