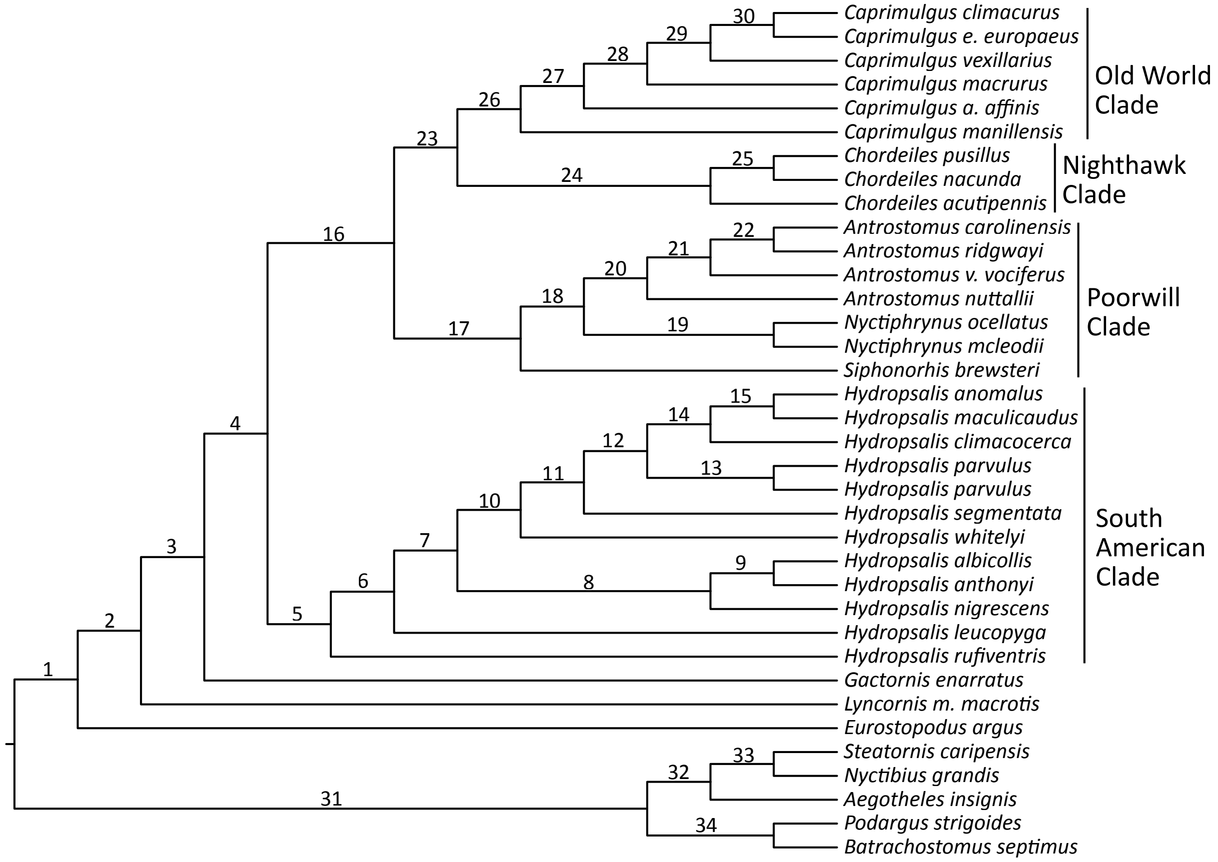
Supplementary Materials for
"A multi-gene estimate of higher-level phylogenetic relationships among nightjars (Aves: Caprimulgidae)" White, ND, GF Barrowclough, JG Groth & MJ Braun

Supplemental Material Table S1. Nodal support values for partitioning schemes with identical topologies, under both GTR + I + G and PartitionFinder-selected model (where applicable, format GTR + I + G / PartitionFinder). Nodes numbered as shown in A), bootstrap support values listed in table B). Nodes constituting the major clades of the tree are given a name. Schemes are numbered: 1-Unpartitioned, 2-Coding vs. non-coding, 3-By gene, 4-Coding positions vs. non-coding, 5-Nuclear vs. mitochondrial vs. non-coding, 6-Nuclear vs. mitochondrial vs. introns vs. UTR, and 7-PartitionFinder. Major clades are abbreviated as follows: O = Old World Clade, P = Poorwill Clade, N = Nighthawk Clade, SA = South American Clade.

A



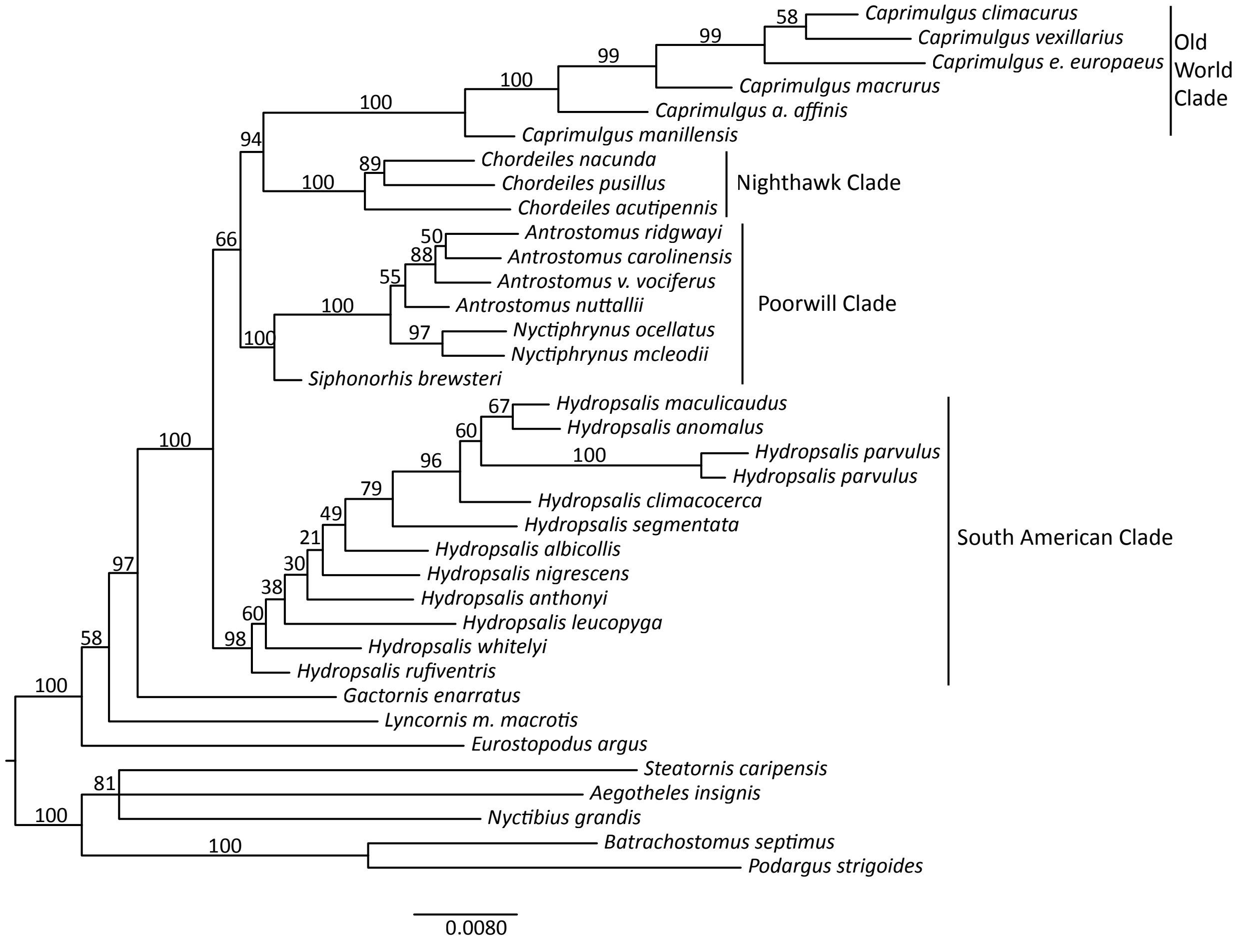
B

		Partitioning Schemes						
Node #	**Node Name**	**1**	**2**	**3**	**4**	**5**	**6**	**7**
1	Caprimulgidae	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
2	*Eurostopodus* (all other)	55	56 / 54	59 / 68	58 / 66	56 / 68	69 / 64	67 / 63
3	*Euro* (*Lyncornis* (all other))	97	97 / 98	95 / 98	99 / 98	96 / 97	98 / 98	100 / 98
4	*Euro* (*Lync* (*Gactornis* (all other)))	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
5	SA	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
6		63	66 / 59	83 / 82	72 / 75	74 / 62	68 / 68	77 / 80
7		56	72 / 63	72 / 73	68 / 68	62 / 62	61 / 62	68 / 65
8		69	70 / 69	73 / 73	70 / 73	61 / 67	65 / 60	77 / 74
9		77	77 / 76	83 / 81	82 / 81	79 / 70	71 / 70	77 / 84
10		83	90 / 83	91 / 85	90 / 86	81 / 82	79 / 89	87 / 87
11		88	88 / 88	88 / 86	87 / 85	87 / 89	81 / 81	87 / 89
12		97	94 / 96	98 / 94	97 / 98	92 / 94	98 / 96	95 / 96
13	Two *H. parvulus* samples	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
14	*H.clim* (*H.anom* , *H.mac*)	n/a	47 / 59	52 / 54	55 / 56	54 / 58	45 / 53	68 / 63
15	(*H.anom* , *H.mac*)	n/a	53 / 56	48 / 49	50 / 50	54 / 58	55 / 52	62 / 63
16	SA (P , N , O)	68	74 / 79	86 / 78	66 / 75	72 / 78	81 / 79	80 / 87
17	P	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
18	*Nyctiphrynus* / *Antrostomus* split	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
19		100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
20		96	96 / 91	85 / 91	90 / 96	89 / 92	94 / 87	88 / 91
21		92	94 / 94	92 / 95	95 / 93	94 / 97	95 / 94	90 / 93
22		98	98 / 99	100 / 100	100 / 99	99 / 99	100 / 100	100 / 99
23	(N , O)	97	99 / 99	98 / 98	99 / 94	98 / 96	97 / 96	97 / 96
24	N	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
25		100	100 / 99	100 / 99	100 / 100	100 / 100	100 / 100	100 / 100
26	O	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
27		99	100 / 99	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
28		100	99 / 99	99 / 100	99 / 99	99 / 99	100 / 98	100 / 100
29		100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
30		83	82 / 68	63 / 72	81 / 82	71 / 67	74 / 76	63 / 68
31	Outgroups	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100
32	*Aegotheles* (*Nyctibius* , *Steatornis*)	70	69 / 66		61 / 63	71 / 77	68 / 67	63 / 53
33	(*Nyctibius* , *Steatornis*)	59	39 / 43		28 / 48	42 / 34	50 / 47	47 / 40
34	(*Podargus* , *Batrachostomus*)	100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100	100 / 100

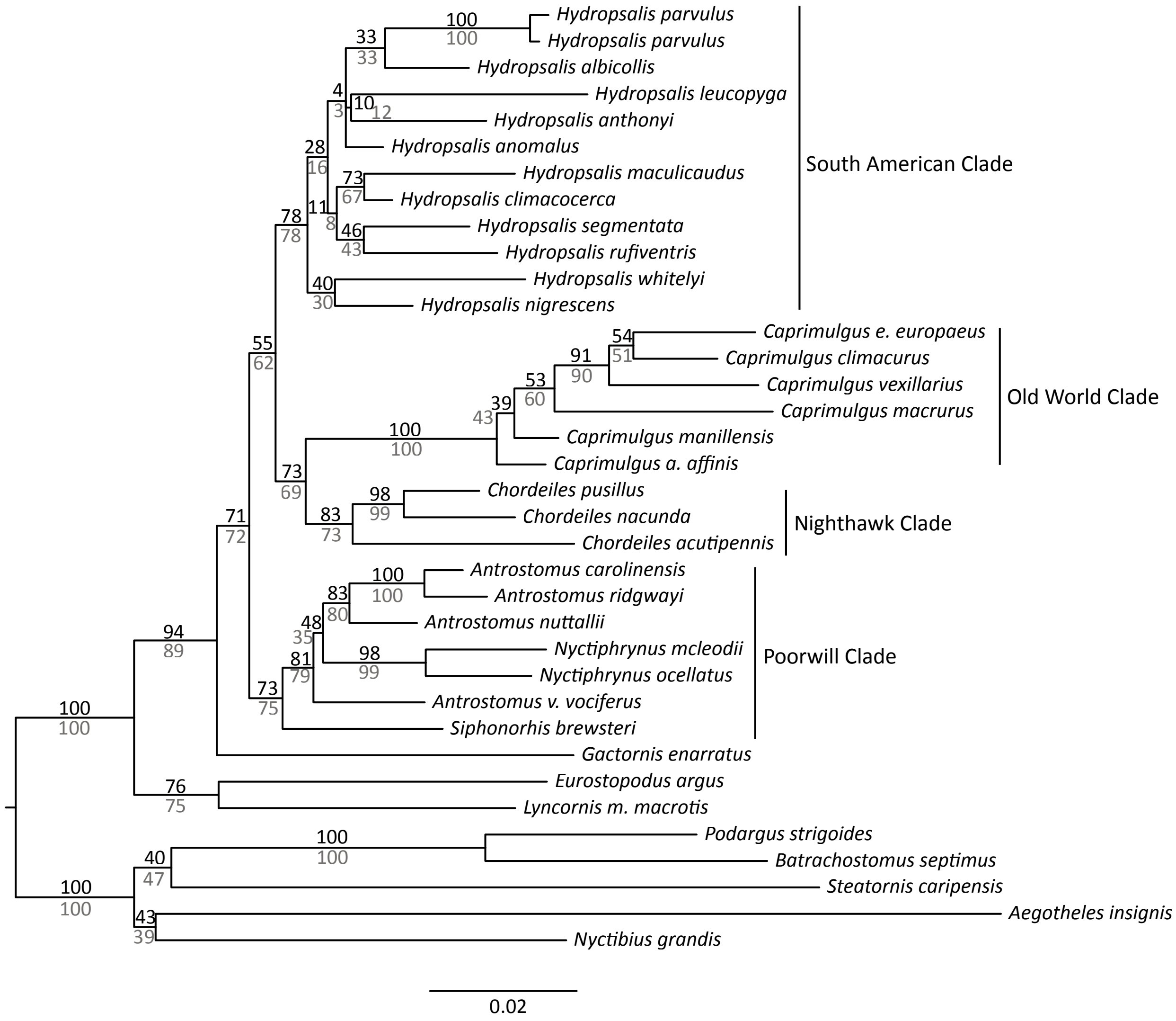
Supplemental Material Table S2. Bootstrap support values at congruent nodes across different analyses of the Caprimulgidae phylogeny, as numbered in Supplemental Material Table S1 A). 'This Study' refers to the analysis of PartitionFinder partitions under the model chosen by that software (presented in Figure 4 of the main text). Nodes constituting the major topology of the tree are given a name. Outgroups excluded due to differences in taxon selection between studies. Major clades are abbreviated as follows: O = Old World Clade, P = Poorwill Clade, N = Nighthawk Clade, SA = South American Clade. Cells shaded gray represent nodes that showed increased bootstrap support in this study over all previous studies (7 nodes had 100% support in all studies).

Node #	**Node Name**	**This study**	**Han et al.**	**Barrowclough et al.**	**Sigurdsson & Cracraft**
1	Caprimulgidae	100	100	100	99
2	*Eurostopodus* (all other)	63	59		< 60
3	*Euro* , *Lyncornis* (all other)	98	84		87
4	*Euro* , *Lync* , *Gactornis* (all other)	100	100	100	100
5	SA	100	100		100
6		80	< 50		< 60
7		65	< 50		< 60
8		74	< 50		100
9		84	84		93
10		87	93		100
11		89			95
12		96	100		96
13		100			100
14		63			
15		63			
16	SA (P , N , O)	87		< 50	< 60
17	P	100	90	100	99
18	*Siphonorhis* basal in P	100	99		99
19	*Nyctiphrynus*	100	100		100
20	*Antrostomus*	91	96	52	100
21		93	56	87	
22		99	100		
23	(N , O)	96	69	93	95
24	N	100	100	100	100
25		100	94		100
26	O	100	100	100	100
27		100	< 50		
28		100		100	
29		100	99	100	
30		68	82		
		Nodes shared with this study	24	11	22
		Bootstrap 100% in both	7	7	7
		Bootstrap Increased in this study	12	4	9
		Bootstrap Decreased in this study	4	0	5

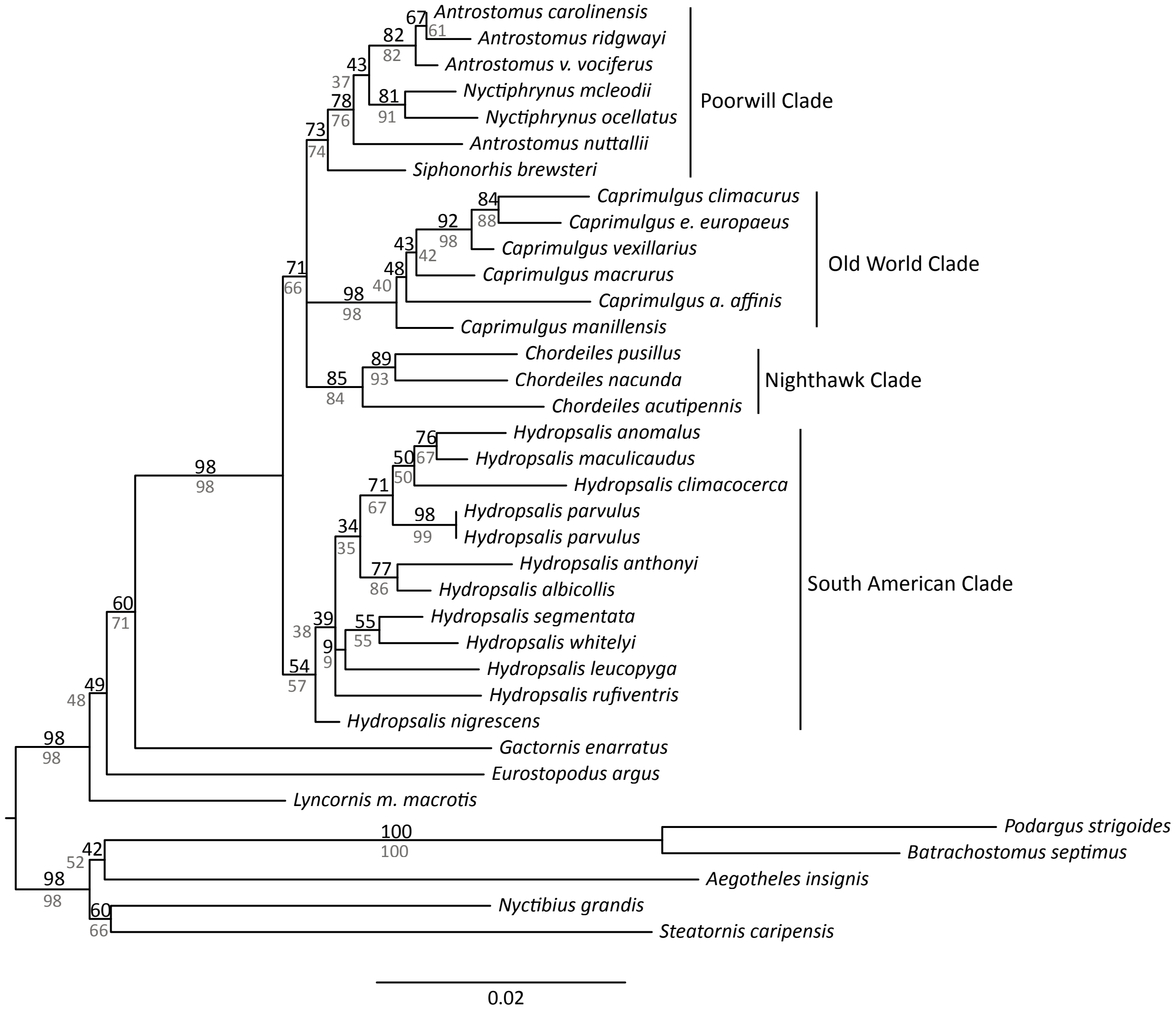
Supplemental Material Figure S1. Maximum likelihood analysis of RAG-1. Bootstrap support values shown for analysis under GTR + I + G. Scale units are substitutions per site.



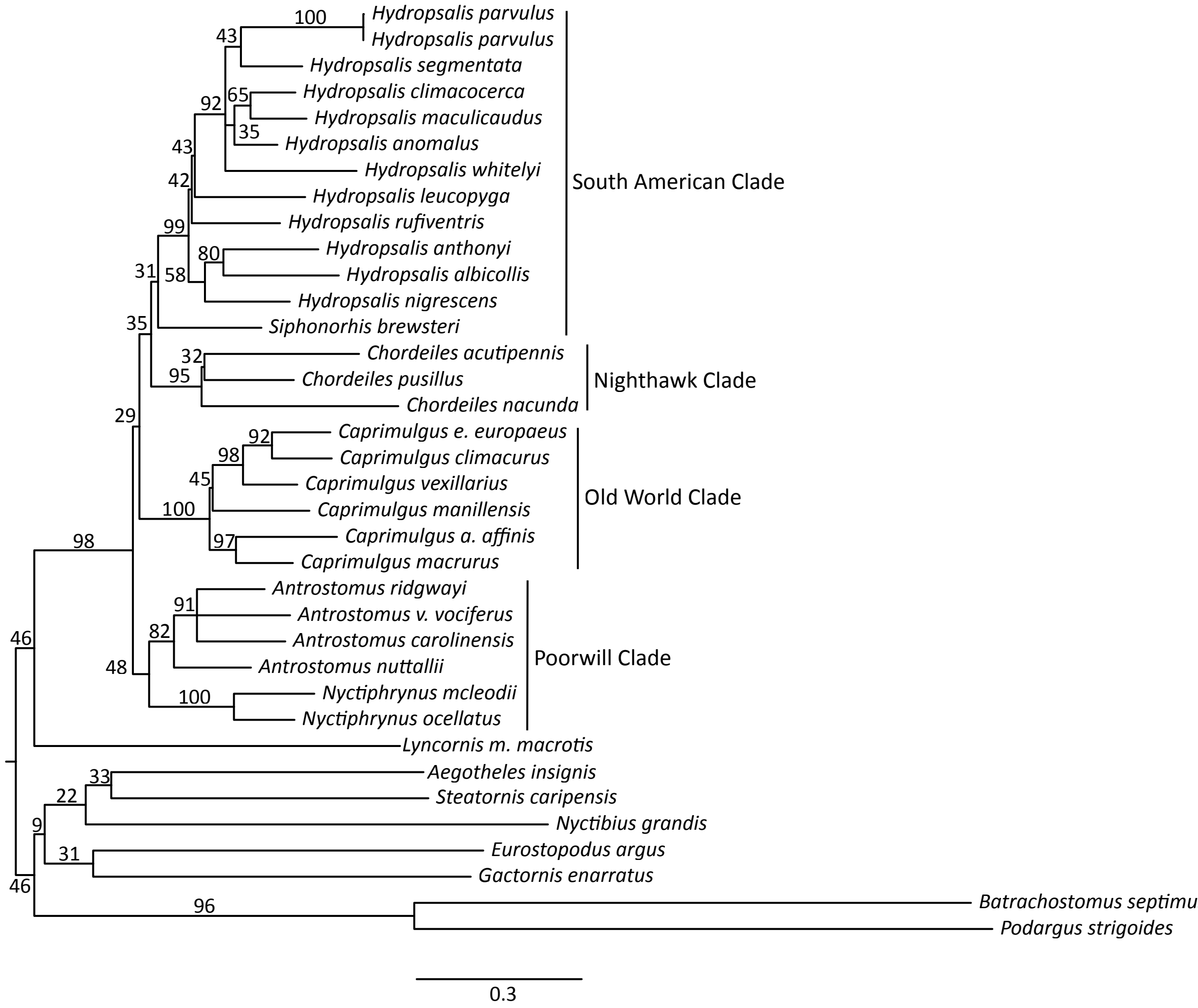
Supplemental Material Figure S2. Maximum likelihood analysis of GH. Bootstrap support values shown above nodes for analysis under GTR + I + G (black), below for analysis under model selected by PartitionFinder (grey) by AICc. Topologies were identical. Scale units are substitutions per site.



Supplemental Material Figure S3. Maximum likelihood analysis of MYC. Bootstrap support values shown above nodes for analysis under GTR + I + G (black), below for analysis under model selected by PartitionFinder (grey) by AICc. Topologies were identical. Scale units are substitutions per site.



Supplemental Material Figure S4. Maximum likelihood analysis of MT-CYB. Bootstrap support values shown for analysis under GTR + I + G. Scale units are substitutions per site.



Supplemental Material Figure S5. SVDquartets analysis cladogram with bootstrap support values.