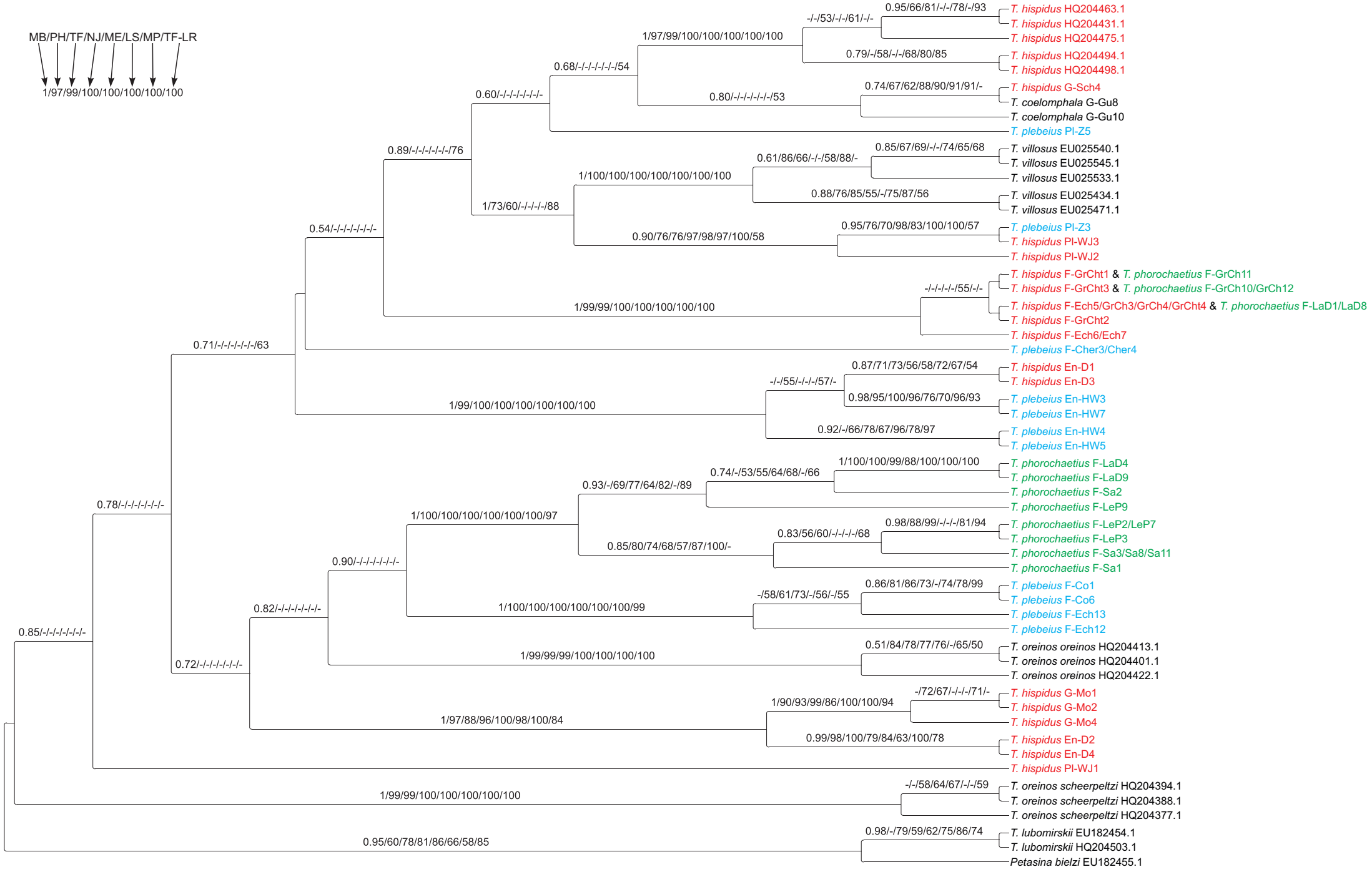Figure S1. The Bayesian cladogram for *COI* gene sequences assigned to *Trochulus*. Two sequences of *Trochulus lubomirskii* (= *Trichia lubomirskii* = *Plicuteria lubomirskii*) and one *Petasina bielzi* were also included as out-group. Labels for *T. hispidus*, *T. plebeius*, *T. phorochaetius* were coloured in red, blue, and green, respectively. Additional acronyms at the species name or ampersand symbol "&" indicate 100% sequence identity for the joined names. Numbers at nodes, in the order shown, correspond to posterior probabilities estimated in MrBayes (MB), as well as bootstrap support values calculated in PhyML (PH), TreeFinder (TF), and PAUP using neighbour joining (NJ), minimum evolution (ME), weighted least squares (WLS) and maximum parsimony (MP) methods. Additionally, support values obtained by Local Rearrangements-Expected Likelihood Weights method in TreeFinder (TF-LR) were shown. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were omitted or indicated by a dash "-".