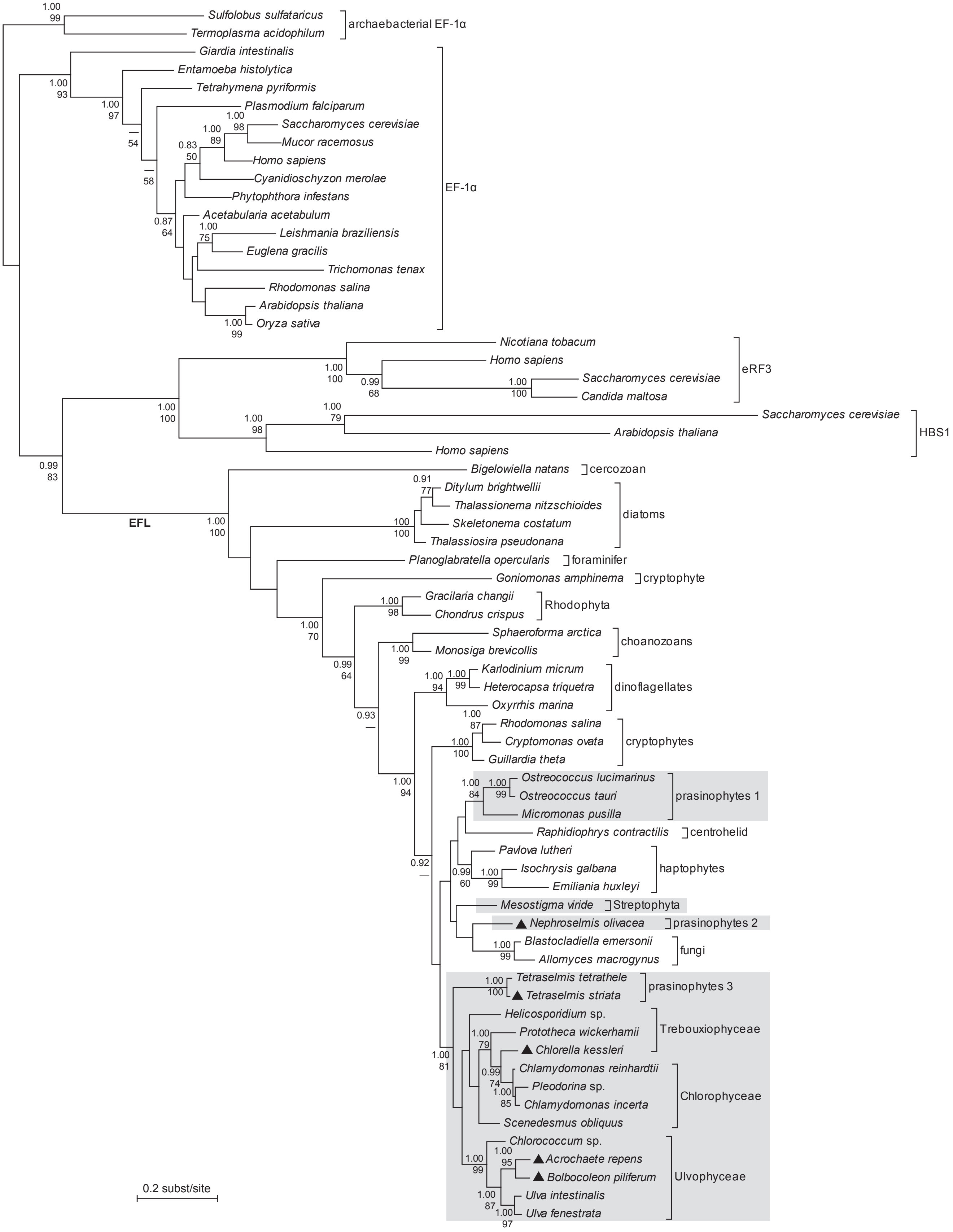

Figure S2. Phylogeny inferred from amino-acid sequences of EFL and related subfamilies of the GTPase translation factor superfamily with Bayesian techniques. Sequences belonging to the green plant lineage are in gray boxes. The green plant EFL sequences seem to form separate lineages. Numbers at nodes indicate posterior probabilities (top) and ML bootstrap values (bottom); values below respectively 0.9 and 50 are not shown.