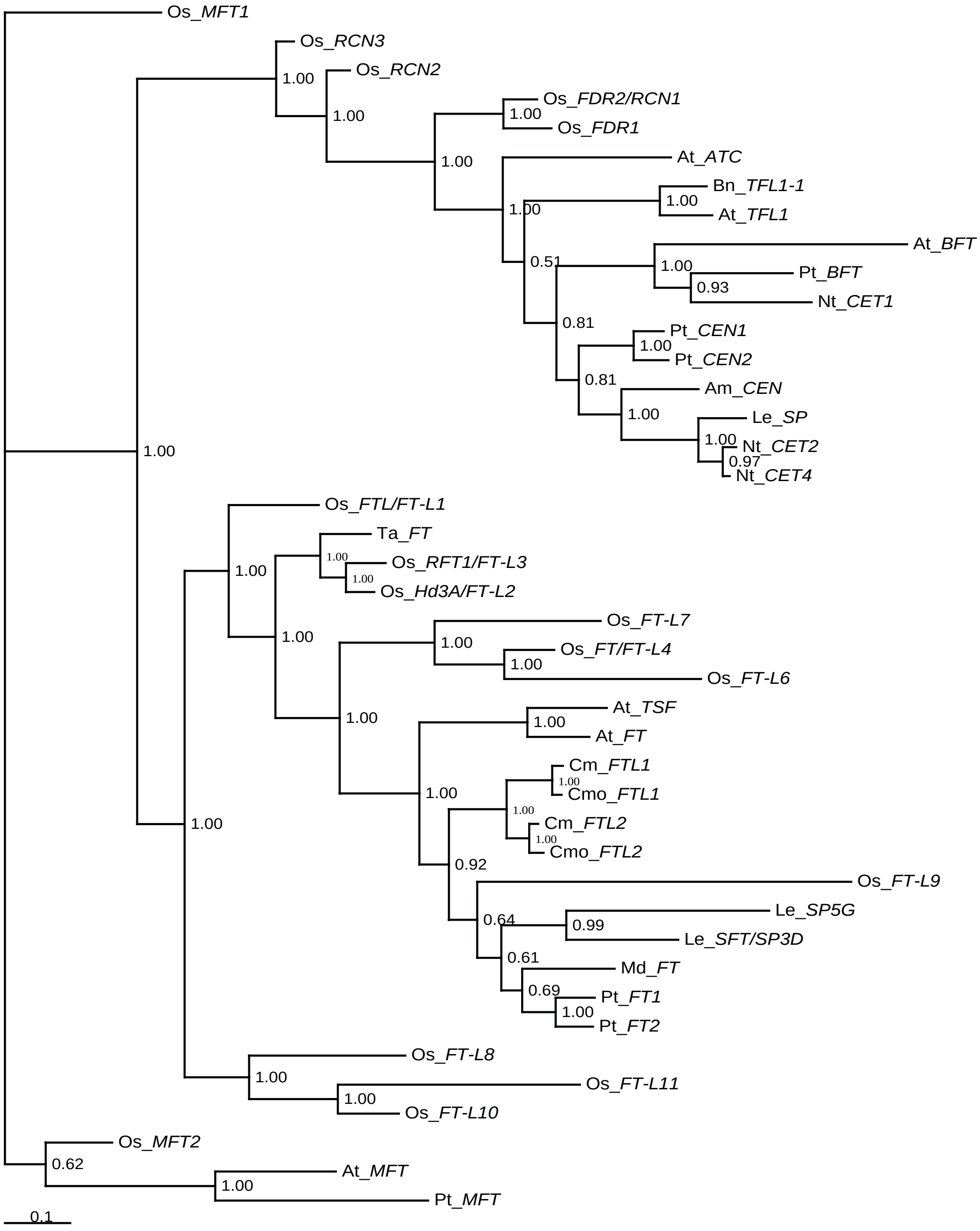

Supplemental Figure 3: Bayesian phylogenetic analysis of 40 FT-TFL family members in Angiosperms. Maximum likelihood methods were implemented in MrBayes 3.0B4 using the GTR model of nucleotide substitution. Three million generations were run, sampling every 100 generations, and a consensus tree was drawn after the first 10,000 trees were discarded. Interior branch numbers represent Bayesian posterior probabilities. The genes and their accession numbers are found in Supplemental Table 1. Abbreviations for species are: *Cucurbita maxima* (Cm), *Cucurbita moschata* (Cmo), *Antirrhinum majus* (Am), *Arabidopsis thaliana* (At), *Brassica napus* (Bn), *Lycopersicon esculentum* (Le), *Malus x domestica* (Md), *Nicotiana tabacum* (Nt), *Oryza sativa* (Os), *Populus trichocarpa* (Pt), *Triticum aestivum* (Ta).