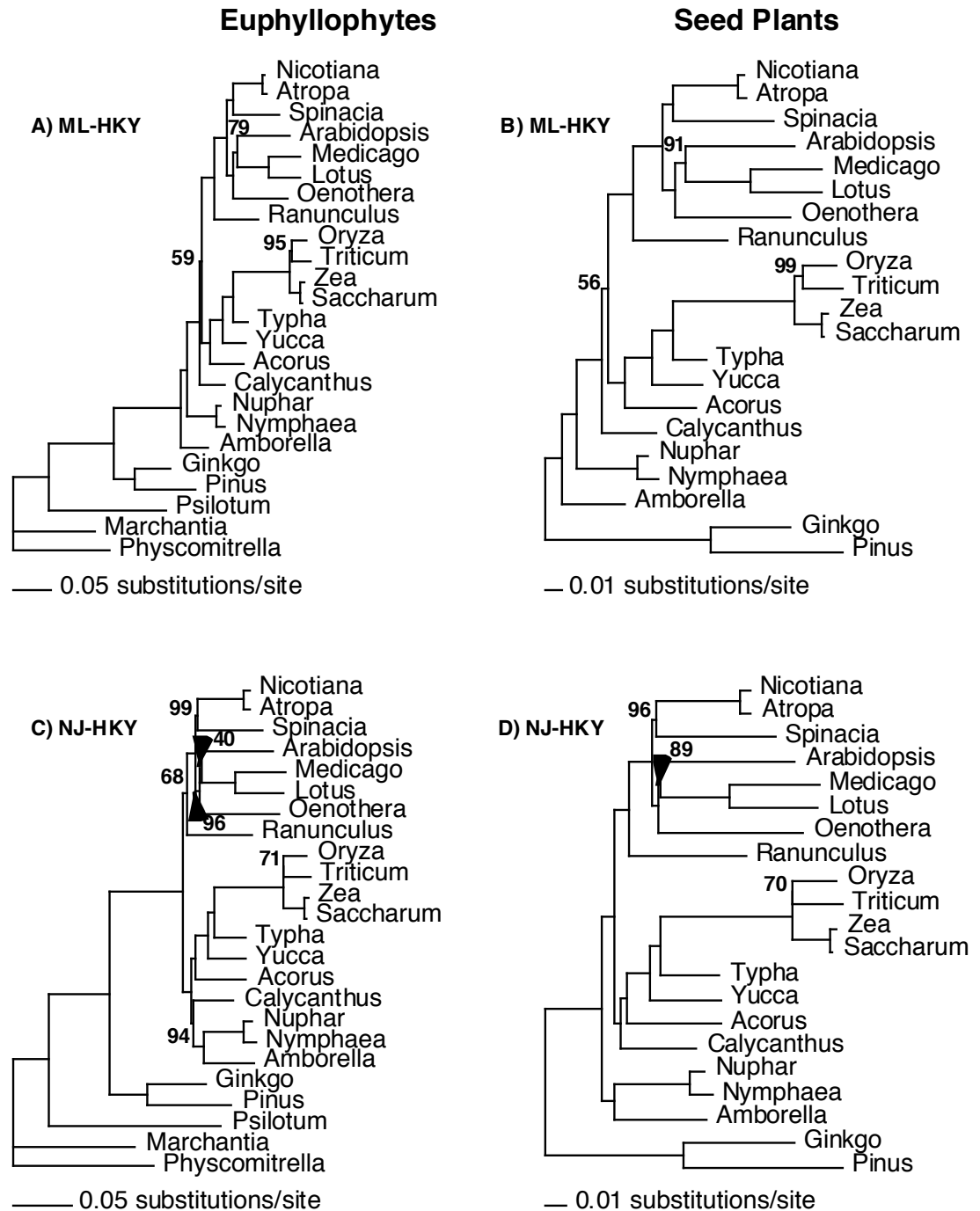
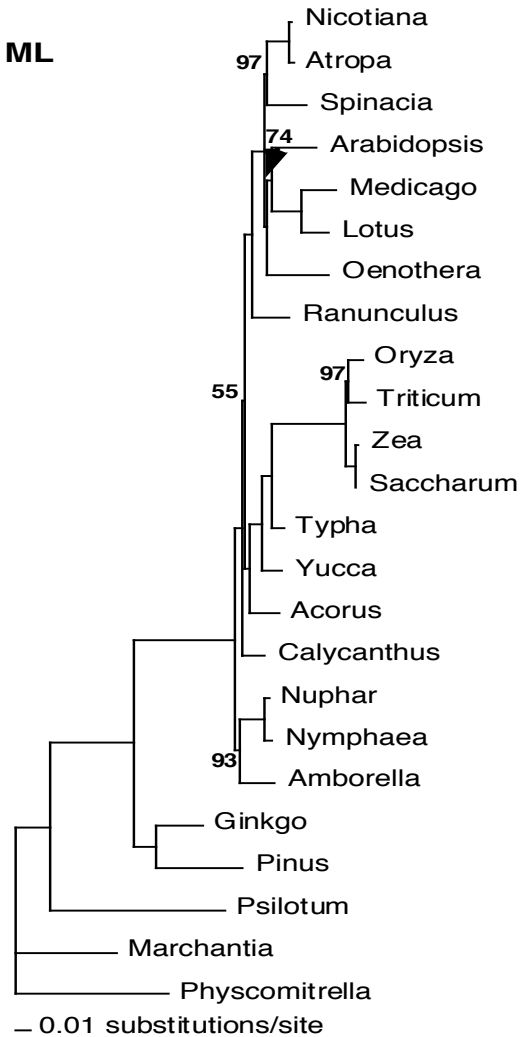


Supplemental Figure 1. ML and NJ phylogenies recovered using the HKY substitution model without correction for among-site variation. Comparison of ML (A and B) and NJ phylogenies (C and D) estimated from alignments including euphyllphytes (A and C) or just seed plant sequences (B and D) shows that the NJ analyses run under the simple HKY model are influenced by the inclusion or exclusion of distant outgroup sequences. Bootstrap values are not shown for nodes with 100% support.

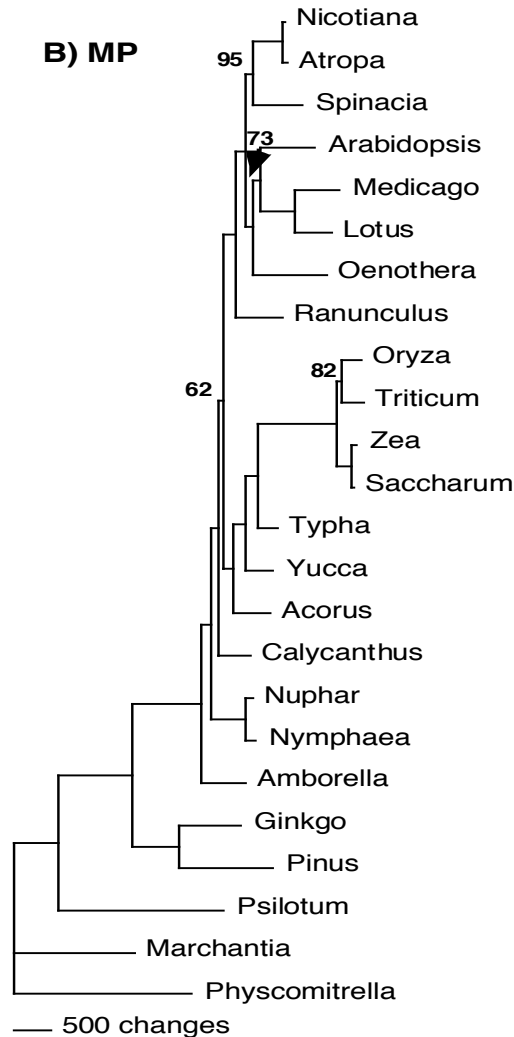


Codon Pos 1 & 2

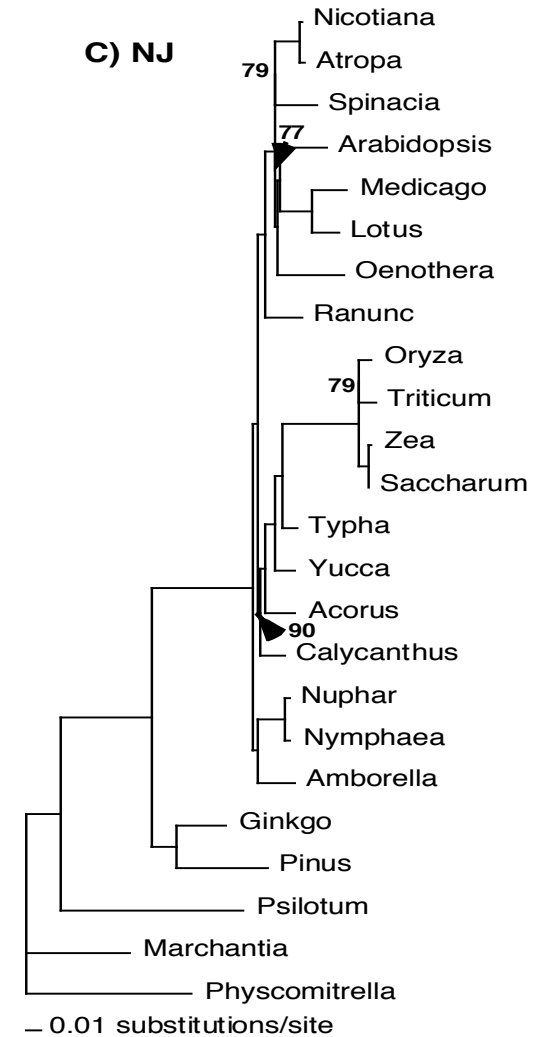
A) ML



B) MP



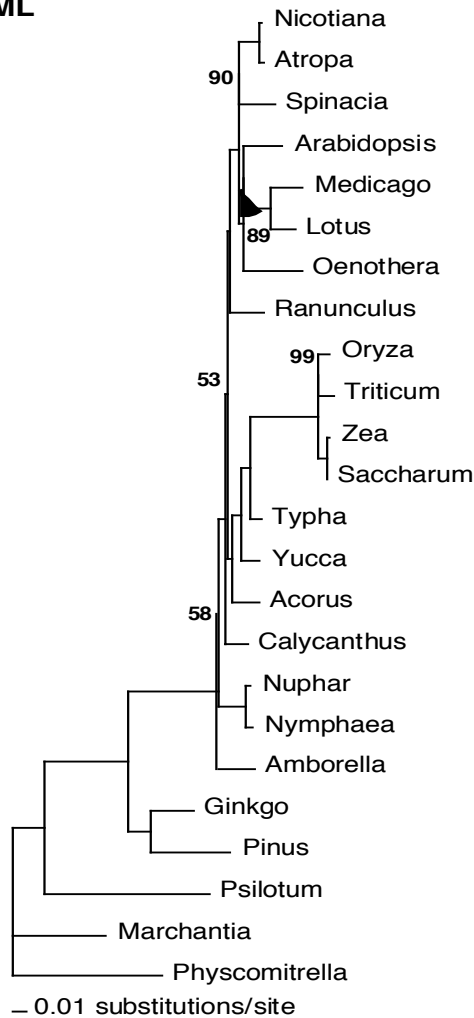
C) NJ



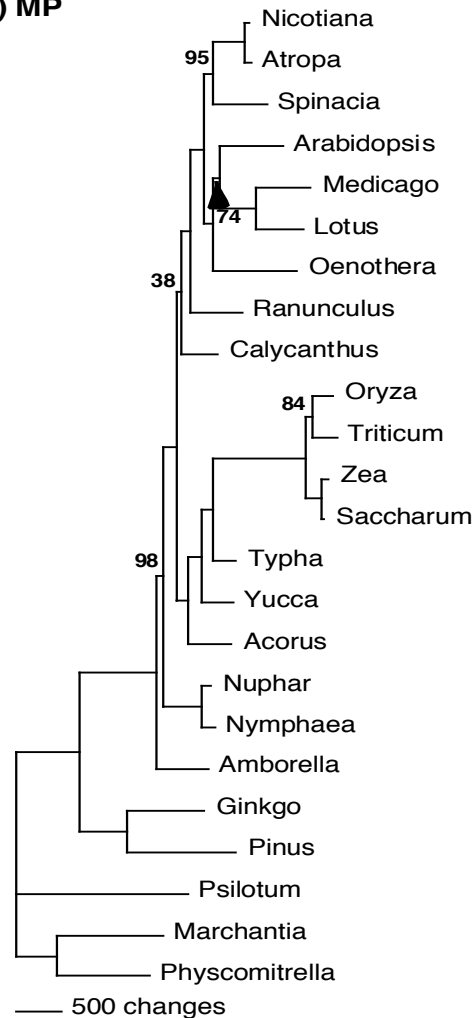
Supplemental Figure 2. ML (A), MP (B) and NJ (C) phylogenies with bootstrap values from analyses of 1st and 2nd codon positions in the nucleotide alignments are very similar to those estimated with all three codon positions (fig. 4). The bootstrap value increased for the water lilies + *Amborella* clade in the ML analysis and the poorly supported placement of *Calycanthus* relative to the eudicots and monocots changed in the MP analysis. ML and NJ analyses performed using the HKY+ Γ +I model as described in text. Bootstrap values are not shown for nodes with 100% support.

AA alignment

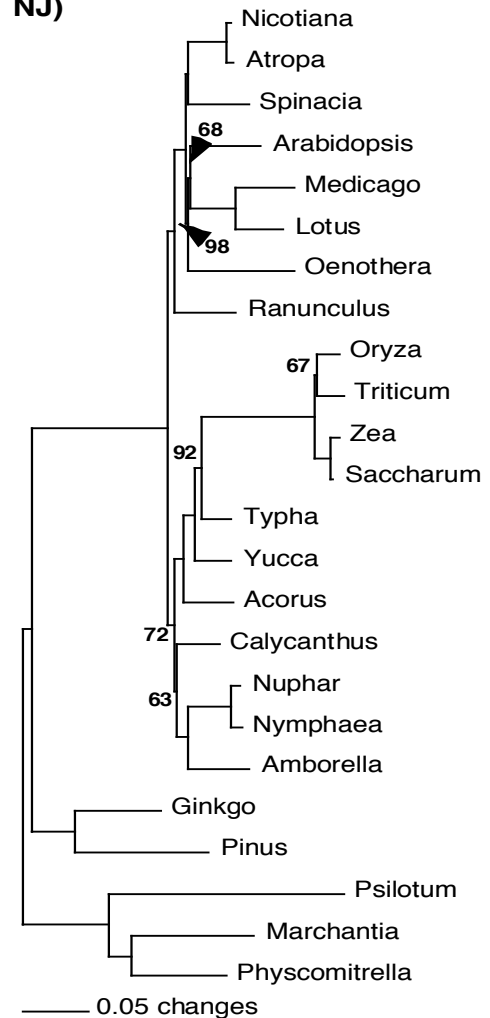
A) ML



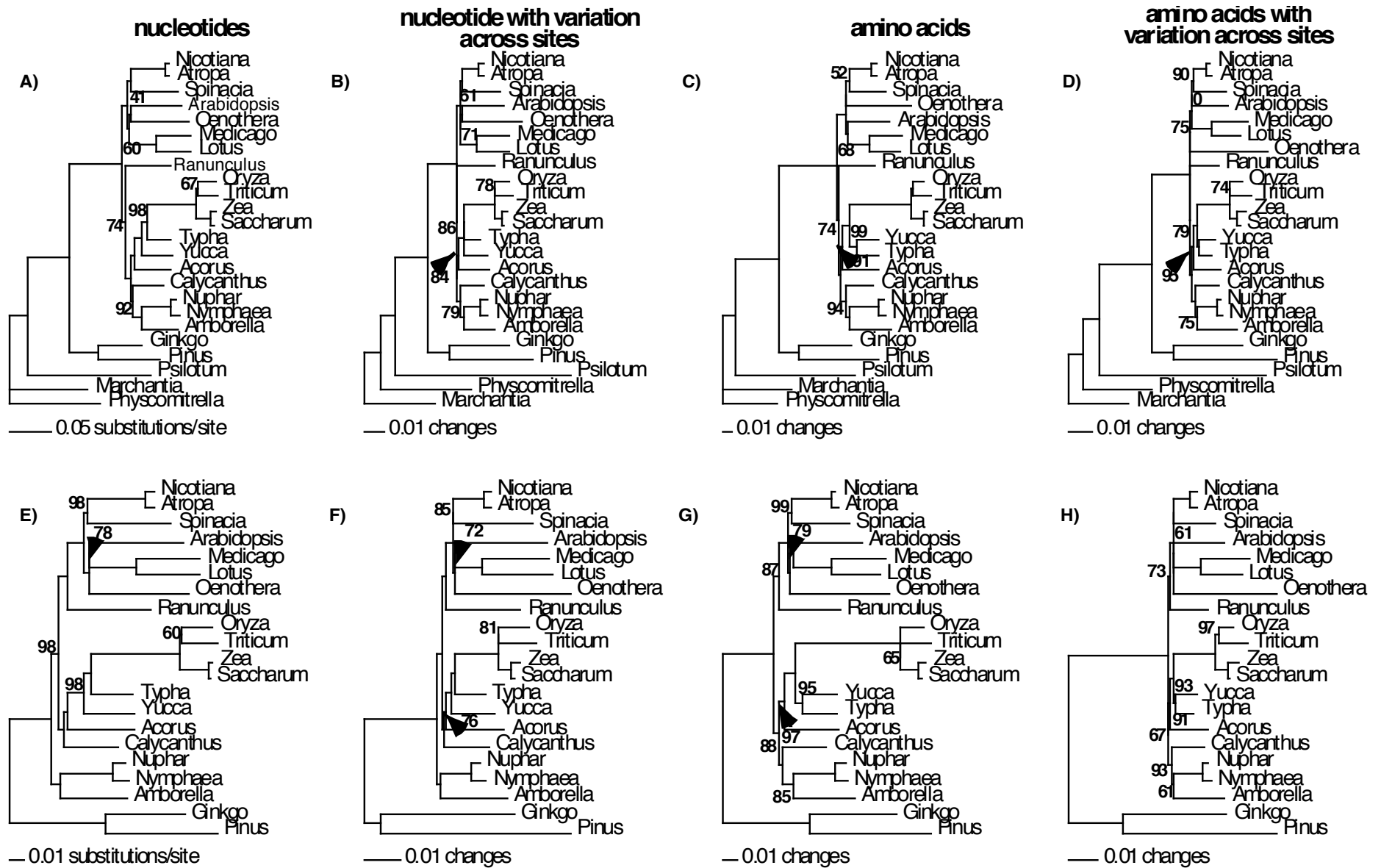
B) MP



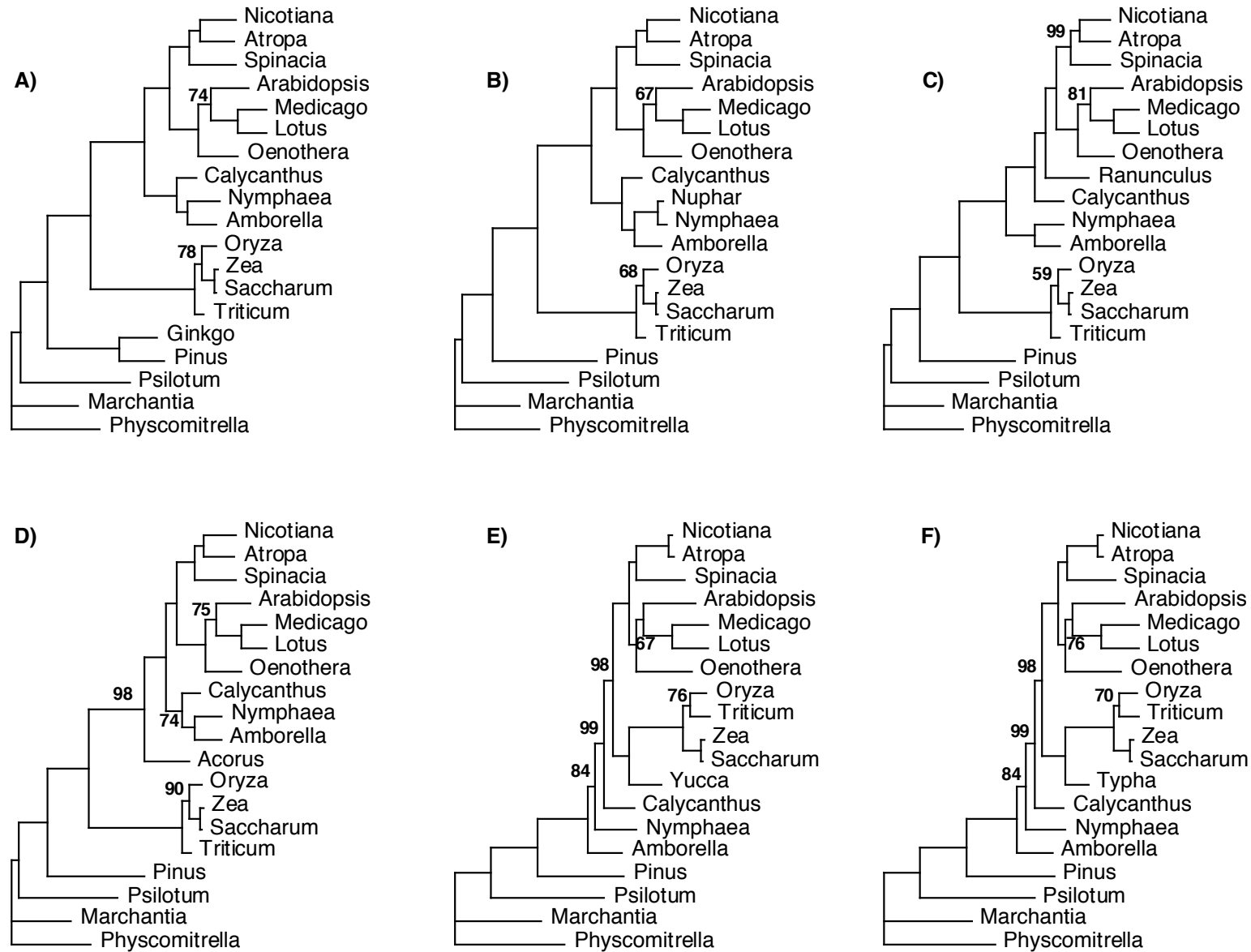
NJ)



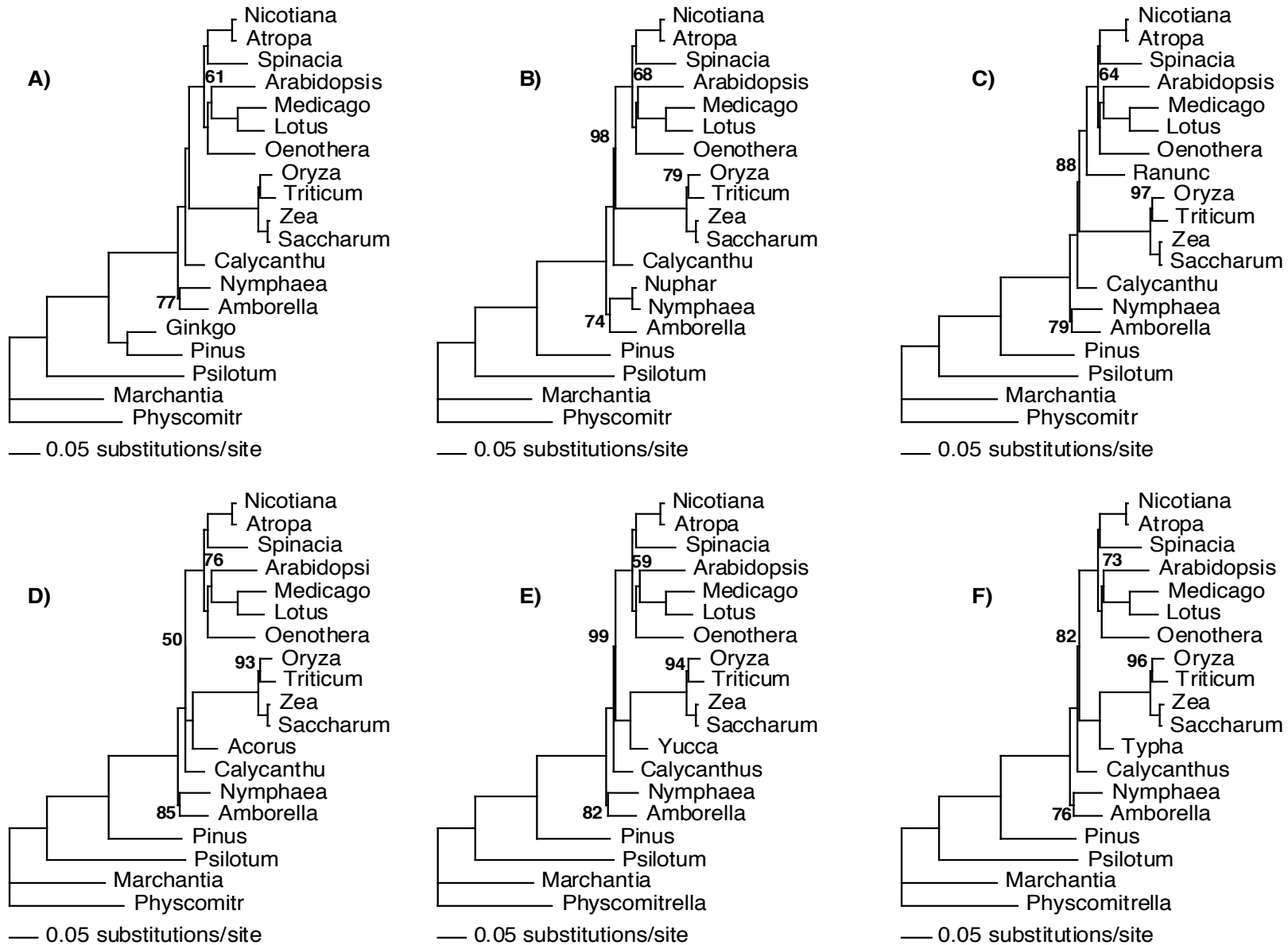
Supplemental Figure 3. The results of ML (A) and NJ (C) analyses of amino acid alignment differ slightly from those estimated with the complete nucleotide alignment (fig. 4). The ML analysis (JTT+ Γ +I) returns poor support of *Amborella* as sister to all other angiosperms, and the NJ analysis (JTT+ Γ) places eudicots as sister to the remaining angiosperms. A NJ analysis restricted to the seed plants returns relationships identical to those for seed plants shown in figure 4C. Bootstrap values are not shown for nodes with 100% support.



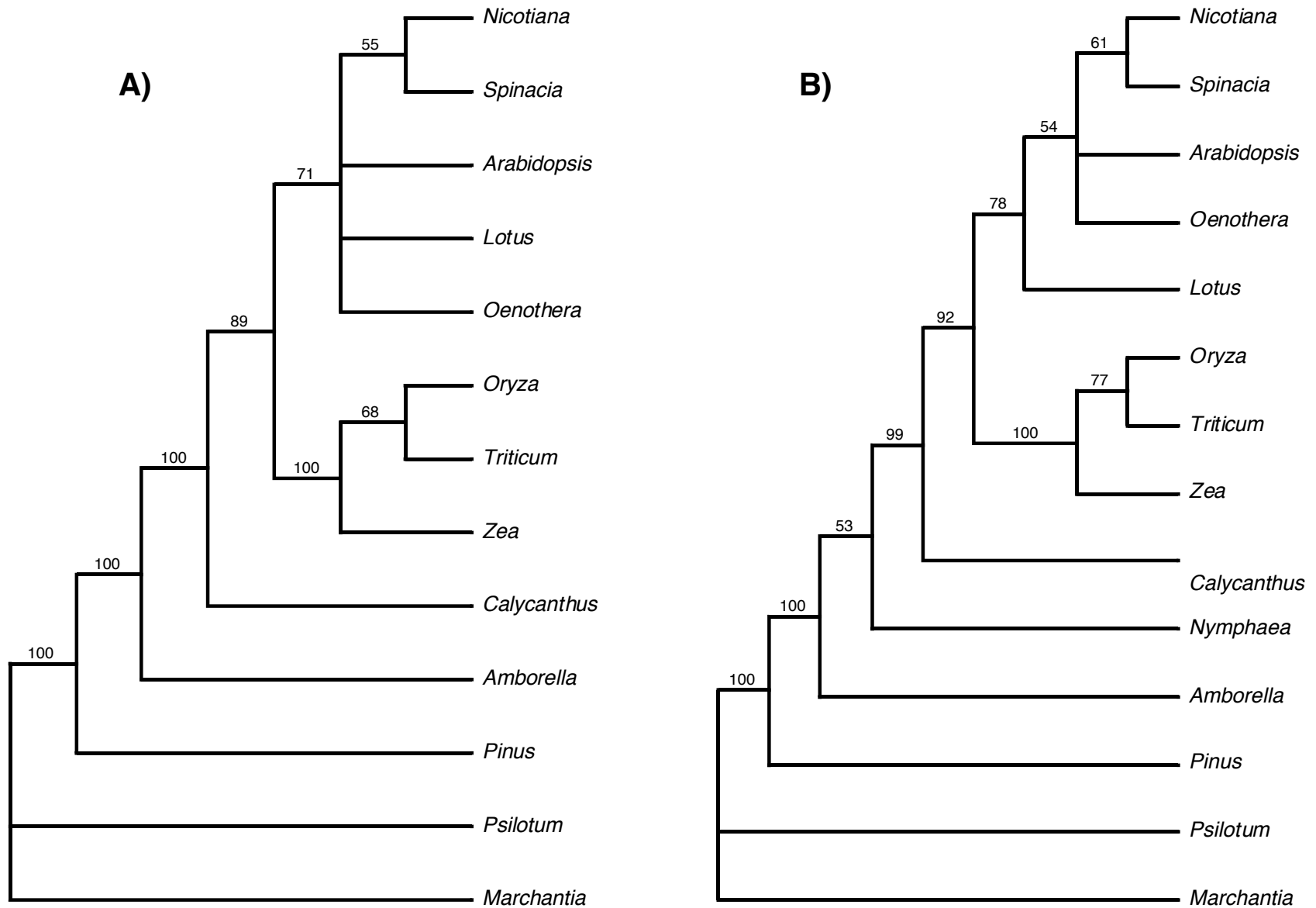
Supplemental Figure 4. Phylogenies resulting from analyses performed on the complete nucleotide and amino acid alignments (ungapped) using LogDet corrected distances place core eudicots as sister all other angiosperms including *Ranunculus* (A-D). Whereas analyses restricted to the seed plant nucleotide alignment recover relationships identical to those for seed plants shown in figure 4C (E and F), the eudicots are placed sister to the remaining angiosperms in analyses of the amino acid alignment for seed plants (G and H). Topologies are identical for LogDet analyses performed with (B, D, F and H) and without (A, C, E and G) variation rates across sites (see text). Bootstrap values shown for nodes where less than 100%.



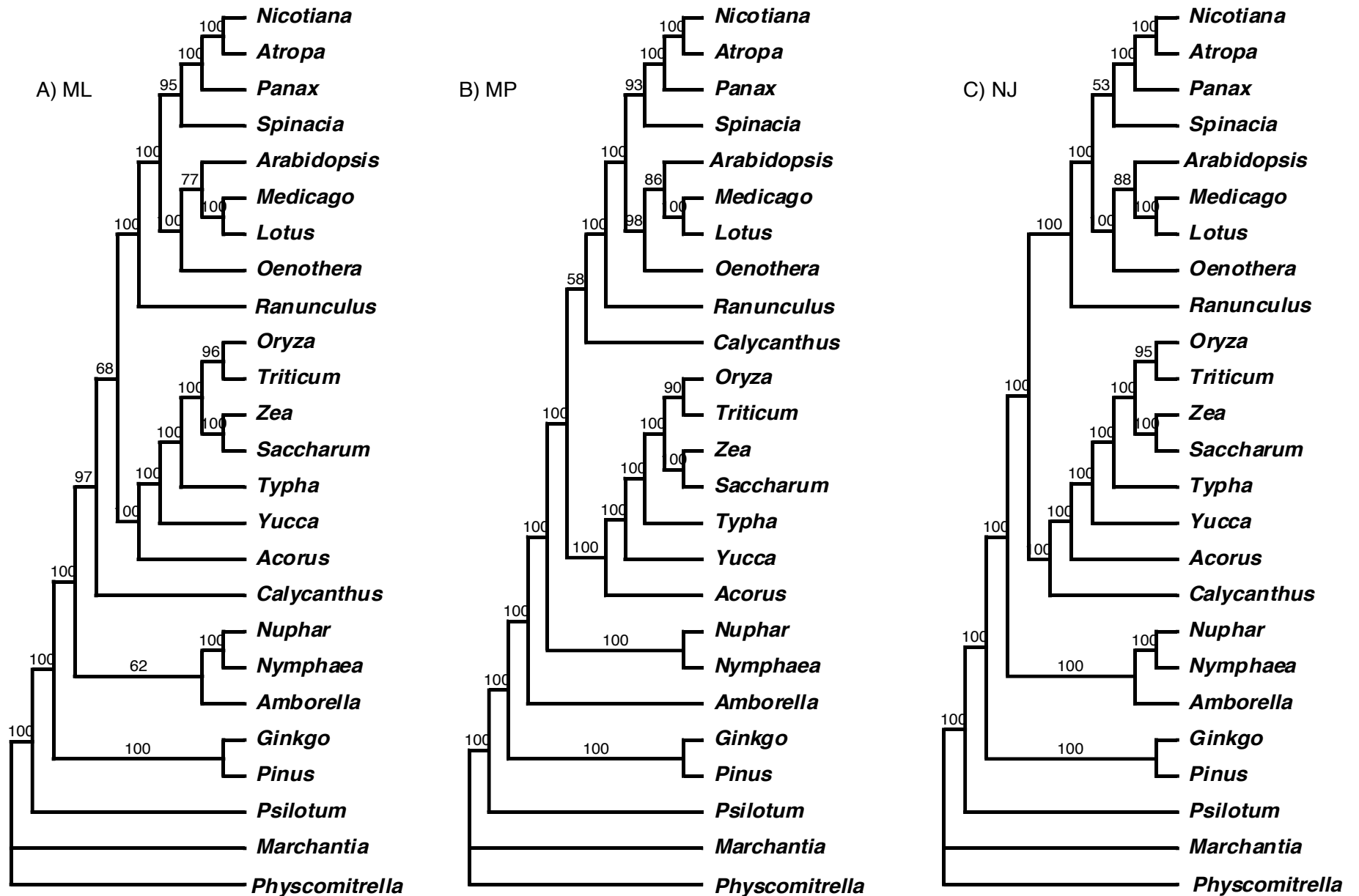
Supplemental Figure 5. Phylogenies from MP analyses adding *Ginkgo* (A), *Nuphar* (B), *Ranunculus* (C), *Acorus* (D), *Yucca* (E) and *Typha* (F) one at a time to a 61 gene nucleotide alignment of previously available plastid genomes. Bootstrap values shown for nodes where less than 100%.



Supplemental Figure 6. Phylogenies from ML analyses adding *Ginkgo* (A), *Nuphar* (B), *Ranunculus* (C), *Acorus* (D), *Yucca* (E) and *Typha* (F) one at a time to a 61 gene nucleotide alignment of previously available plastid genomes. The HKY+ Γ +I substitution model was used in all analyses. Bootstrap values shown for nodes where less than 100%.



Supplemental Figure 7. Parsimony bootstrap consensus trees of indel characters, using taxon sets from A) Goremykin et al. (2003) and B) Goremykin (2004). For analysis A, one MP tree was obtained (115 steps; CI=0.9111; RC = 0.8856) with *Amborella* the first branching angiosperm, while B obtained two MP trees at 127 steps (CI=9134; RC = 0.8560), one with *Amborella* and one with *Amborella* + *Nymphaea* as the earliest angiosperm branch.



Supplemental Figure 8. Bootstrap consensus phylogenies for ML, MP and NJ analyses of nucleotide alignment including 61 genes from *Panax schinseng* plastid genome sequence (Kim and Lee 2004) are consistent with those shown in figure 4. All analyses performed as described in text.