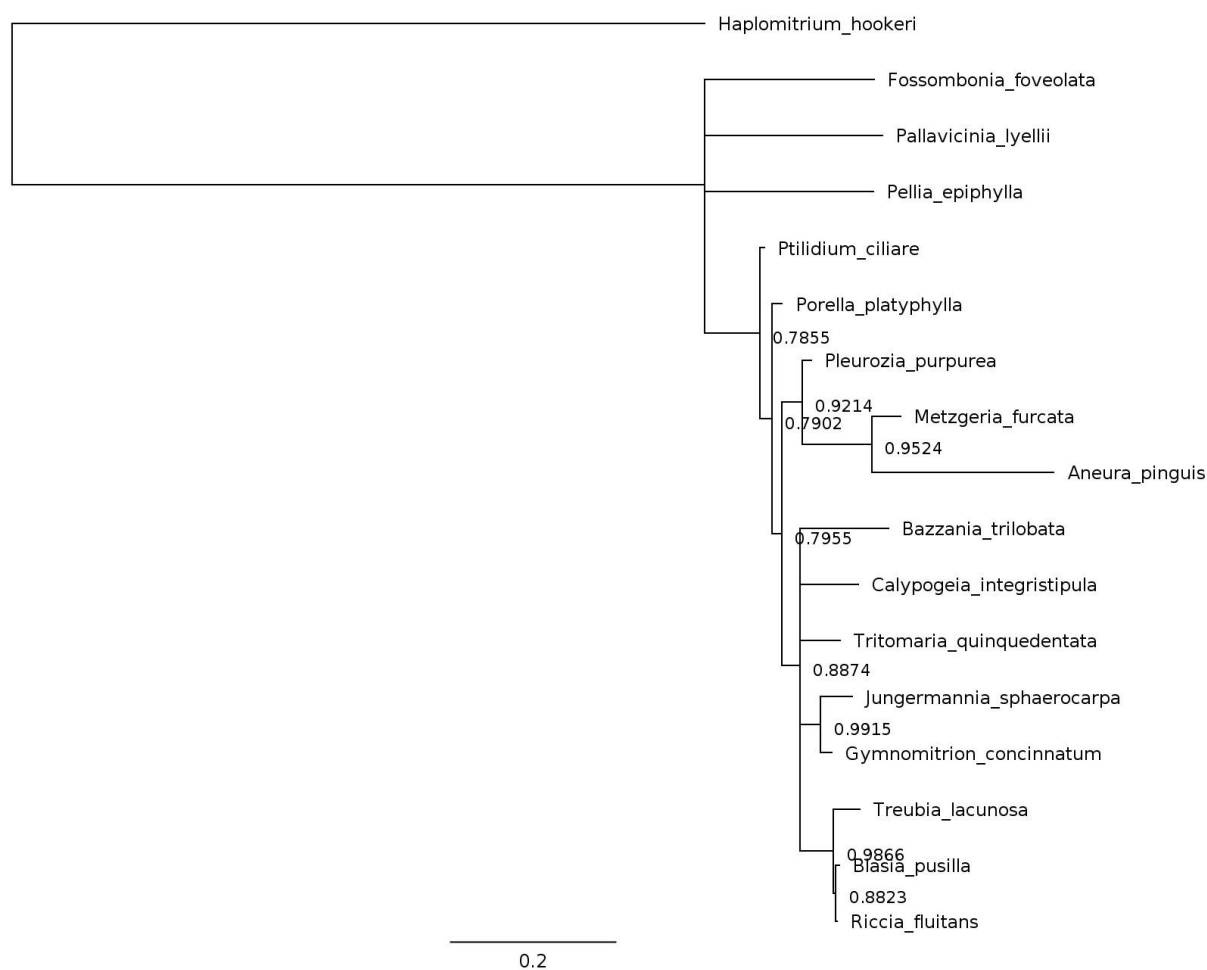


**Figure S1.** Phylogenetic relationships of 37 species of liverworts and mosses based on 33 concatenated mitochondrial protein-coding sequences. The phylogenetic tree was obtained as a result of Maximum Likelihood analysis. The bootstrap values are shown at the nodes. The scale bar indicates the number of substitutions per nucleotide position.





**Figure S3.** Phylogenetic relationships of 17 species liverworts based on binary-state matrix of predicted C-to-U editing sites positions. The phylogenetic tree was obtained as a result of Bayesian analysis. The posterior probability values are shown at the nodes. The scale bar indicates the number of substitutions per nucleotide position.