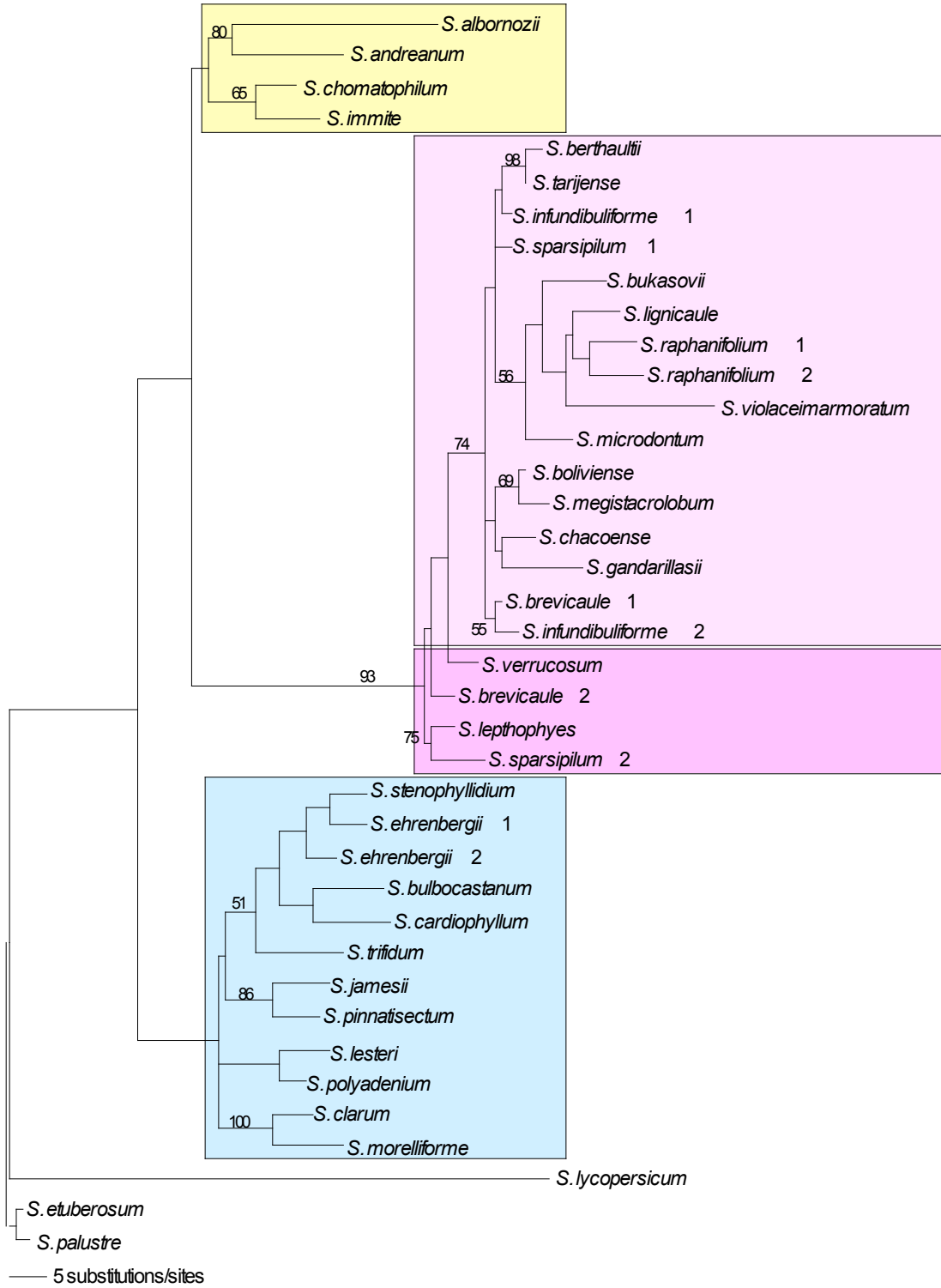
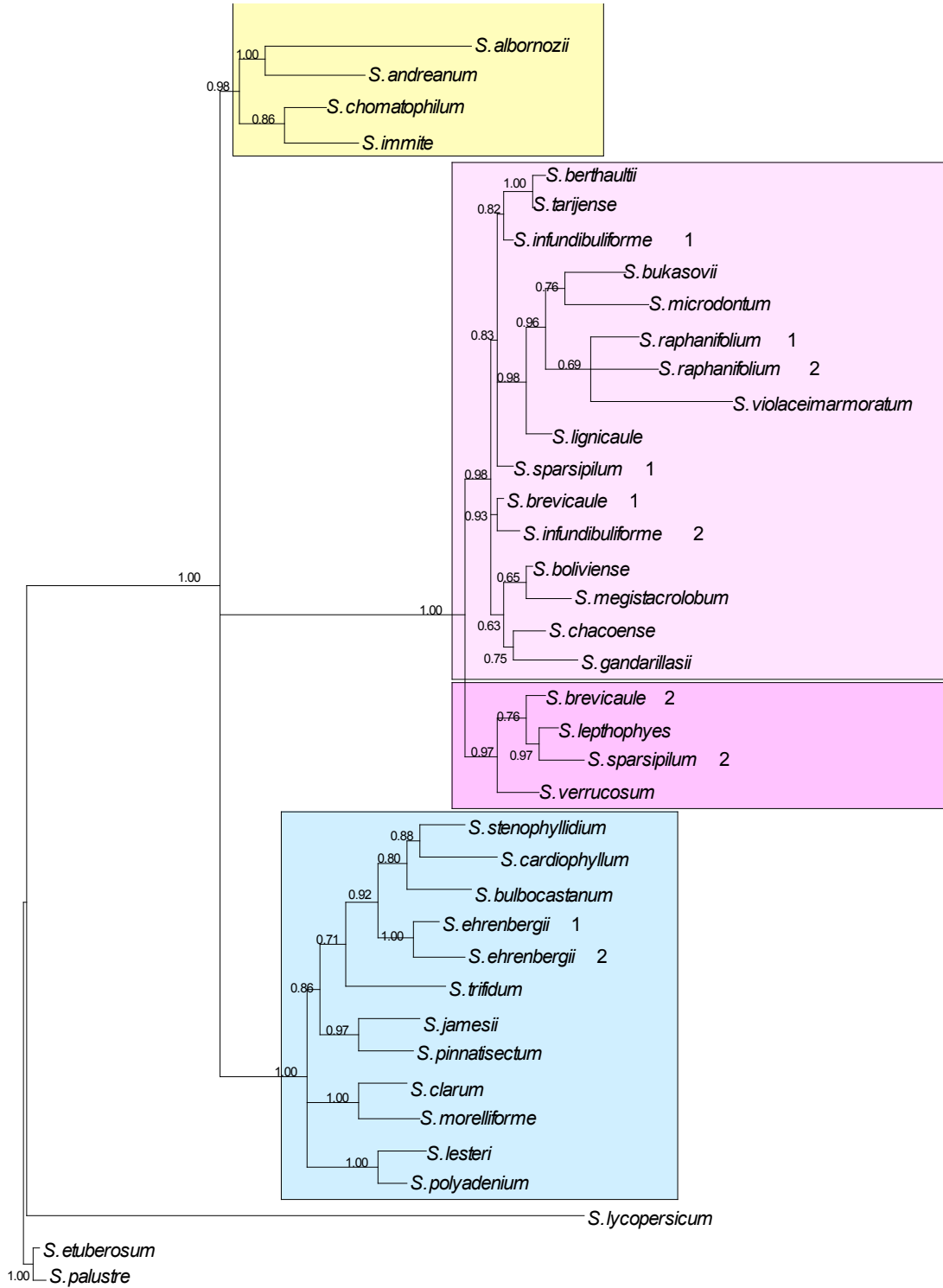


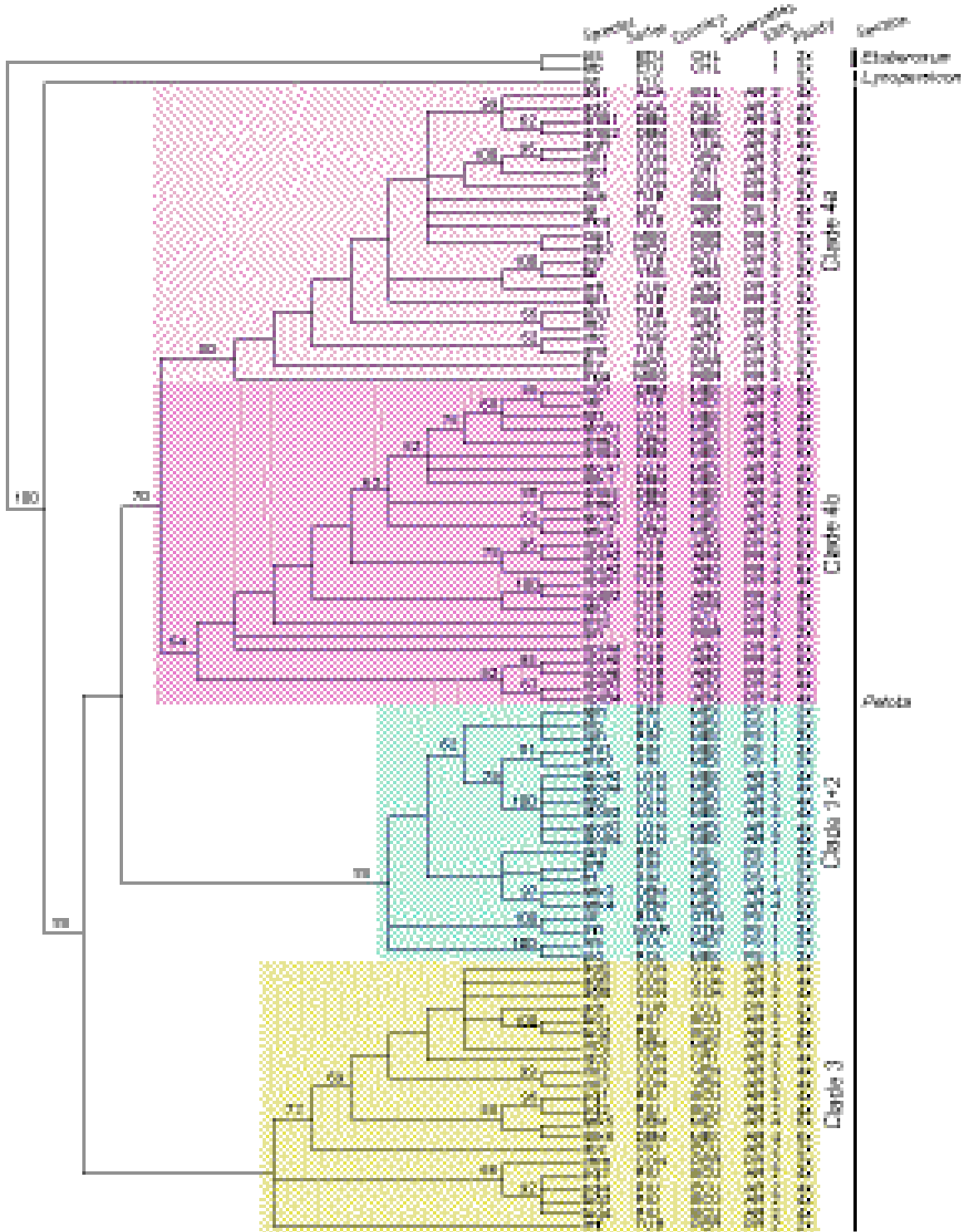
SUPPLEMENTARY FIGURE 1. Maximum likelihood phylogram for diploid species (substitution model GTR + I + Γ , $-\ln L=4619.667$). Bootstrap values higher than 50% are indicated above branches. Numbers after species names indicate allelic variants.



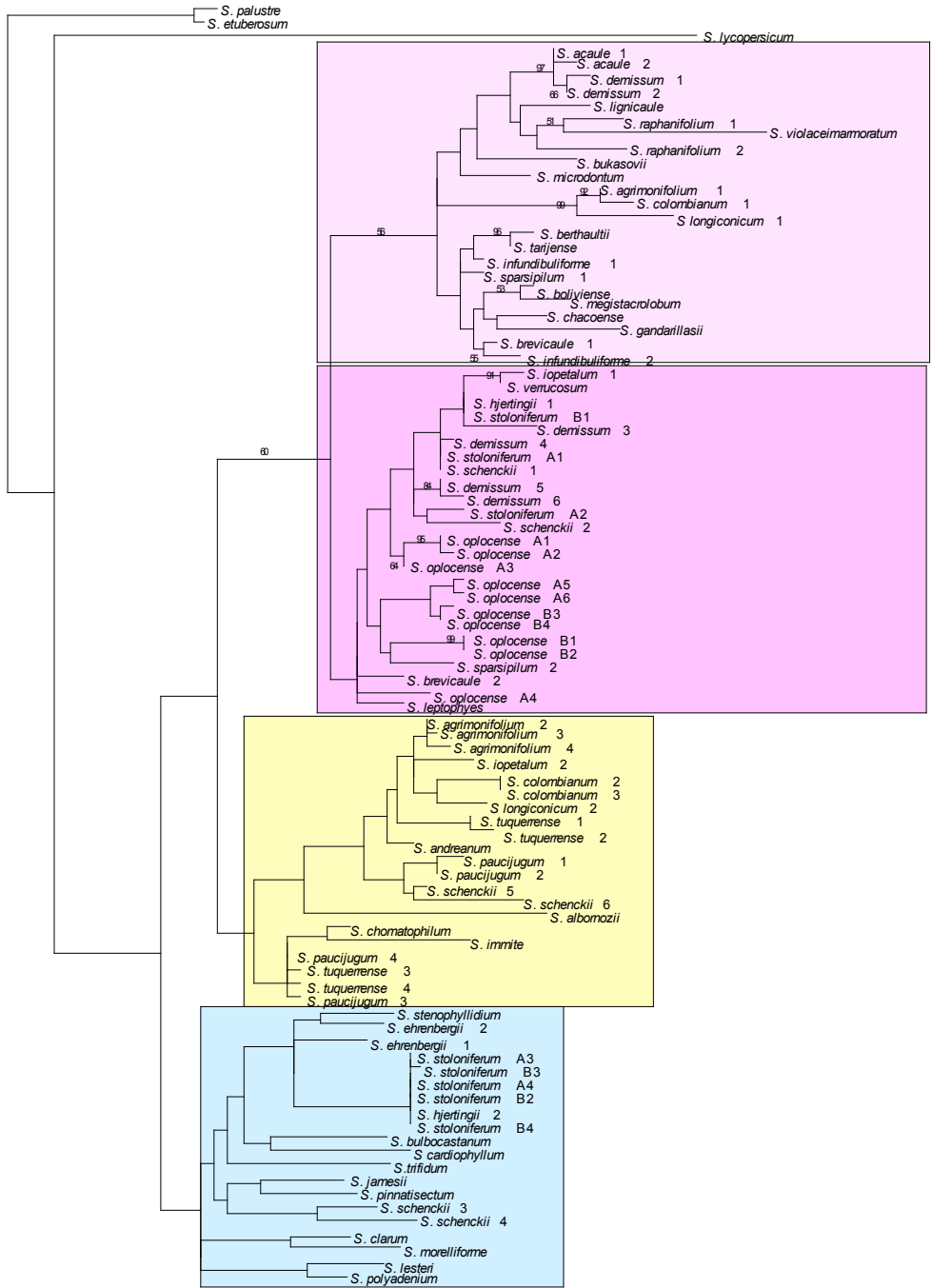
SUPPLEMENTARY FIGURE 2. Bayesian phylogram of diploid species. Posterior probability values are indicated for nodes with a probability value greater than 0.50. Numbers after the species names indicate allelic variants.



SUPPLEMENTARY FIGURE 3. Strict consensus of 9482 equal-length trees (L=712, CI=0.680, RI=0.846) of diploid and polyploid species. Bootstrap values higher than 50% are indicated above branches. Numbers after the 3-letter species codes indicate allele variants. Letters after the species acronym indicate another accession for the same species.



SUPPLEMENTARY FIGURE 4. Maximum likelihood phylogram of diploid and polyploid species. Branches are drawn in proportion to the substitutions per site assuming the GTR+I+ Γ model. Bootstrap values higher than 50% are indicated above branches. Numbers after species names indicate allele variants. Letters after the species name indicate another accession for the same species.



— 0.001 substitutions/site