

Figure S1. Comparison of tandemly duplicated *cytb* to CR segment with its first copy for *Nestor notabilis*, *Nymphicus hollandicus*, *Calyptorhynchus baudinii*, *Probosciger aterrimus*, *Eolophus roseicapilla*, *Cacatua moluccensis* and *Cacatua pastinator* mitogenomes. Dots in the sequence of the second copy indicate residues identical with the first copy. Cytochrome b genes (in the 1st copies) and *cytb* pseudogene (in the 2nd copies) are marked in red, *tRNA-Thr* copies are marked in green, *tRNA-Pro* copies are marked in yellow, *ND6* genes and *ND6* psuedogenes (in some 2nd copies) are marked in blue, *tRNA-Glu* genes and *tRNA-Glu* pseudogenes (in some 2nd copies) are marked in grey, two copies of control region are in red font.

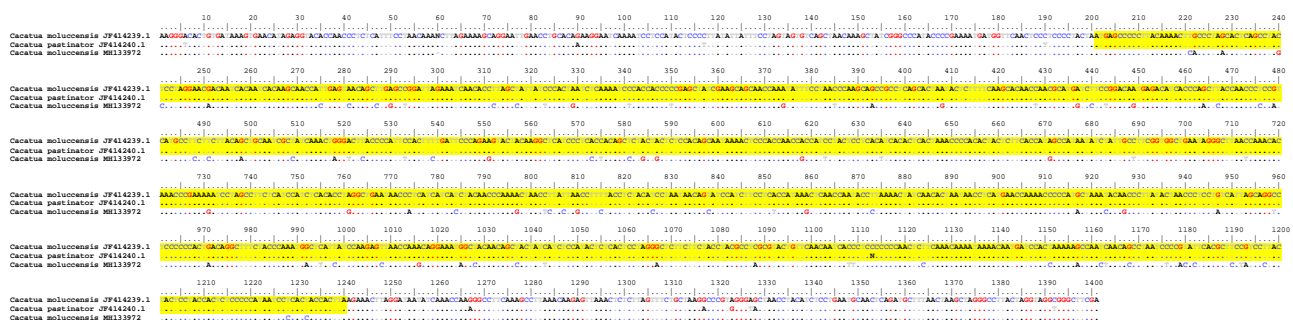


Figure S2. Comparison of *ND2* gene and adjacent sequences from *Cacatua moluccensis* mitogenome sequenced in this study (MH133972) with corresponding sequences from previously obtained *Cacatua moluccensis* (JF414239.1) and *Cacatua pastinator* (JF414240.1) mitogenomes. Regions flanking *ND2* gene are identical between *Cacatua moluccensis* mitogenomes but not the *ND2* gene itself. Interestingly, this gene from the previously obtained *Cacatua moluccensis* mitogenome occurred to be identical with the gene from previously sequenced *Cacatua pastinator* mitogenome. The identical sequences are marked in yellow.



Figure S3. Alignments of selected fragments from mitogenomes of *Prioniturus luconensis* (KM611473.1), *Forpus passerinus* (KM611470.1), *Psittacus erithacus* (KM611474.1), *Poicephalus gulielmi* (MF977813) and *Neophema chrysogaster* (NC\_019804.1). The following sequences are aligned: the last 177 nucleotides of gene *cytb* and the last 144 nucleotides of CR1 from *Prioniturus luconensis* (A); the first 123 nucleotides of CR1 and gene *ND6* from *Forpus passerinus* (B); the first 68 nucleotides of CR1 and gene *ND6* from *Psittacus erithacus* (C); the last 178 nucleotides of CR1 and gene *cytb* from *Psittacus erithacus* (D); the last 170 nucleotides of CR1 and gene *cytb* from *Poicephalus gulielmi* (E); CR fragment (NC\_019804.1; positions 10786 - 11181) and gene *cytb* from *Neophema chrysogaster* (F). Dots indicate residues identical in the compared sequences.

**A**

CCAAAAACCCCTACAAAGGCCCCACCACAGGTGGAGGGCCTTATTAACCATTAATAGCCCCATATAGTGGACCCCCCTTACCCCCAACGGCATAATATGAGCAGGCCTATGG  
GCTATGTATATAGTACATTATTATATGGTCCTTAAACATTATATTAAGCTCCTTGTAAGATTAAATATTCATGTTCTACGGACTATTATATGTAACGGGCAATAAACGATAC  
AGCTCTATTTTGGTTTCAAGGGTTAGTAGCAACTTCATGCTCTTAGGTGATGTCACGACCGGTTATGGCACCTCCACCGACCTTCTACTTTGGTATTATTCGTTTAAATGGTCGCTG  
GACATAGTCTTAAACACTTCTATCACCTCTAAATTACCAATACCCAGTAAAAGATCAACAAAGGATGTAGGAAAAATTTCCAATAAACCTTTGTCAAACGTAAACAAACGTACAAAA  
CAAACACGAAACAAACAAACGTTACTACTCGAATTATGAATCTTCATAAAACGTTGCTCACTACTCGAAGCTTCCATTCACTTATCTAAATGTTTGACGCTTTATTTTGTATTATT  
TAATTTAATCTTTAACCCCAACCGCATCCATGAATCTGCCCTCCCTACCCCATGATATCA (AGGTCCCCCAACCCAAGCTTGAGGGGCTAGCTACCTAAGTCCCACCGTACA  
ACCCCT) (AGGCCCCCCAACCTAAGCTTGAGGGGCTAGCTACCTTAATCCACCGTACAACCTCCCT) (AGGCCCCCTAACCCAAGCTTGAGGGGCTAGCTACCTAAGTCCCAC  
CCGTACAACCCCT) (AGGCCCCCTAACCCAAGCTTGAGGGGCTAGCTACCTAAGTCCCACCGTACAACCCCT) (AGGCCCCCTAACCCAAGCTTGAGGGGCTAGCTACCTTA  
ATCCACCGTACAACCCCT) (AGGCCCCCTAACCCAAGCTTGAGGGGCTAGCTACCTAAGTCCCACCGTACAACCTCCCT) (AGGCCCCCCAACCTAAGCTTGAGGGGCTAGCT  
ACCTAAGTCCCACG) ACACACTACATGAGGGGCCCCATCAACCATTAATAGCCCCATACAGTGGACCCCCCTTACCCCCAACGGCATAATATGAGCAGGCCTATGGGTATGT  
ATATAGTACATTATTATGGTCCTTAGTACATTATATTAAGCTTCTTAAAGACTAAATGTTTCATGTTCTATAGATTACTATATGTAACCGGCAATAACGATACAGCTCTA  
TTTGTGTTTCAAGGGTTAGTAGCAACTTCATGCTCTTAGGTGATGTCACGACCTGCTCTAAAGATCAGTAGTAACCTCATGCTCTTAAGTCATACCTAGTACTTCTCCAAAGGACT  
GGTAGCAACTTCATGCTTCTAAGTCATATCCAGCACTGCTCTAAGGACTGGTAGCAGTTCATGCTCCCAGGTATACACGACATAATCGGGTATTCACGATGCTTCTCGGCG  
TTCTCATGCTTGTATACAATGATTTCGTATAATTAGACGGCAGGTAGAGTACCCCAATCCTCCCGCAGGGAACGGACGGCGCTCCATGCACACATGTCATATCTAGCCCACTCAA  
CCGATTATGAGTCCGGTCTTCCCTCGACTGGCGGTGCTGCATAGTCTGAGGACTACAATTGGTTGGTACACCATGGACTTTTCATTTCACGTAGCGCTAGTTTCAAGTATCCGG  
TTATCTATTGATGGGCTTCTCAGAGAAATCCCTACTCAACGTATGGAAGACGACAGCTACTAGCTTCAAGGCCATTCTTTCCCCCTACACCTGACACTACTTTCGACTTTG  
GGTACCTCTGGTCTCGGTACGGCCATGAGCTCCTTAATTGAGCTTCTTATTATCTTCAAAGTCATCACTTCTAGTCTGAGTACATTTTGCTCTTAATCTCGGCCCTCTTAT  
GGTCTCTATAGAGCCTTGCTTCTCTTTTCTGGTCTTTCACTGACACTCCAGTGCTCACAGGCGCATACTATTGTTGAGATGTACATTATGCCCTTCGTCTCTGCTGT  
GGTCTCAGGAGCTAATTAATGATATGGCTTAAATGCGGGGCGCTCATTTTTTACACTGATGCACCTTTGTCTTACACTTGGTTATGGCACCTCCACGACCTTCTACTTGGTA  
TTATTCGTTTAAATGGTCGCTGGACATAGTCTTAACACTTCTATCACCTCTAAATACCAATACCAAGATCCAGTAAAAGATCAACAAAGGATGTAGGAAAAATTTCCAATAAACCTTTGTC  
AAACGTAACAAACGTACAAACAAACACGAAACAAACAAACGTTACTACTCGAATTATGAATCTTCATAAAACGTTGCTCACTACTCGAAGCTTCCATTCACTTATCTAAATGT  
TTGACGTTTATTTGTTTATTTAATTTAATCTTTAACCCCAACCGCATCCATGAATCTGCCCTCCCTACCCAATACCTACACTGCCCAATAGCATAAACCAACAAACAAACAA  
GCAGGTACCT

**B**

	10	20	30	40	50	
Repeat 1st	AGGTCCCCCAACCCAAGCTTGAGGGGCTAGCTACCTAAGTCCCACCGTACAAC-CCCT					
Repeat 2nd	...C.....T.....T.A.....T.....					
Repeat 3rd	...C.....T.....T.....T.....					
Repeat 4th	...C.....T.....T.....T.....					
Repeat 5th	...C.....T.....T.A.....T.....					
Repeat 6th	...C.....T.....T.....T.....					
Repeat 7th	...C.....T.....T.....T.....					

**C**

	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240
N. chrysogaster CR2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
N. chrysogaster CR1	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480
N. chrysogaster CR2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
N. chrysogaster CR1	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720
N. chrysogaster CR2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
N. chrysogaster CR1	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960
N. chrysogaster CR2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
N. chrysogaster CR1	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
N. chrysogaster CR2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
N. chrysogaster CR1	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440
N. chrysogaster CR2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
N. chrysogaster CR1	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
	1450	1460	1470	1480																				
N. chrysogaster CR2	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....
N. chrysogaster CR1	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....

Figure S4. Reannotated control region (CR) of *Neophema chrysogaster*. (A) The mitochondrial sequence originally annotated as control region (JX133087.1; positions 10,155 - 12,658). Two control regions are marked in red fonts and the *cytb* pseudogene in yellow. Its 7 repeats are in brackets. (B) Comparison of seven repeats included in the *cytb* pseudogene. Dots in the 2<sup>nd</sup> to 7<sup>th</sup> repeats indicate residues identical with the first repeat (1<sup>st</sup>). (C) The alignment of two newly identified control regions. Dots indicate residues identical in the compared sequences.





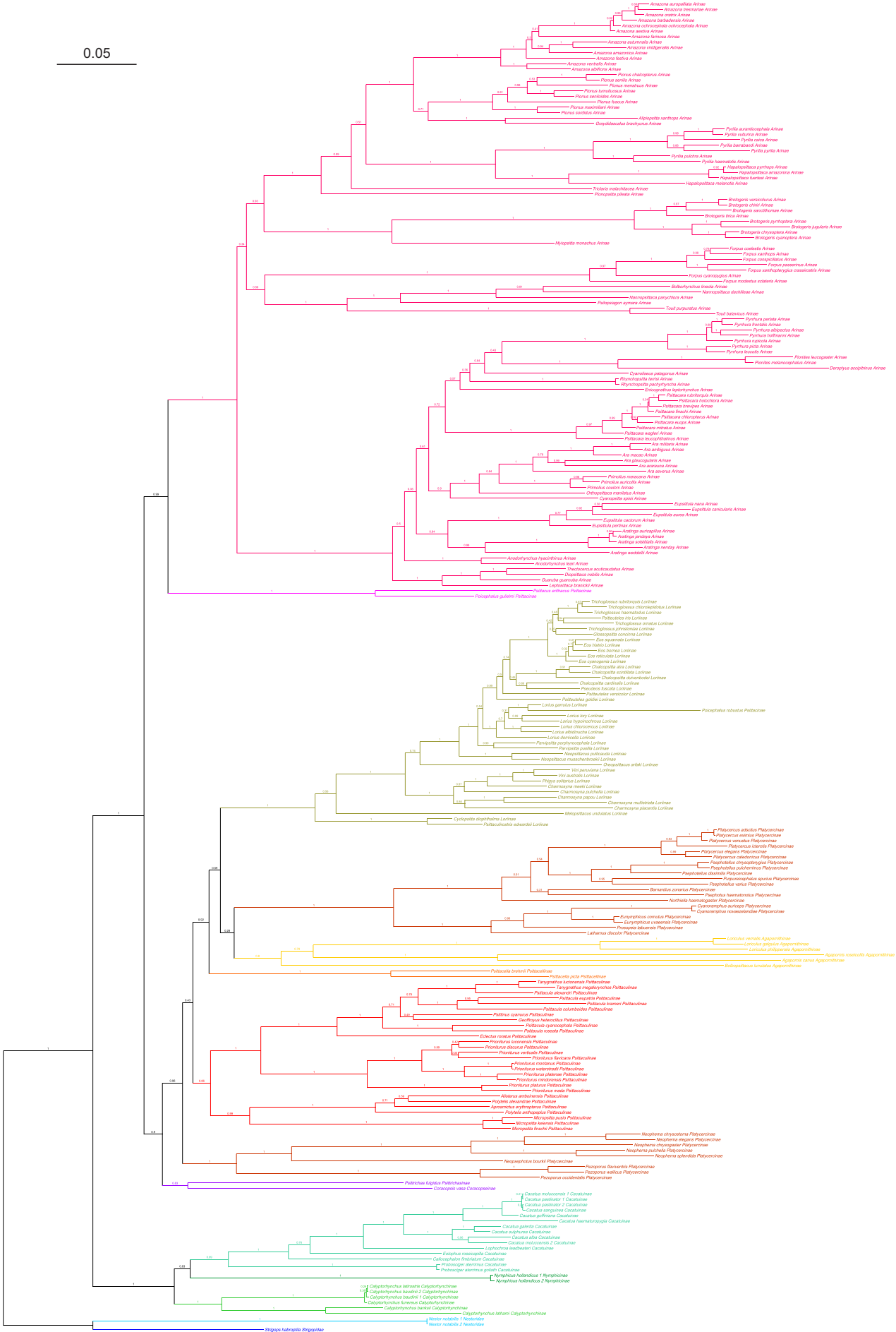


Figure S7. Phylogenetic tree (phylogram) obtained in MrBayes based on ND2 sequences. The values at nodes indicate posterior probabilities.

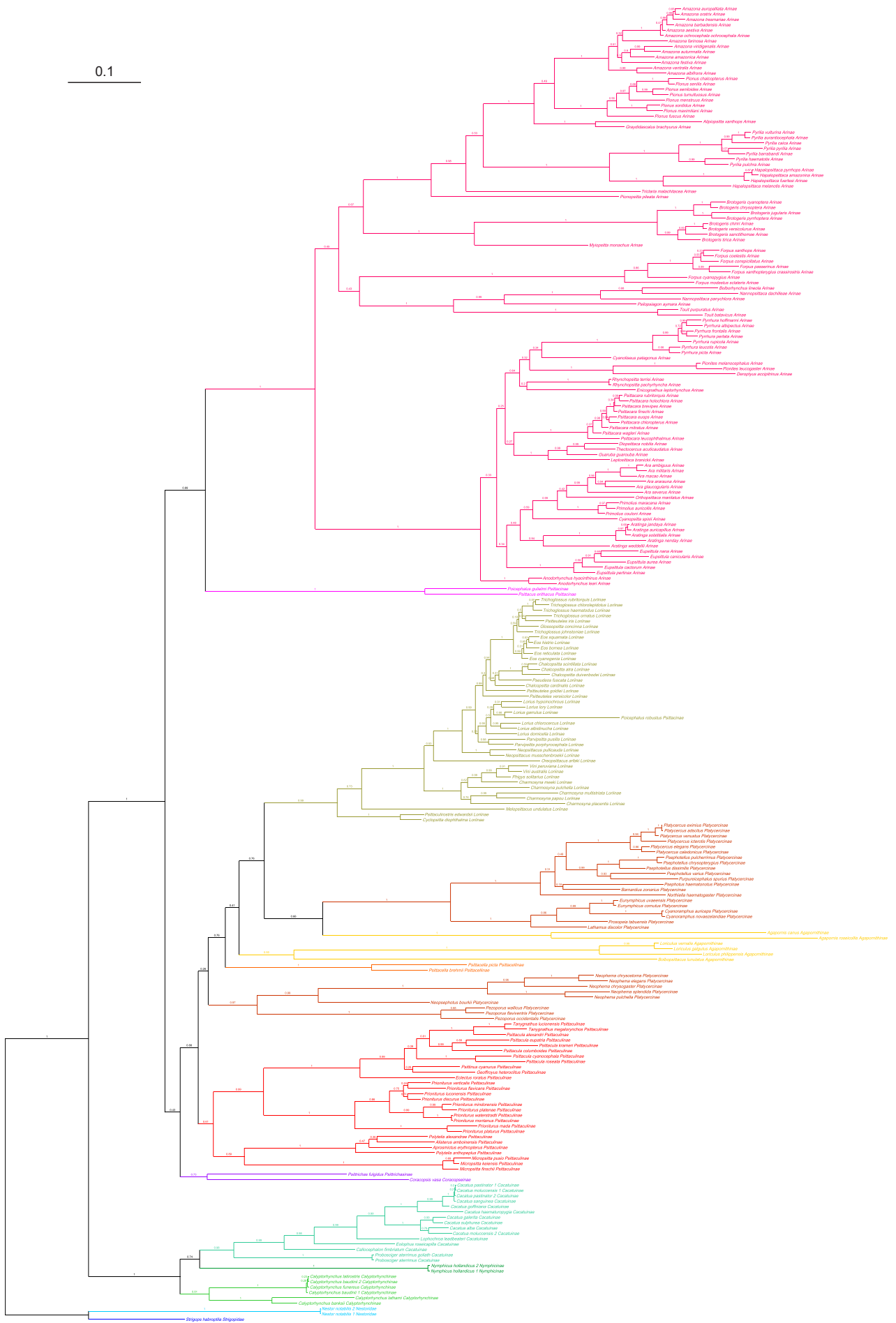


Figure S8. Phylogenetic tree (phylogram) obtained in PhyloBayes based on ND2 sequences. The values at nodes indicate posterior probabilities.



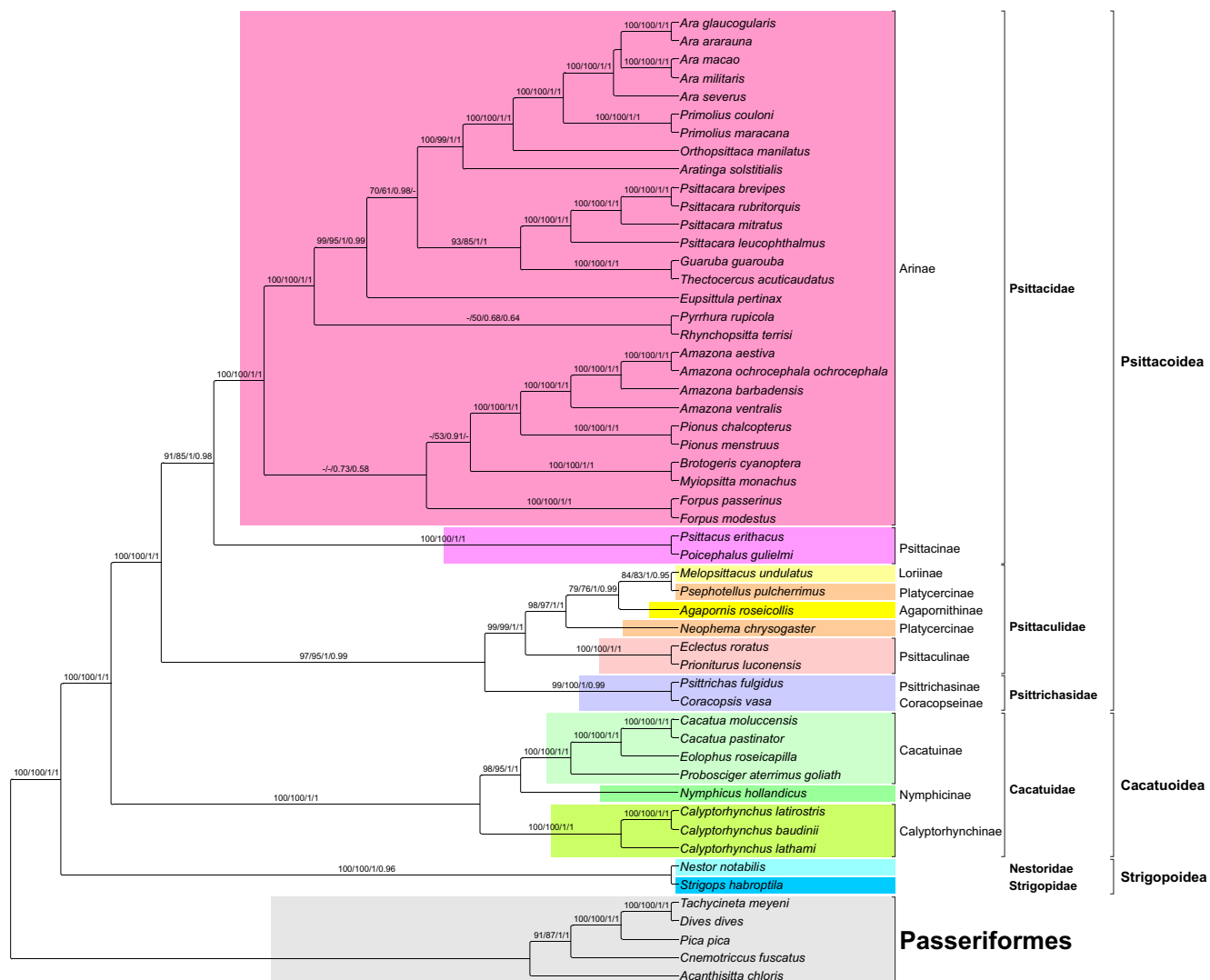


Figure S9. Phylogenetic tree (cladogram) obtained in IQ-Tree based on 37 mitochondrial genes. The values at nodes, in the order shown, indicate SH-aLRT (SH) and non-parametric bootstrap (BP) percentages calculated in IQ-TREE as well as posterior probabilities found in MrBayes (MB) and PhyloBayes (PB). The posterior probabilities < 0.5 and the percentages < 50% were omitted or indicated by a dash “-”.

0.05



Figure S10. Phylogenetic tree (phylogram) obtained in IQ-Tree based on 37 mitochondrial genes. The values at nodes, in the order shown, indicate SH-aLRT (SH) and non-parametric bootstrap (BP) percentages.

0.05

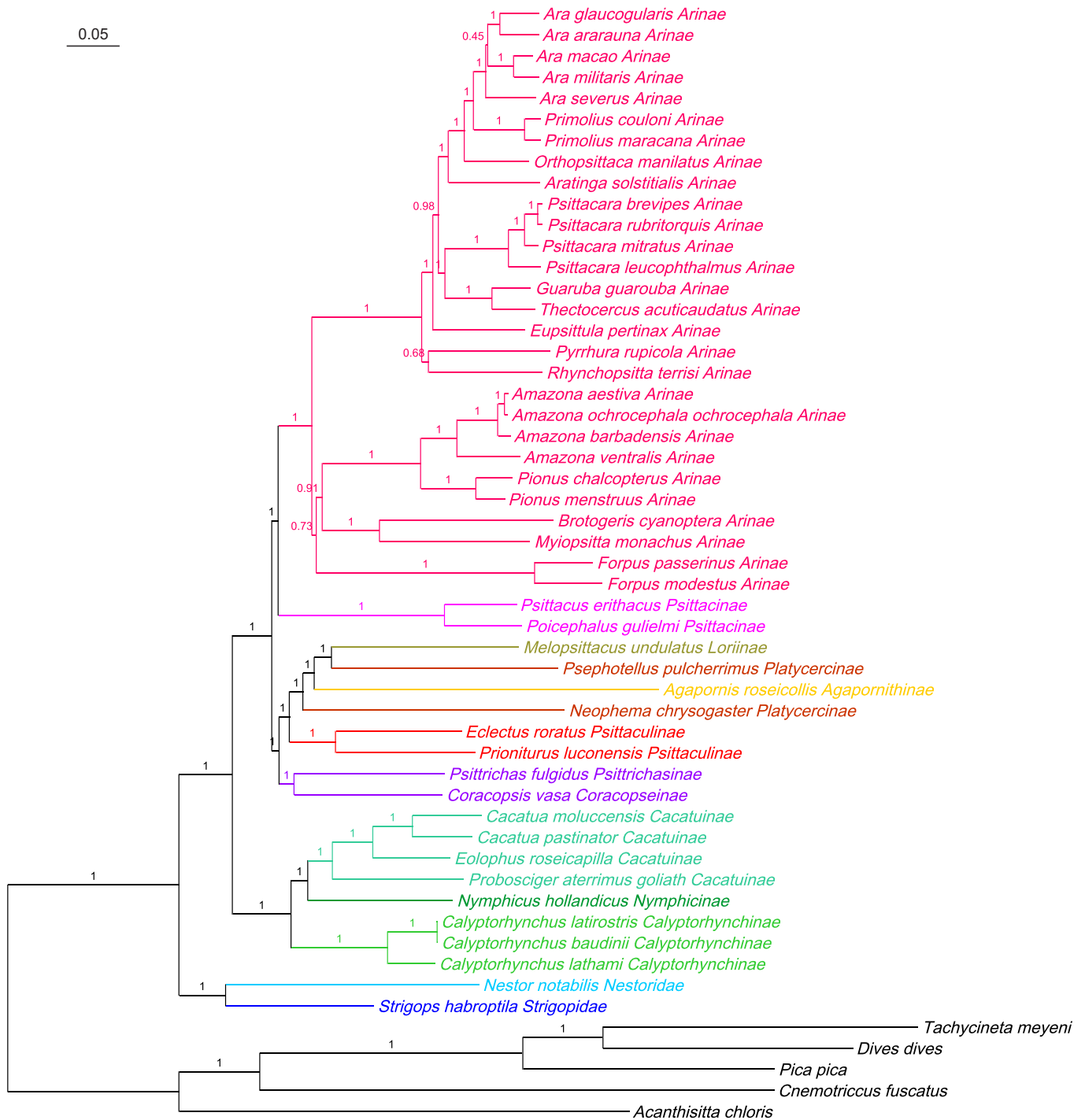


Figure S11. Phylogenetic tree (phylogram) obtained in MrBayes based on 37 mitochondrial genes. The values at nodes indicate posterior probabilities.

0.1

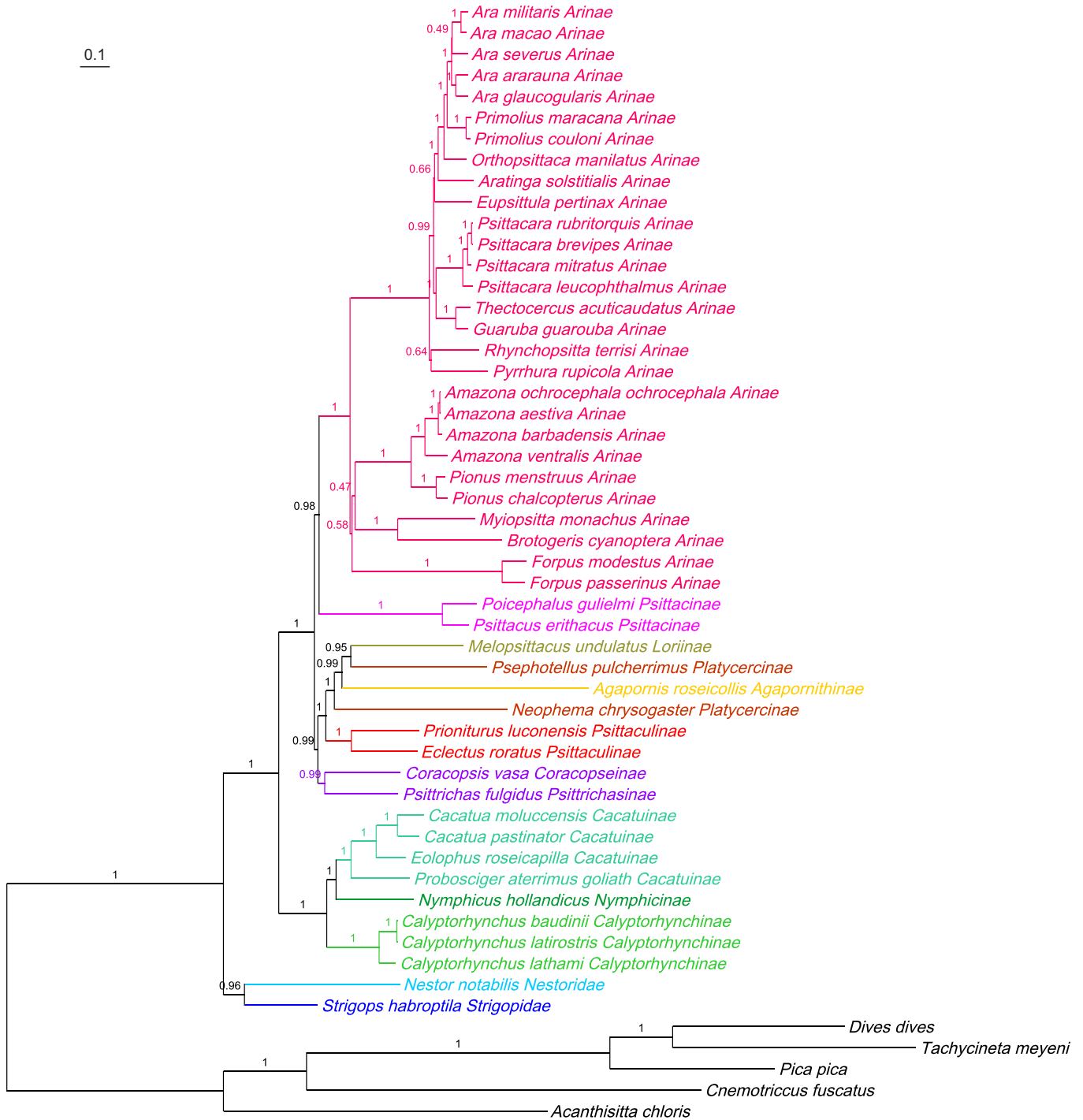


Figure S12. Phylogenetic tree (phylogram) obtained in PhyloBayes based on 37 mitochondrial genes. The values at nodes indicate posterior probabilities.



