

Supplementary Materials for “On the Taxonomic History and True Identity of the Collared Titi, *Cheracebus torquatus* (Hoffmannsegg, 1807) (Platyrrhini, Callicebinae)” by Hazel Byrne, Anthony B. Rylands, Stephen D. Nash and Jean Philippe Boubli

Molecular Dataset and Phylogenetic Analyses

We collected all currently available sequence data for *Cheracebus* for three mitochondrial regions including the complete cytochrome *b* (CYTB) locus, partial cytochrome oxidase I (COI) locus, and the non-coding D-Loop region. Some of these sequences were unpublished but all were generated previously for other studies/projects following the protocol described in Byrne *et al.* (2018). References for the primer sequences are as follows: CYTB (Byrne *et al.* 2016); COI (Ward *et al.* 2005); and D-Loop (Oliveira *et al.* 2011). For the highly variable D-Loop region, we included sequences from only *Cheracebus* taxa in our data matrix. For COI and CYTB, we also included published sequences for *Plecturocebus grovesi* and *Plecturocebus donacophilus*, as well as one representative from each of the genera of Pitheciinae (*Pithecia*, *Cacajao*, *Chiropotes*). GenBank accession numbers for all sequences are presented below in Table S2.

Each locus was aligned independently using the MUSCLE algorithm in Geneious R7.1 (Biomatters) and subsequently combined in a matrix with a total alignment length of 2,517 bp (Dataset B). A matrix comprised of only CYTB and COI was also generated with a total alignment length of 1,800 bp (Dataset A). Thirty *Cheracebus* individuals are represented in these alignments. We used the GTR + G (gamma) substitution model for each COI + CYTB codon position partition, and for a D-Loop partition. Phylogenetic inference was conducted using maximum-likelihood and Bayesian methods. For maximum-likelihood inferences, we used the program RAxML v.8.2.12 and estimated support using the rapid-bootstrapping algorithm (`-f a -x` option) for 1000 non-parametric bootstrap replicates (Stamatakis *et al.* 2008; Stamatakis, 2014). Bayesian analyses were performed using MrBayes 3.2.7 (Ronquist *et al.* 2012). MCMC (Markov Chain Monte Carlo) convergence was checked after two independent four-chain runs of 2 million generations after a burn-in of 10%.

Table S2 List of the GenBank accession numbers for all sequences. In bold are the newly generated sequences.

Species	Sample ID	COI	CYTB	D-Loop
<i>Cheracebus lugens</i> (LJ)	CTGAM733	MT465106	MT461034	MT461044
<i>Cheracebus lugens</i> (LJ)	CTGAM734	MT465107	MT461039	--
<i>Cheracebus lugens</i> (LJ)	CTGAM753	MT465108	MT461035	MT461045
<i>Cheracebus lugens</i> (RN)	JPB81	KU694203	MT461029	MT461046
<i>Cheracebus lugens</i> (RN)	CRB2696	--	DQ337710	--
<i>Cheracebus lugens</i> (RN)	CRB2697	--	DQ337709	--
<i>Cheracebus lugens</i> (RN)	CRB2698	--	DQ337708	--
<i>Cheracebus lugens</i> (RN)	CRB2837	--	DQ337707	--
<i>Cheracebus lugens</i> (LN)	CCM105	MT465105	MT461028	MT461043
<i>Cheracebus lugens</i> (LN)	JPB108	MT465109	MT461030	MT461047
<i>Cheracebus lugens</i> (LN)	JPB111	MT465110	MT461040	MT461048
<i>Cheracebus lugens</i> (LN)	JPB119	KU694204	KU694251	MT461049
<i>Cheracebus lugens</i> (LN)	JPB121	MT465111	MT461031	MT461050
<i>Cheracebus lugens</i> (LN)	JPB123	MT465112	MT461032	MT461051
<i>Cheracebus lugens</i> (LN)	JPB124	KU694205	KU694252	MT461052
<i>Cheracebus lugens</i> (LN)	JPB136	KU694206	KU694253	MT461053
<i>Cheracebus lugens</i> (LN)	JPB160	MT465113	MT461036	MT461054
<i>Cheracebus lugens</i> (LN)	JPB161	MT465114	MT461037	MT461055
<i>Cheracebus lugens</i> (LN)	GenBank	KC592393	KC592393	KC592393
<i>Cheracebus lugens</i> (LN)	CRB2205	--	AF524888	--
<i>Cheracebus lugens</i> (LN)	CRB2433	--	AF524889	--
<i>Cheracebus lugens</i> (LN)	CRB2570	--	DQ337711	--
<i>Cheracebus lugens</i> (LN)	CRB2667	--	DQ337712	--
<i>Cheracebus torquatus</i> (fka <i>purinus</i>)	CTGAM154	KU694207	KU694254	MT461056
<i>Cheracebus torquatus</i> (fka <i>purinus</i>)	CTGAM195	KU694208	KU694255	MT461057
<i>Cheracebus torquatus</i> (fka <i>purinus</i>)	CTGAM209	KU694209	KU694256	MT461058
<i>Cheracebus torquatus</i> (fka <i>purinus</i>)	GenBank	--	AF524890	--
<i>Cheracebus lucifer</i>	CTGAM726	MT465103	MT461033	--
<i>Cheracebus lucifer</i>	CTGAM727	MT465104	MT461038	MT461042
<i>Cheracebus lucifer</i>	CTGAM703	MH101708	MH101710	MT461041
<i>Plecturocebus grovesi</i>	RVR22	KU694222	KU694272	--
<i>Plecturocebus donacophilus</i>	GenBank	FJ785423	FJ785423	--
<i>Pithecia pithecia</i>	GenBank	JF459229	KR902424	--
<i>Cacajao calvus</i>	GenBank	NC021967	NC021967	--
<i>Chiropotes israelita</i>	GenBank	NC024629	NC024629	--

Supplementary Figure Legends

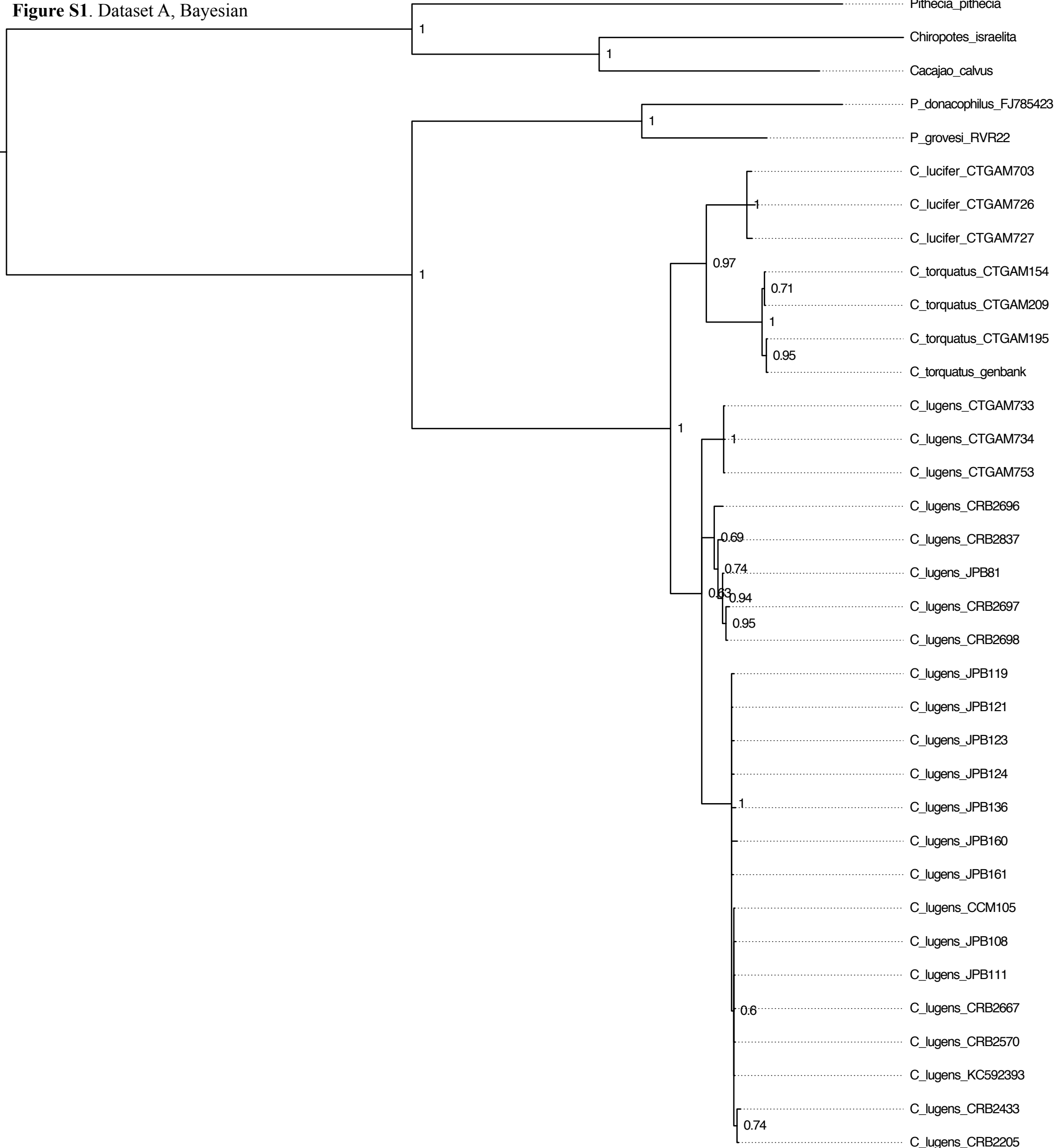
Figure S1. Phylogenetic trees inferred from the mitochondrial Dataset A based on Bayesian methods

Figure S2. Phylogenetic trees inferred from the mitochondrial Dataset B based on Bayesian methods

Figure S3. Phylogenetic trees inferred from the mitochondrial Dataset A based on maximum likelihood methods

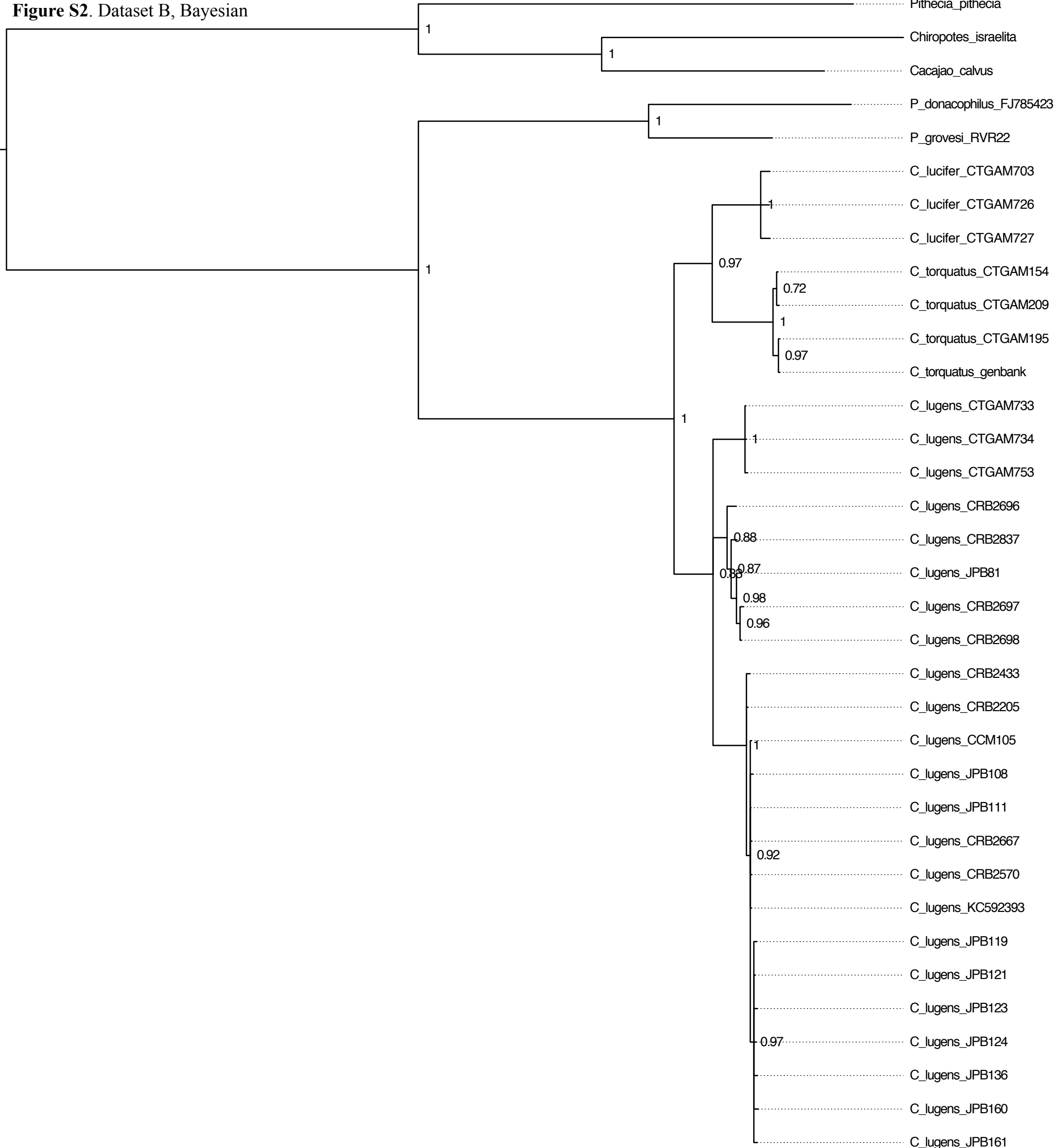
Figure S4. Phylogenetic trees inferred from the mitochondrial Dataset B based on maximum likelihood methods

Figure S1. Dataset A, Bayesian



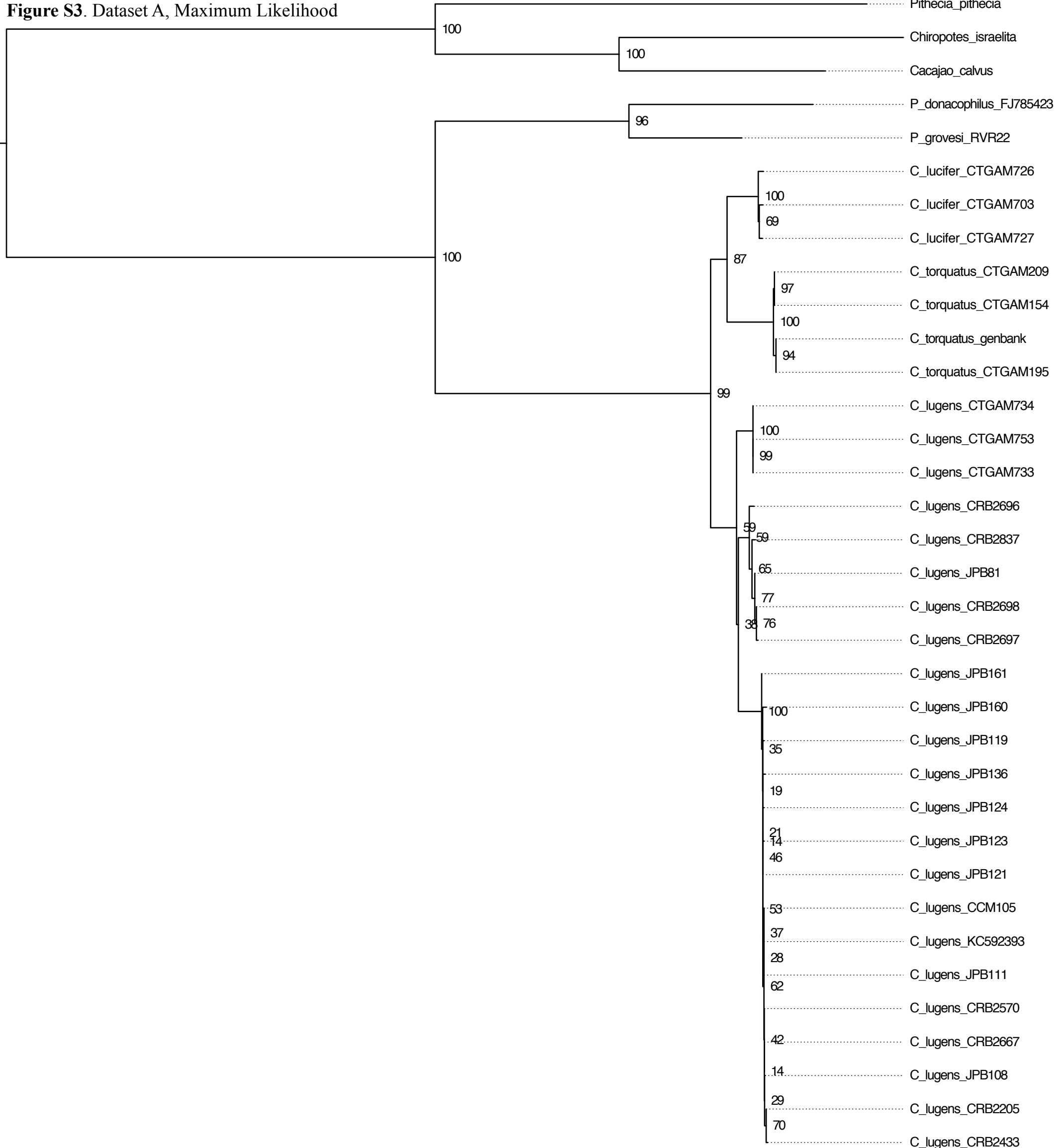
0.1

Figure S2. Dataset B, Bayesian



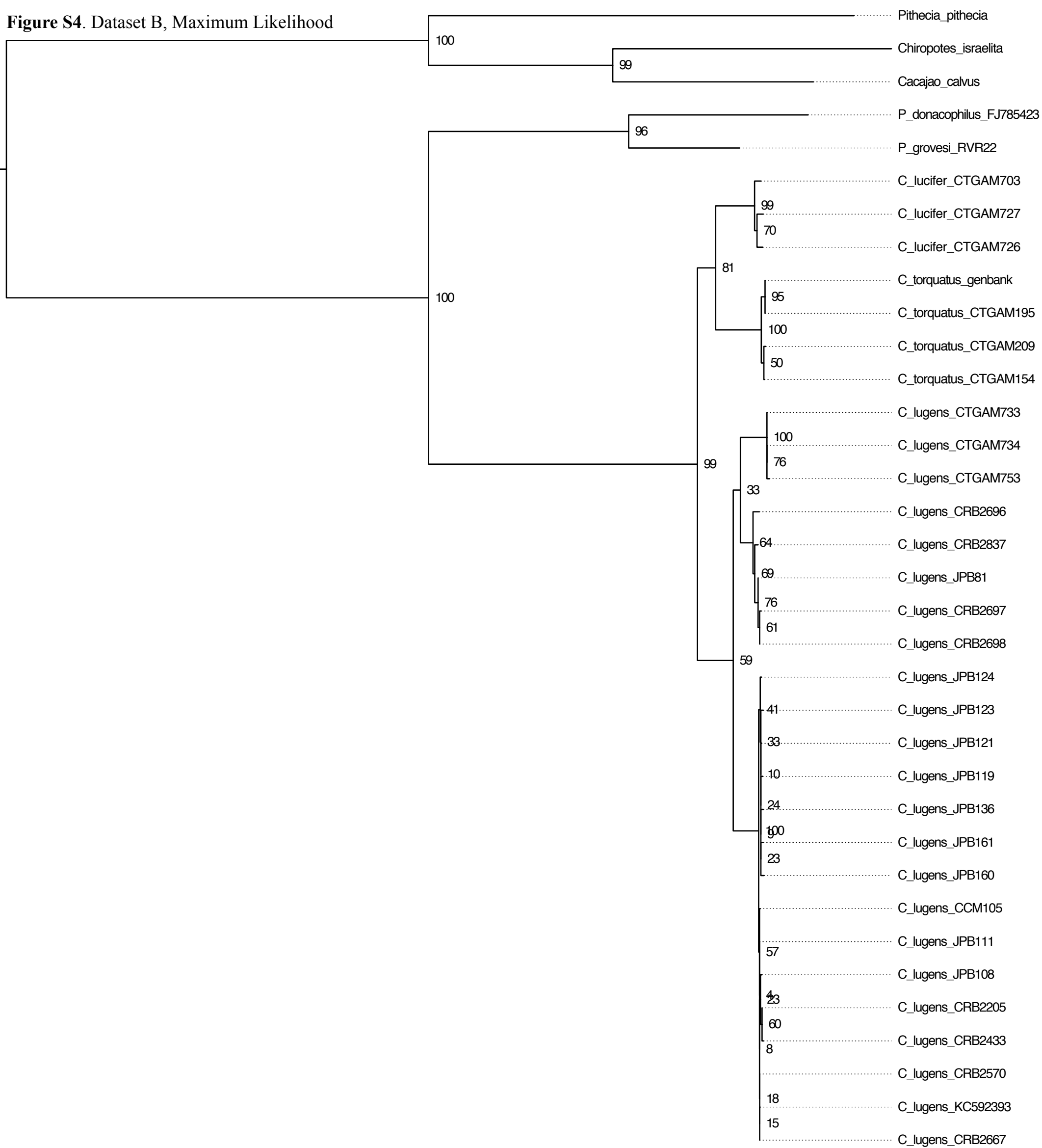
0.2

Figure S3. Dataset A, Maximum Likelihood



0.08

Figure S4. Dataset B, Maximum Likelihood



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