

**Supplementary file 4.** Bayesian majority-rule consensus tree of the *Ocotea* complex (Lauraceae) derived from the analysis of nuclear ribosomal ITS sequence data (269 terminals by 918 aligned sites) showing the placement of the morphologically enigmatic new species *Ocotea bilocellata* within the *Ocotea minarum* group (sensu Trofimov et al. 2019). Posterior probabilities from 0.5 to 1.0 are shown as color gradient from red to black as well as values on the branches. GenBank accession numbers and vouchers follow the terminal taxon labels.

