

Fig. S1. Maximum likelihood tree based on nucleotides; partitioning by gene and GTR substitution model for all partitions

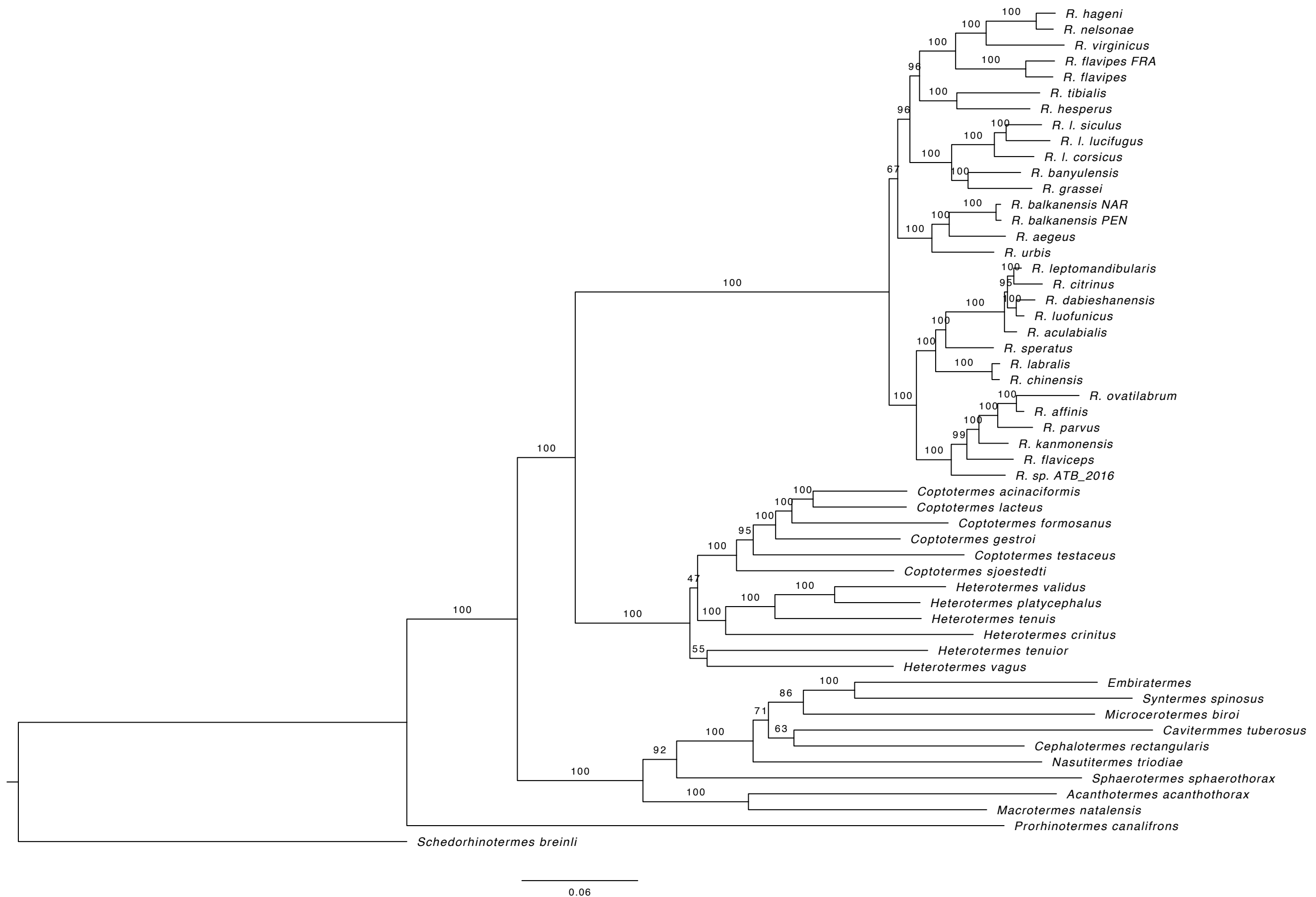


Fig. S2. Maximum likelihood tree based on nucleotides; partitioning by gene and best substitution models estimated by Model Finder

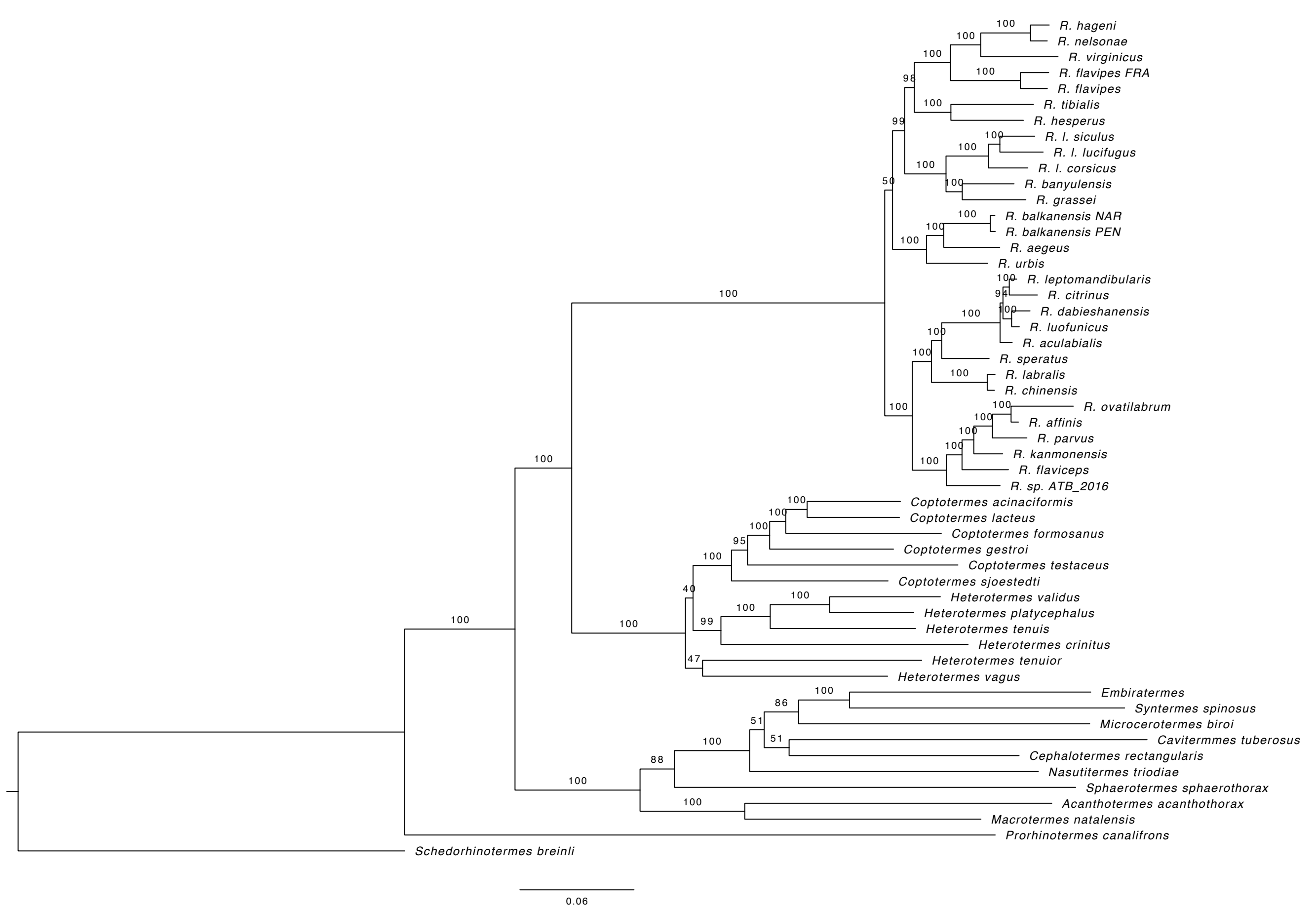


Fig. S3. Maximum likelihood tree based on nucleotides; partitioning by gene, allowing merging of partitions and best substitution models estimated by Model Finder

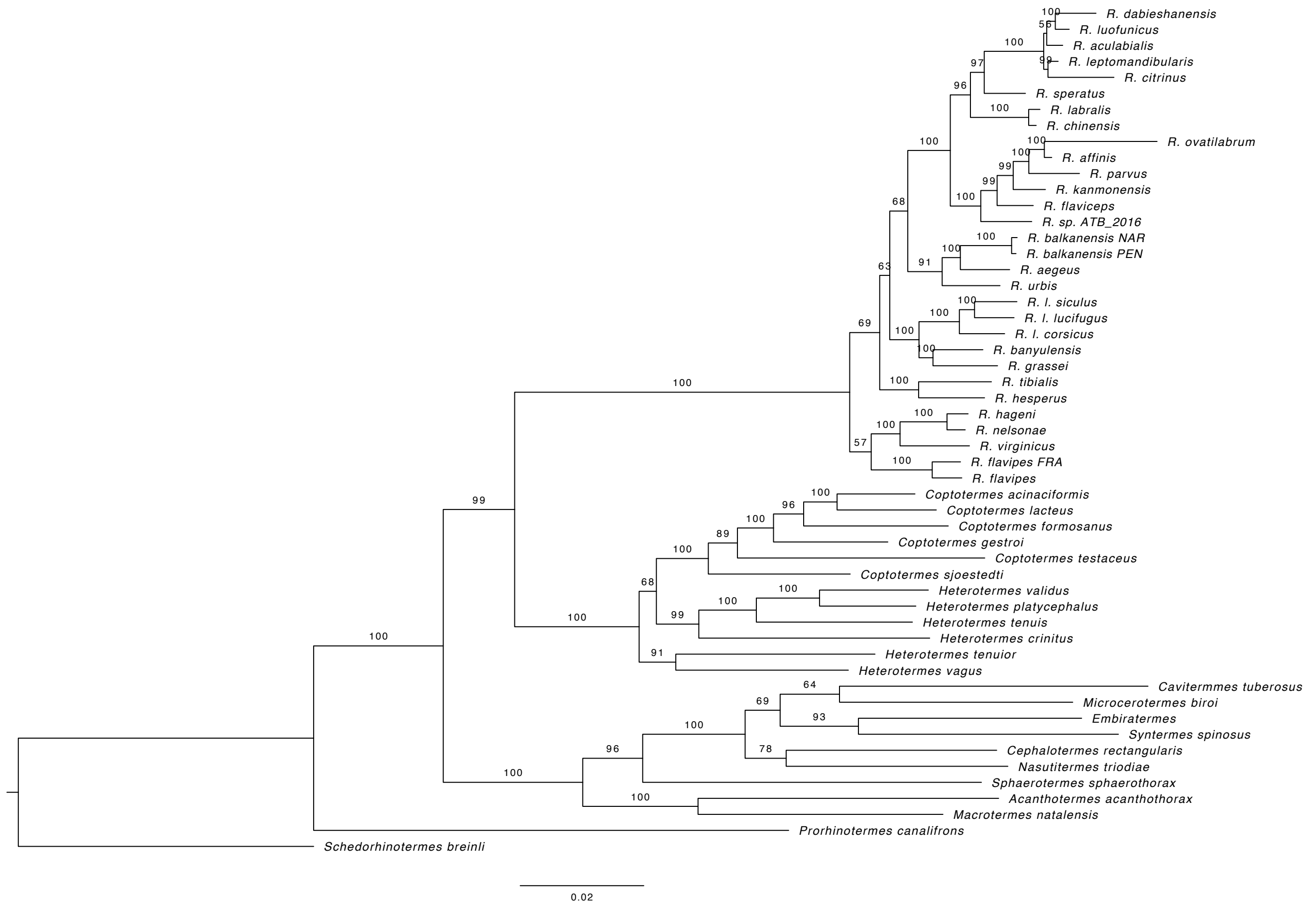


Fig. S4. Maximum likelihood tree based on nucleotides; partitioning by gene, excluding the 3rd codon position, and GTR substitution model for all partitions

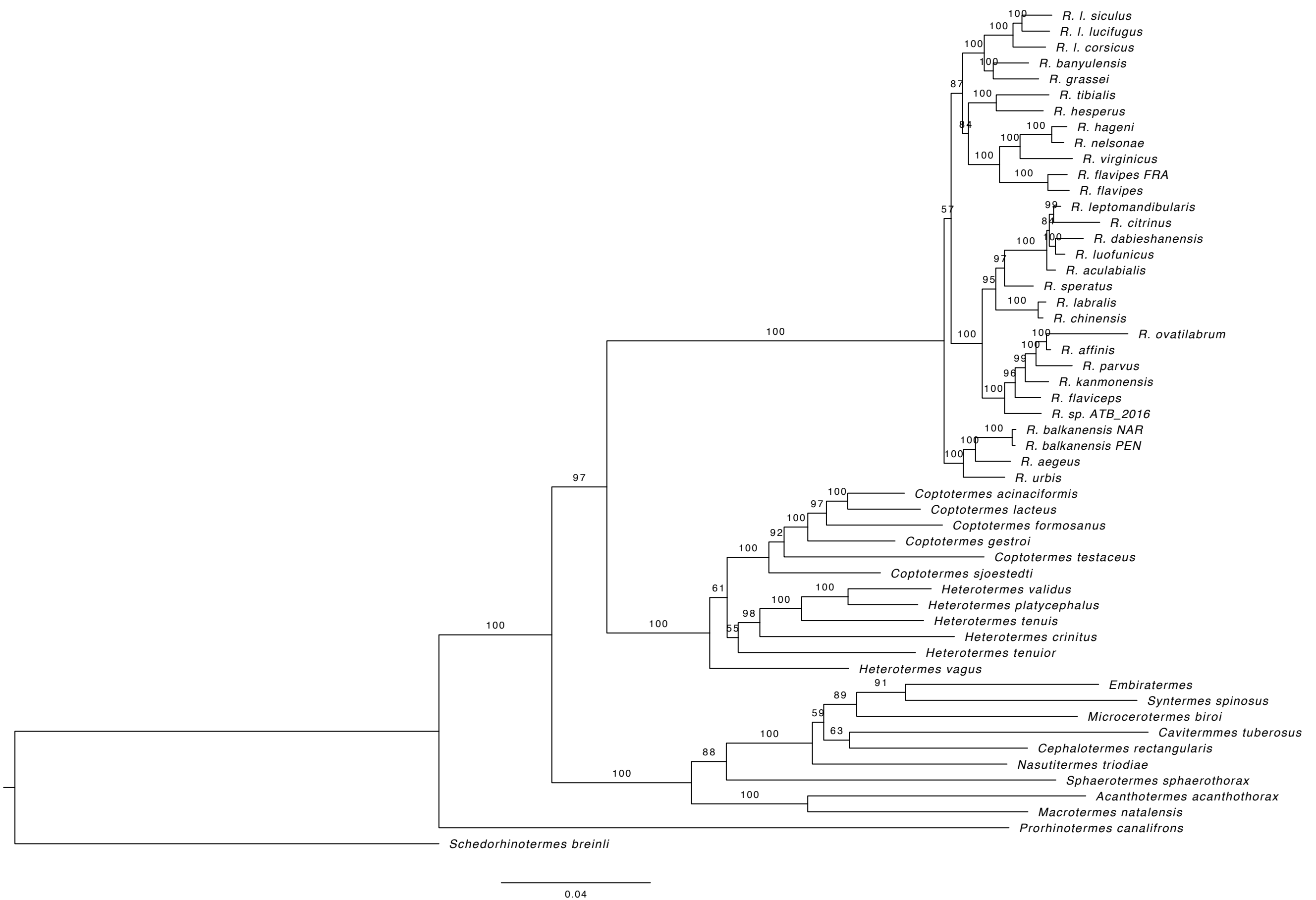


Fig. S5. Maximum likelihood tree based on nucleotides; partitioning by gene, excluding the 3rd codon position, and best substitution models estimated by Model Finder

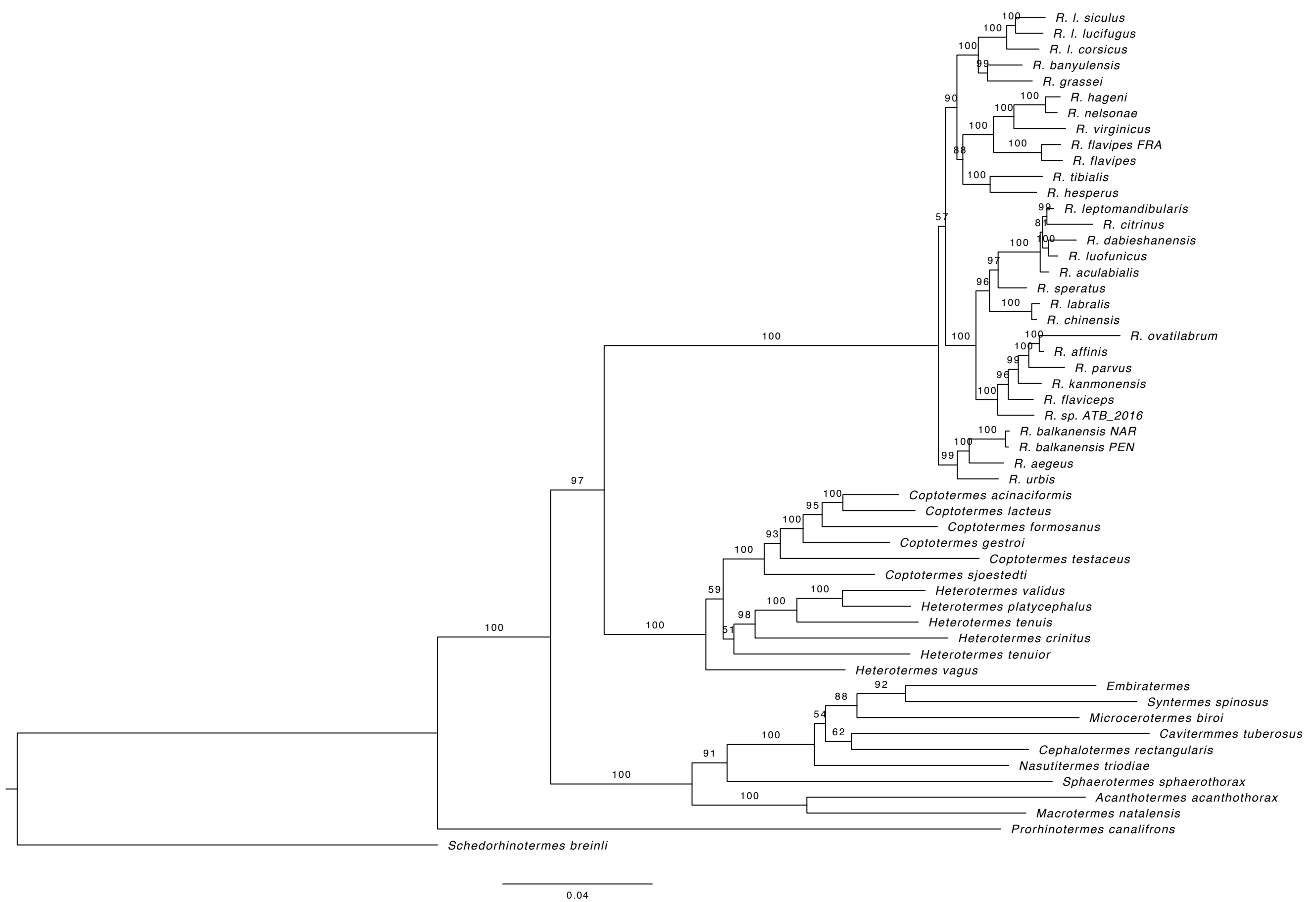


Fig. S6. Maximum likelihood tree based on nucleotides; partitioning by gene, excluding the 3rd codon position, allowing merging of partitions and best substitution models estimated by Model Finder

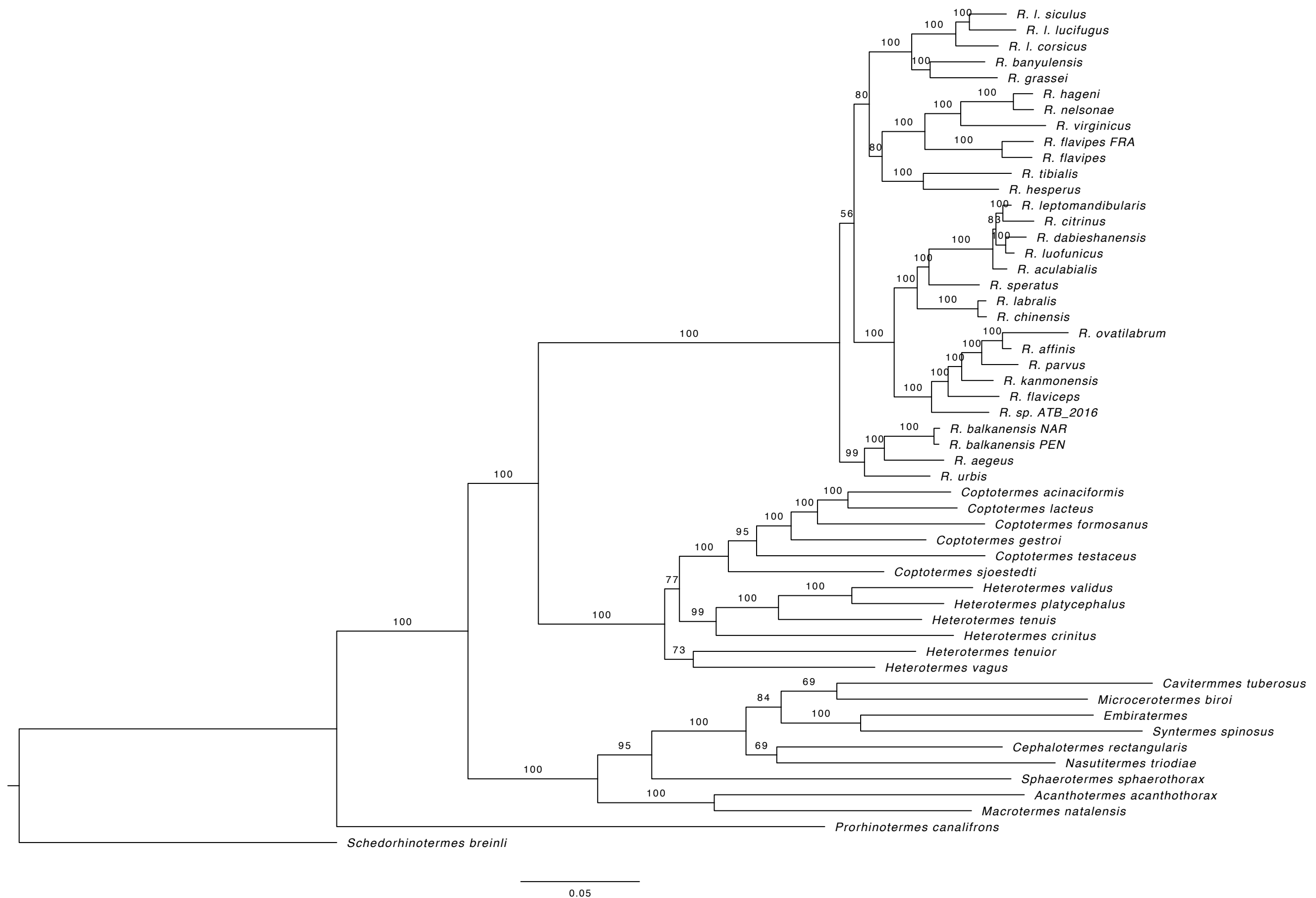


Fig. S7. Maximum likelihood tree based on nucleotides; partitioning by codon positions and GTR substitution model for all partitions

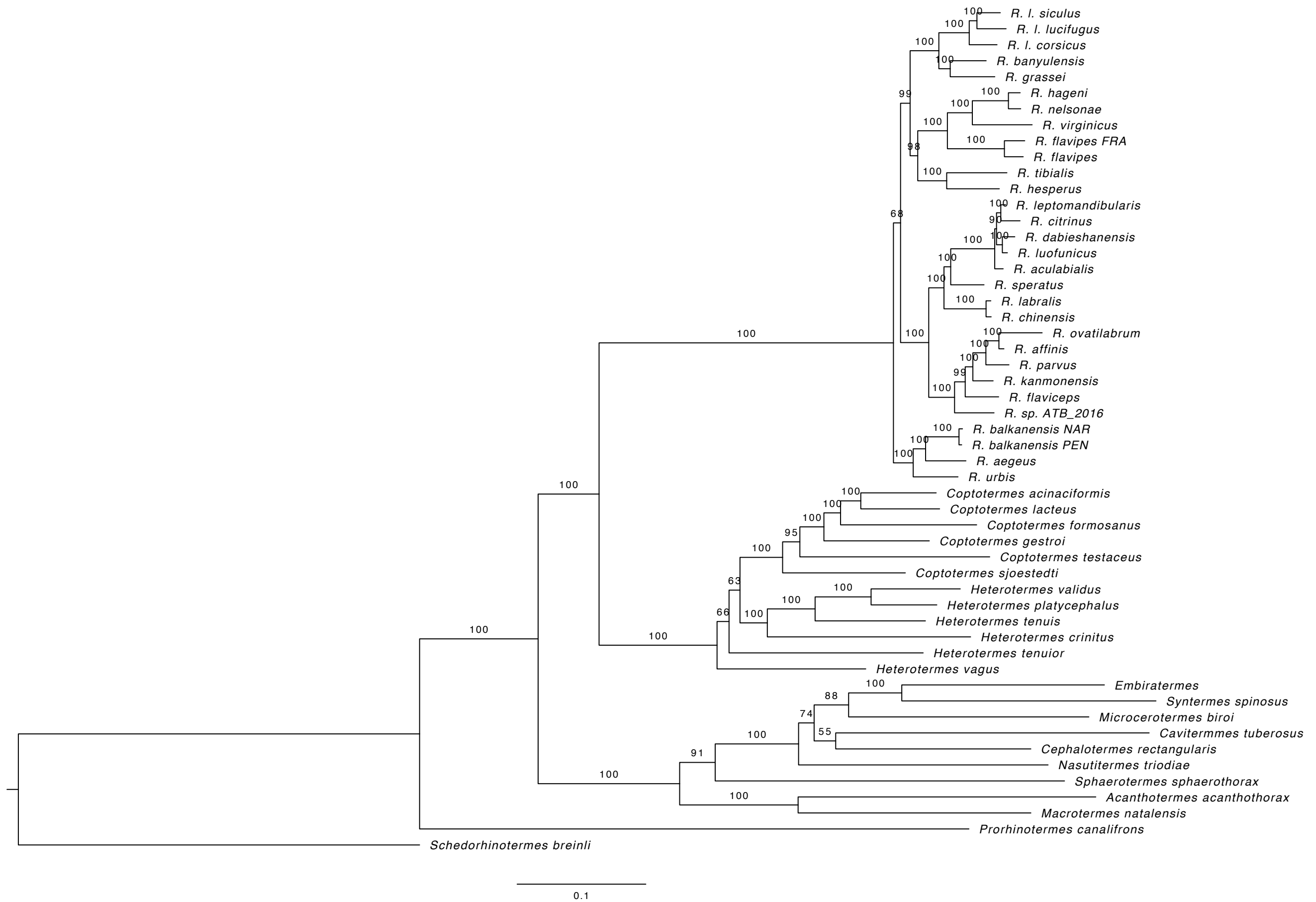


Fig. S8. Maximum likelihood tree based on nucleotides; partitioning by codon positions and best substitution models estimated by Model Finder



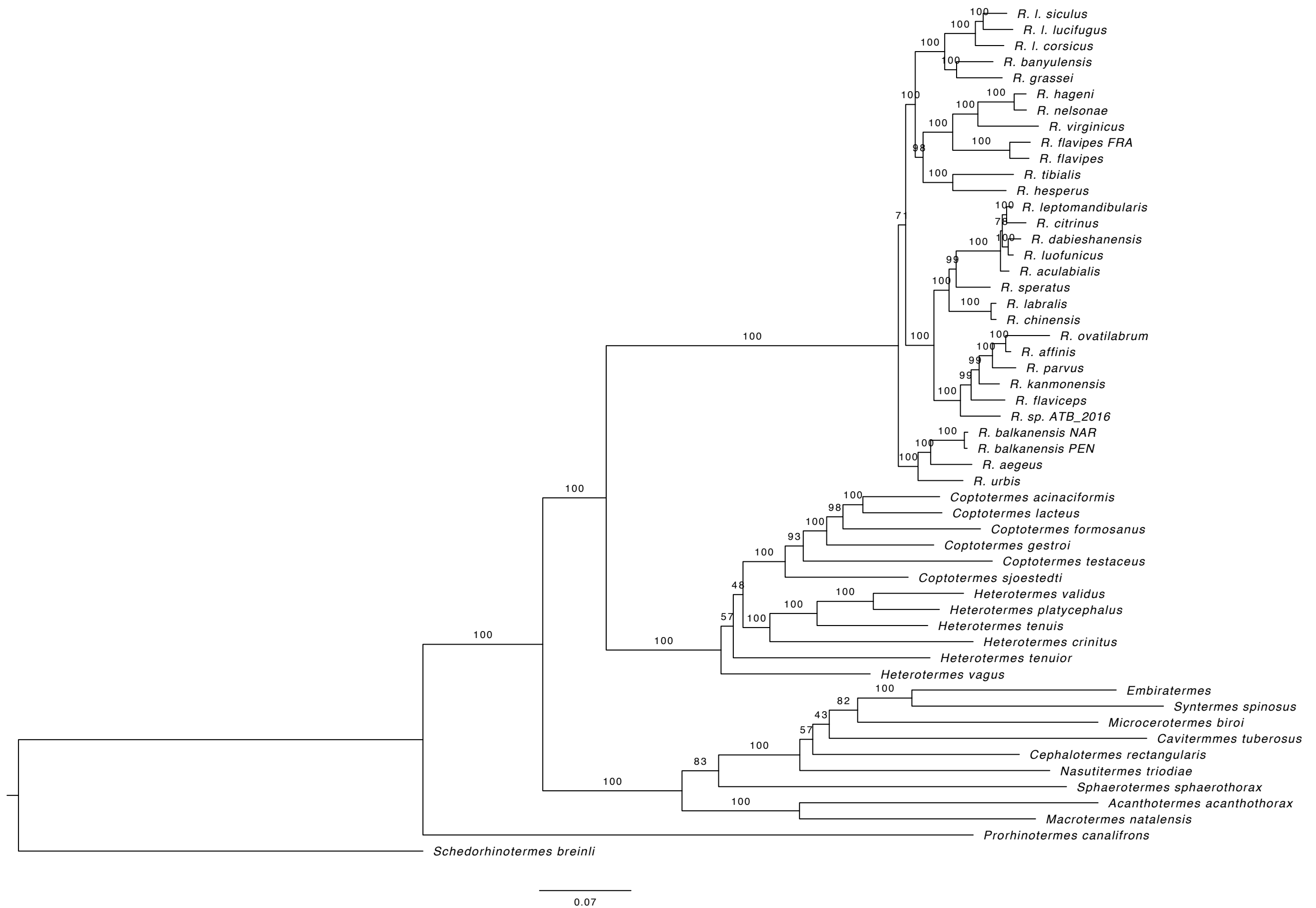


Fig. S9. Maximum likelihood tree based on nucleotides; partitioning by codon positions, allowing merging of partitions and best substitution models estimated by Model Finder

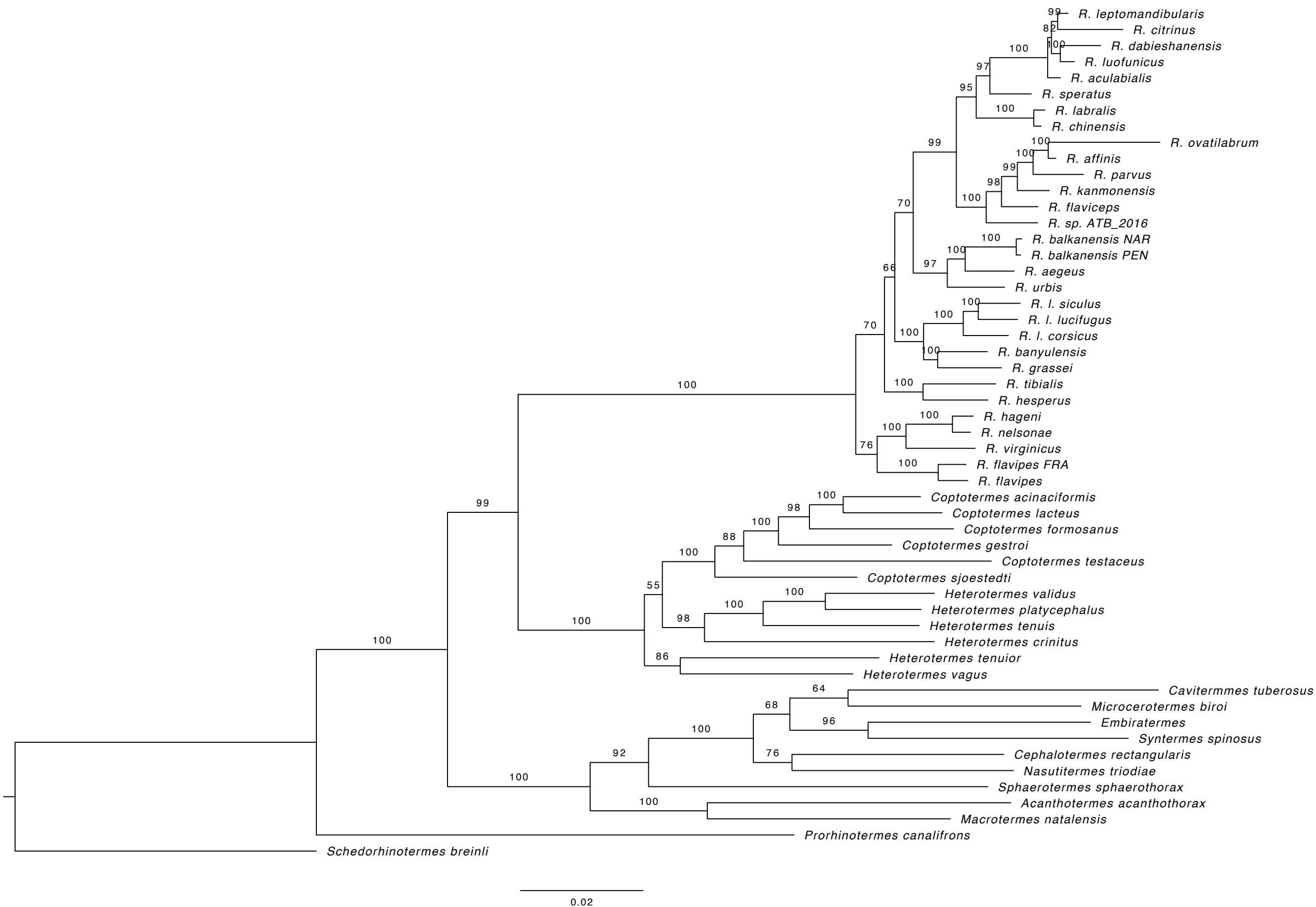


Fig. S10. Maximum likelihood tree based on nucleotides; partitioning by codon positions, excluding the 3rd codon position, and GTR substitution model for all partitions

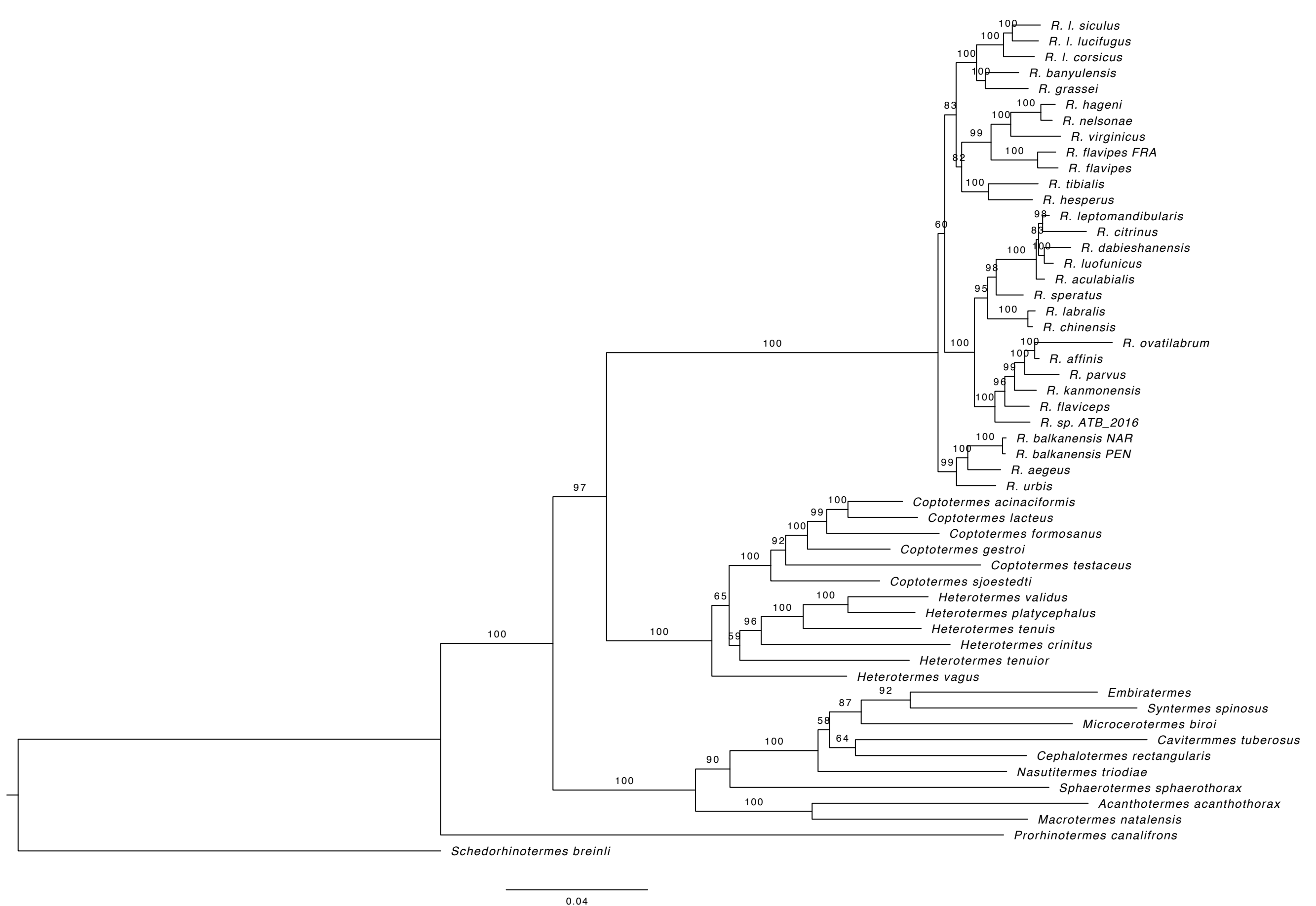


Fig. S11. Maximum likelihood tree based on nucleotides; partitioning by codon positions, excluding the 3rd codon position, and best substitution models estimated by Model Finder

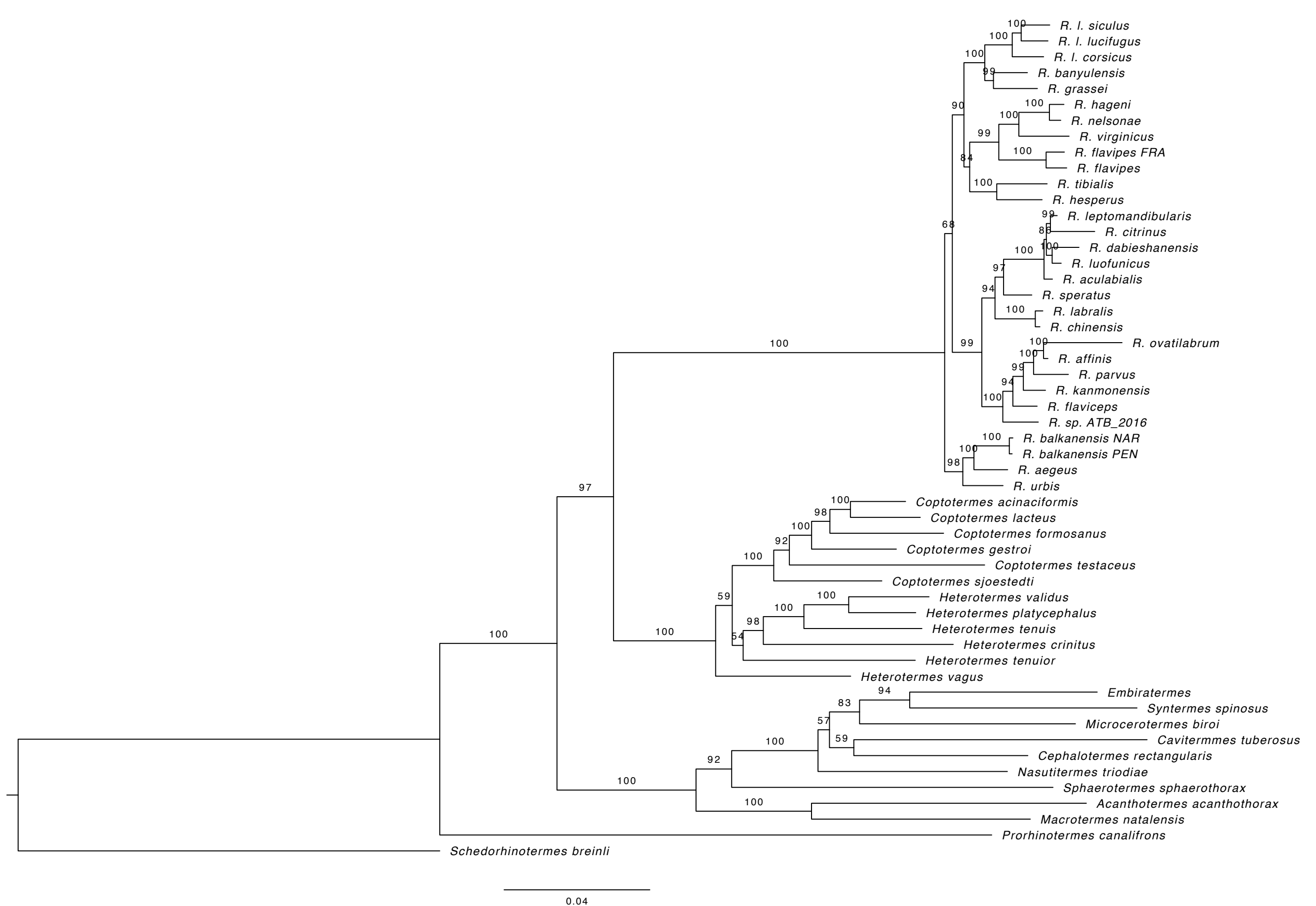


Fig. S12. Maximum likelihood tree based on nucleotides; partitioning by codon positions, excluding the 3rd codon position, allowing merging of partitions and best substitution models estimated by Model Finder

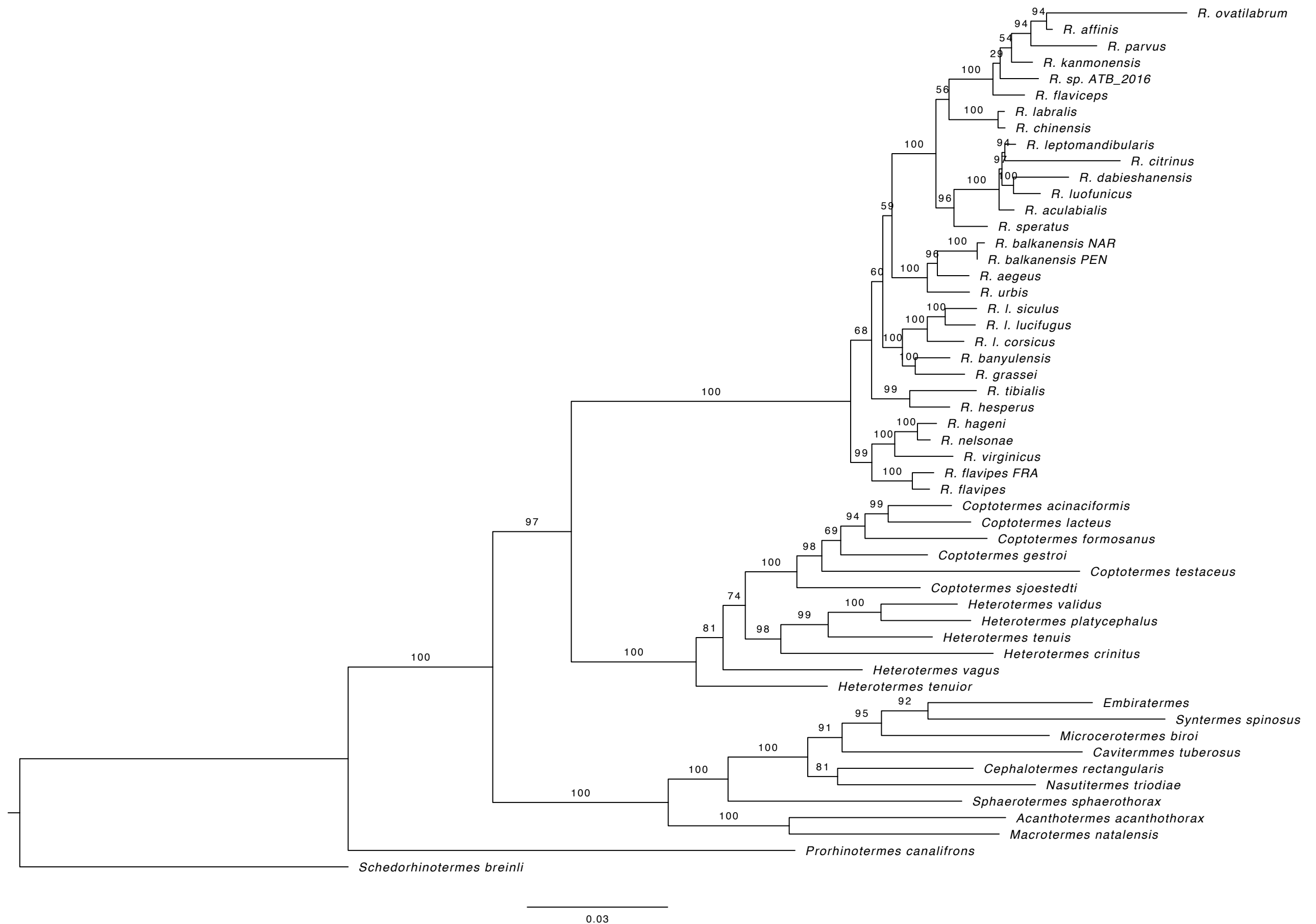


Fig. S13. Maximum likelihood tree based on amino acids; partitioning by gene and LG substitution model for all partitions

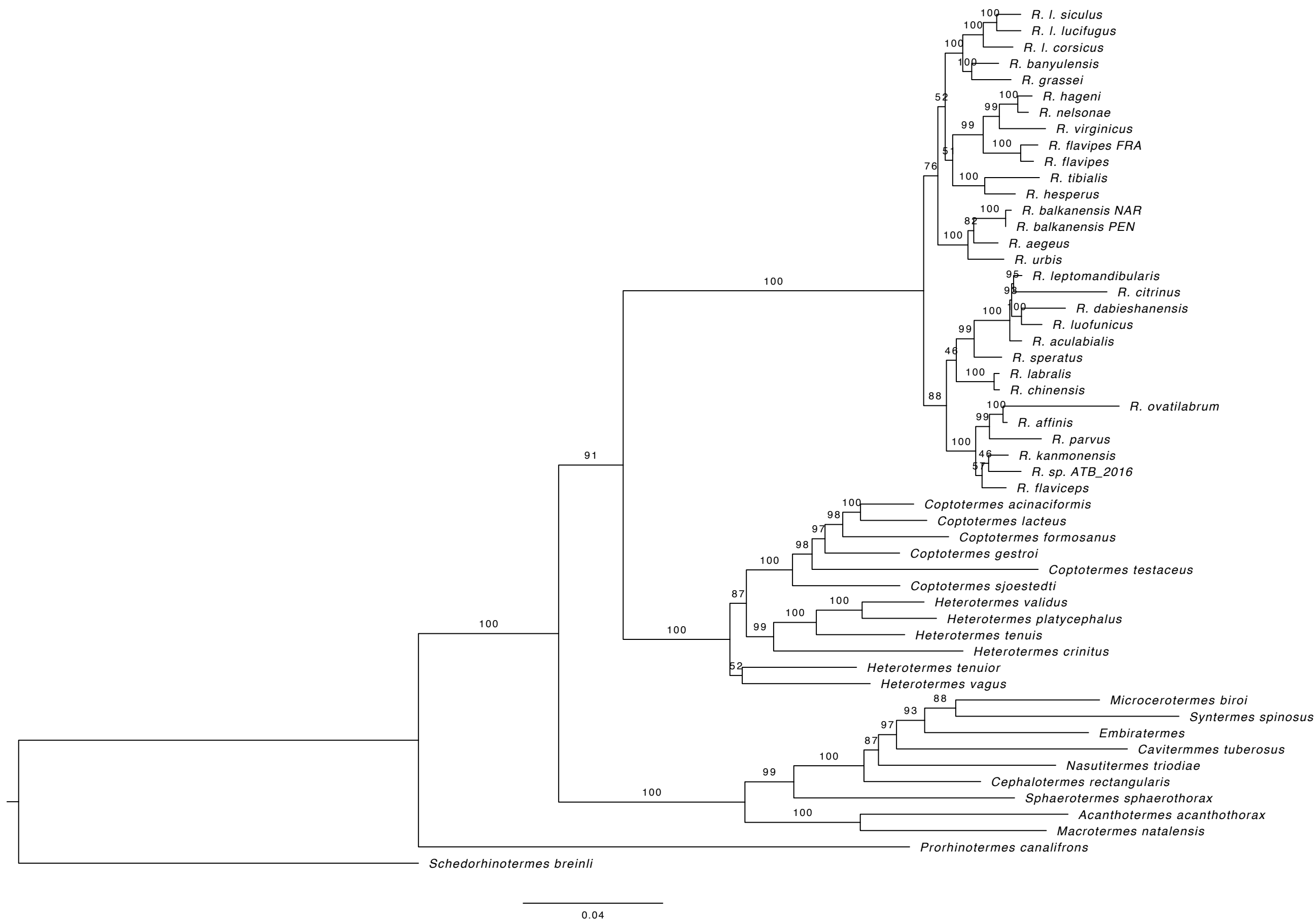


Fig. S14. Maximum likelihood tree based on amino acids; partitioning by gene and best substitution models estimated by Model Finder

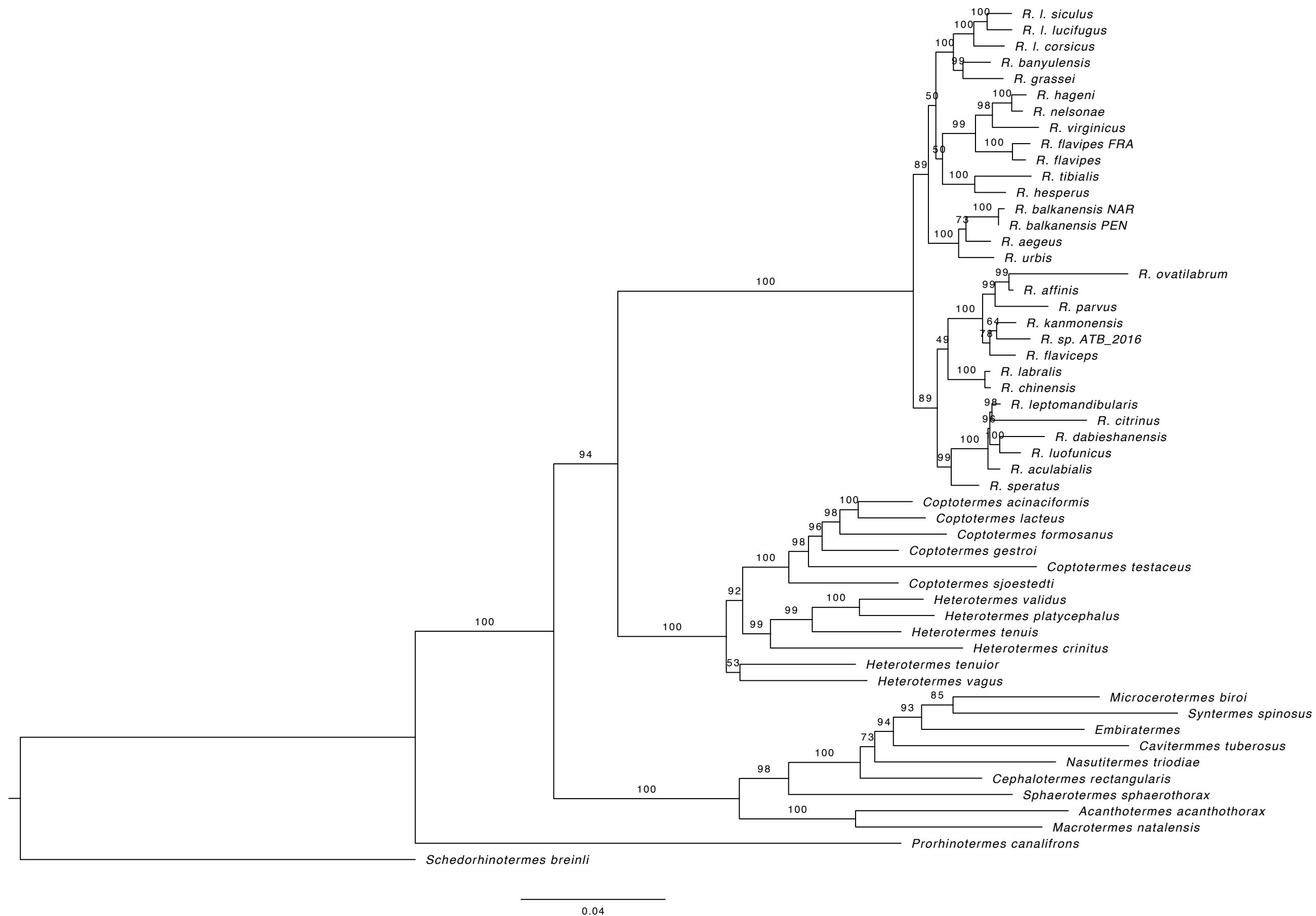


Fig. S15. Maximum likelihood tree based on amino acids; partitioning by gene, allowing merging of partitions and best substitution models estimated by Model Finder

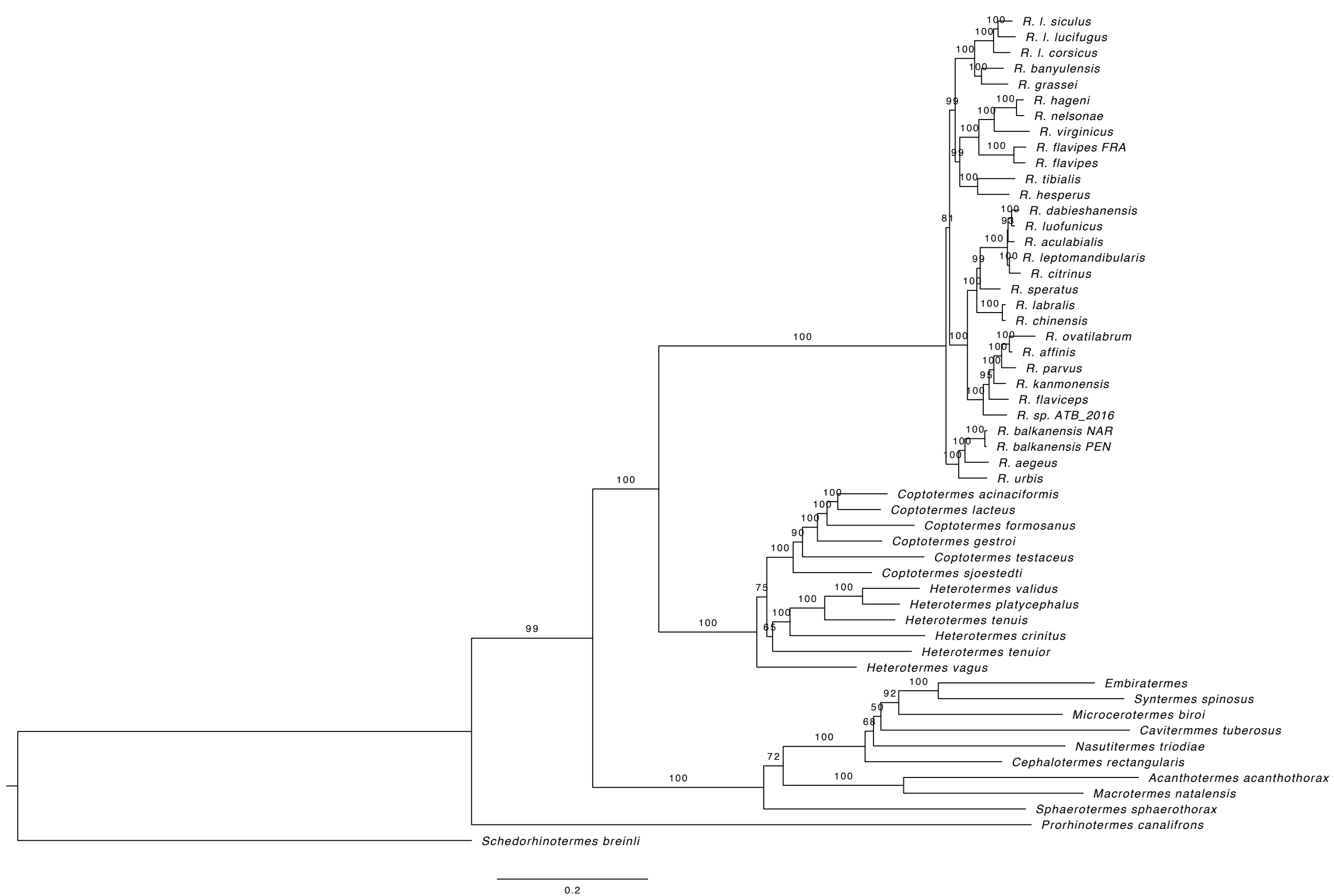


Fig. S16. Maximum likelihood tree based on nucleotides and mixture models



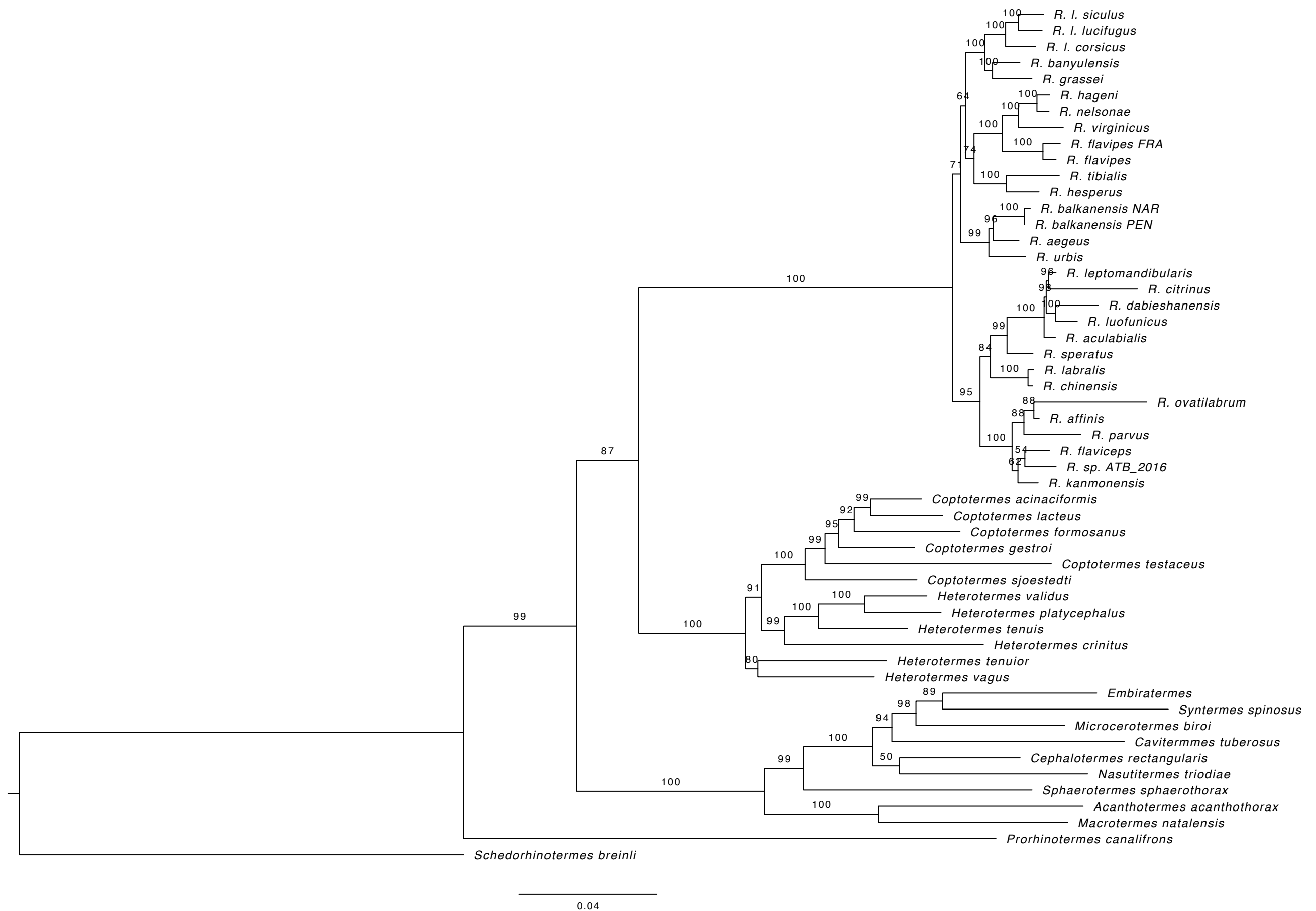


Fig. S17. Maximum likelihood tree based on amino acids and mixture models

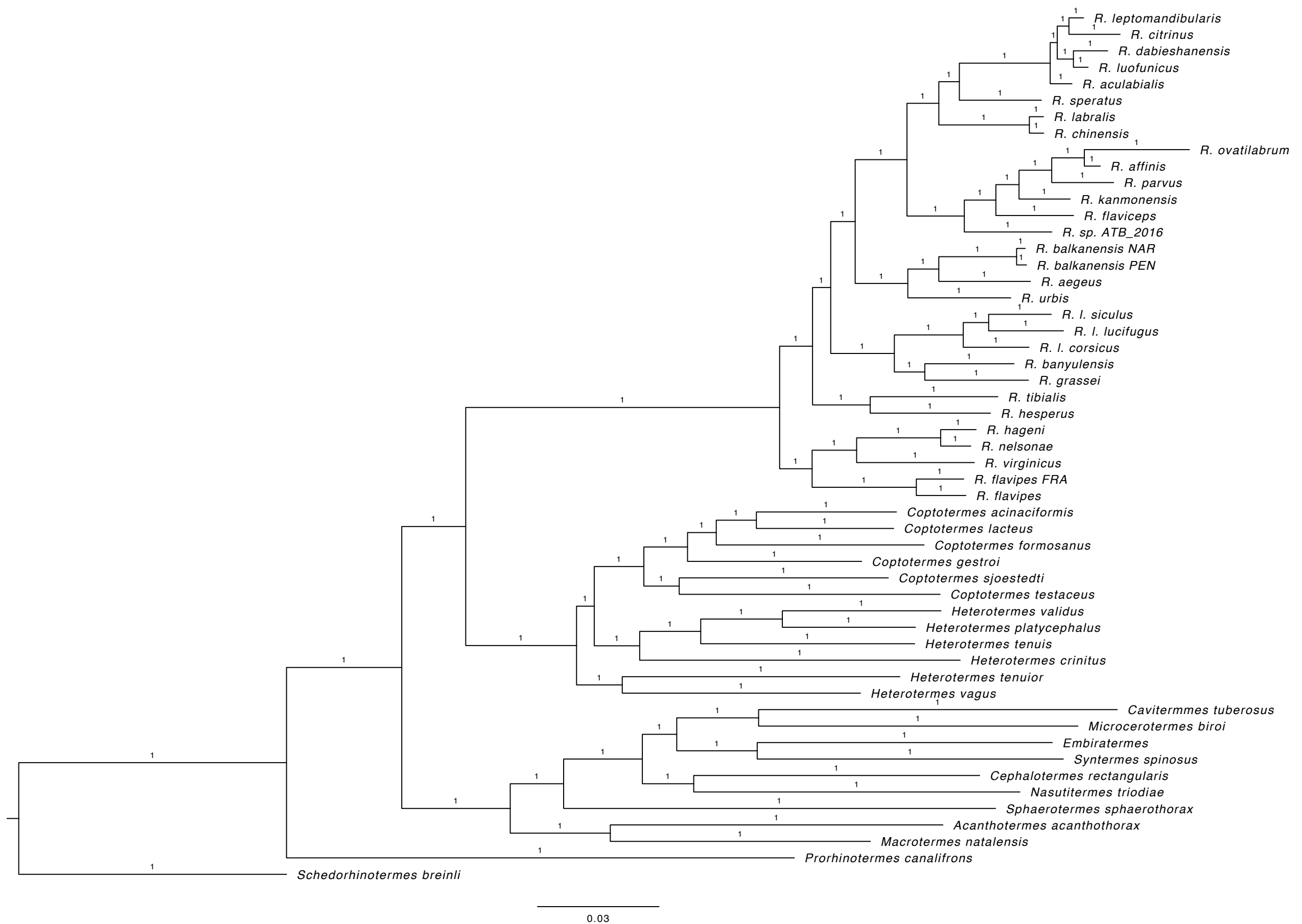


Fig. S18. Bayesian Inference based on nucleotides; partitioning by gene and GTR substitution model for all partitions

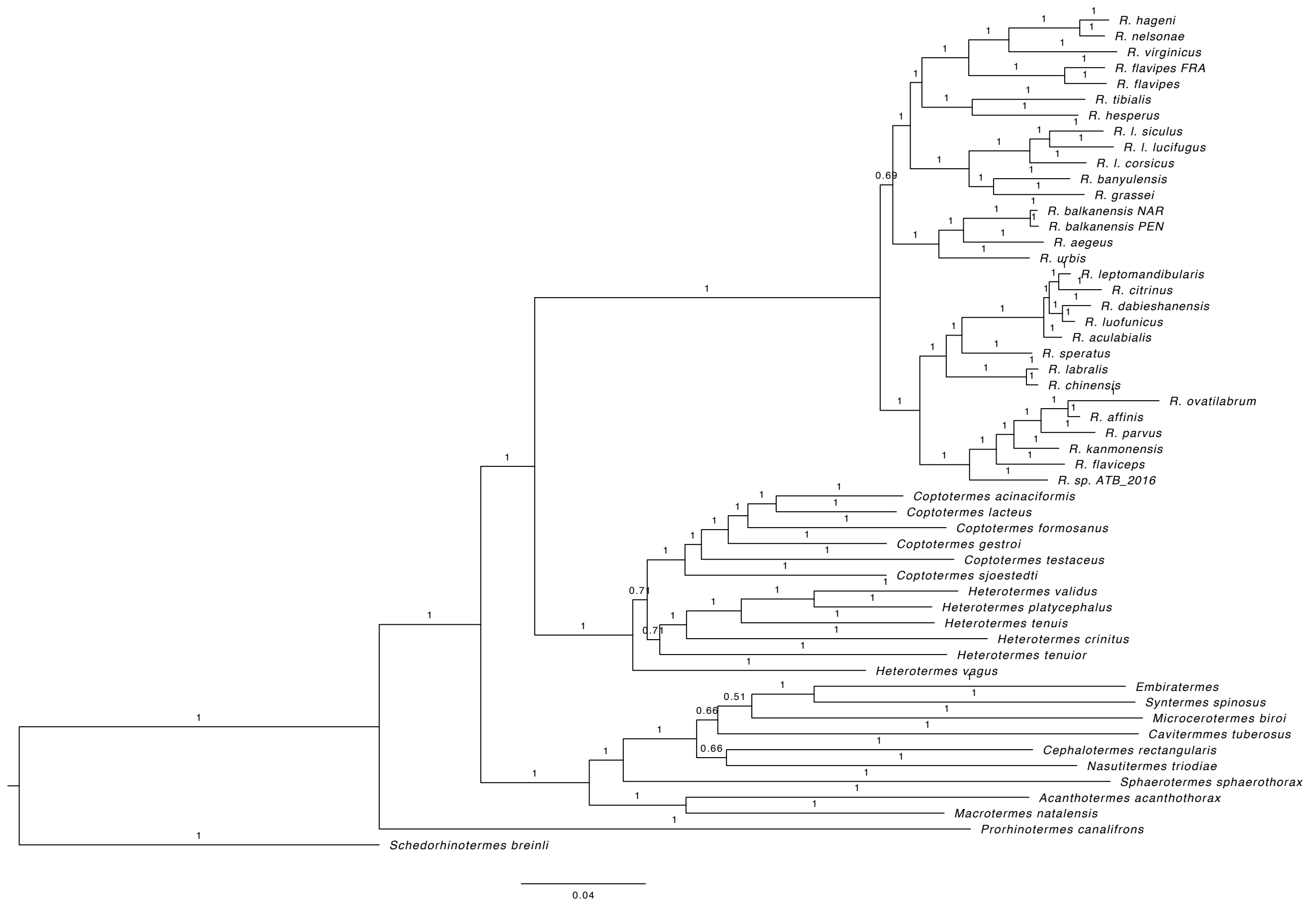


Fig. S19. Bayesian Inference based on nucleotides; partitioning by gene and best substitution models estimated by Partition Finder

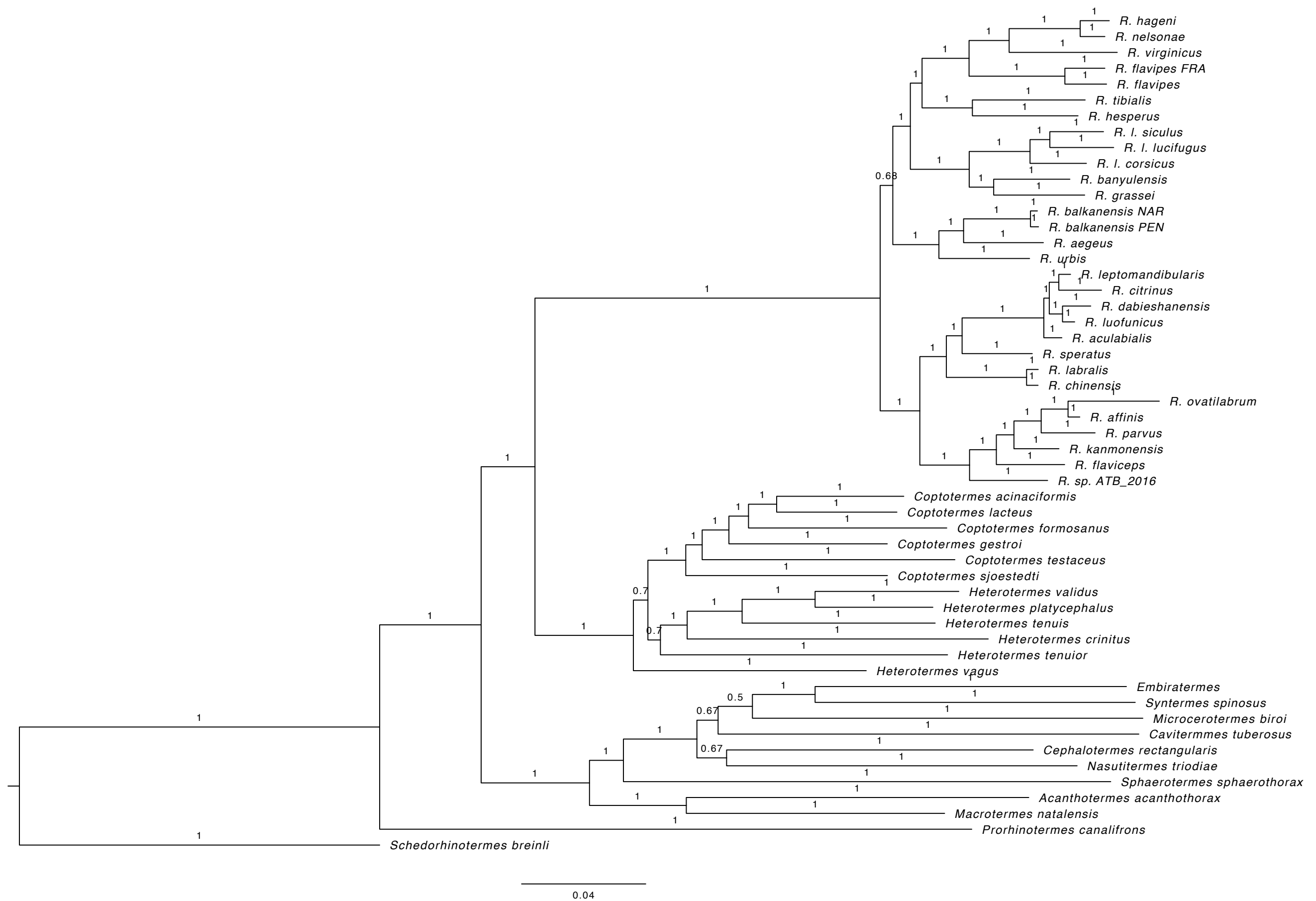


Fig. S20. Bayesian inference based on nucleotides; partitioning by gene, allowing merging of partitions and best substitution models estimated by Partition Finder





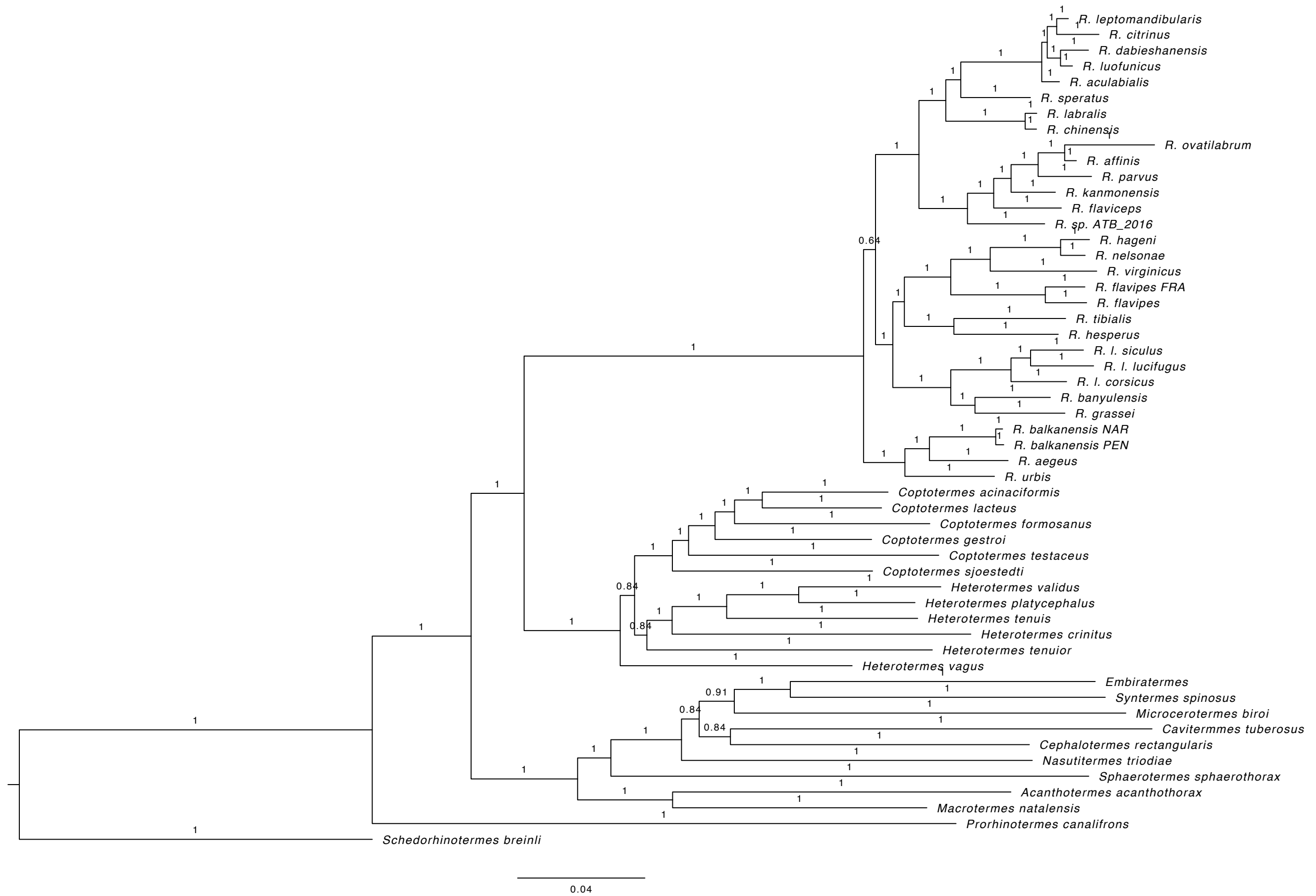


Fig. S23. Bayesian inference based on nucleotides; partitioning by codon positions, allowing merging of partitions and best substitution models estimated by Partition Finder

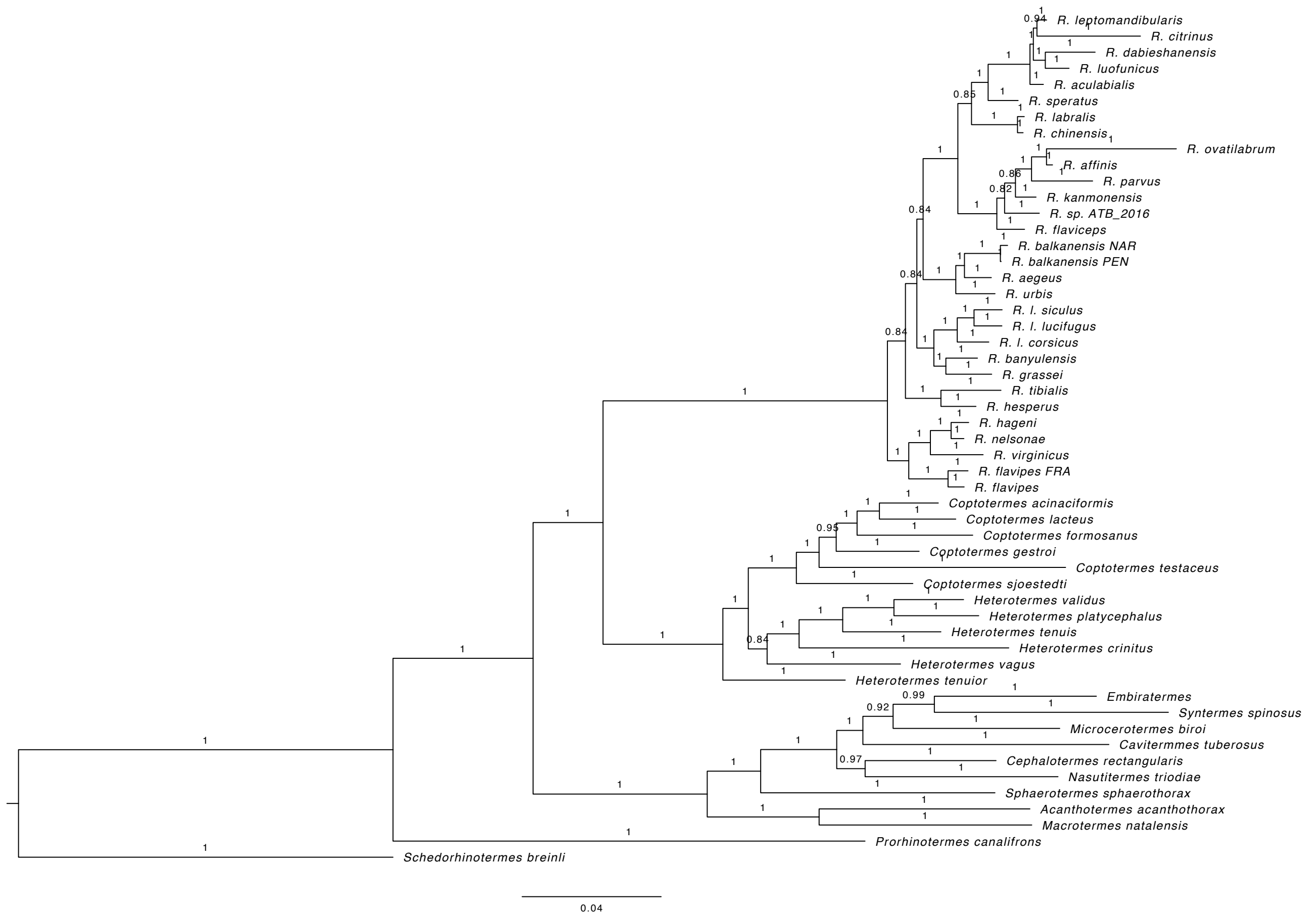


Fig. S24. Bayesian inference based on amino acids; partitioning by gene and LG substitution model for all partitions



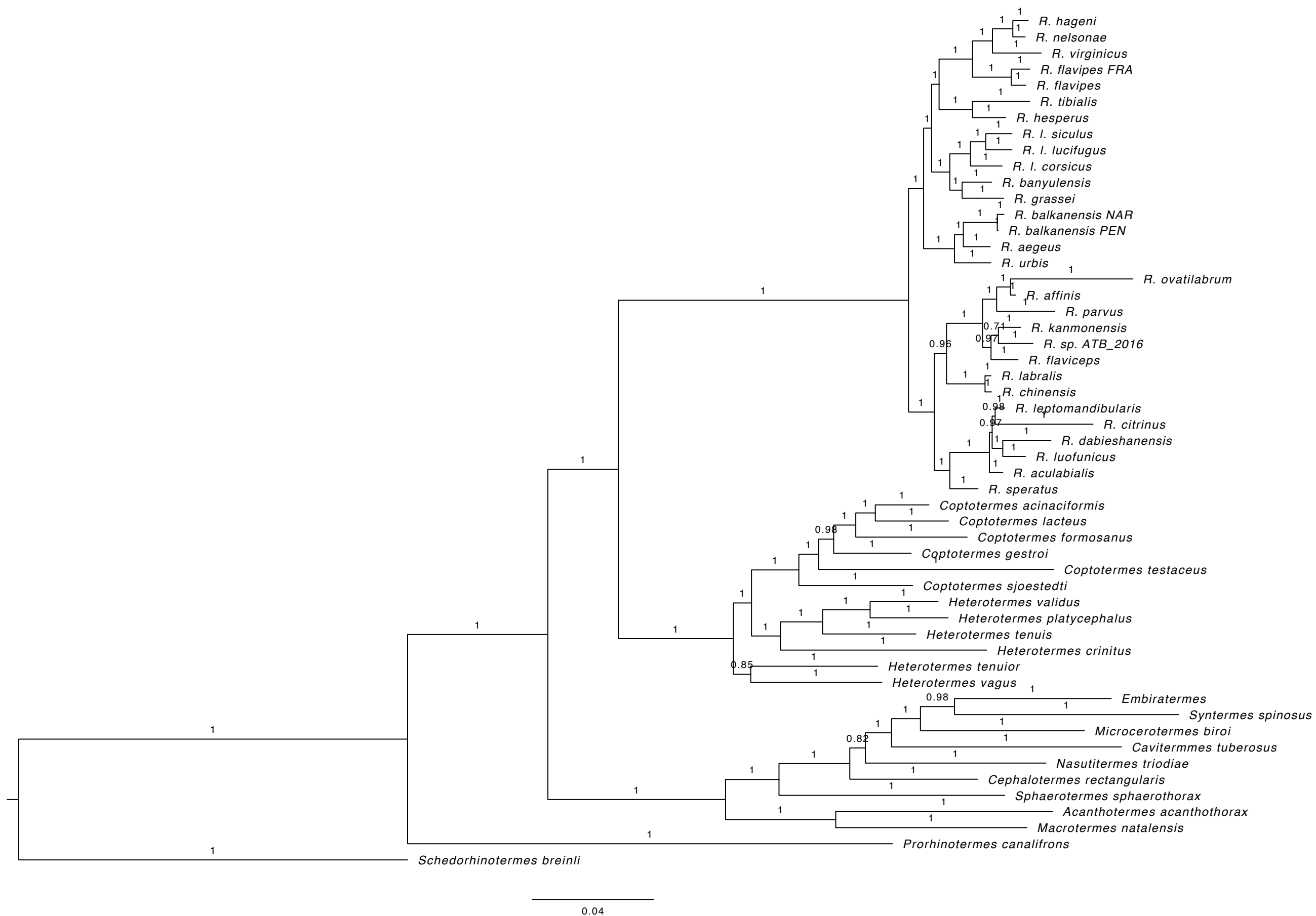
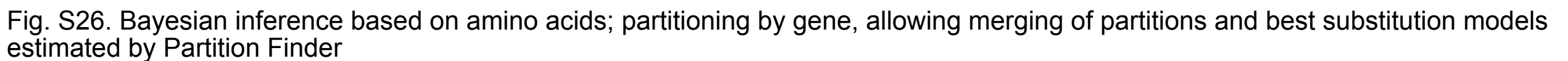


Fig. S25. Bayesian inference based on amino acids; partitioning by genes and best substitution models estimated by Partition Finder



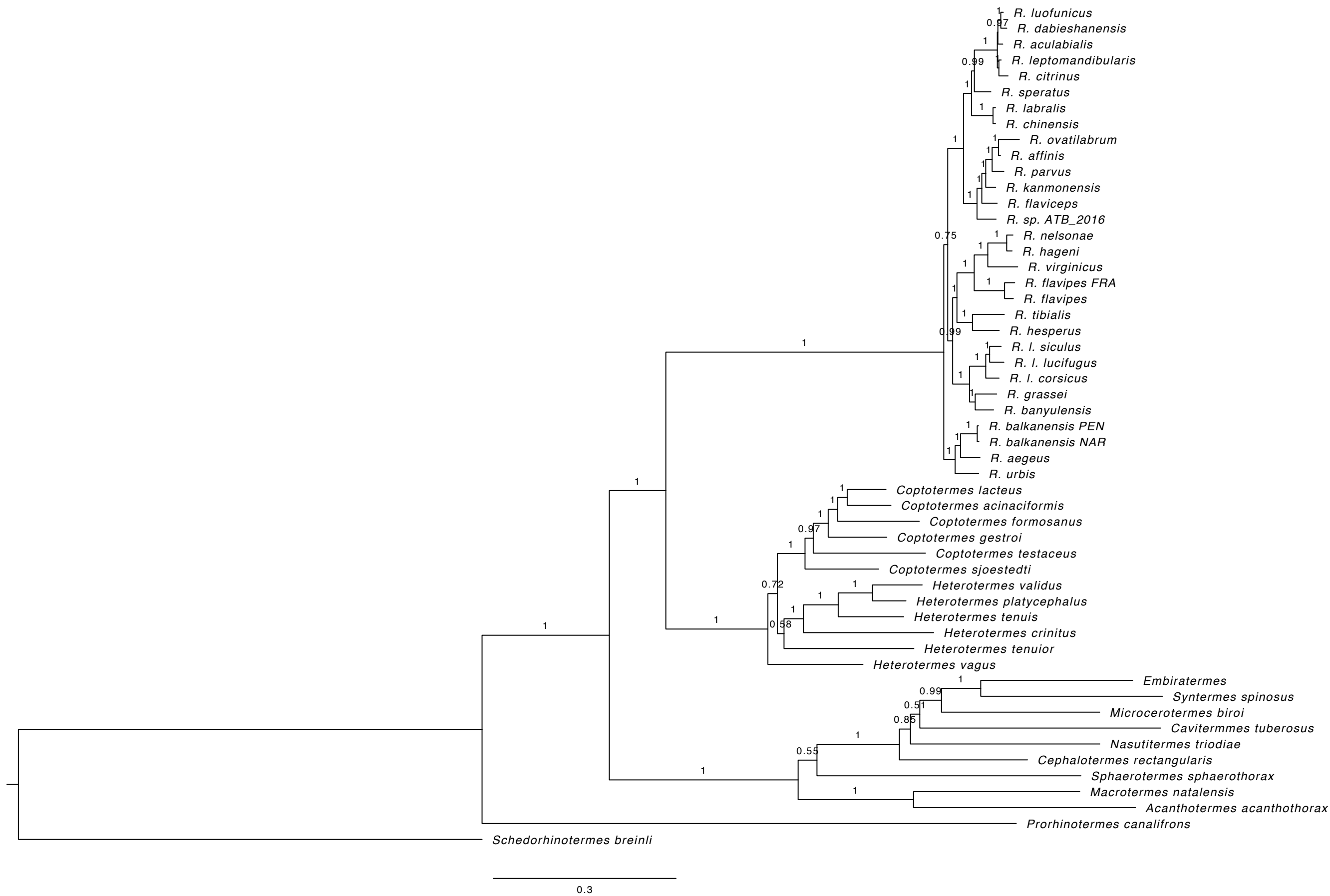


Fig. S27. Bayesian inference based on nucleotides and mixture models

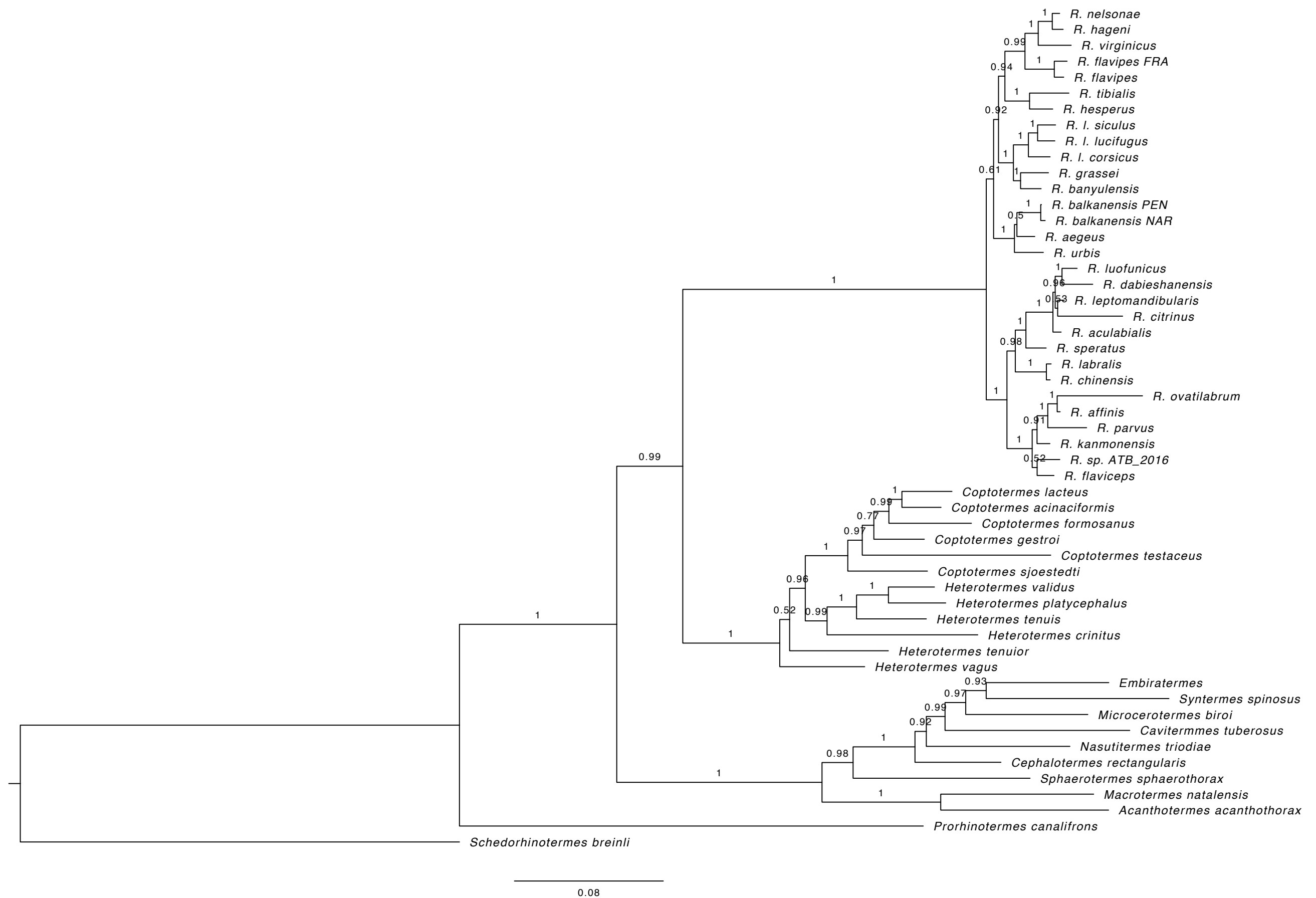


Fig. S28. Bayesian inference based on amino acids and mixture models

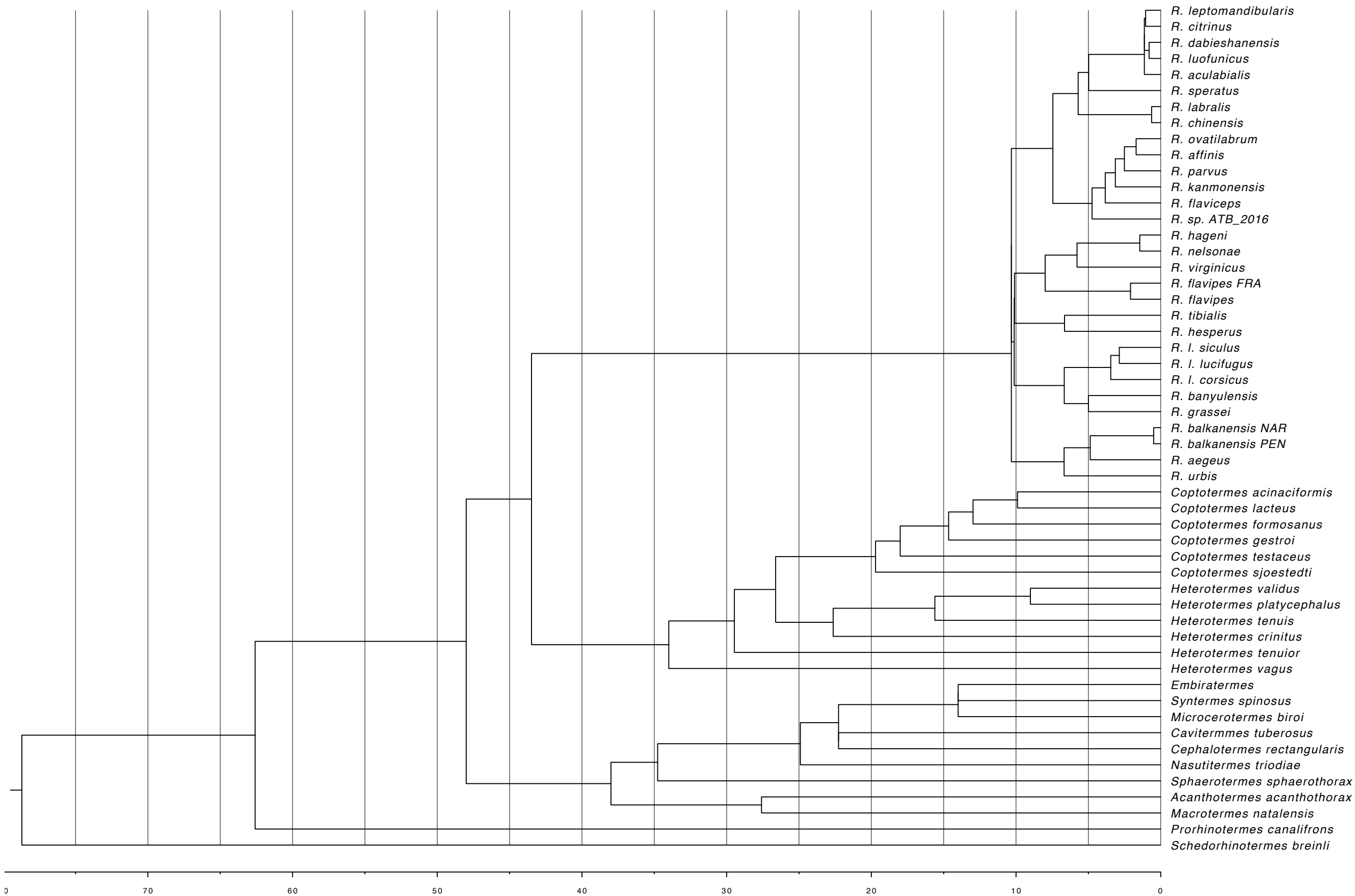


Fig. S29. Time tree inferred on nucleotides, partitioning by codon positions, allowing merging of partitions and best substitution models estimated by Model Finder. The time scale below represent million years before the present.

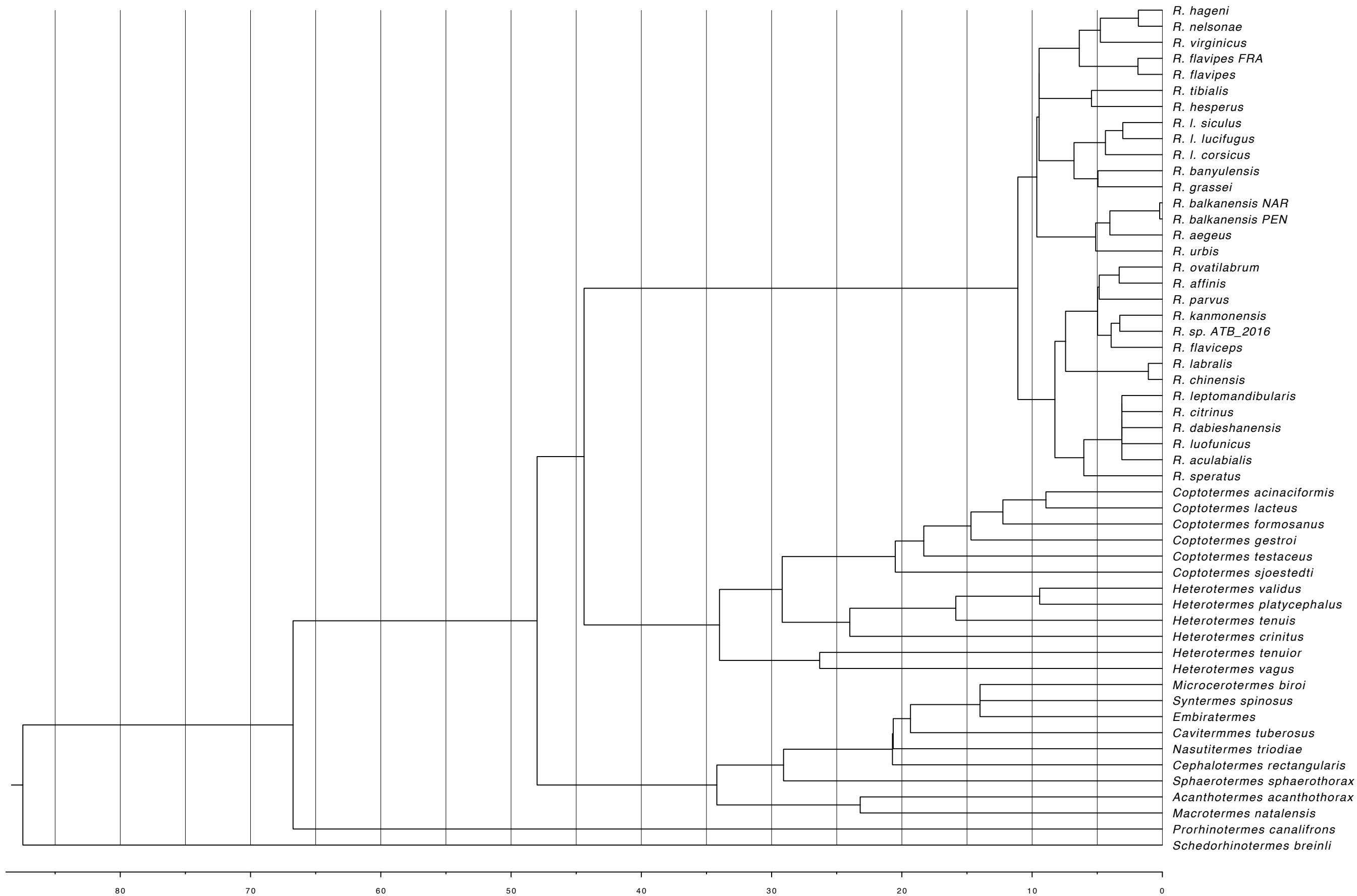


Fig. S30. Time tree inferred on amino acids; partitioning by gene, allowing merging of partitions and best substitution models estimated by Model Finder. The time scale below represent million years before the present.