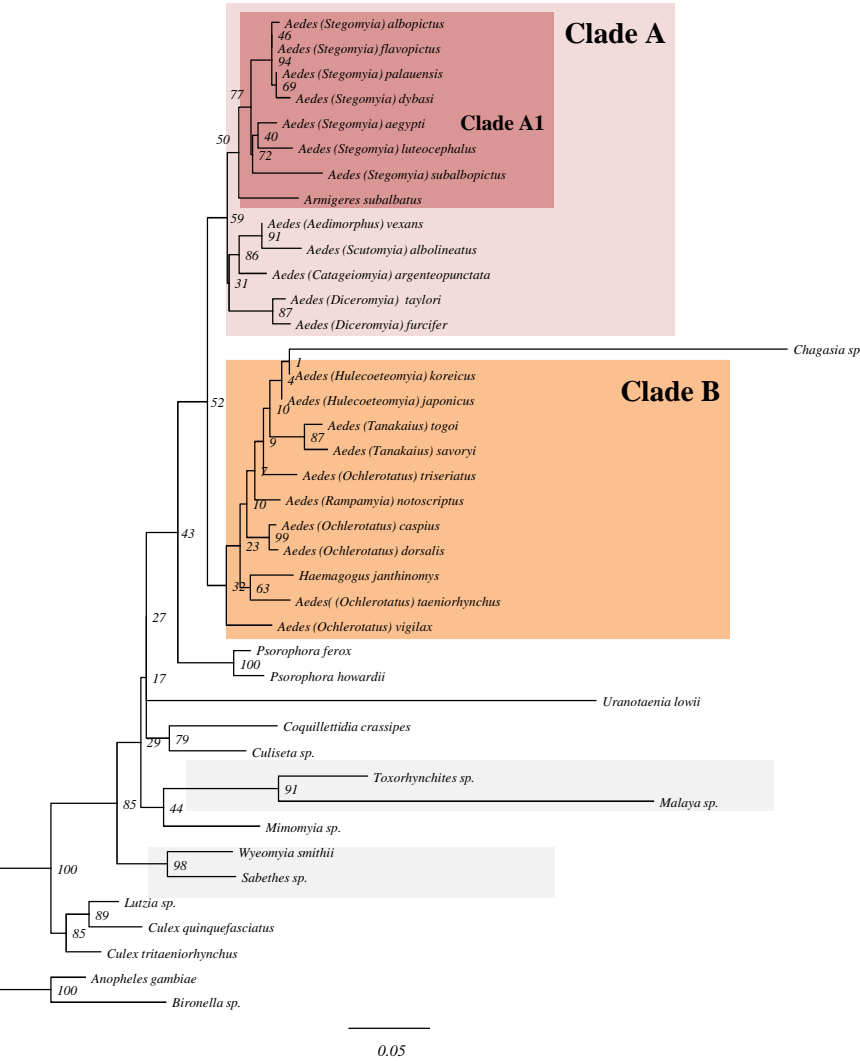
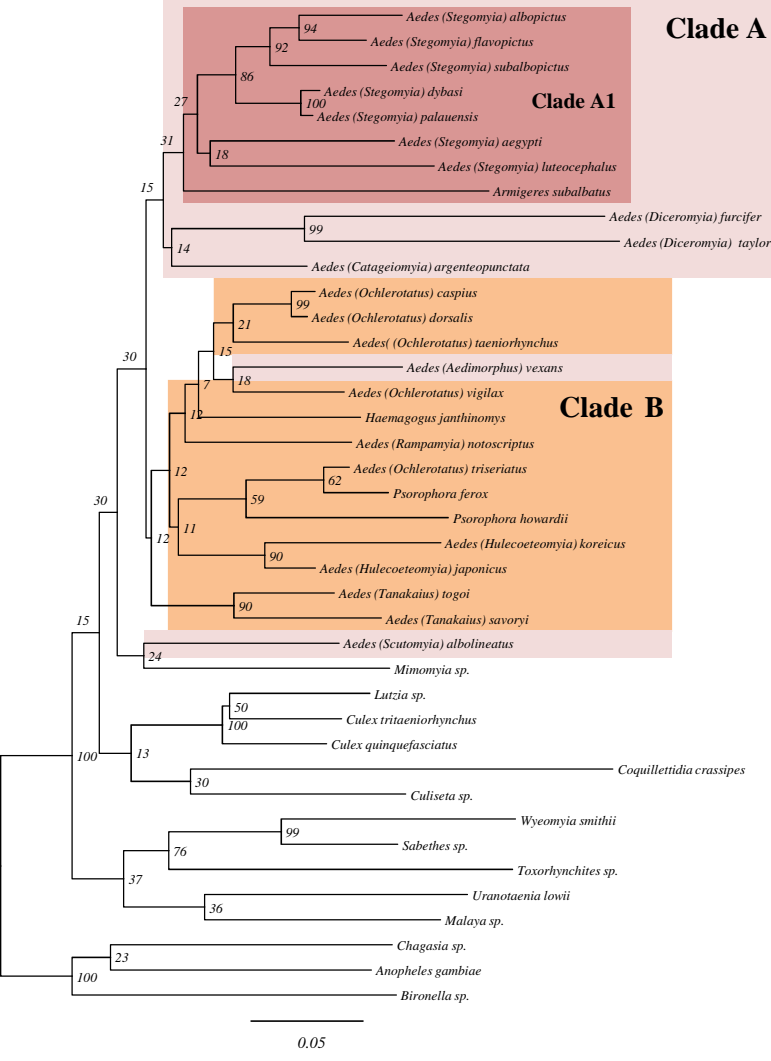


Supplementary figure S1: Maximum Liklehood analyses using RAXML and GTR+G

a. nuclear

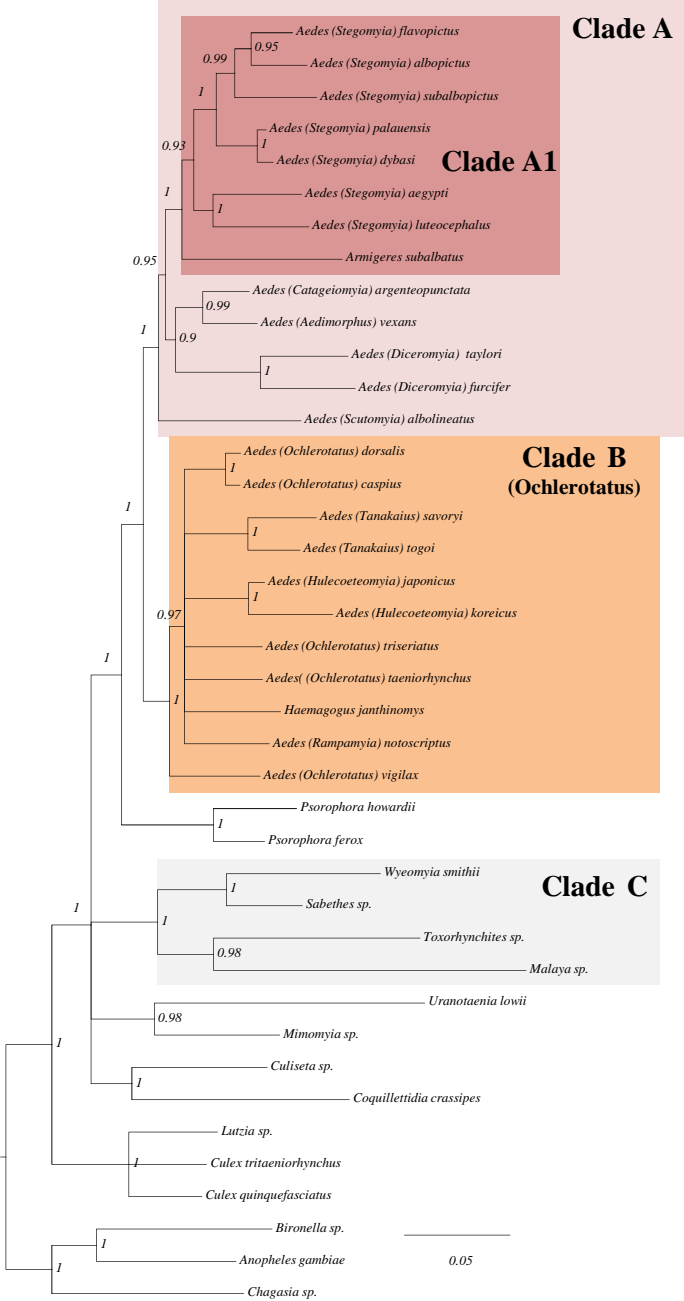


b. mitochondrial

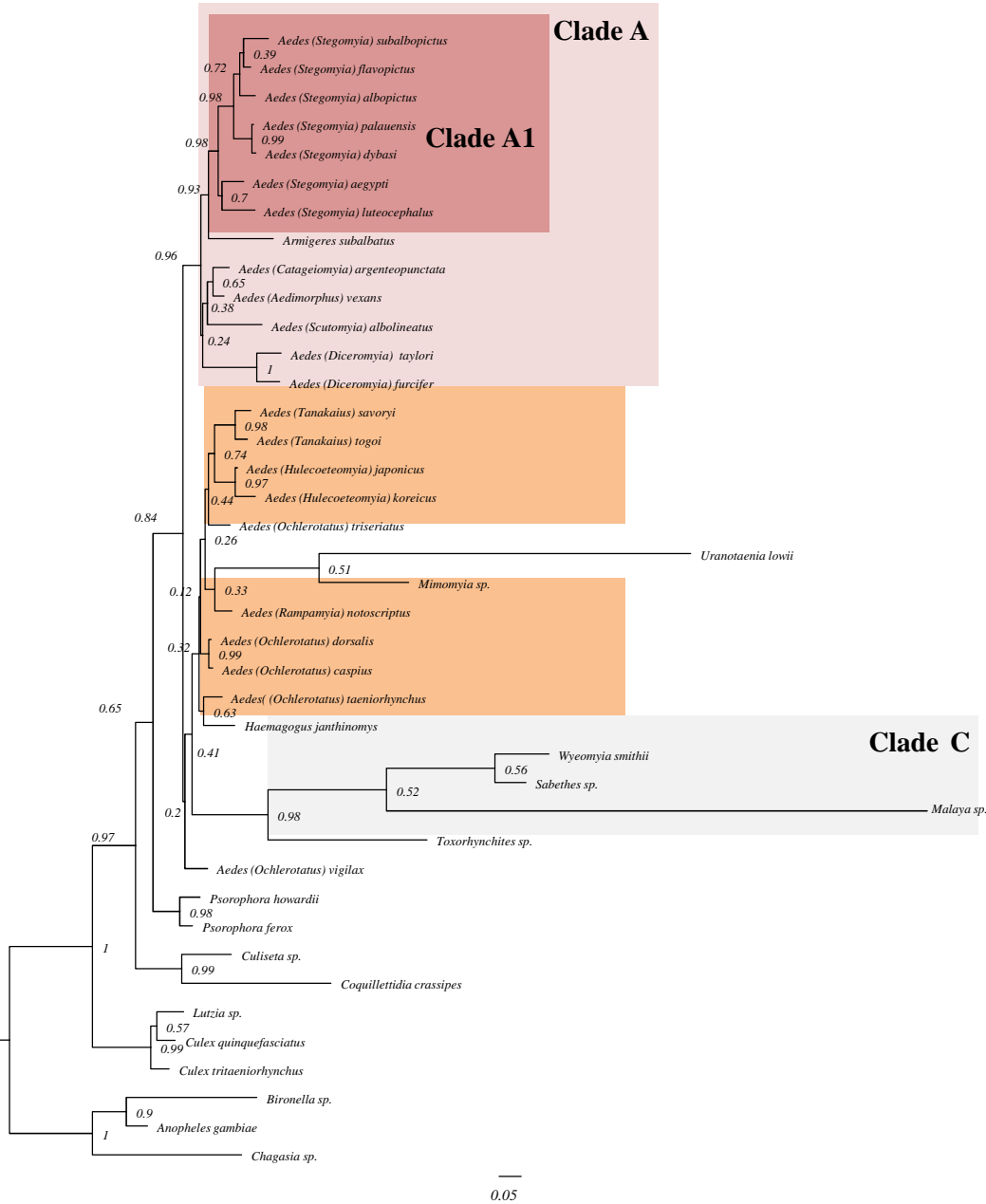


Supplementary figure S2: Bayesian trees of concatenated datasets

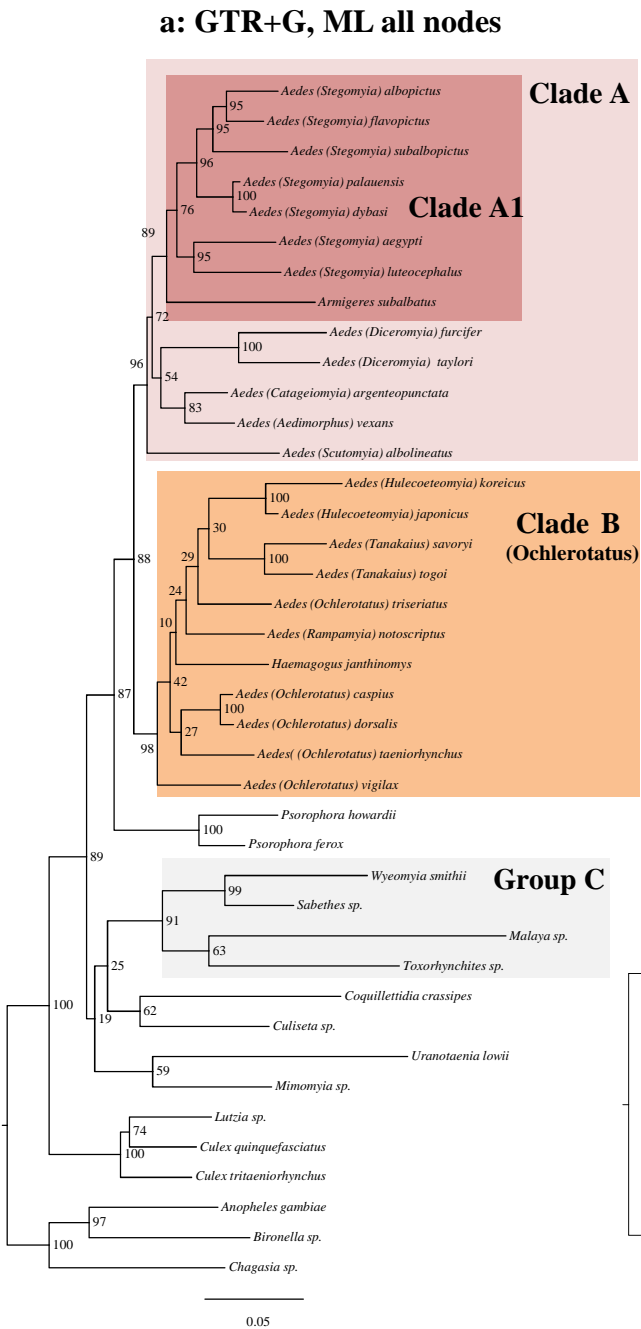
a: GTR+G Bayesian



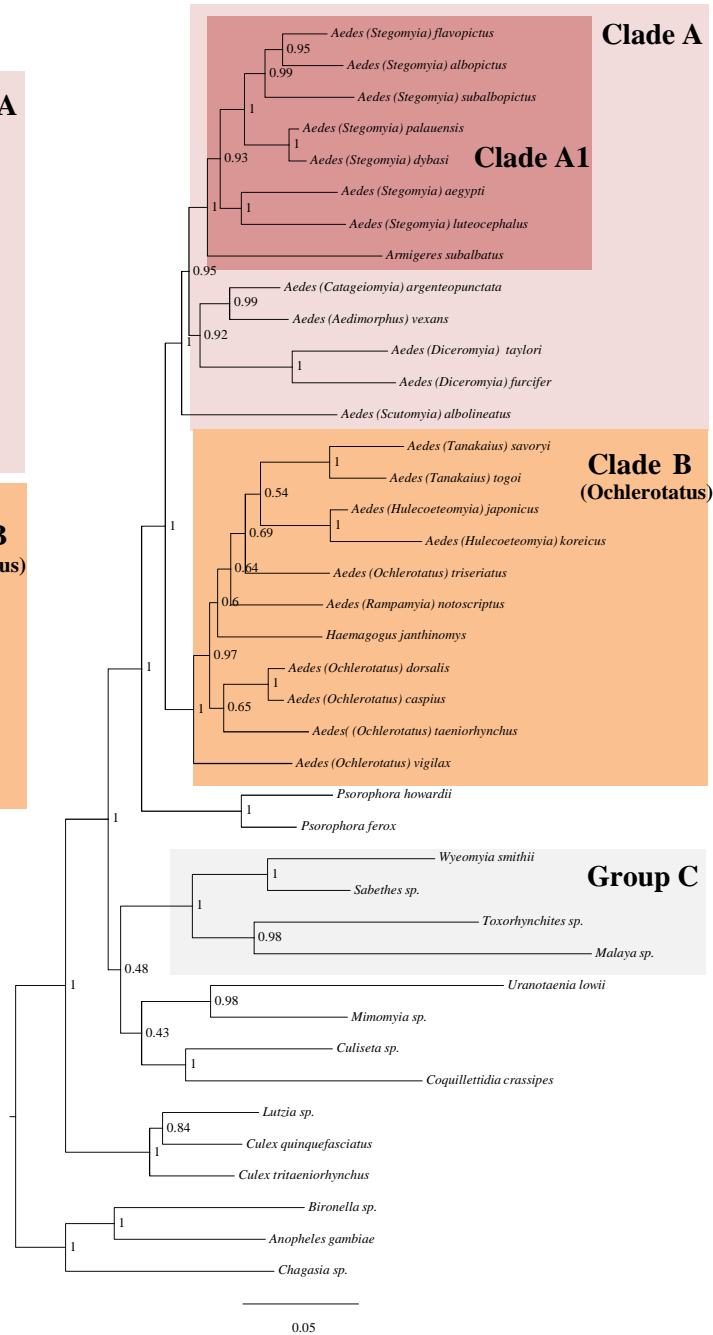
b: CAT+G Bayesian



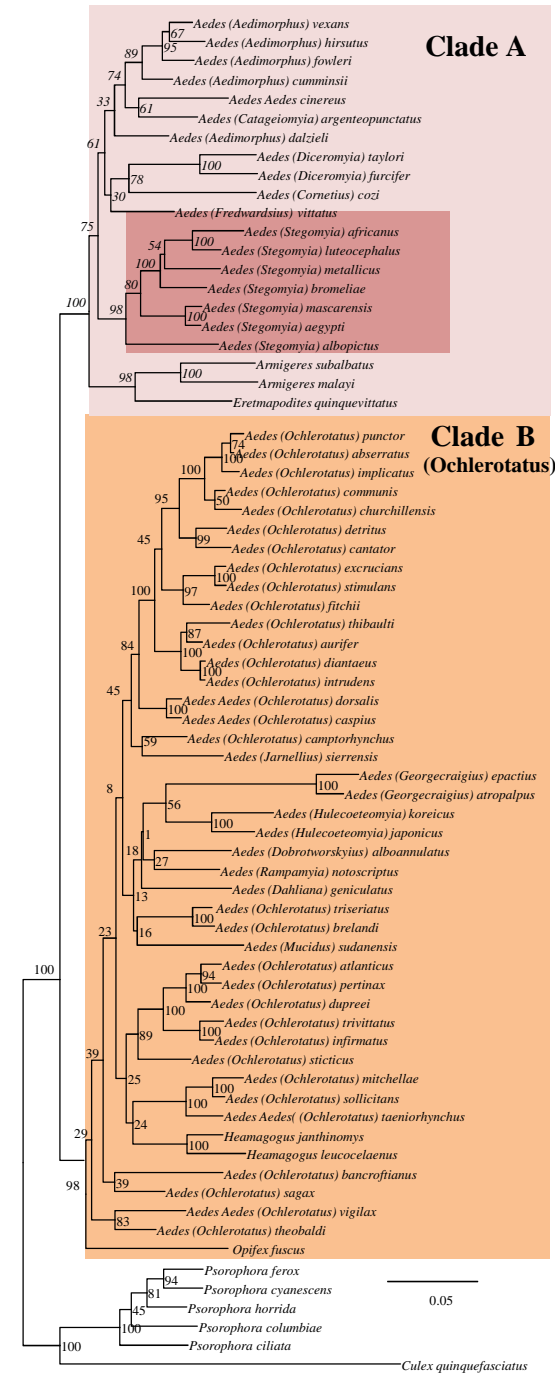
Supplementary figure S3: concatenated dataset, full trees



b: GTR+G, Phylobayes all nodes

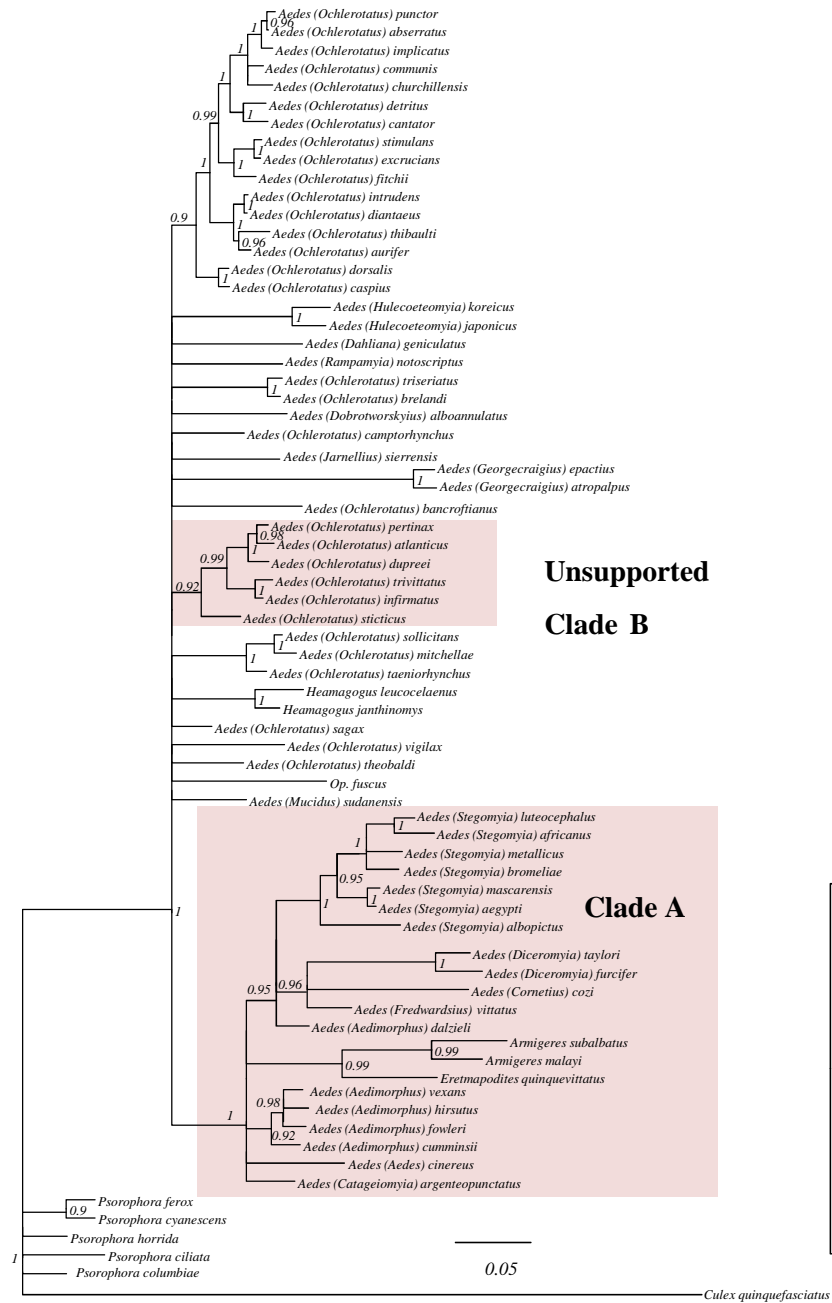


c: GTR+G, ML Soghigian dataset

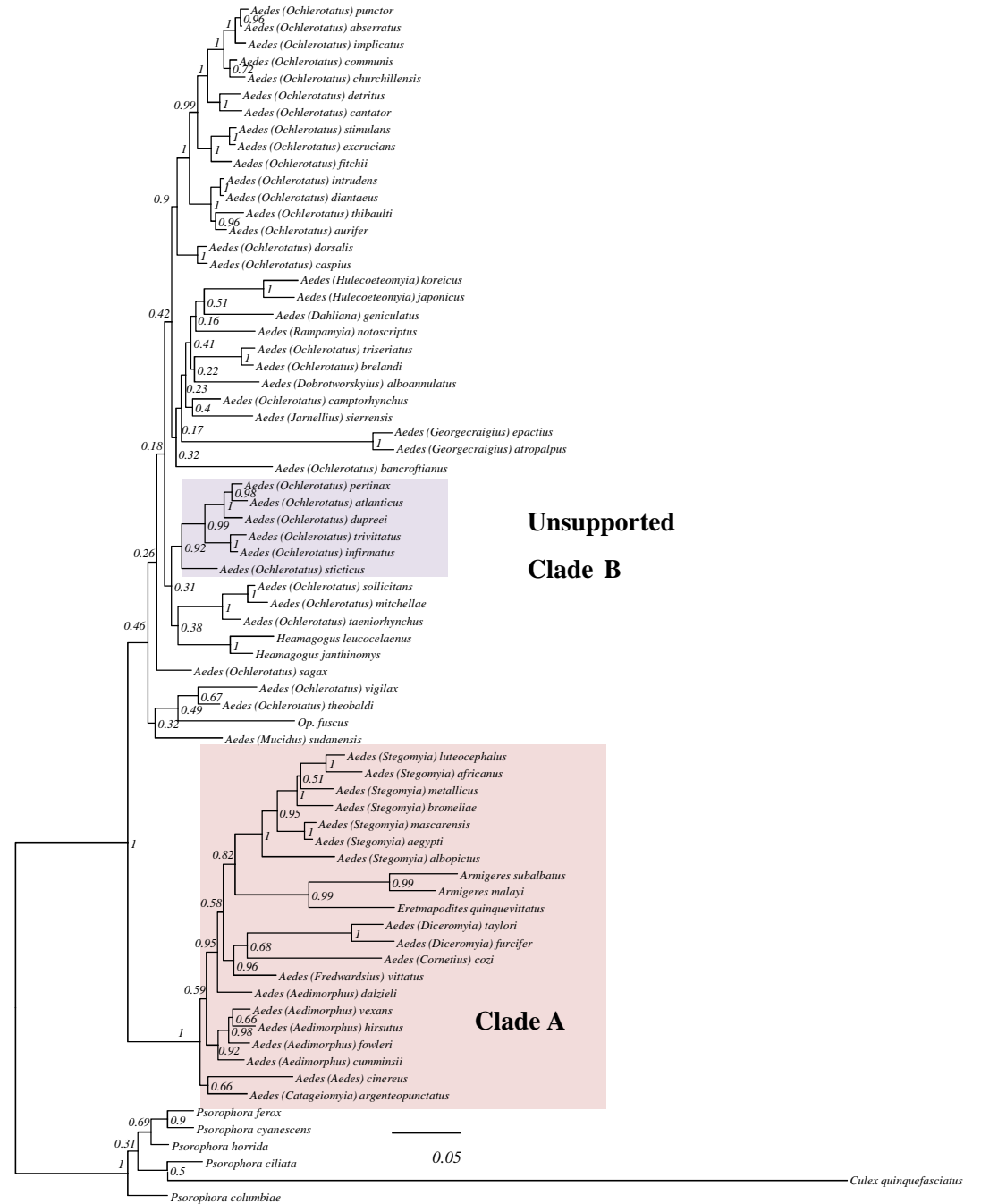


Supplementary figure S4: Soghigian dataset CAT+G full trees

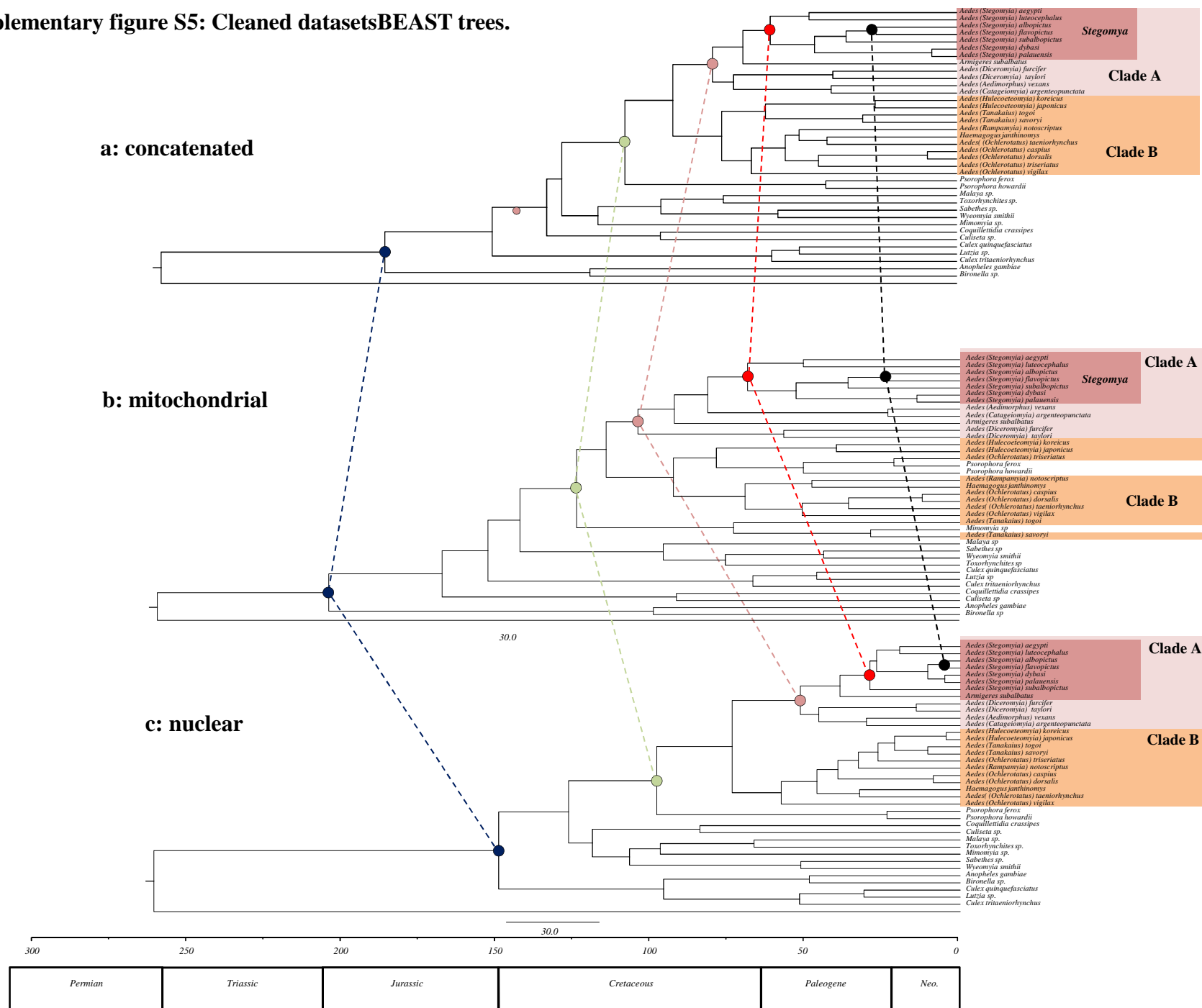
a: Bayesian CAT+G, collapsed



B: Bayesian CAT+G, full

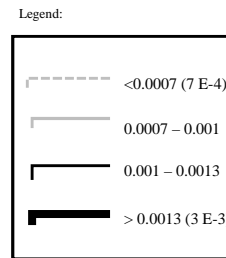
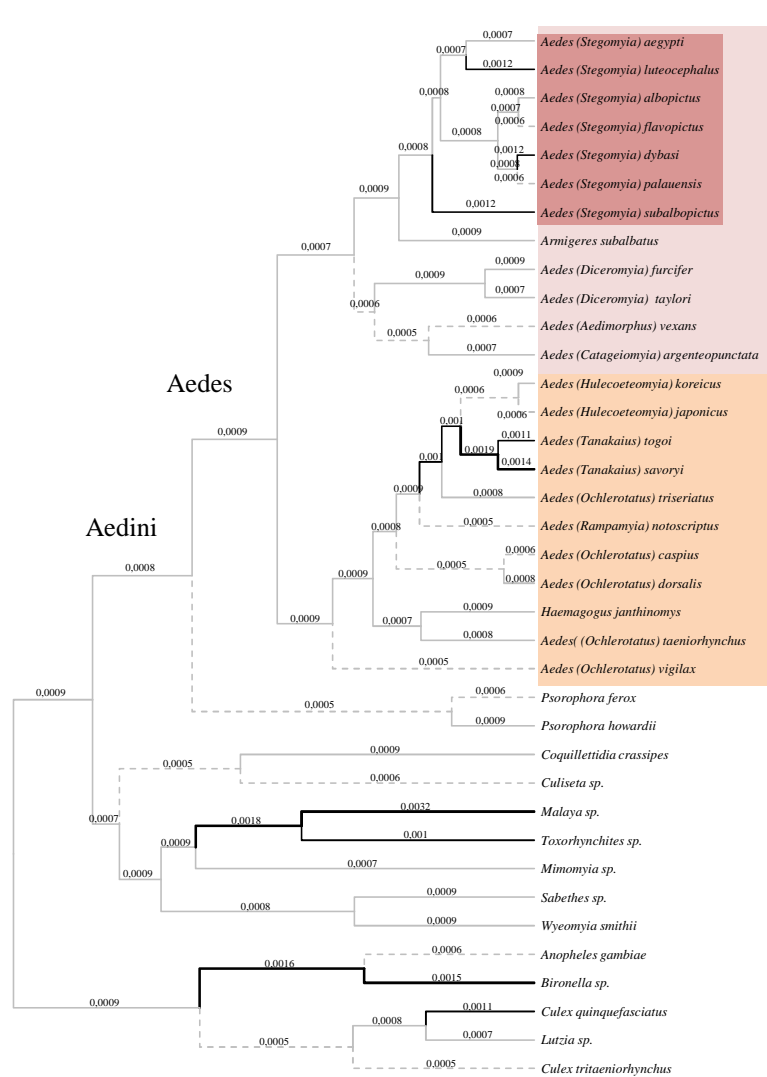


Supplementary figure S5: Cleaned datasetsBEAST trees.

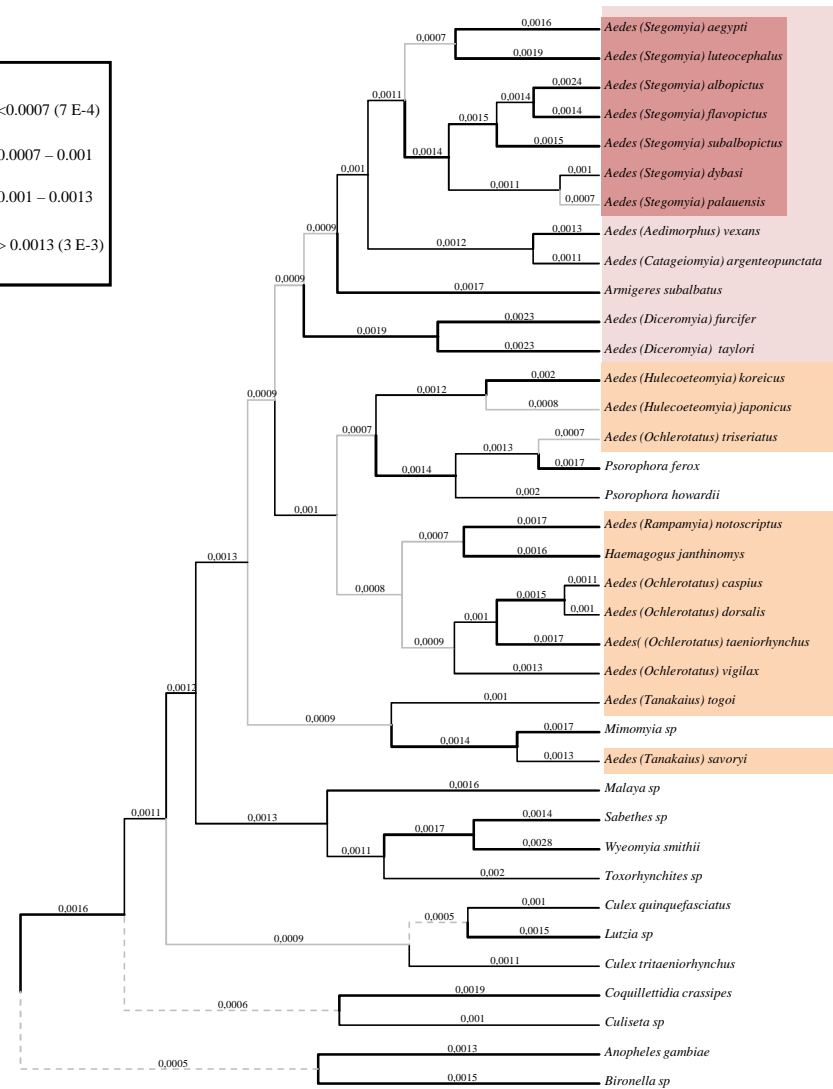


Supplementary figure S6: Cleaned datasets BEAST trees. Posterior mean rates at nodes

a. nuclear

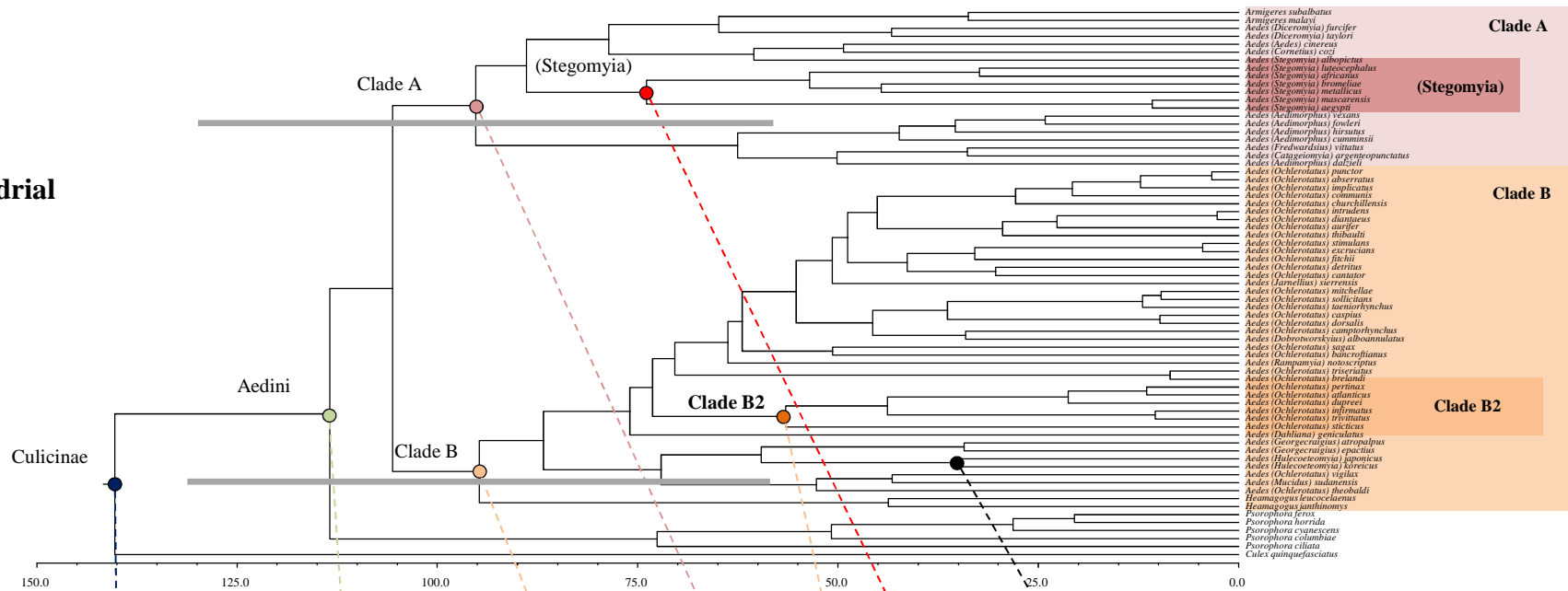


b. mitochondrial

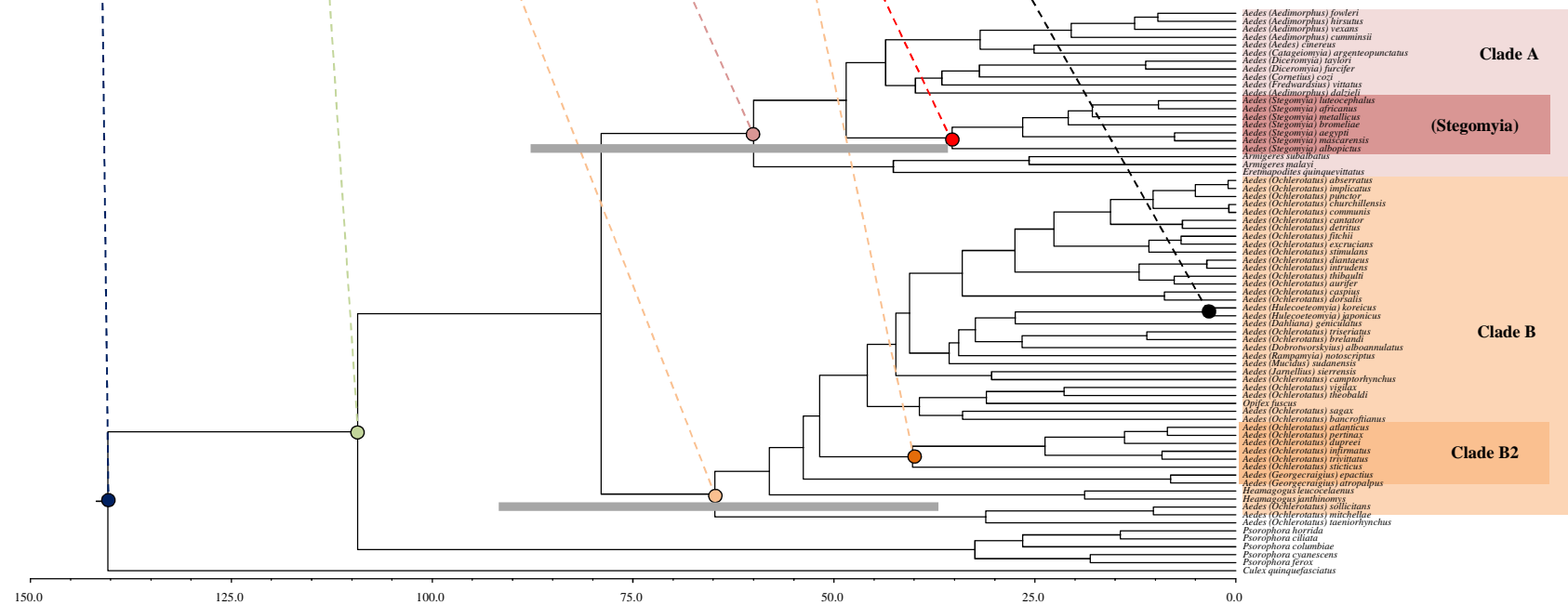


Supplementary figure S7: Partitioned Soghigian BEAST trees.

a: mitochondrial

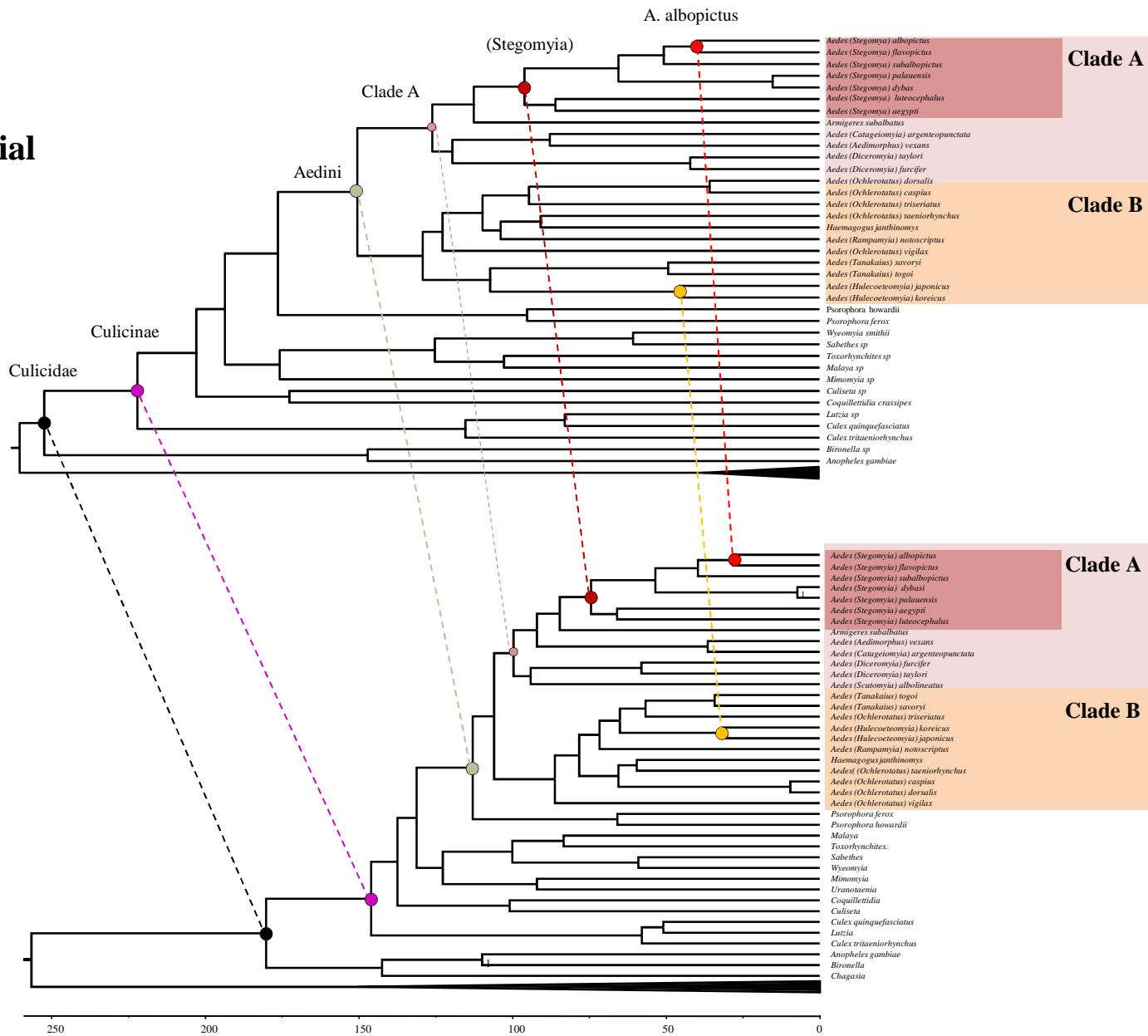


b: nuclear



Supplementary figure S8: Phylobayes timetrees using the CAT+G model

a: mitochondrial



b: nuclear

