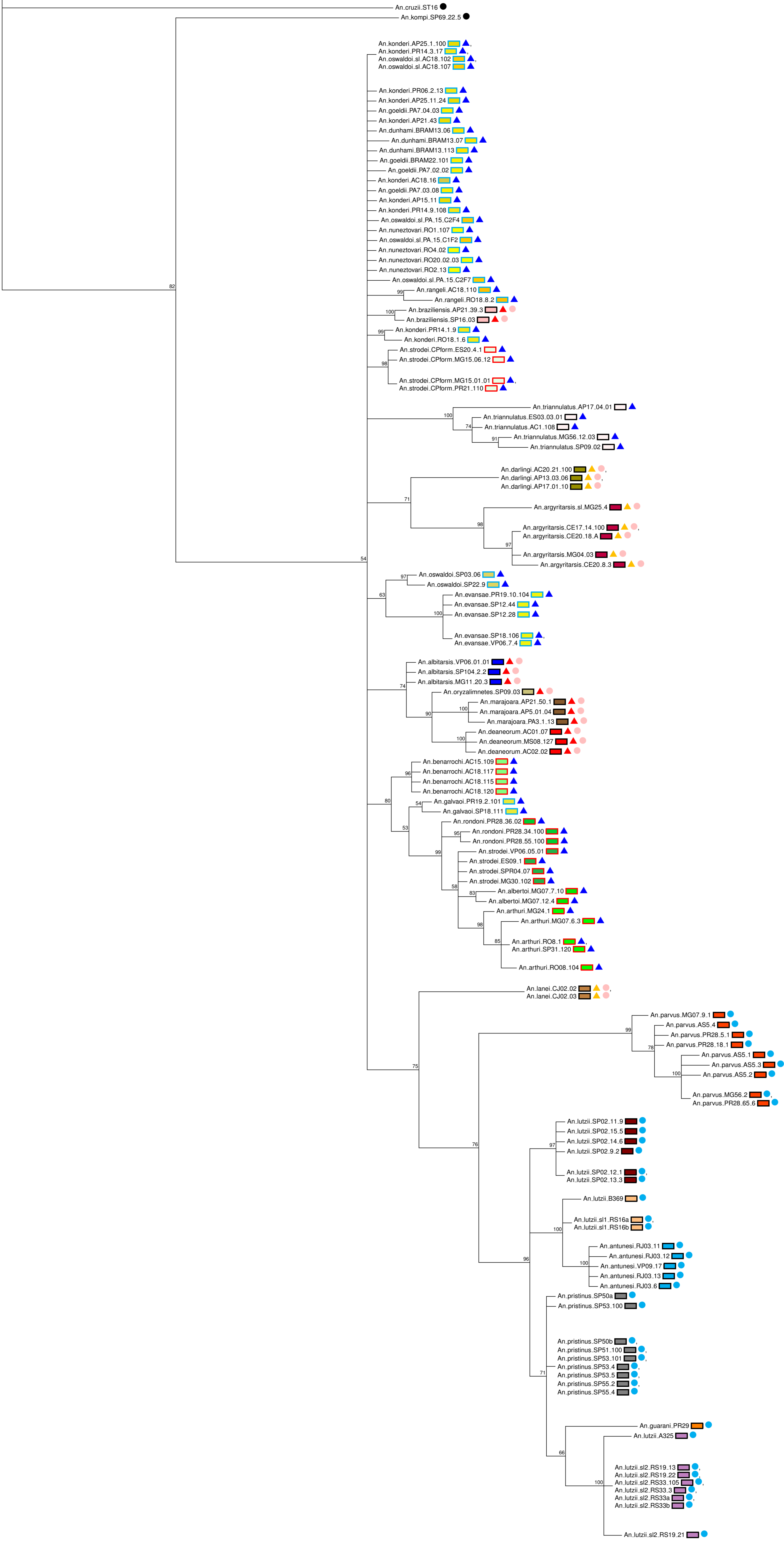
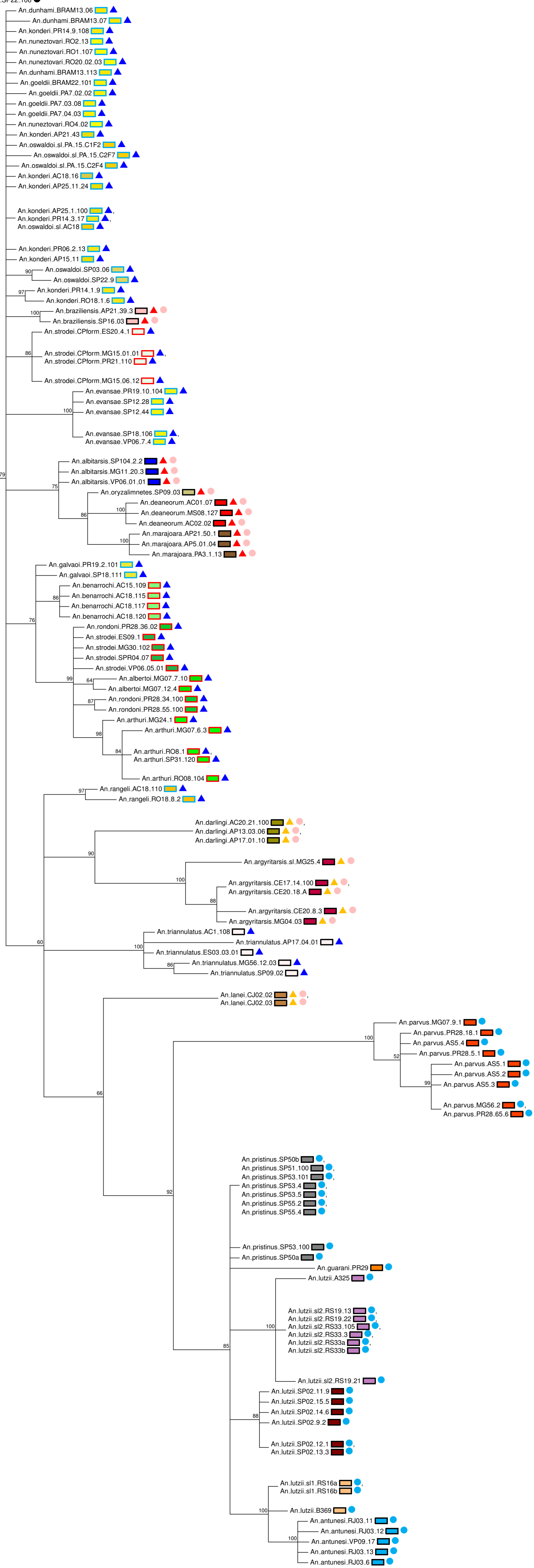


**Figure S2A-C.** Bayesian phylogenetic analysis of protein translations of the three gene regions. MCMC analysis used both MrBayes with the JTT+G model, and p4 with the JTT+F+G model (\*+F implying using empirical frequencies; this model aspect is not available in MrBayes). MrBayes used an MCMCMC with 4 chains, and p4 used a single chain (*ie* no MCMCMC). The consensus tree of the pooled post burnin samples is shown, with internal nodes decorated with posterior probability expressed as percent. Separate results can be seen in Table S5. (A) Analysis of protein translations of all three gene regions, including *An. kompi* in the the outgroup. This used two runs using MrBayes, and 10 runs using p4, both for 10 million generations. The MrBayes runs took 2001 samples and used a burnin of 1501 samples, and the p4 runs took 2000 samples and used a burnin of 1500 samples. (B) Analysis of protein translations of all three gene regions, not including *An. kompi* in the the outgroup. This used two runs for MrBayes, and 5 runs for p4, both for 5 million generations. The MrBayes runs took 1001 samples with a burnin of 751 samples. The p4 runs took 2000 samples and used a burnin of 1500 samples. The polytomy prior was used in p4. (C) Analysis of protein translations of all three gene regions, not including the outgroup. Conditions were the same as for (B) except that 2001 samples were taken in the MrBayes runs, with a burnin of 1501 samples.



An.intermedius.SP22.106

An.cruzi.ST16



Supplementary Figure S4C. Analysis of protein translations of all three gene regions, not including the outgroup.

