Figure S1. Figure illustrating how the estimated genome-wide heterozygosity rate changes with mapping coverage and filtering. Unfilled squares represent the estimated genome-wide rate of heterozygosity when 5bp were removed from both ends of the raw-reads before mapping and filled red circles represents the estimates when 10bp were removed from both ends.

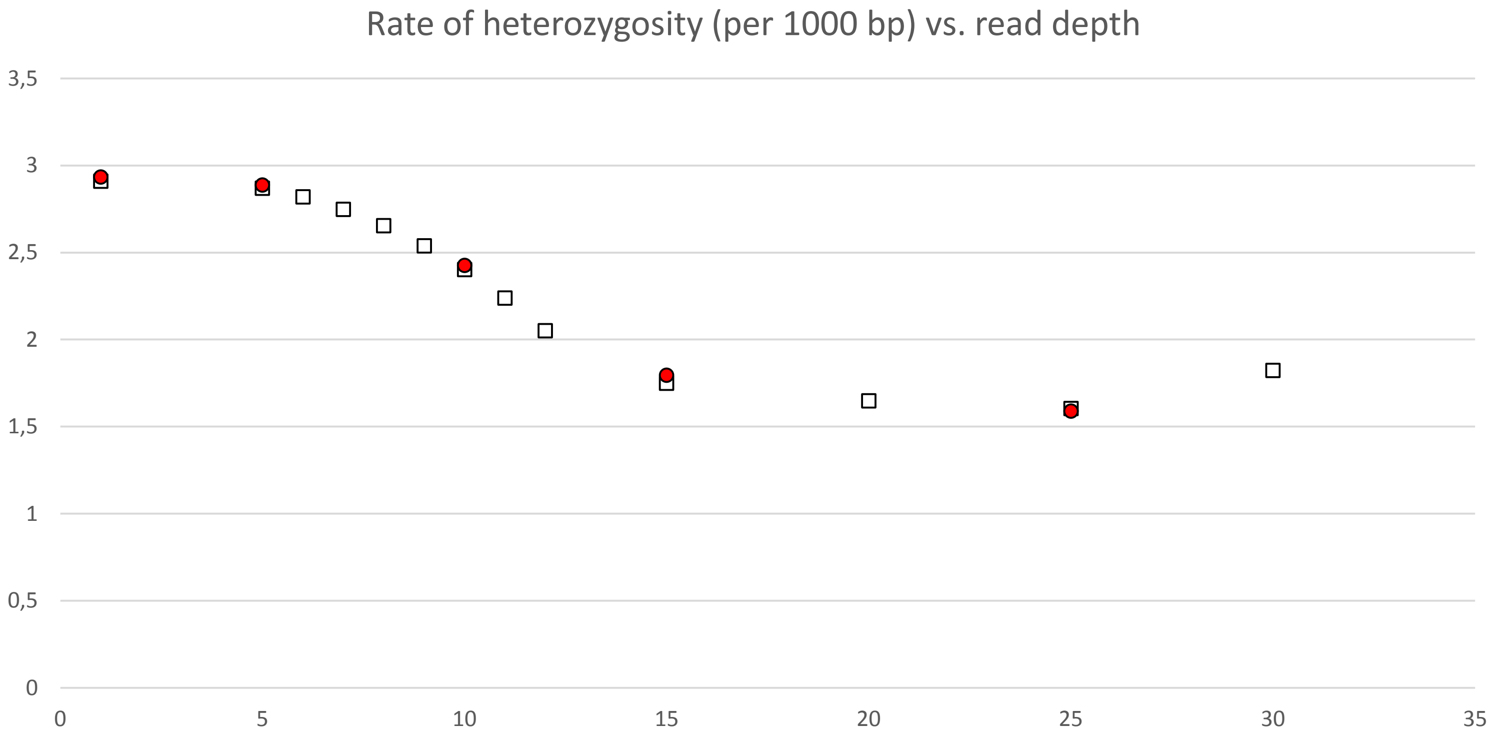

Figure S2. Best-fit maximum-likelihood trees estimated for the nuclear c-mos gene (580 bp) using RAxML. Bootstrap values are indicated at the nodes.

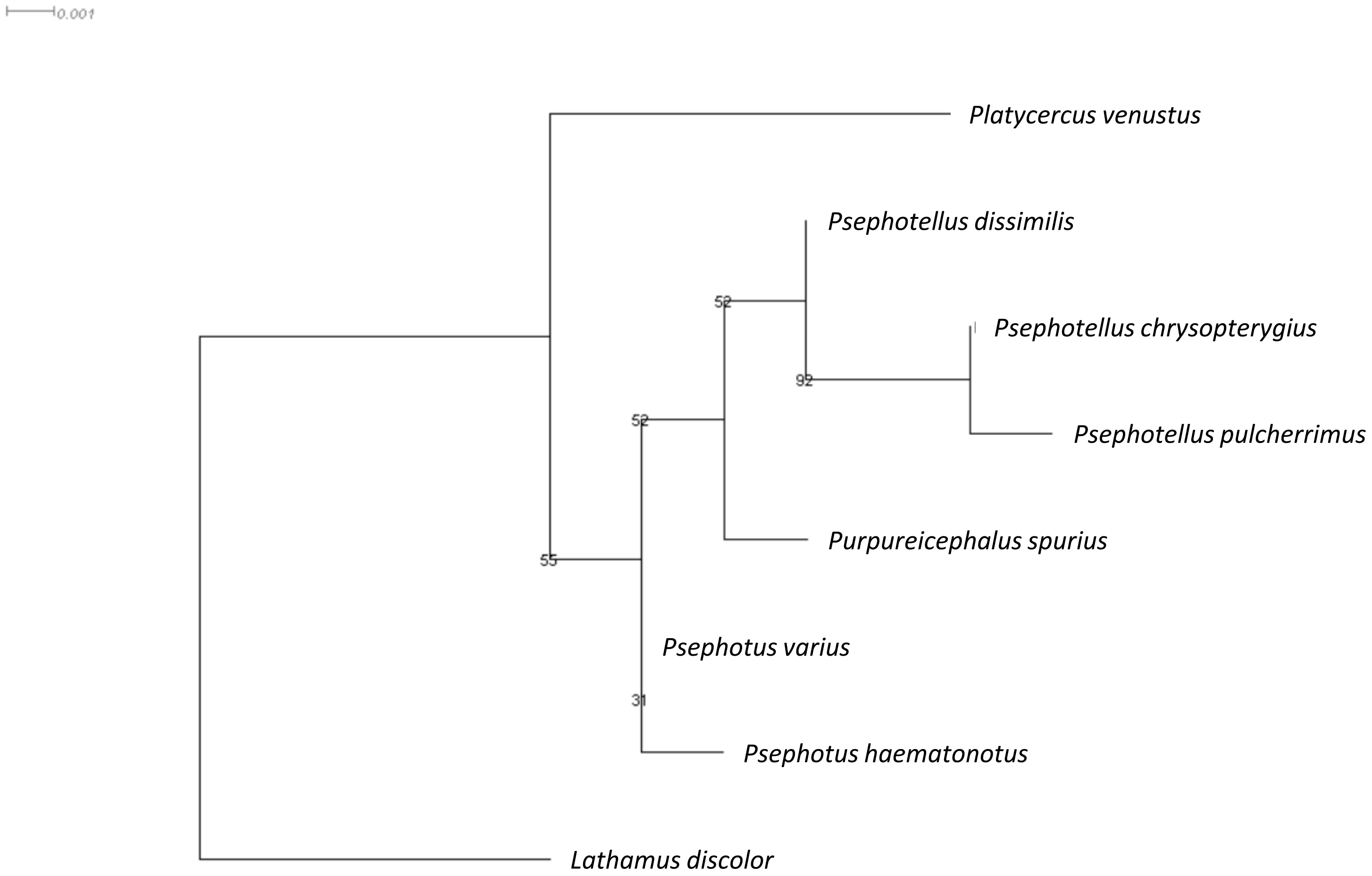

Figure S3. Best-fit maximum-likelihood trees estimated for the nuclear RAG1 gene (1270 bp) using RAxML. Bootstrap values are indicated at the nodes.

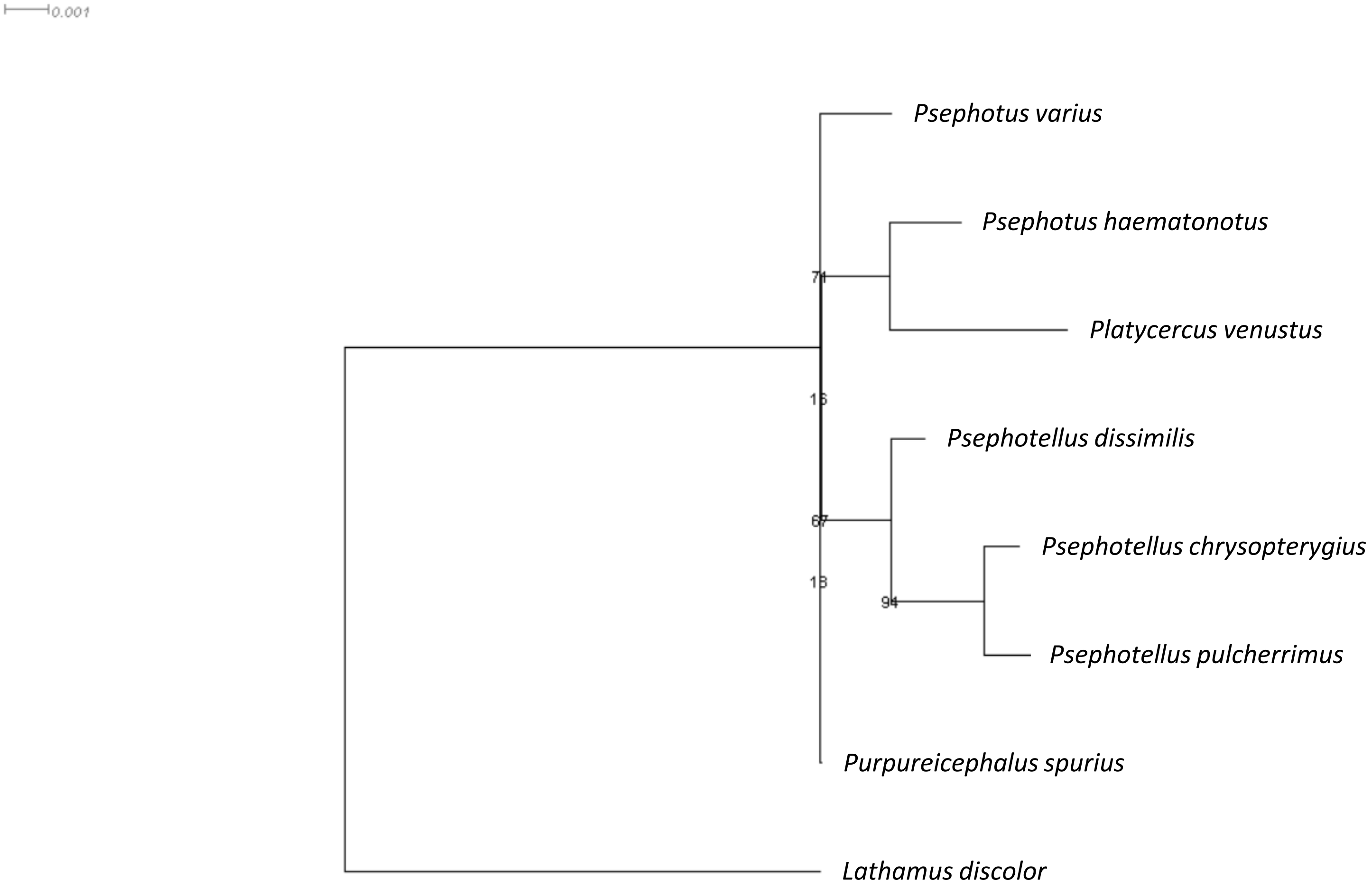

Figure S4. Best-fit maximum-likelihood trees estimated for the nuclear ZENK gene (1103 bp) using RAxML. Bootstrap values are indicated at the nodes.

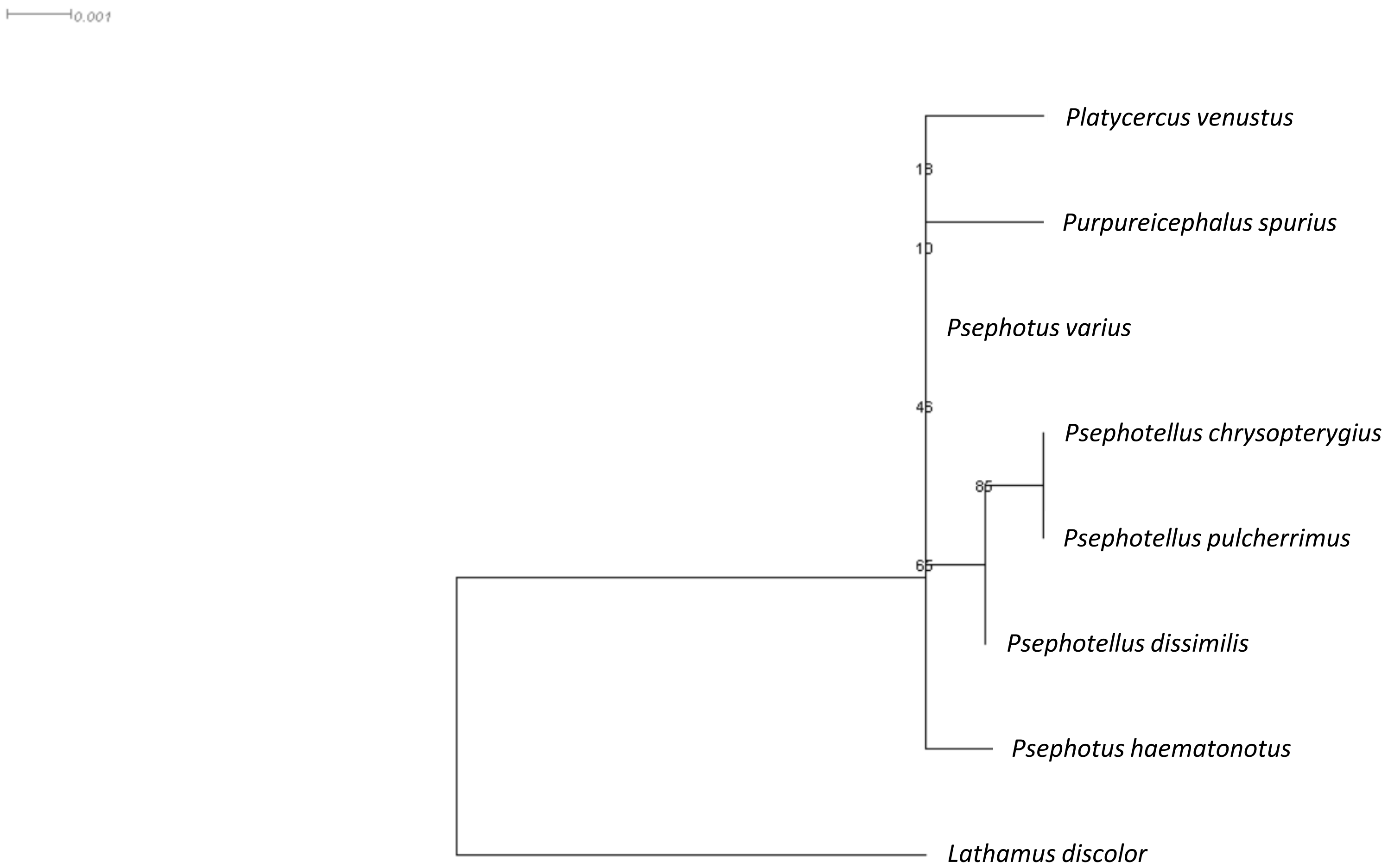

Figure S5. Best-fit maximum-likelihood trees estimated for the mitochondrial cyt *b* gene (876 bp) using RAxML. Bootstrap values are indicated at the nodes.

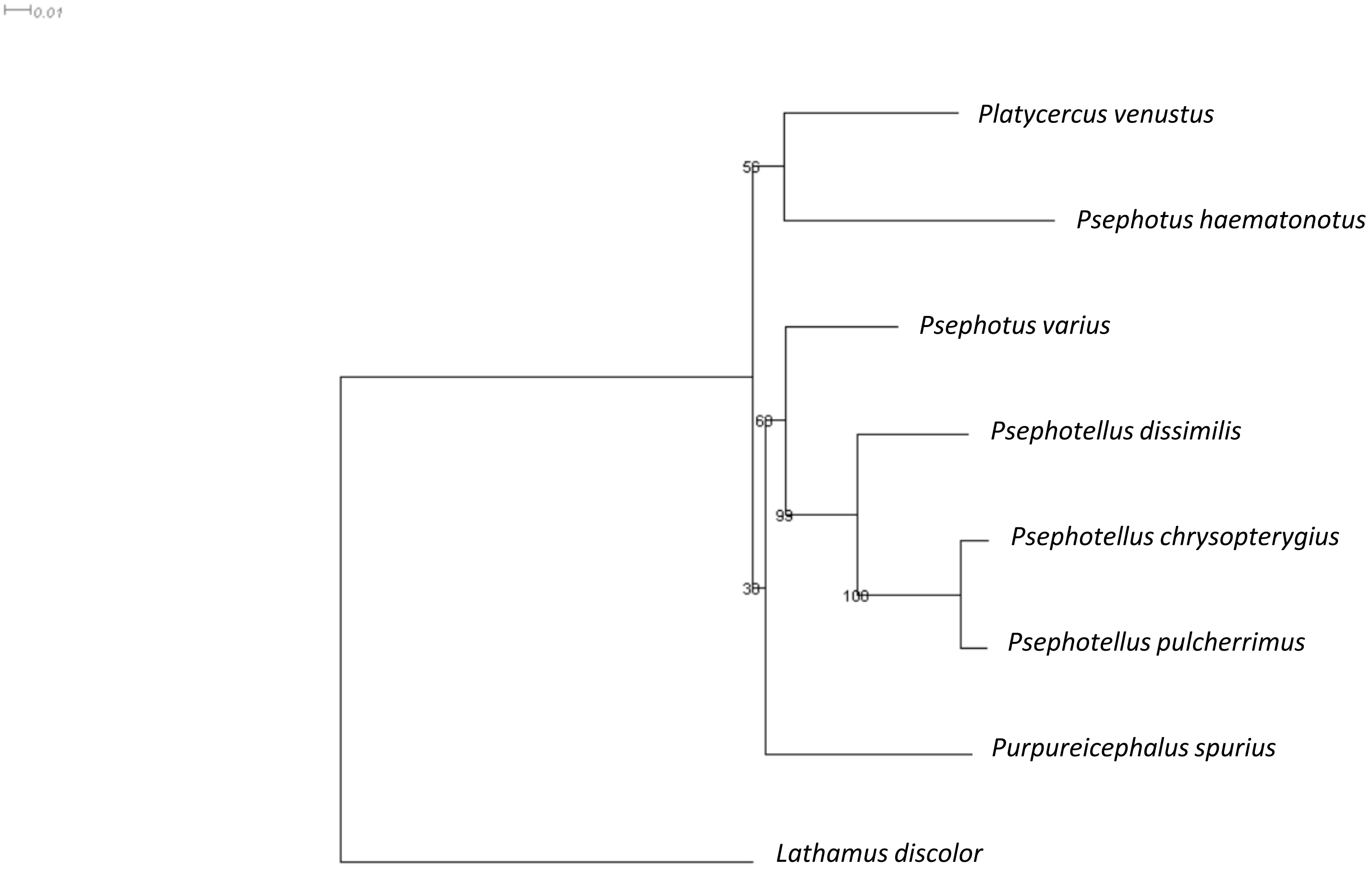

Figure S6. Best-fit maximum-likelihood trees estimated for the mitochondrial ND2 gene (1041 bp) using RAxML. Bootstrap values are indicated at the nodes.

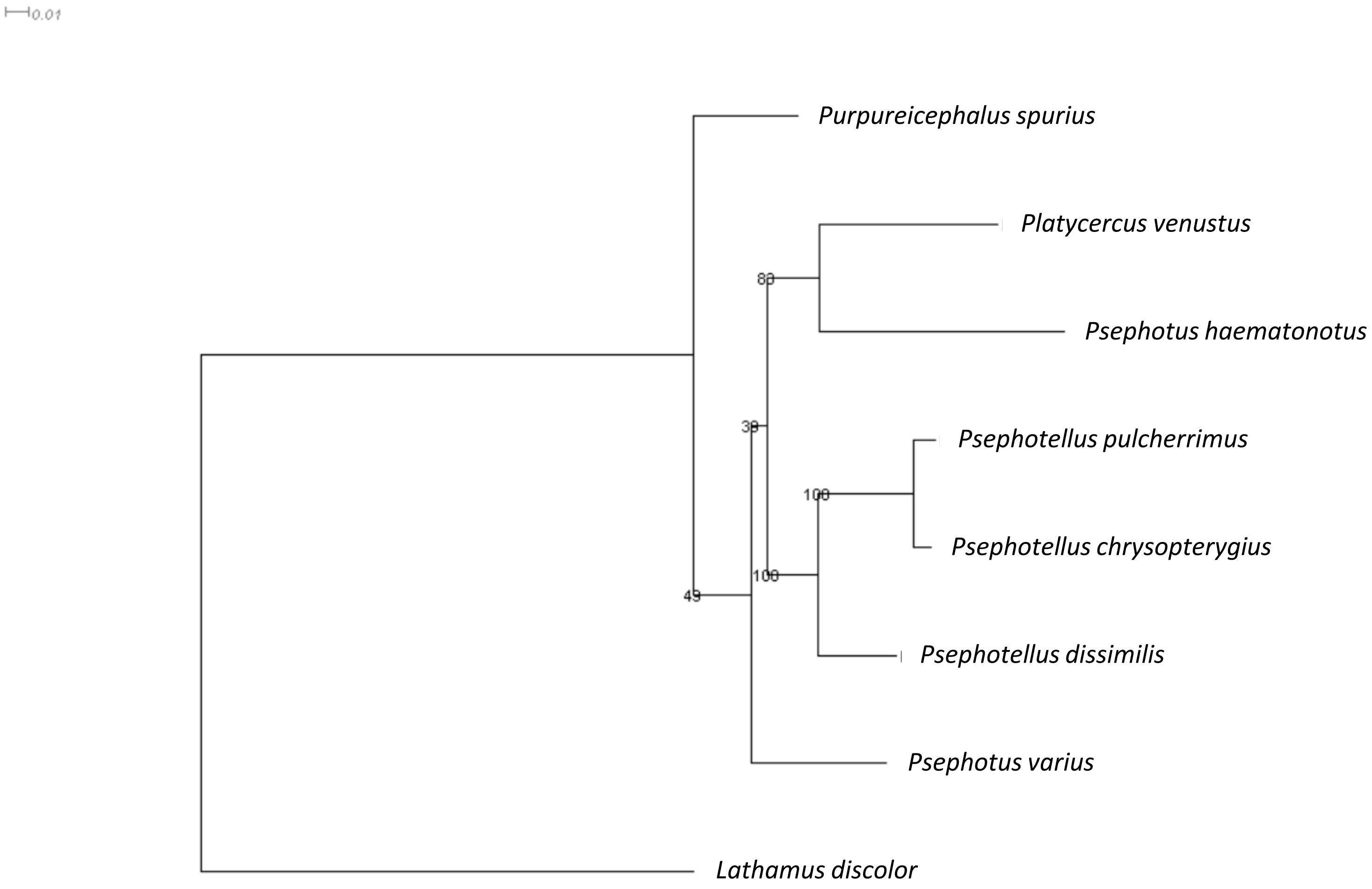

Figure S7. Best-fit maximum-likelihood trees estimated for the concatenated data sets consisting of all five genes (4,870 bp) using RAxML. Bootstrap values are indicated at the nodes.

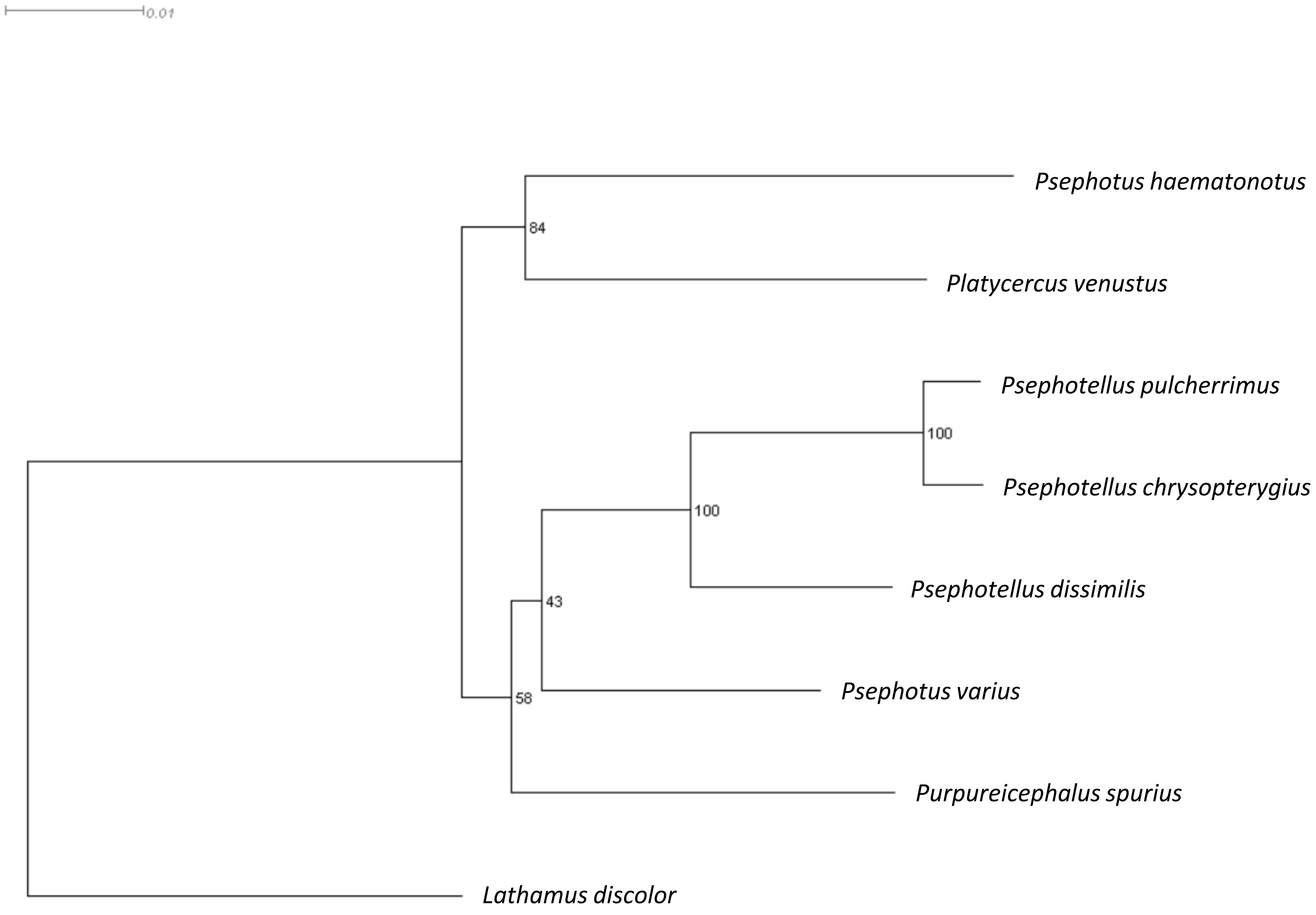

Figure S8. Species tree based on the individual gene trees using MP-EST. Bootstrap values are indicated at the nodes.