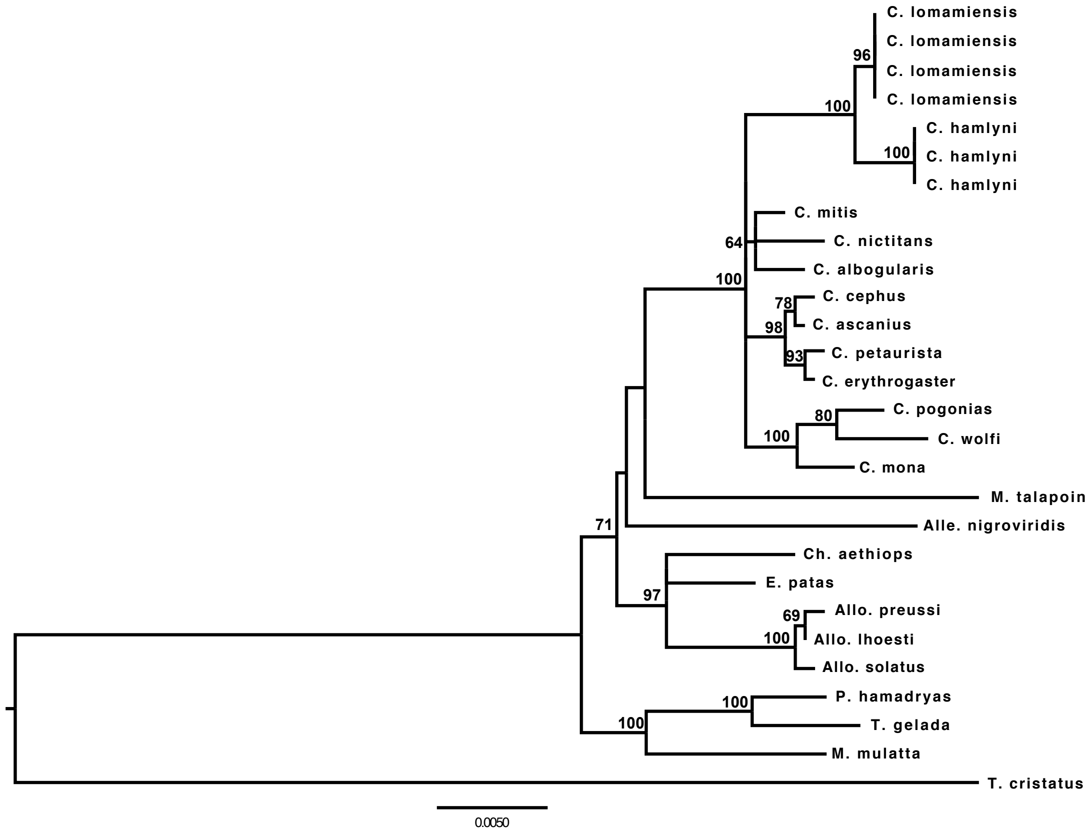

Fig. S1. Maximum likelihood tree, TSPY. Phylogram and bootstrap support values (500 replicates) were inferred using GARLI 0.951. The topology is identical to that inferred using a Bayesian approach (Fig. S2). *Cercopithecus lomamiensis* and *C. hamlyni* are reciprocally monophyletic. The scale at the bottom is in units of nucleotide substitutions per site.