Figure S1. Maximum likelihood phylogenetic tree of 52 taxa based on *rpl32* gene sequence. Bootstrap support values >50% are shown at nodes. Red and black lines indicate nuclear- and plastid-encoded copies of *rpl32* sequences, respectively. Scale bar indicates 0.05 substitutions/site.

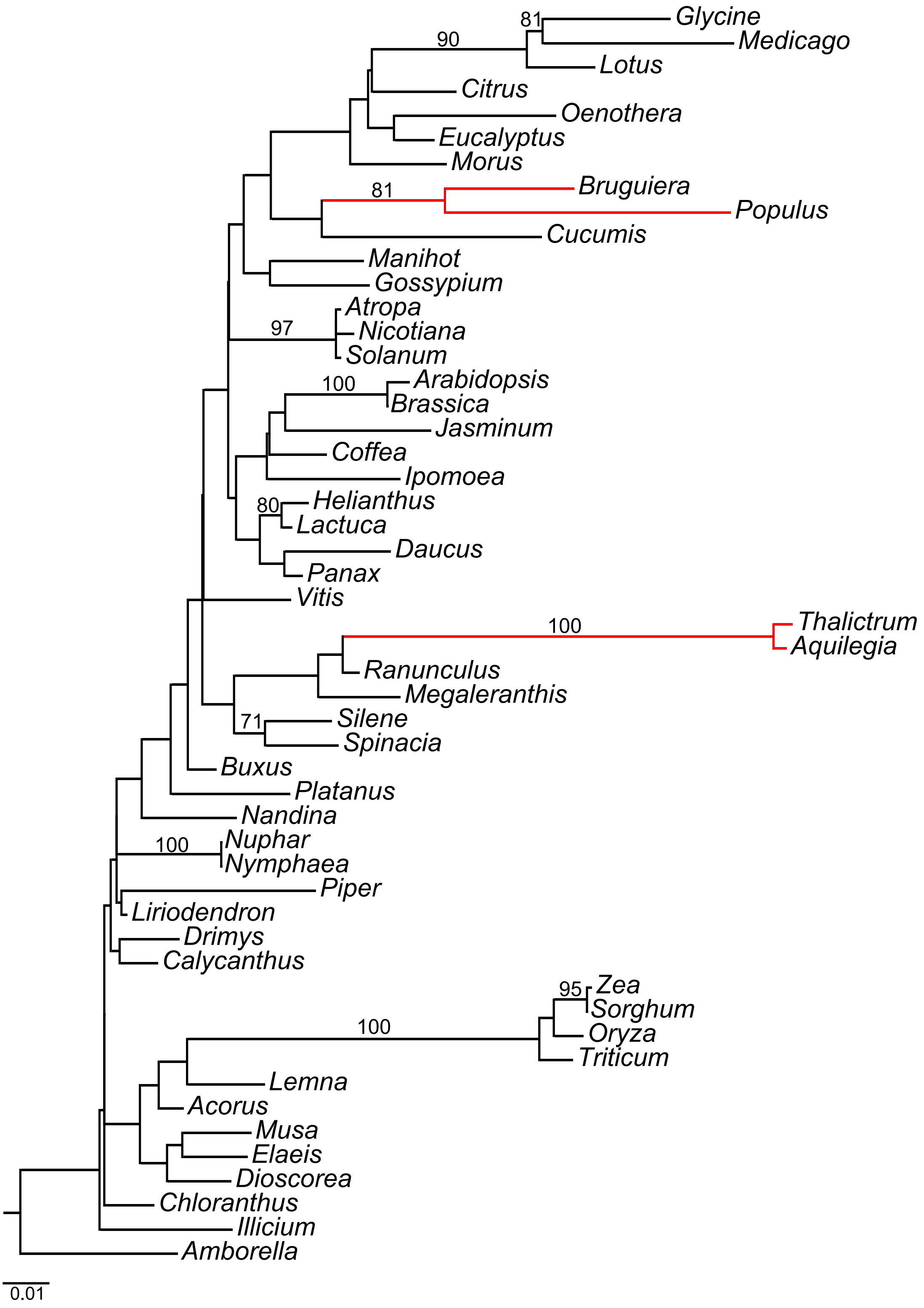

Figure S2. Alignment of the *infA* gene*.* **A.** Nucleotide sequence alignment of nuclear and transcript copies from *Aquilegia*. Intron is highlighted in colors. **B.** Amino acid sequence alignment of the nuclear copies of *rpl32* of *Thalictrum* and *Aquilegia*. Green box indicates plastid transit peptides (TP) that were predicted using TargetP. Red box indicates a conserved domain of translation initiation factor A.

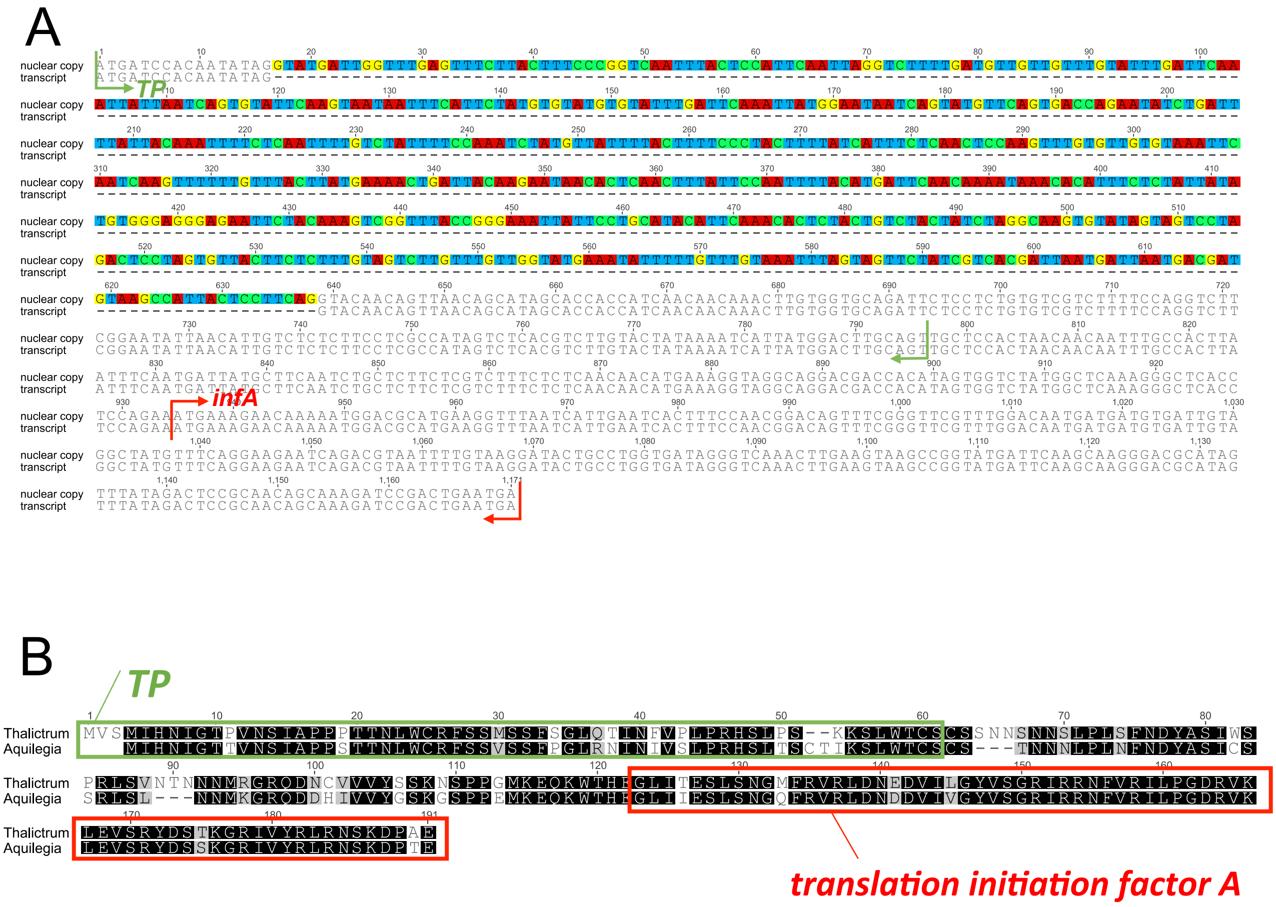

Figure S3. Maximum likelihood phylogenetic tree inferred from 16 genes from 51 taxa of angiosperms used as a constraint tree for rate comparisons. Bootstrap support values >50% are shown at nodes. Scale bar indicates 0.01 substitutions/site.