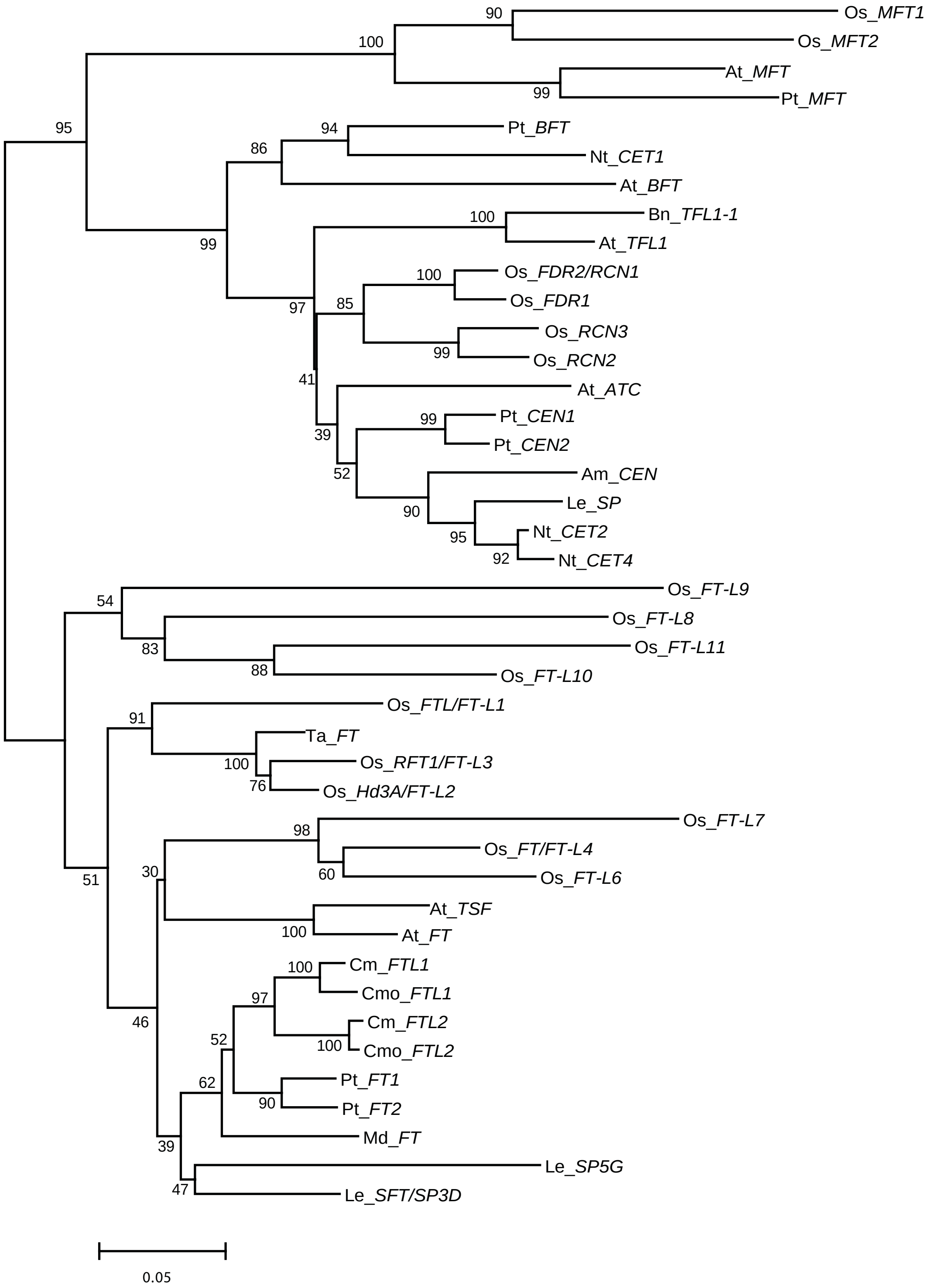

Supplemental Figure 2: NeighborJoining phylogenetic analysis of 40 FT-TFL family members in Angiosperms. The tree was constructed based on a nucleic acid alignment of approximately 500 protein-coding nucleotides, using the neighborjoining method implemented in MEGA 3.1. Numbers at each branch point are the bootstrap values for percentages of 1,000 replicate trees and only values >50% are shown. 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).