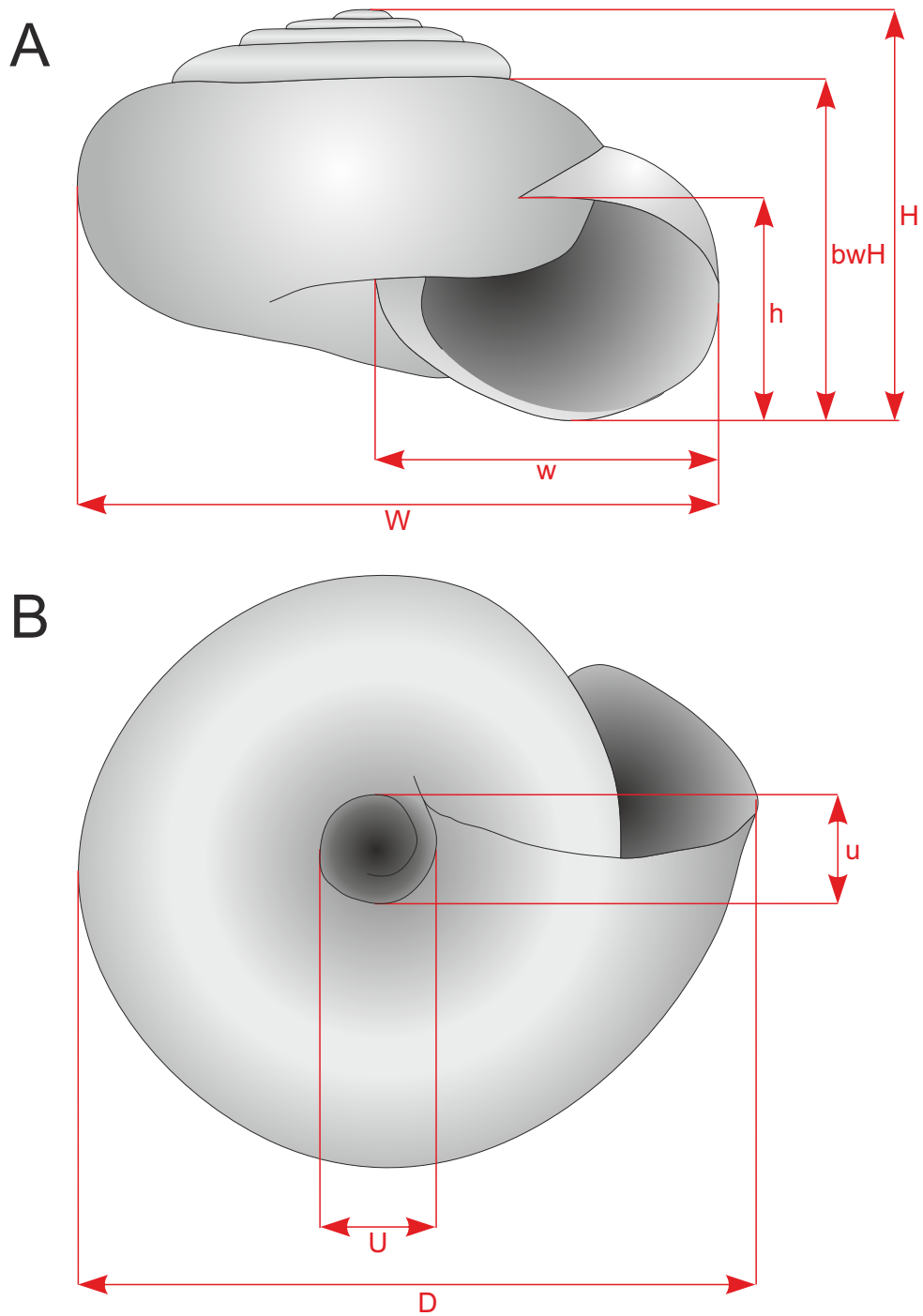
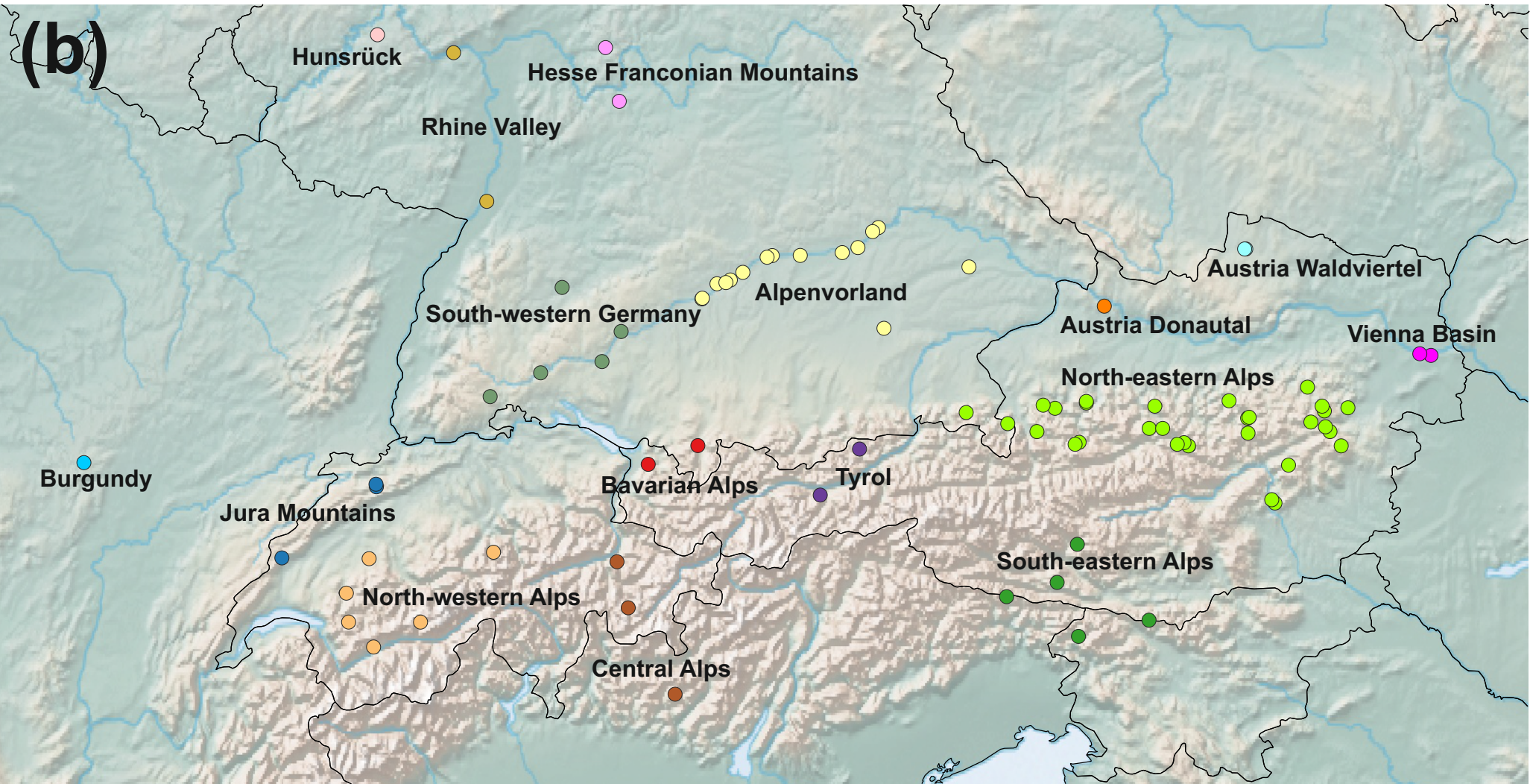
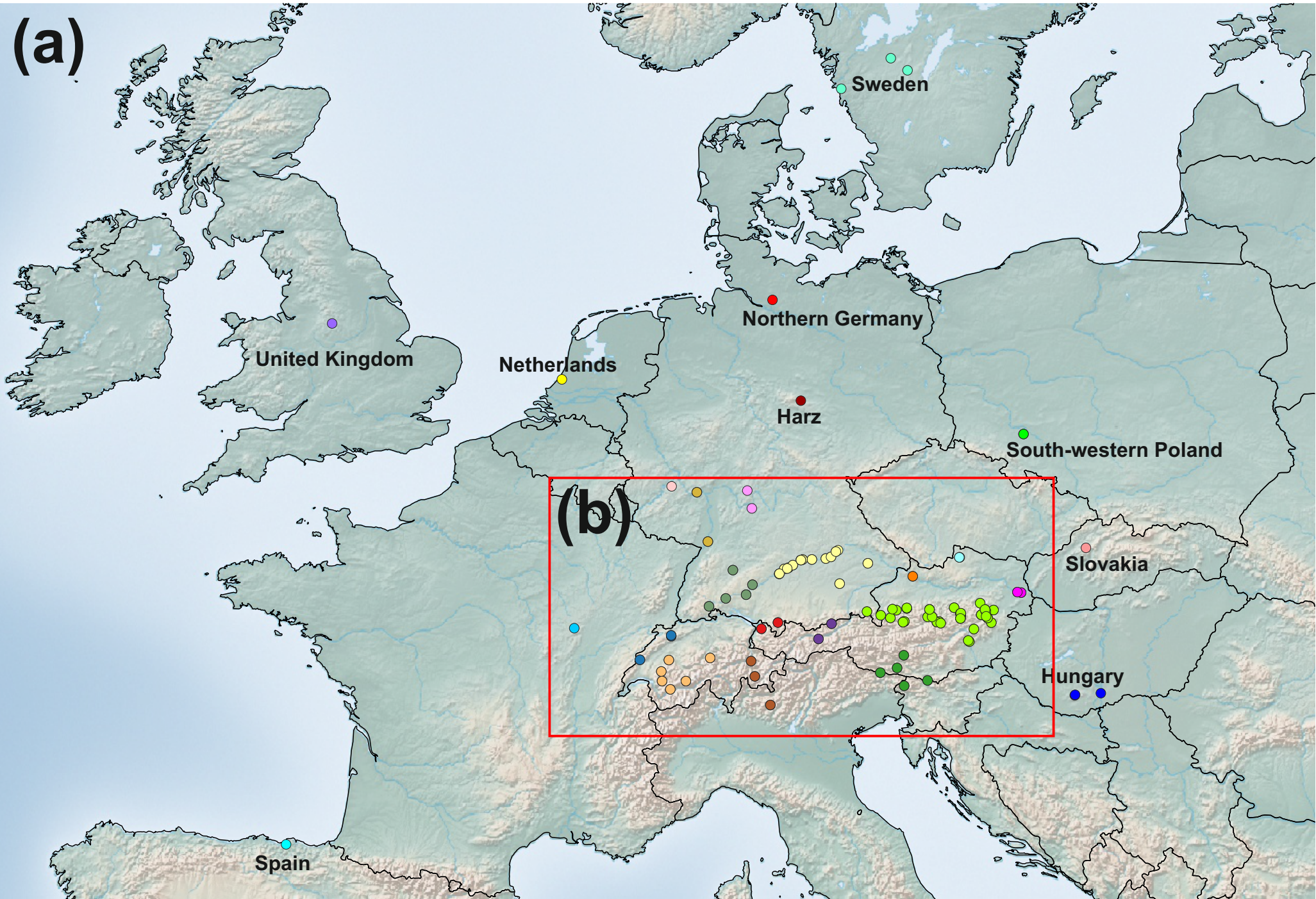


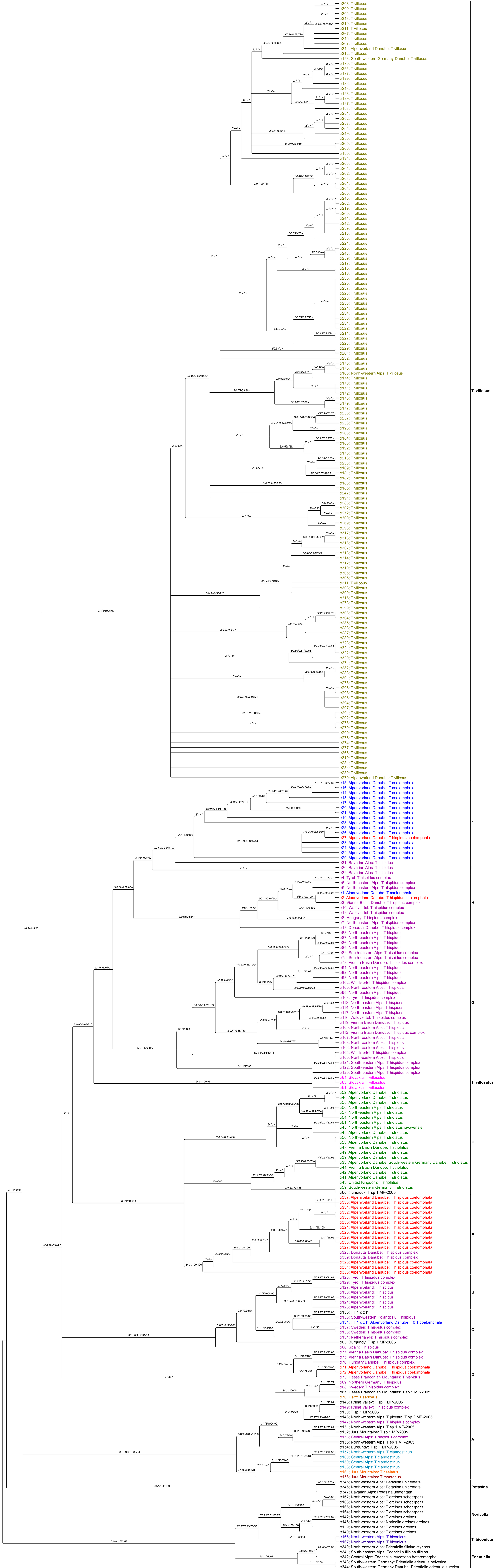
**Fig. S1.** Scheme of shell measurements used in the study; frontal view (A): height (H), width (W), body whorl height (bwH), aperture height (h), aperture width (w); bottom view (B): the umbilicus major diameter (U), the umbilicus minor diameter (u) and the shell diameter (D).



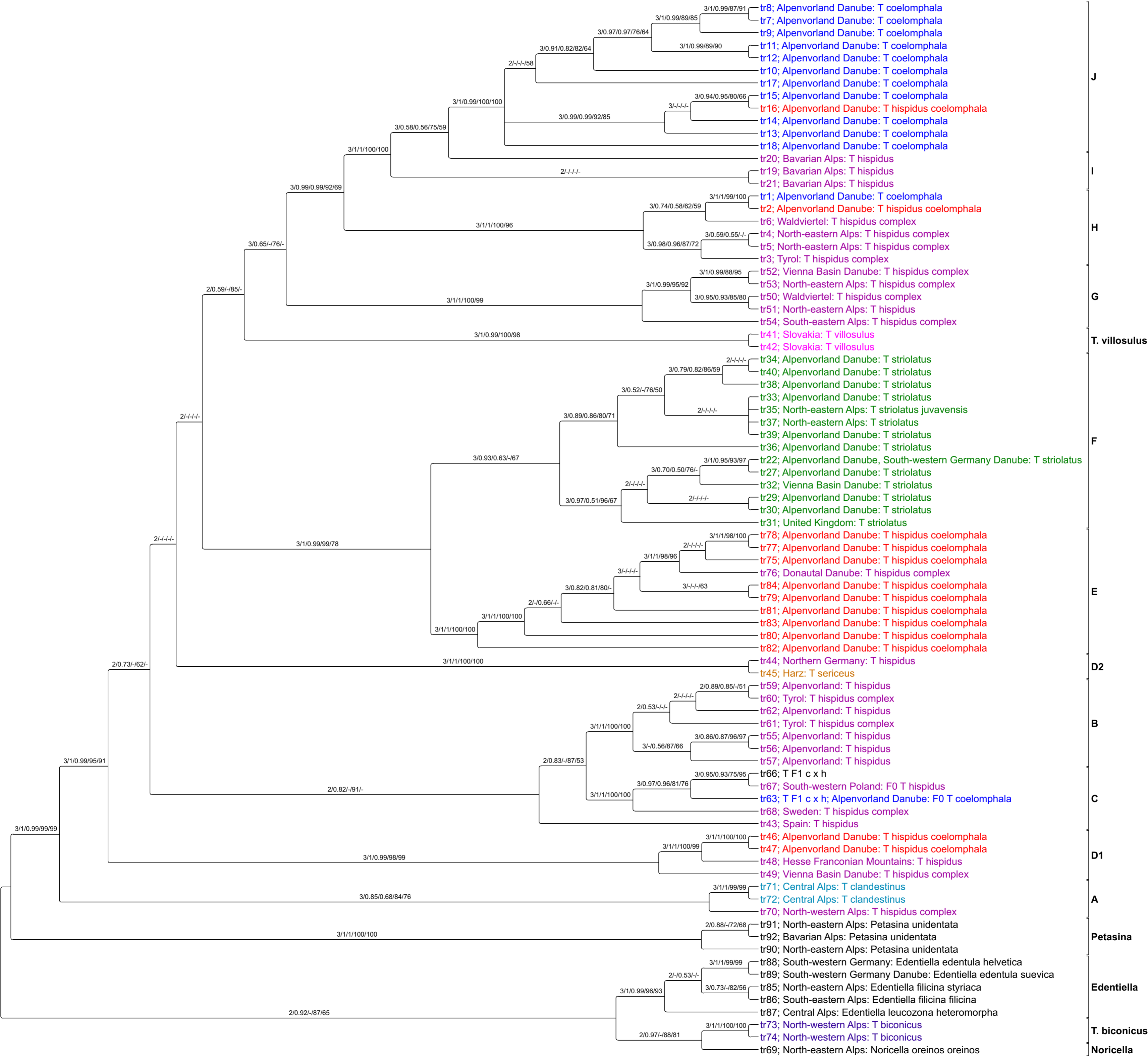
**Fig. S2.** Geographic distribution of samples used in phylogenetic analyses.  
(a) General view. (b) Enlarged view on the Alps and surrounding regions.



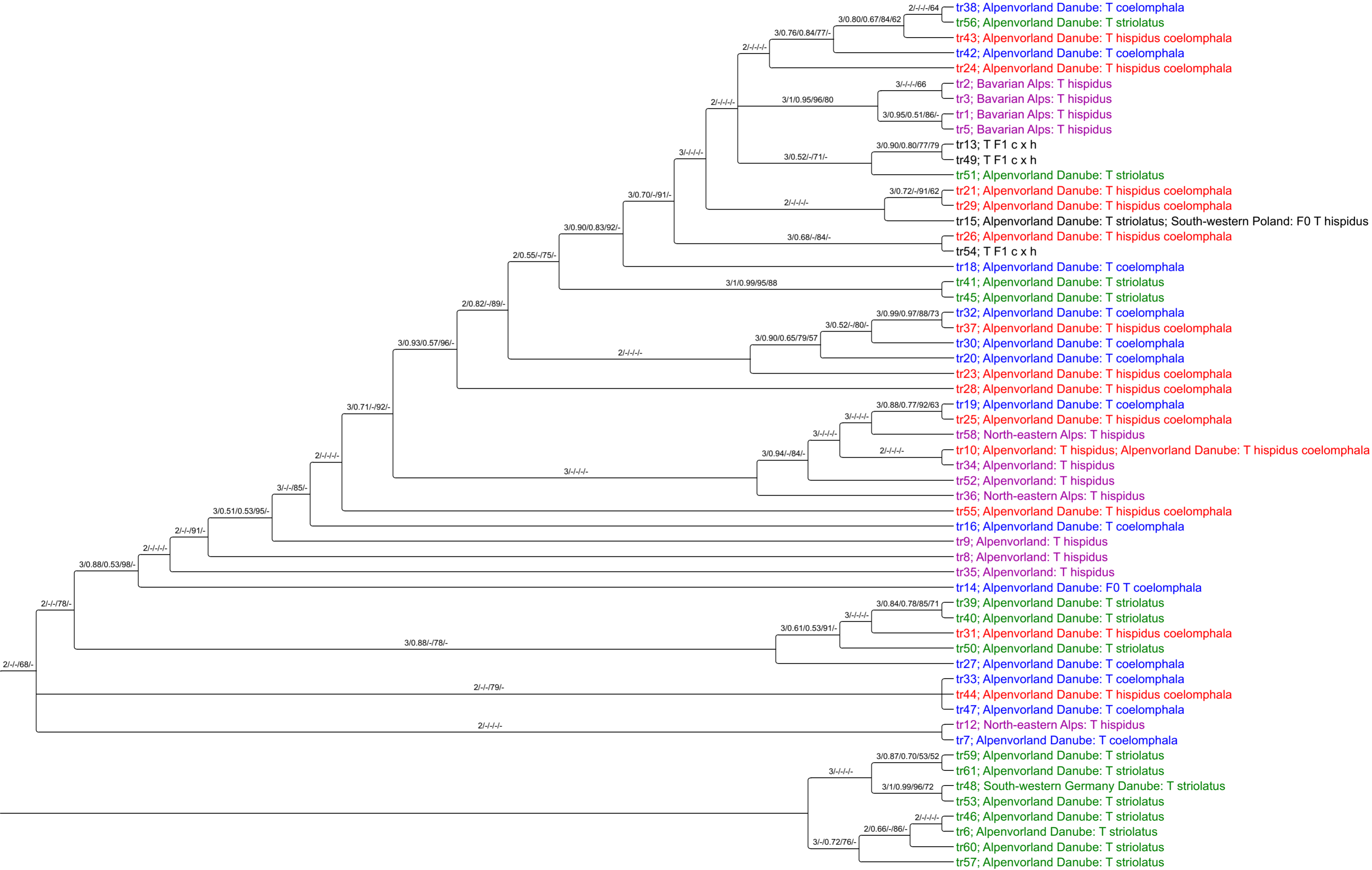
**Fig. S3.** The consensus of trees obtained in three approaches for the alignment of two mitochondrial markers COI+16S rDNA (1) including all available sequences. Numbers at nodes, in the following order correspond to: the number of the trees that contained a given node, posterior probabilities estimated in MrBayes and PhyloBayes as well as support values obtained by the approximate likelihood ratio test based on a Shimodaira-Hasegawa-like procedure and bootstrap method calculated in IQ- TREE. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were indicated by a dash "-".



**Fig. S4.** The consensus of trees obtained in three approaches for the alignment of two mitochondrial markers COI+16S rDNA (2) including the same sequences as in the set of ITS2+28S rDNA (2). Numbers at nodes, in the following order correspond to: the number of the trees that contained a given node, posterior probabilities estimated in MrBayes and PhyloBayes as well as support values obtained by the approximate likelihood ratio test based on a Shimodaira-Hasegawa-like procedure and bootstrap method calculated in IQ- TREE. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were indicated by a dash "-".

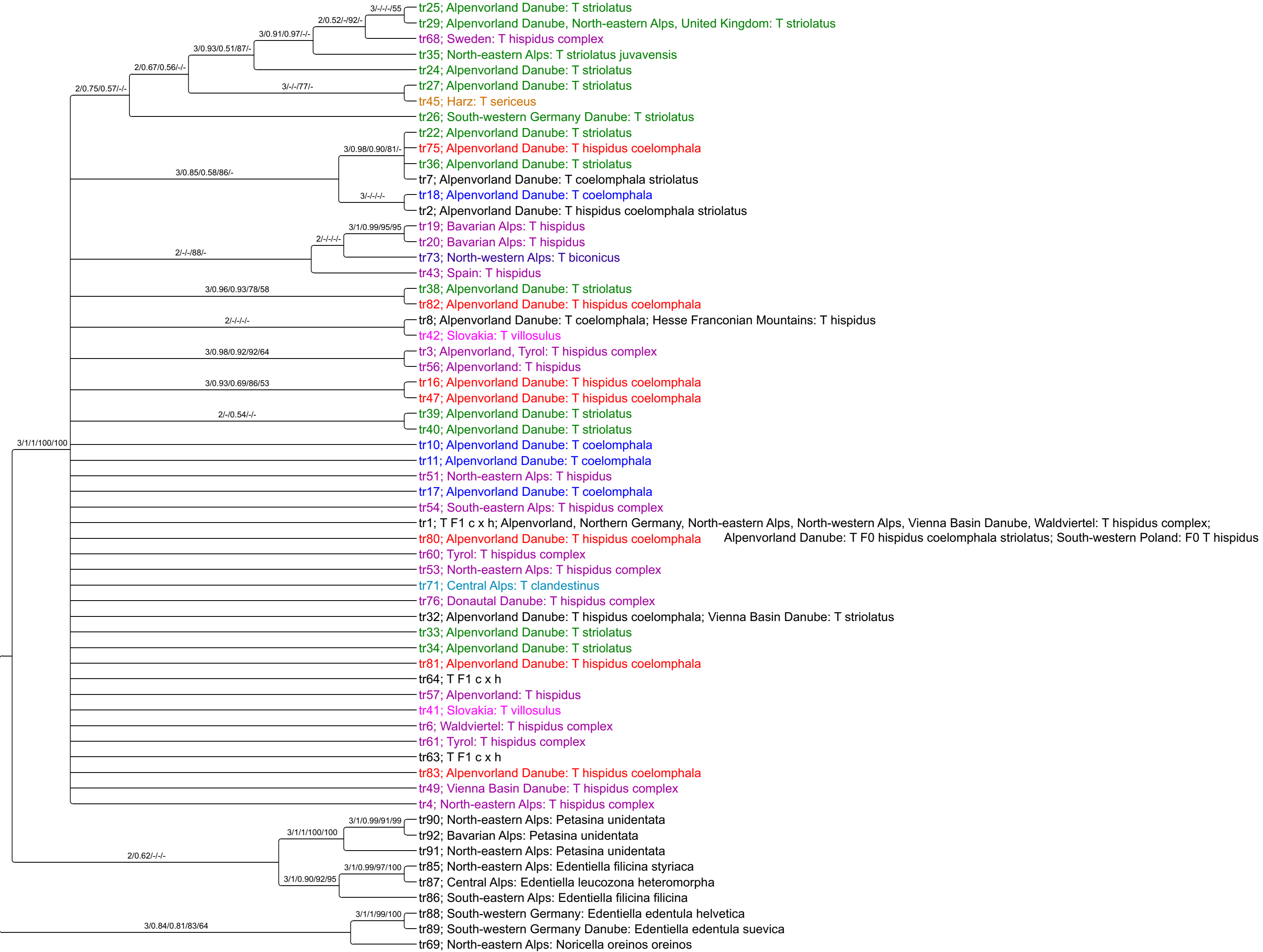


**Fig. S5.** The consensus of trees obtained in three approaches for the alignment of three nuclear markers H3+28S rDNA+ITS2. Numbers at nodes, in the following order correspond to: the number of the trees that contained a given node, posterior probabilities estimated in MrBayes and PhyloBayes as well as support values obtained by the approximate likelihood ratio test based on a Shimodaira-Hasegawa-like procedure and bootstrap method calculated in IQ- TREE. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were indicated by a dash "-".



**Fig. S6.** The consensus of trees obtained in three approaches for the alignment of two nuclear markers ITS2+28S rDNA (1) including all available sequences. Numbers at nodes, in the following order correspond to: the number of the trees that contained a given node, posterior probabilities estimated in MrBayes and PhyloBayes as well as support values obtained by the approximate likelihood ratio test based on a Shimodaira-Hasegawa-like procedure and bootstrap method calculated in IQ- TREE. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were indicated by a dash "-".

**Fig. S7.** The consensus of trees obtained in three approaches for the alignment of two nuclear markers ITS2+28S rDNA (2) including the same sequences as in the set of COI+16S rDNA (2). Numbers at nodes, in the following order correspond to: the number of the trees that contained a given node, posterior probabilities estimated in MrBayes and PhyloBayes as well as support values obtained by the approximate likelihood ratio test based on a Shimodaira-Hasegawa-like procedure and bootstrap method calculated in IQ- TREE. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and



**Fig. S8.** Individual trees obtained for three approaches in MrBayes, PhyloBayes and IQ-TREE for six data sets: *COI+16S rDNA* (1), *ITS2+28S rDNA* (1), *COI+16S rDNA* (2), *ITS2+28S rDNA* (2), *H3+ITS2+28S rDNA* and *COI+16S rDNA+ITS2+28S rDNA*. Numbers at nodes correspond to: posterior probabilities in the case of MrBayes and PhyloBayes as well as support values obtained by the approximate likelihood ratio test based on a Shimodaira-Hasegawa-like procedure and bootstrap method calculated in IQ-TREE. Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were omitted or indicated by a dash "-".

0.0 0.01



COI+ 16S rDNA (1), IQ-TREE



A horizontal number line with a vertical tick mark at the left end labeled 0.0 and a vertical tick mark at the right end labeled 0.005. There are 10 equal intervals between the two ends, marked by 9 intermediate vertical tick marks.

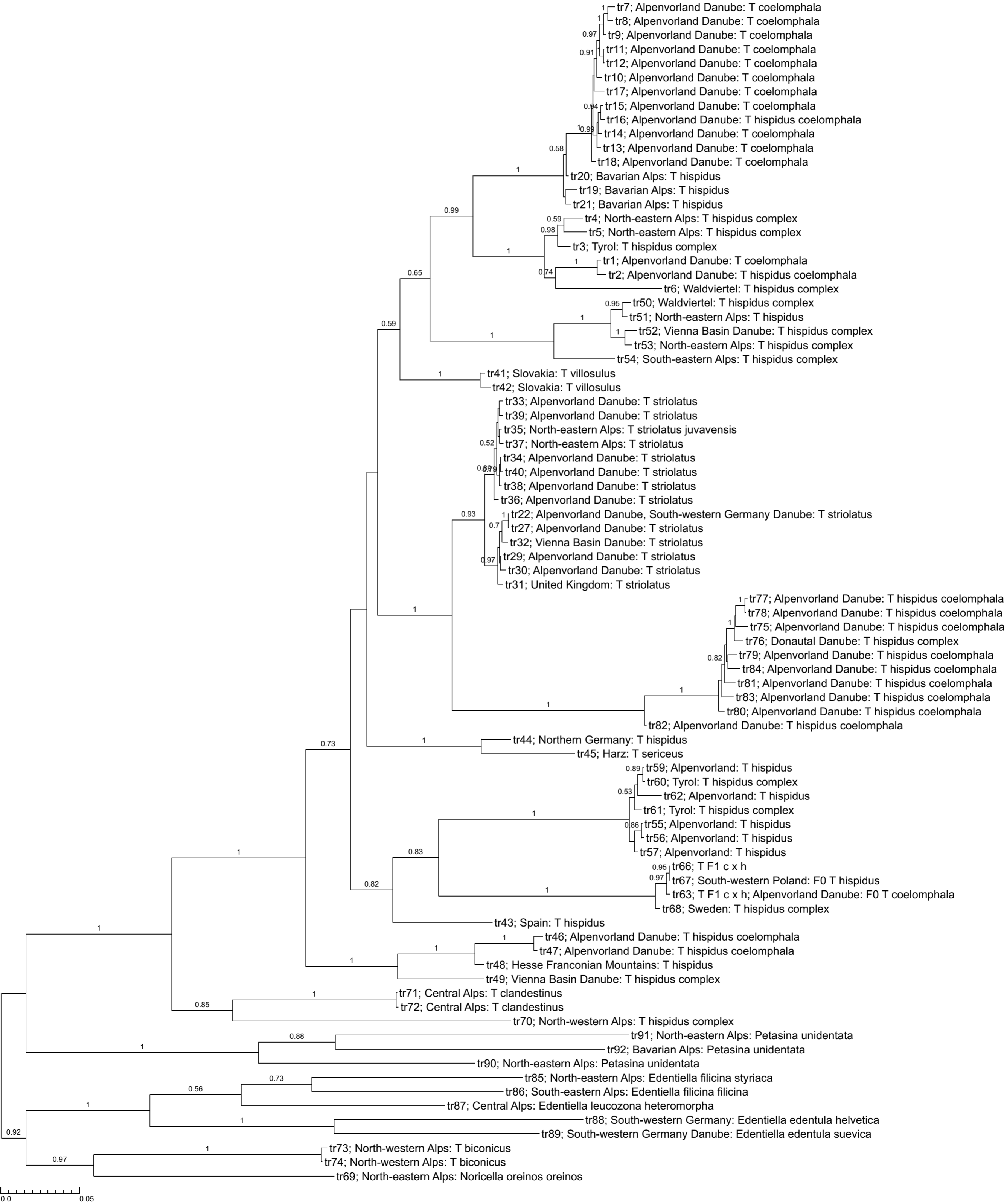
# ITS2+28S rDNA (1), PhyloBayes



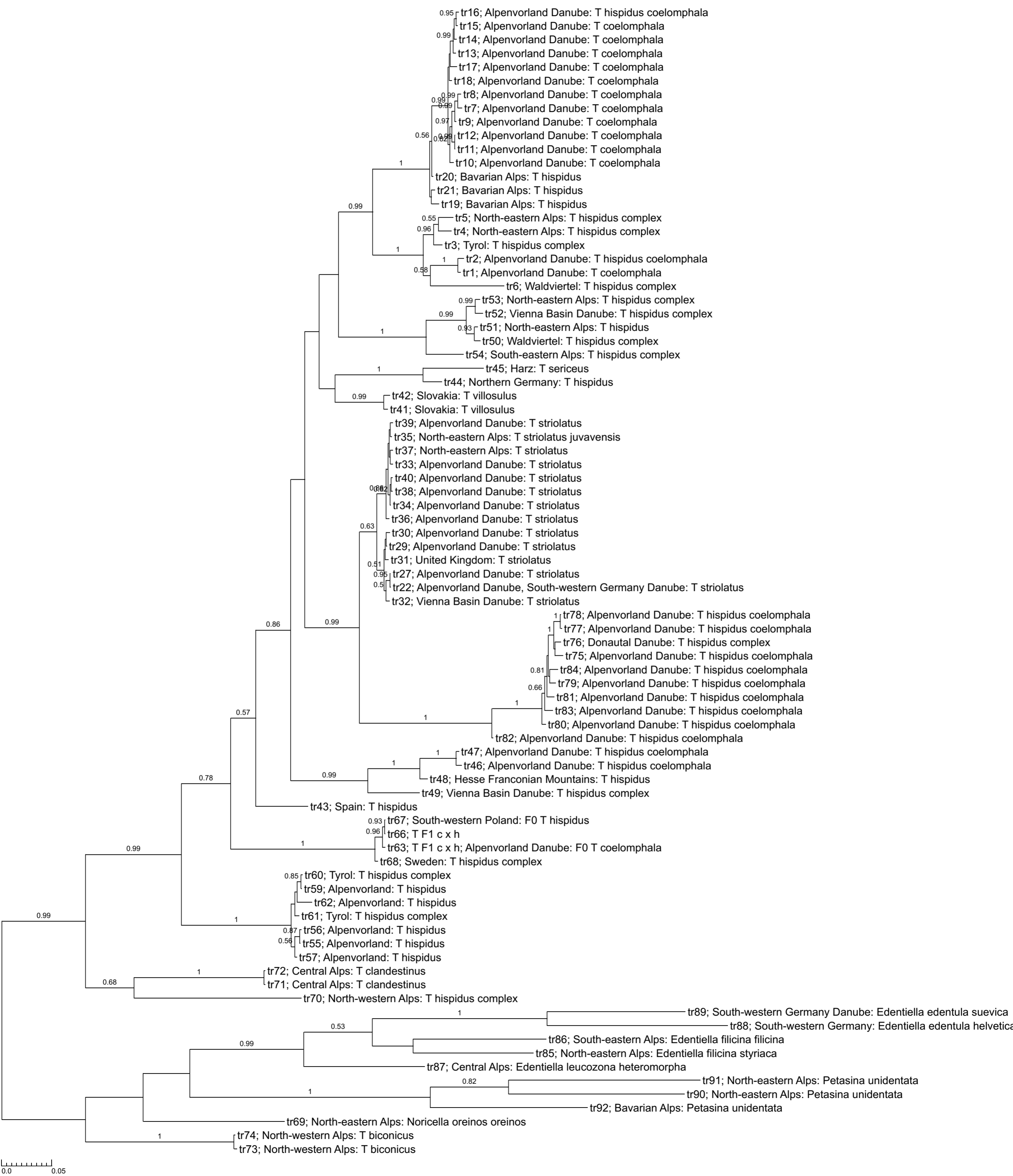
# ITS2+28S rDNA (1), IQ-TREE



# COI+16S *rDNA* (2), MrBayes



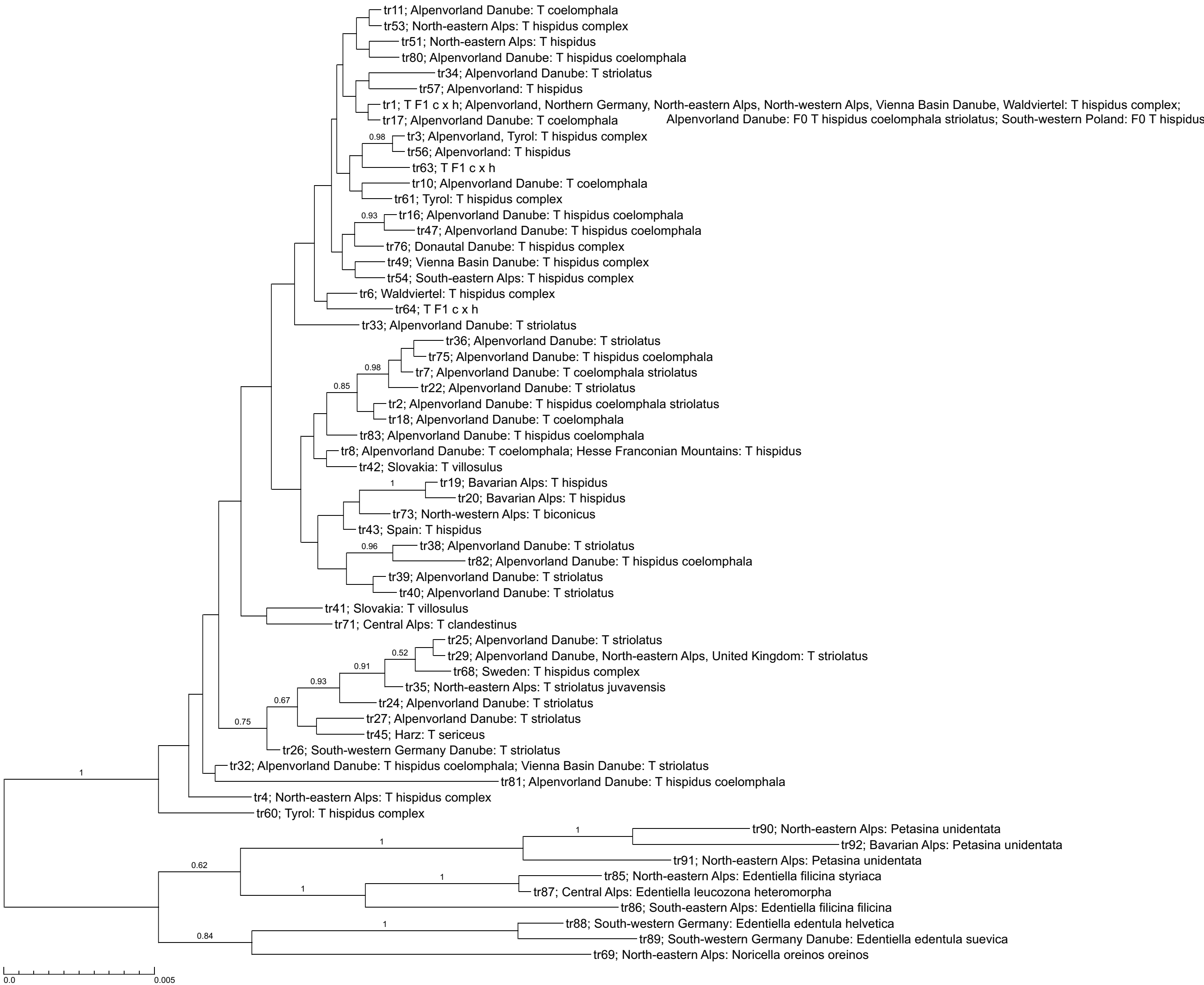
# COI+16S *rDNA* (2), PhyloBayes



# COI+16S *rDNA* (2), IQ-TREE



# ITS2+28S rDNA (2), MrBayes



# ITS2+28S rDNA (2), PhyloBayes

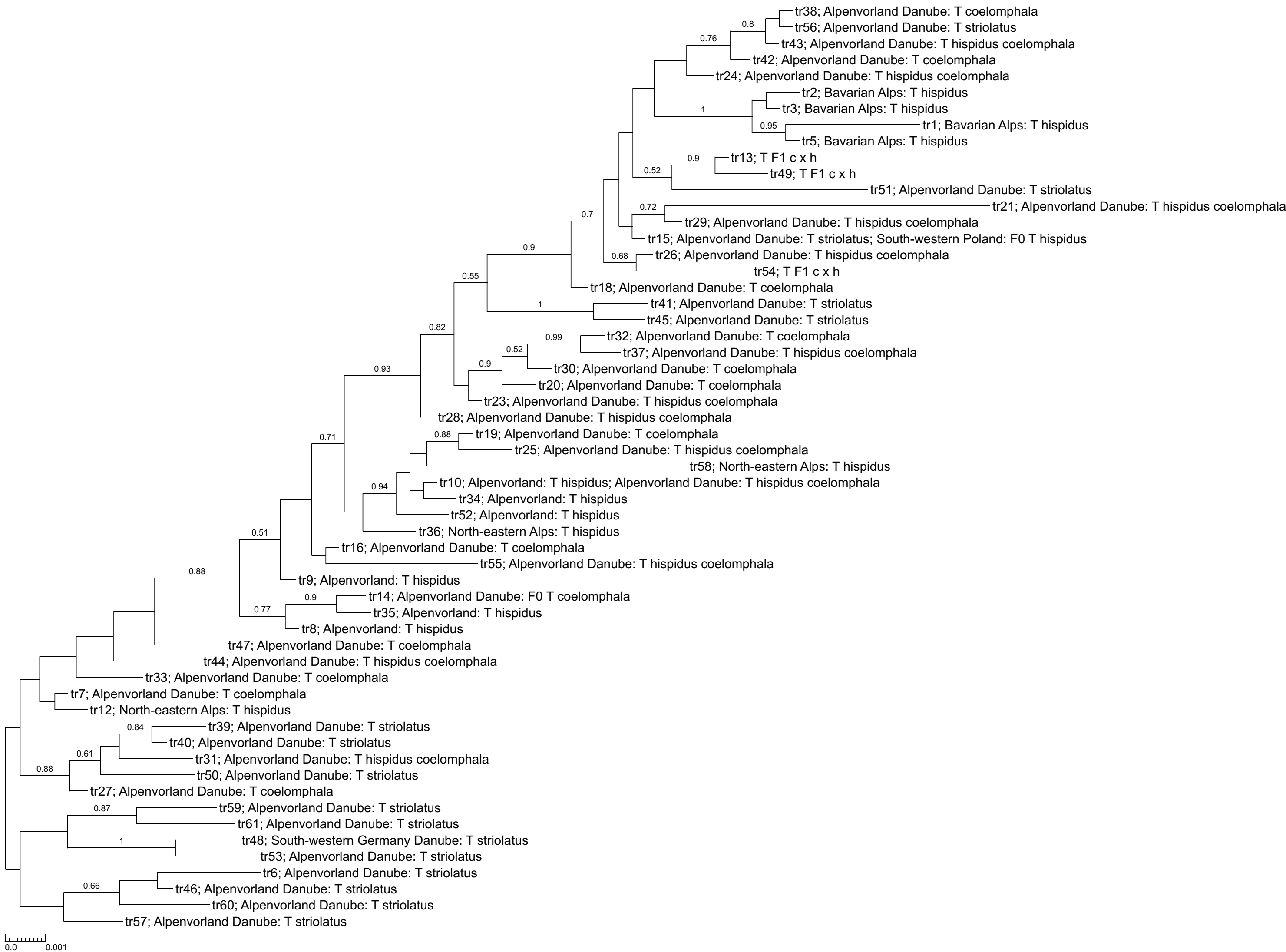


# ITS2+28S rDNA (2), IQ-TREE

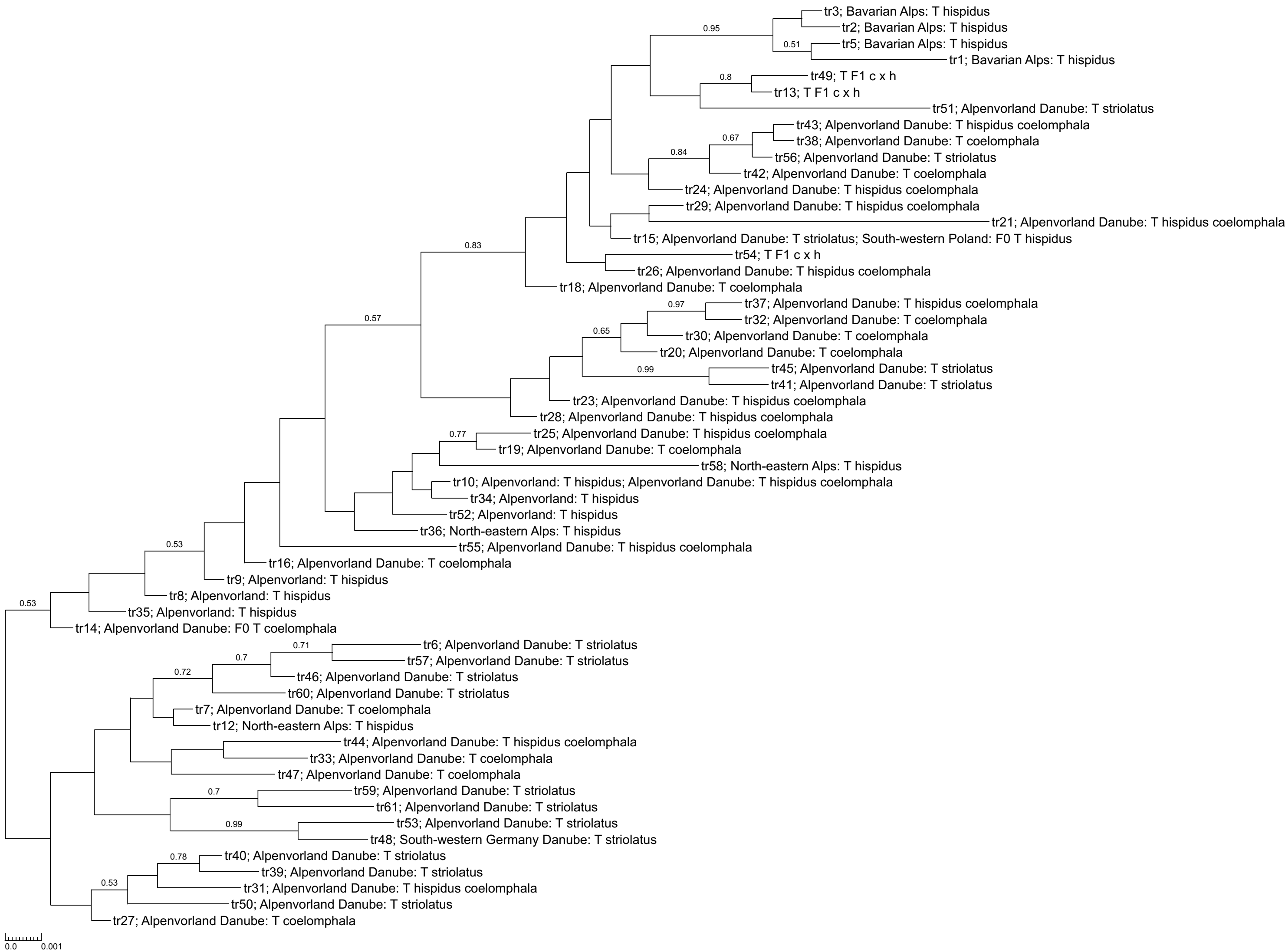


0.0 0.005

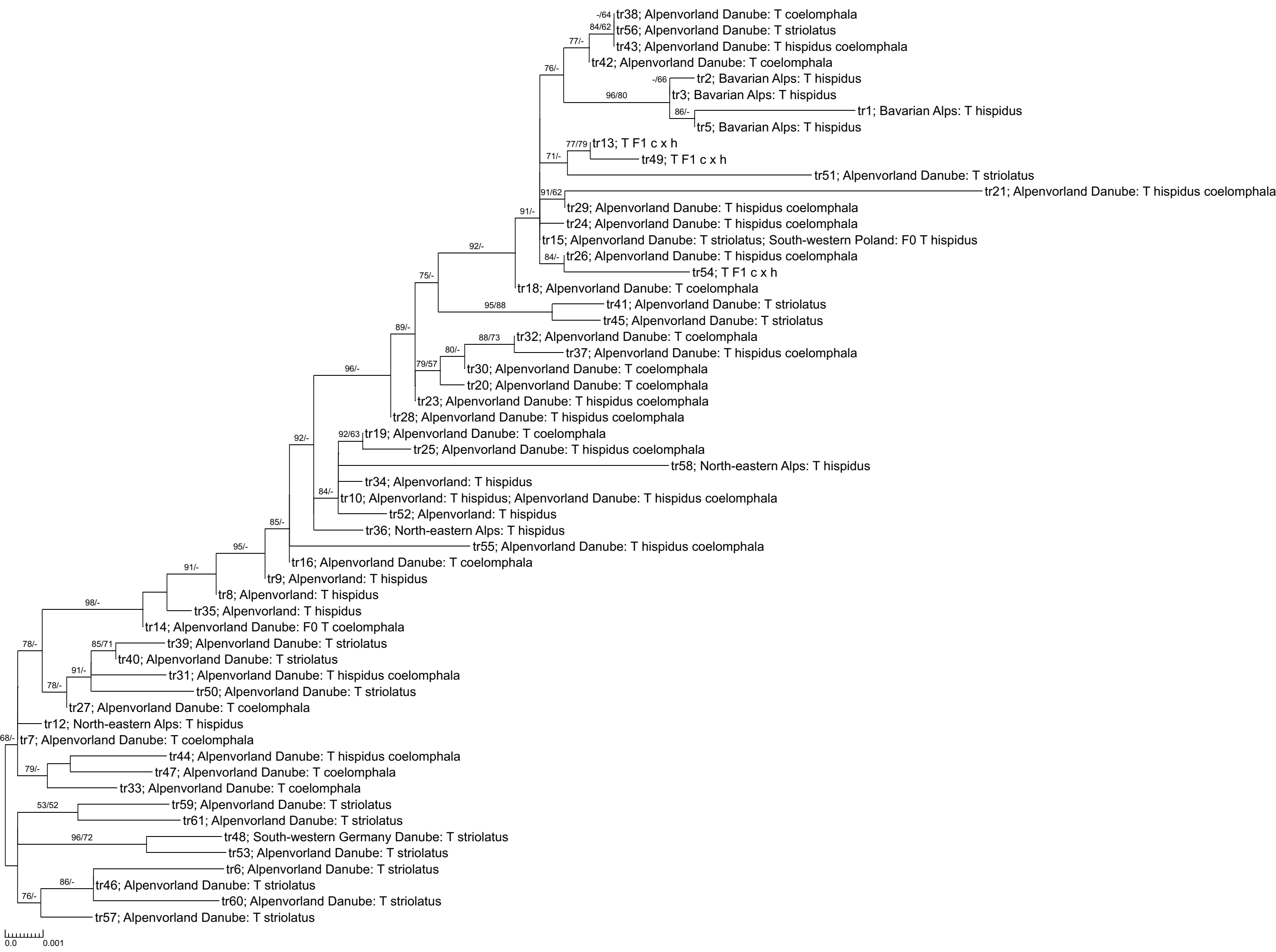
# H3+ITS2+28S *rDNA*, MrBayes



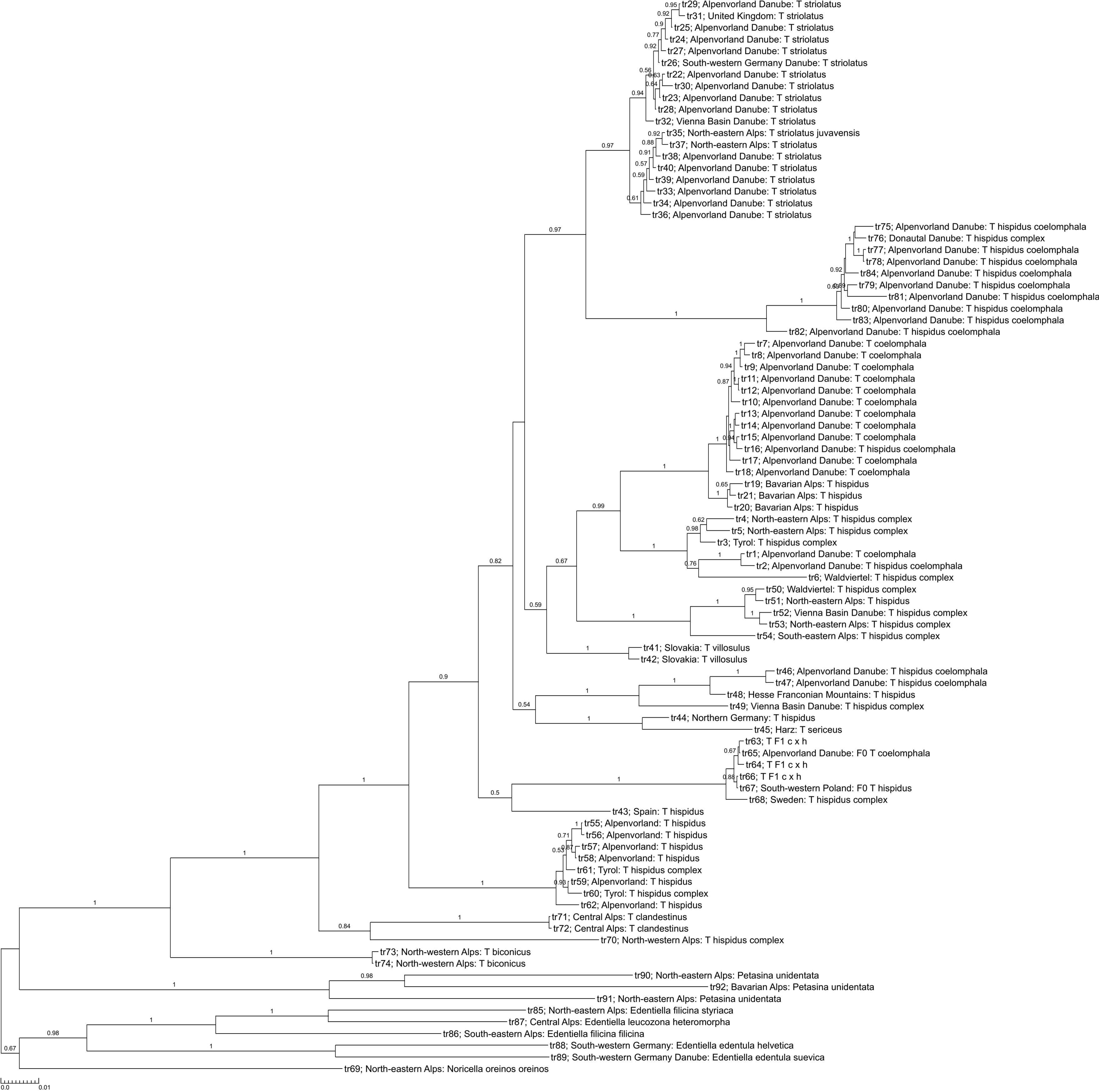
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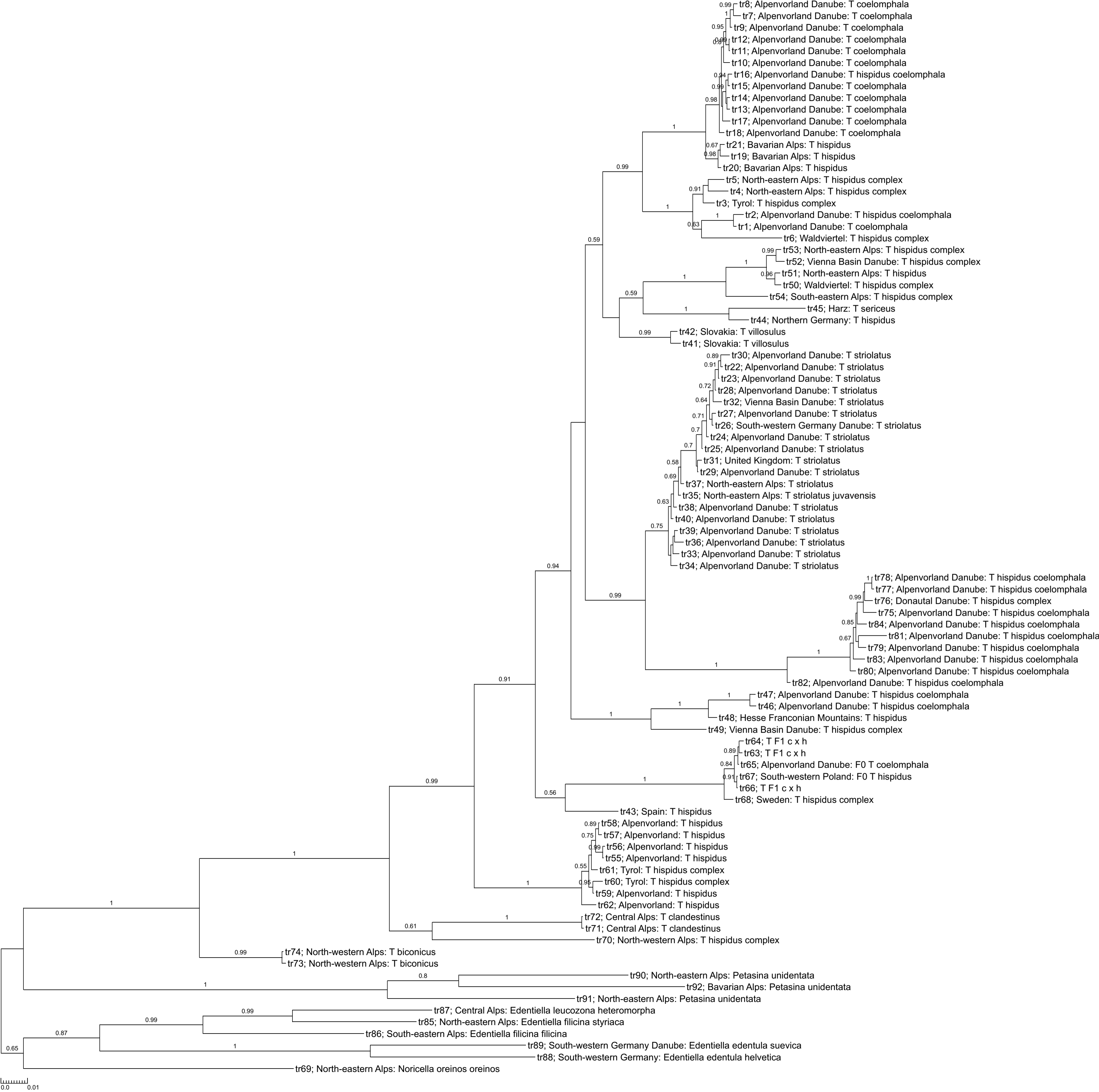
# H3+ITS2+28S *rDNA*, IQ-TREE



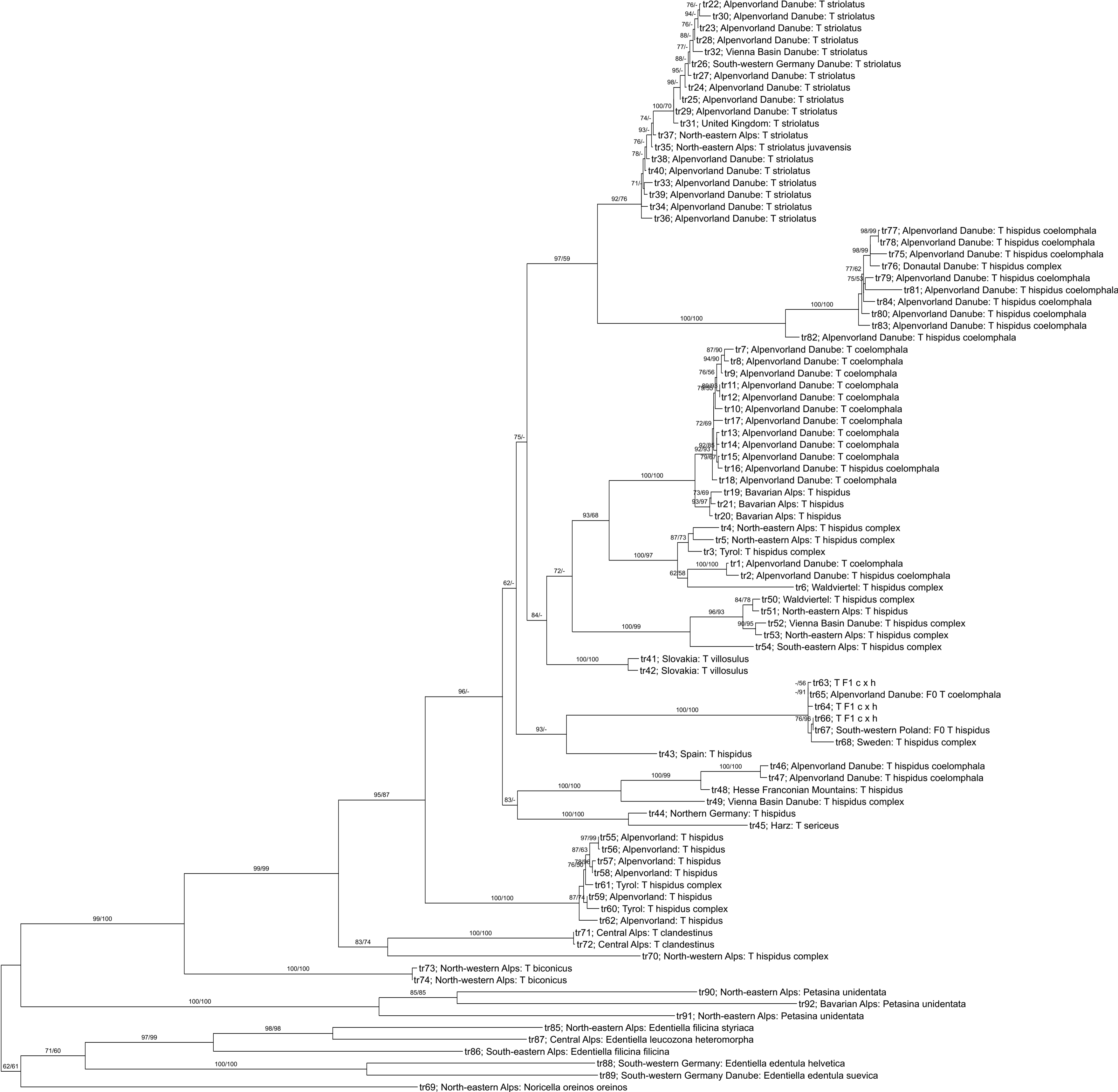
# COI+16S rDNA+ITS2+28S rDNA, MrBayes



# COI+16S rDNA+ITS2+28S rDNA, PhyloBayes



# COI+16S rDNA+ITS2+28S rDNA, IQ-TREE



0.0 0.01