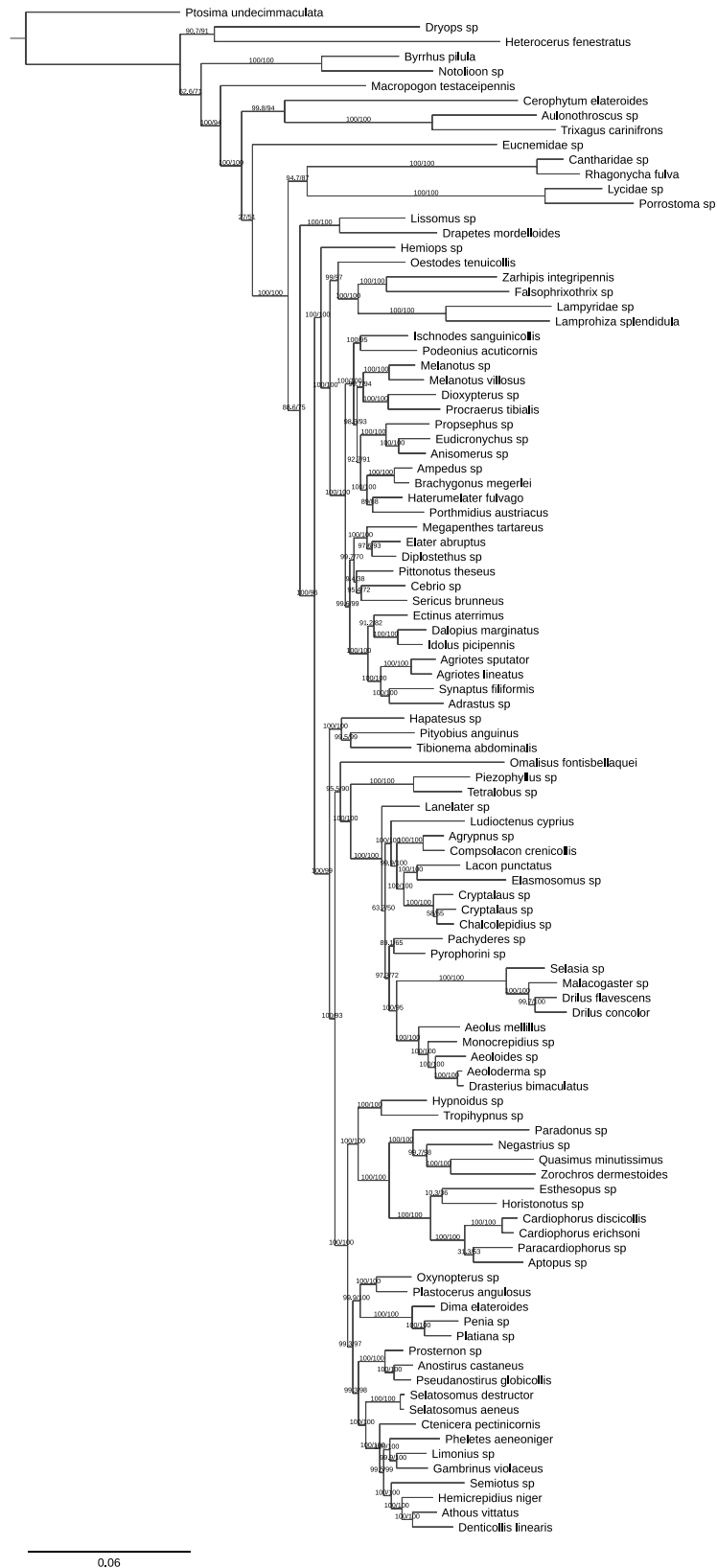
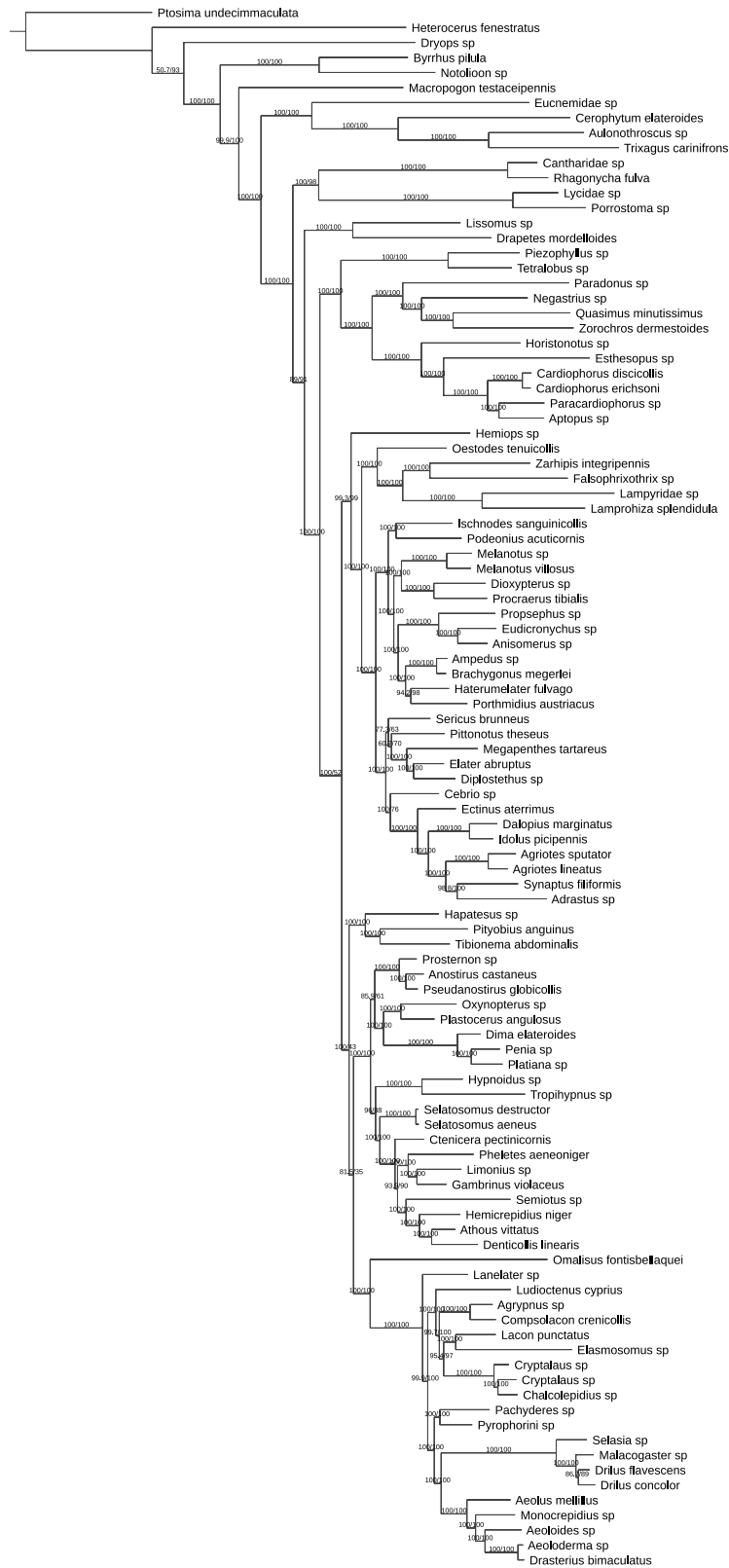


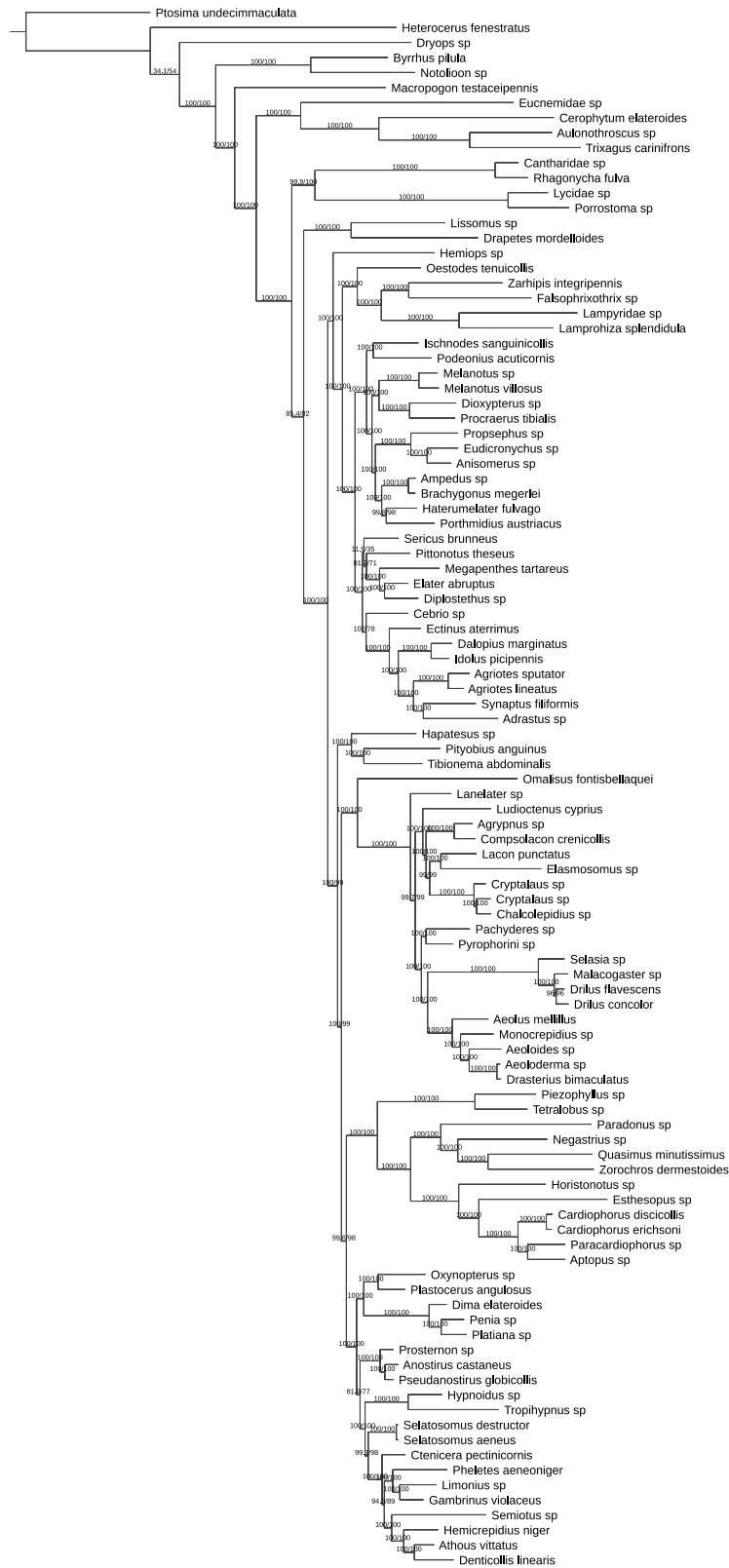
Phylogeny inferred from maximum likelihood analysis of unpartitioned, concatenated amino acid data, 50% completeness matrix (50CU-AA)



Phylogeny inferred from maximum likelihood analysis of partitioned, concatenated amino acid data, 50% completeness matrix (50CP-AA)

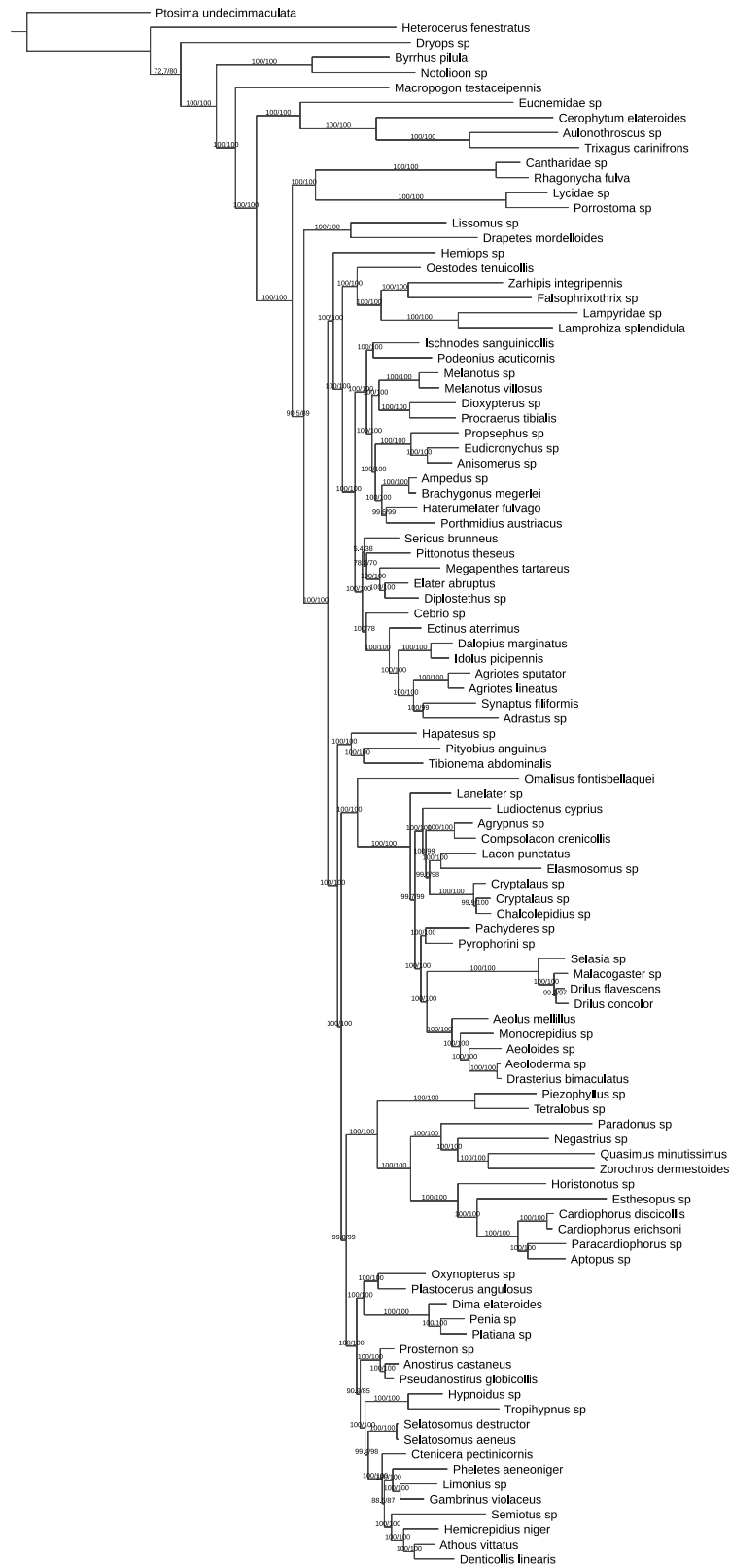


Phylogeny inferred from maximum likelihood analysis of unpartitioned, concatenated nucleotide data, 50% completeness matrix (50CU)

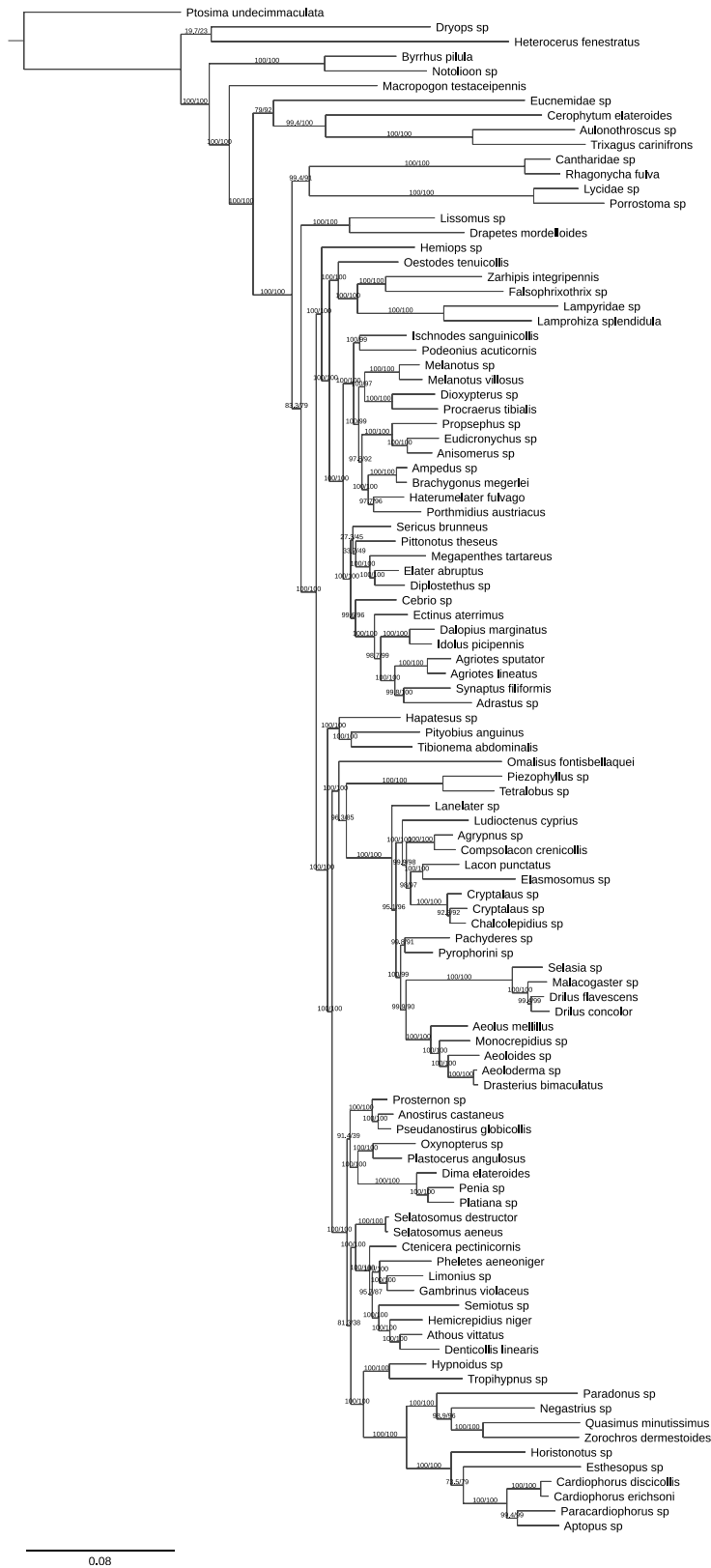


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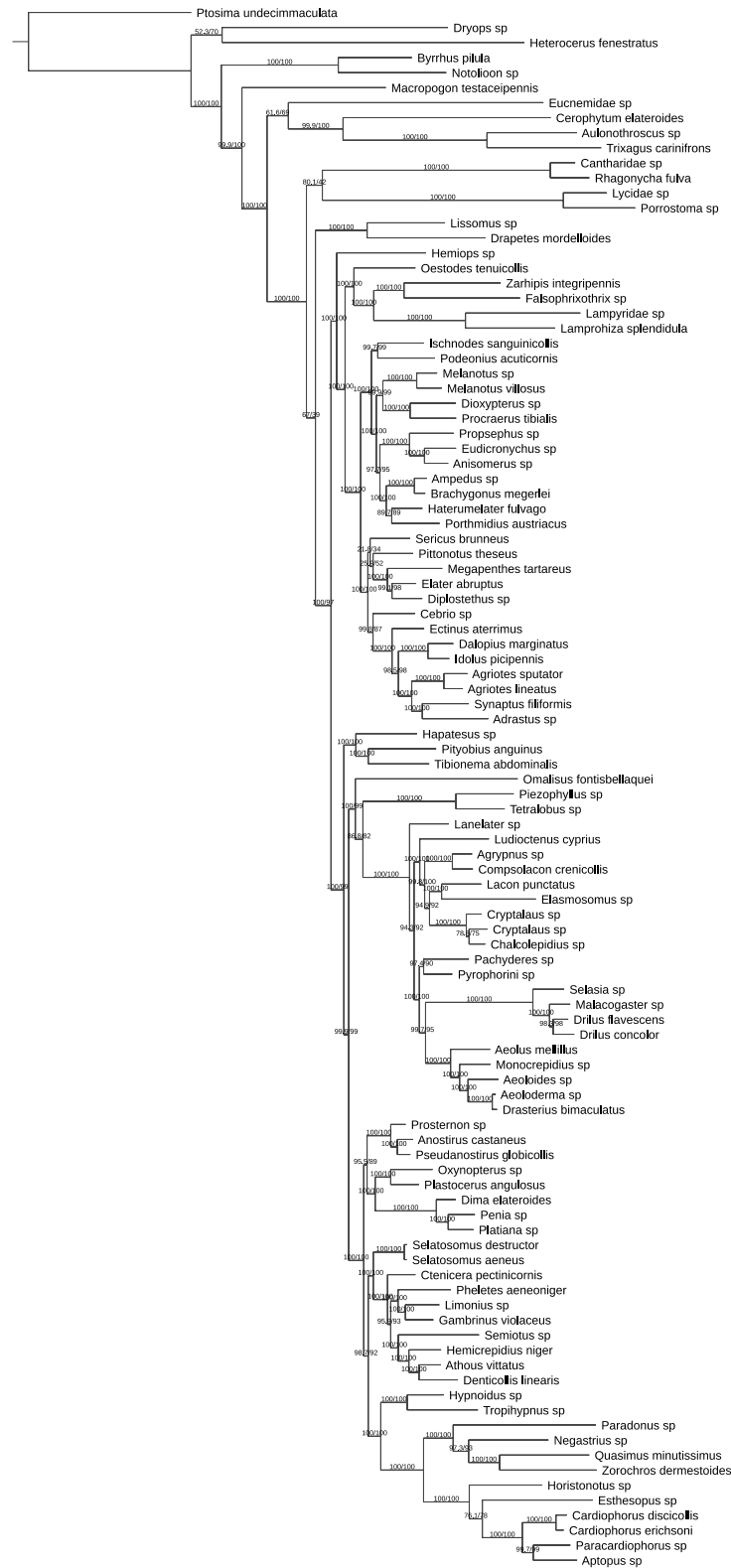
Phylogeny inferred from maximum likelihood analysis of partitioned, concatenated nucleotide data, 50% completeness matrix (50CP)



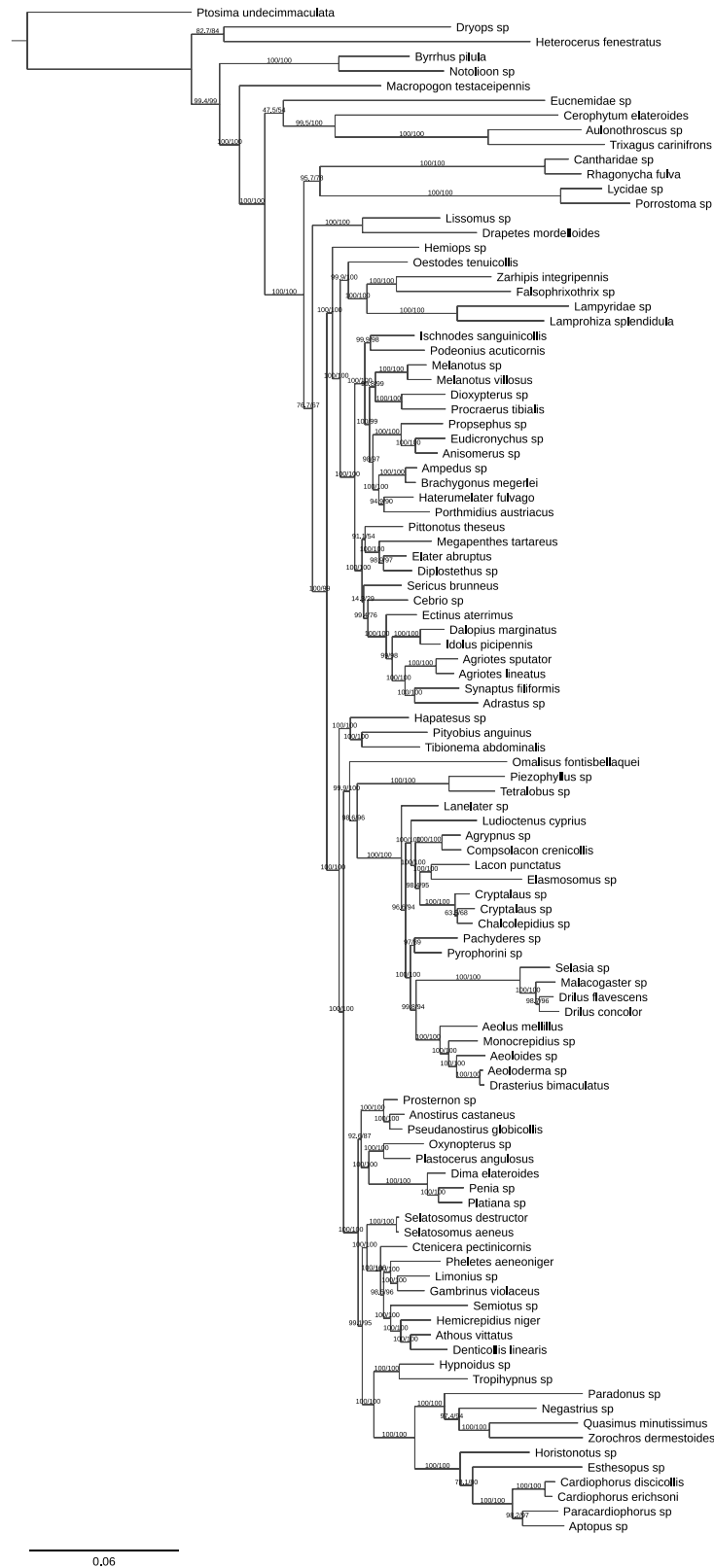
Phylogeny inferred from maximum likelihood analysis of partitioned, concatenated nucleotide data with flanking regions added, 50% completeness matrix (50CPF)



Phylogeny inferred from maximum likelihood analysis of partitioned, concatenated nucleotide data with flanking regions added and third codon positions removed, 50% completeness matrix (50CPF-No3)

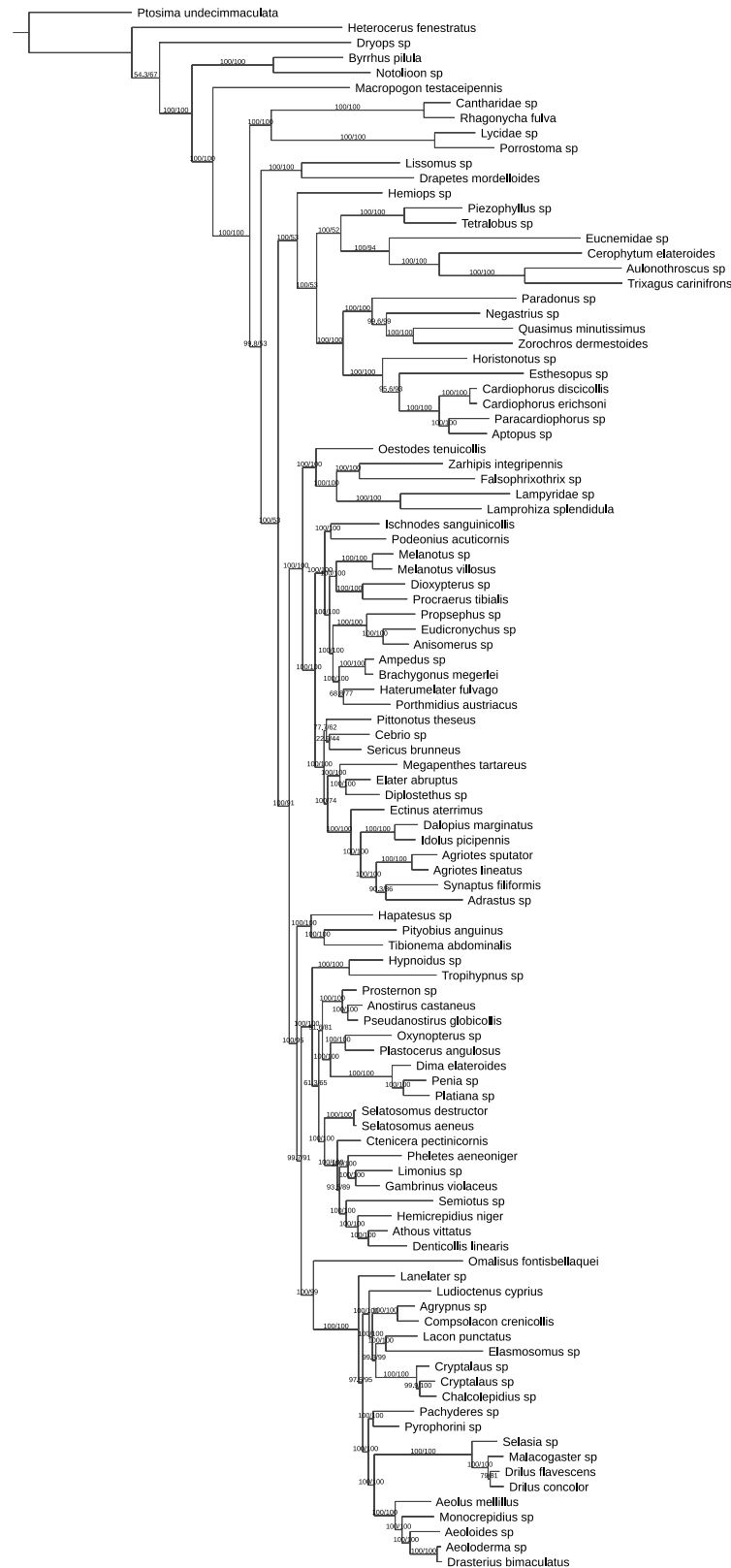


Phylogeny inferred from maximum likelihood analysis of unpartitioned, concatenated nucleotide data with third codon positions removed, 50% completeness matrix (50CU-No3)

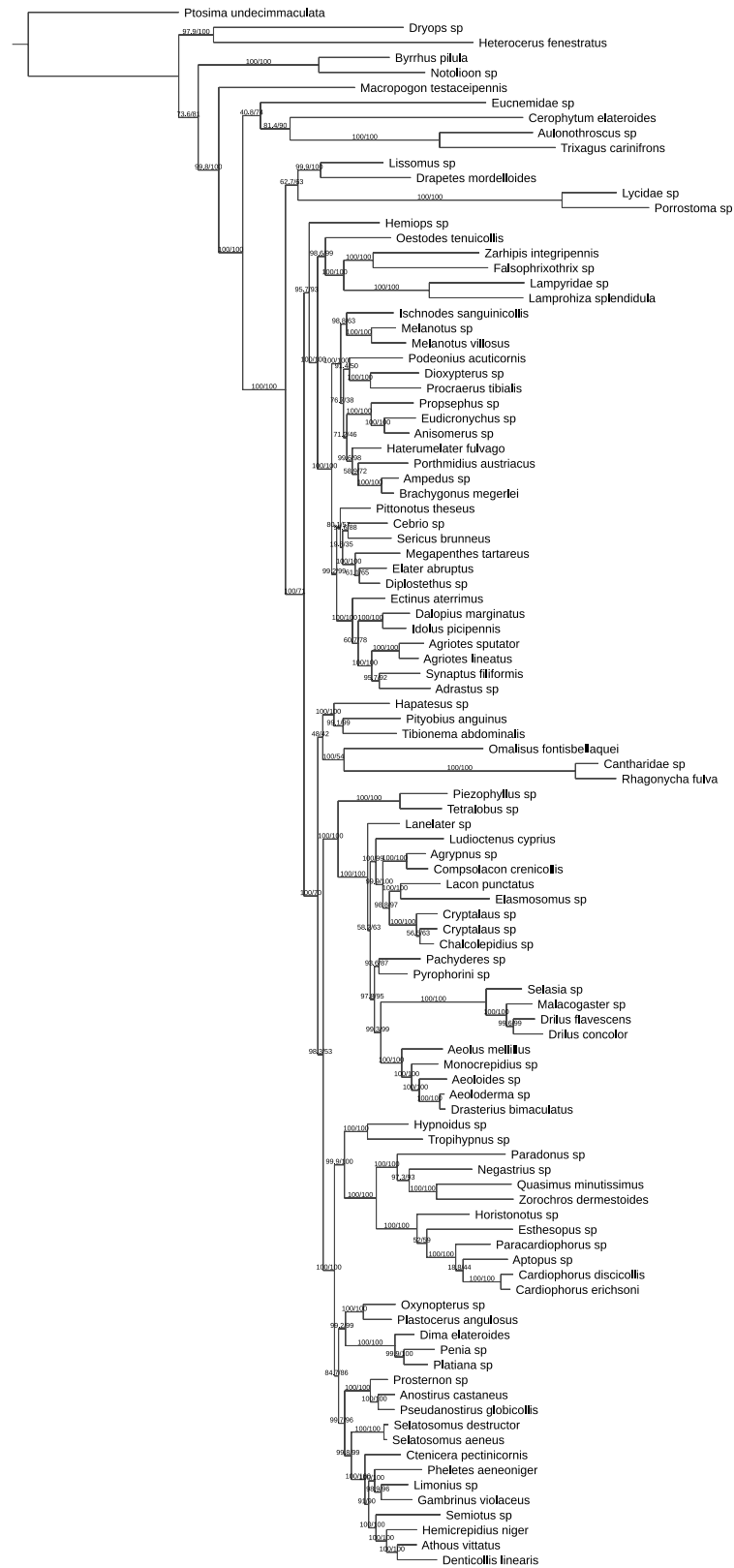


Phylogeny inferred from maximum likelihood analysis of partitioned, concatenated nucleotide data with third codon positions removed, 50% completeness matrix (50CP-No3)

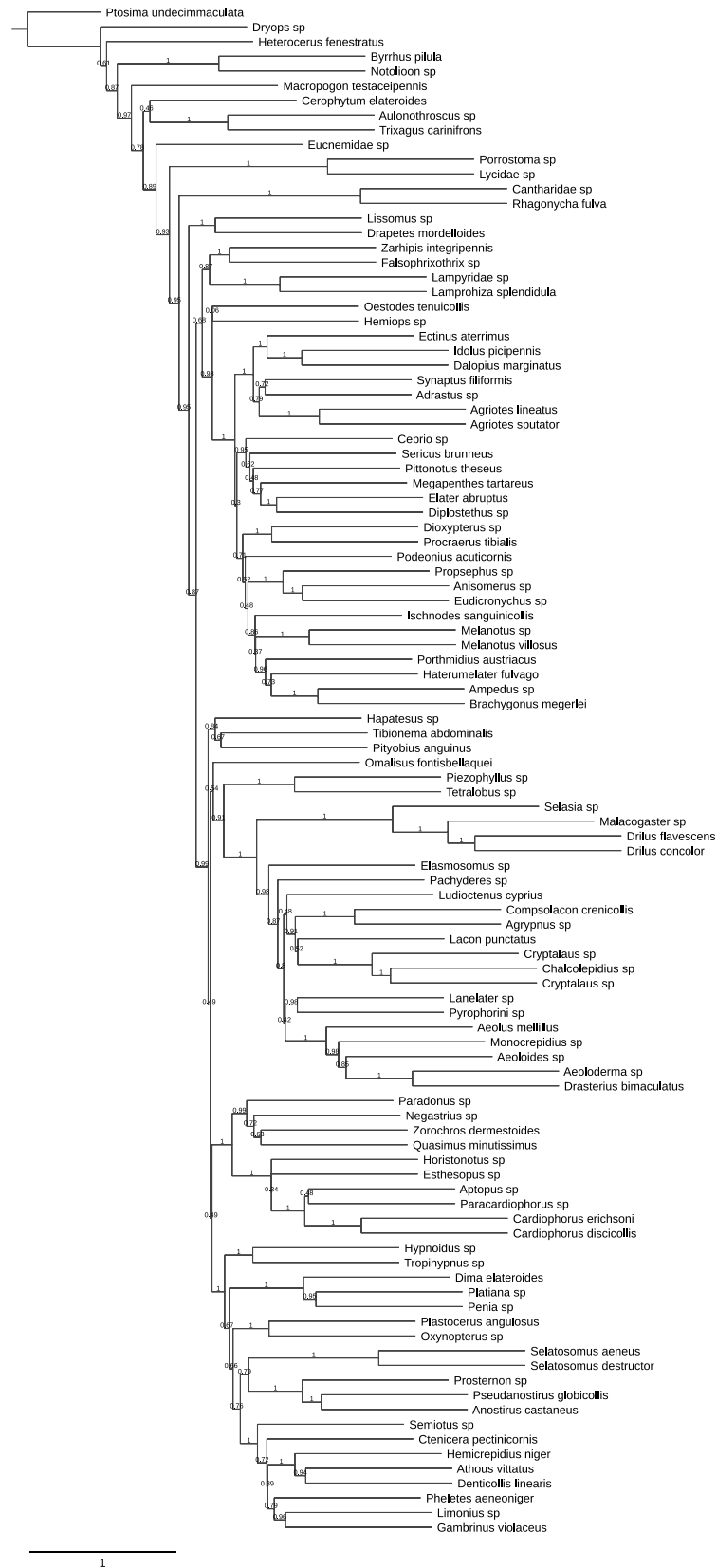




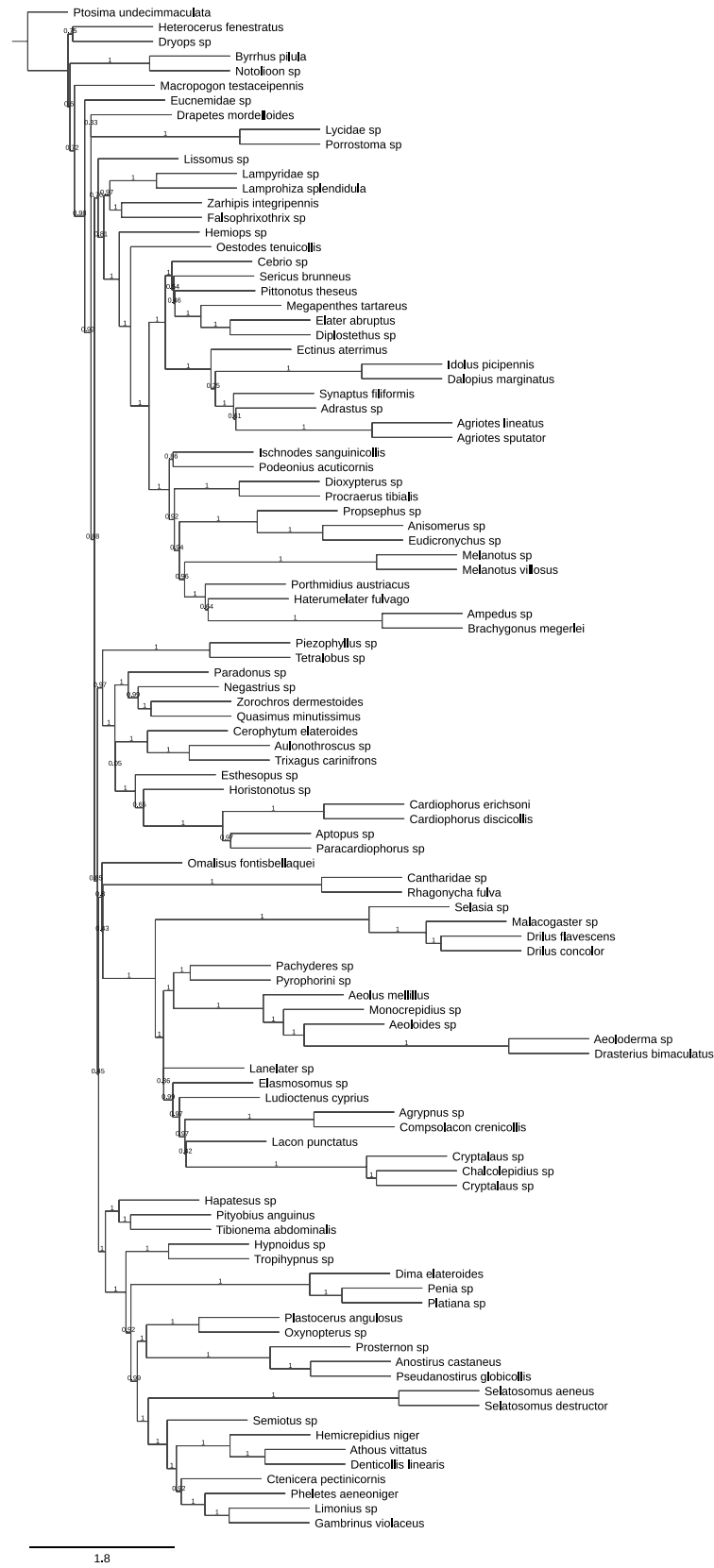
Phylogeny inferred from maximum likelihood analysis of partitioned, concatenated nucleotide data with flanking regions added, 75% completeness matrix (75CPF)



Phylogeny inferred from maximum likelihood analysis of unpartitioned, concatenated amino acid data, 75% completeness matrix (75CU-AA)



Phylogeny inferred from coalescent analysis (ASTRAL-III) of amino acid data, 50% completeness matrix (Astral50-AA)



Phylogeny inferred from coalescent analysis (ASTRAL-III) of nucleotide data, 50% completeness matrix (Astral50)