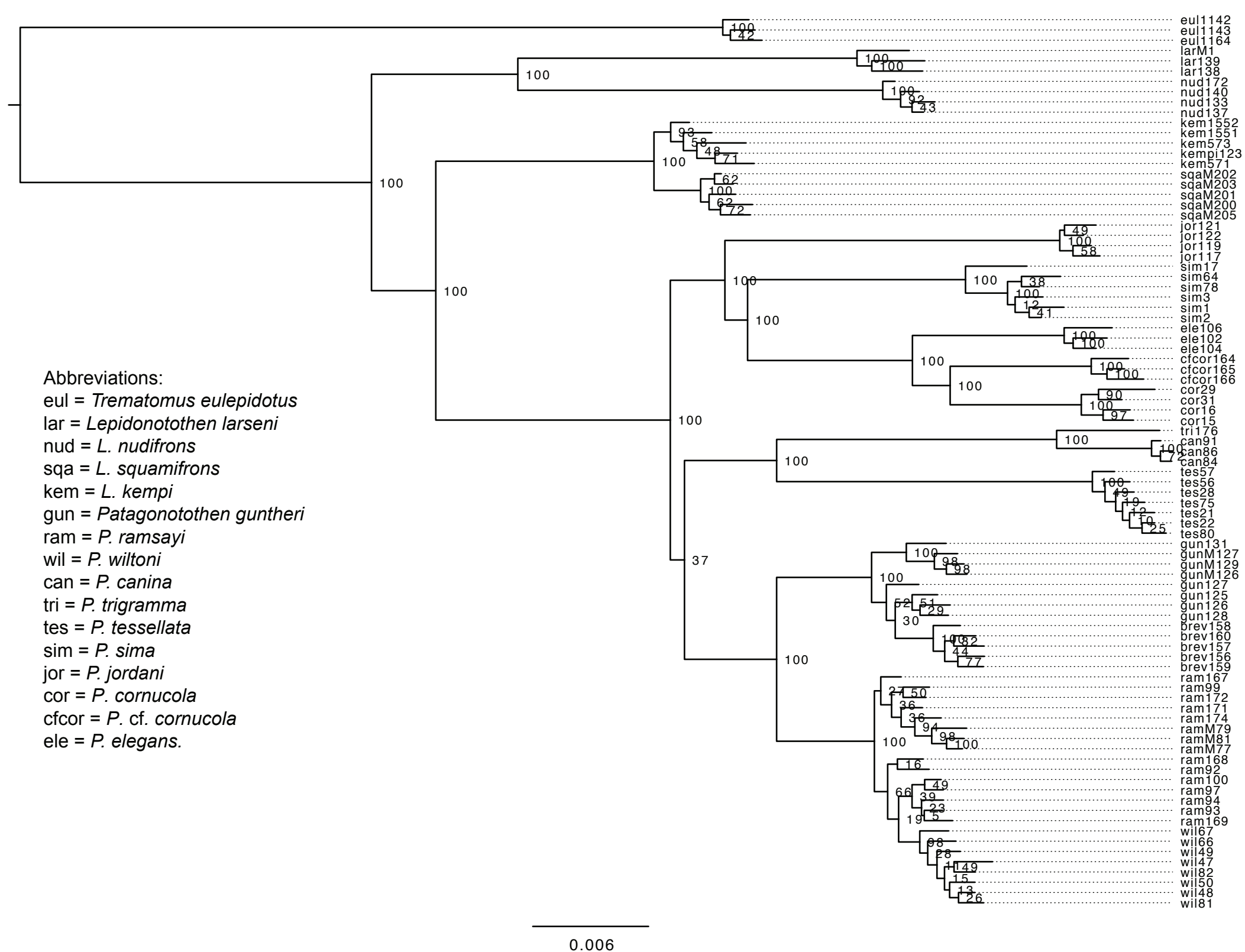




**Additional file 3.** Maximum-likelihood tree based on 18,485 SNPs from 2,914 RAD loci. Distant outgroups (*E. maclovinus*, *H. harpagifer* and *N. coriiceps*) were excluded in order to maximize the recovered number of loci and SNPs. Node labels represent bootstrap support values as obtained with RAxML.