

Figure S1. Phylogenetic trees were constructed using three different algorithms. (a) NJ (neighbor-joining) tree, (b) ML (maximum likelihood) tree, (c) Bayes (Bayesian) tree. Genes were clustered into *FT*-like, *BFT*-like, *TFL*-like, *CEN*-like, and *MFT*-like subfamilies.

