

Supplementary material

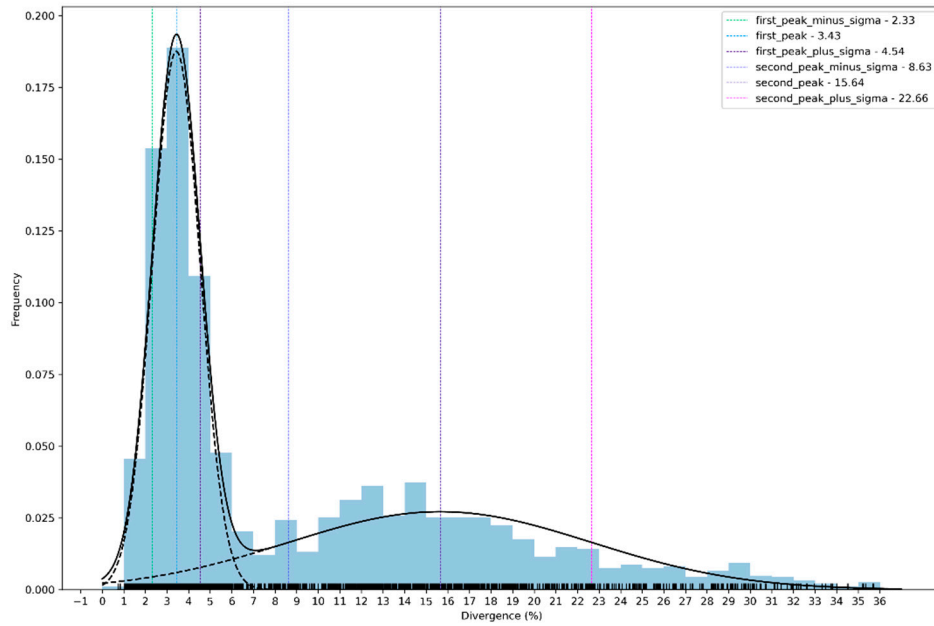
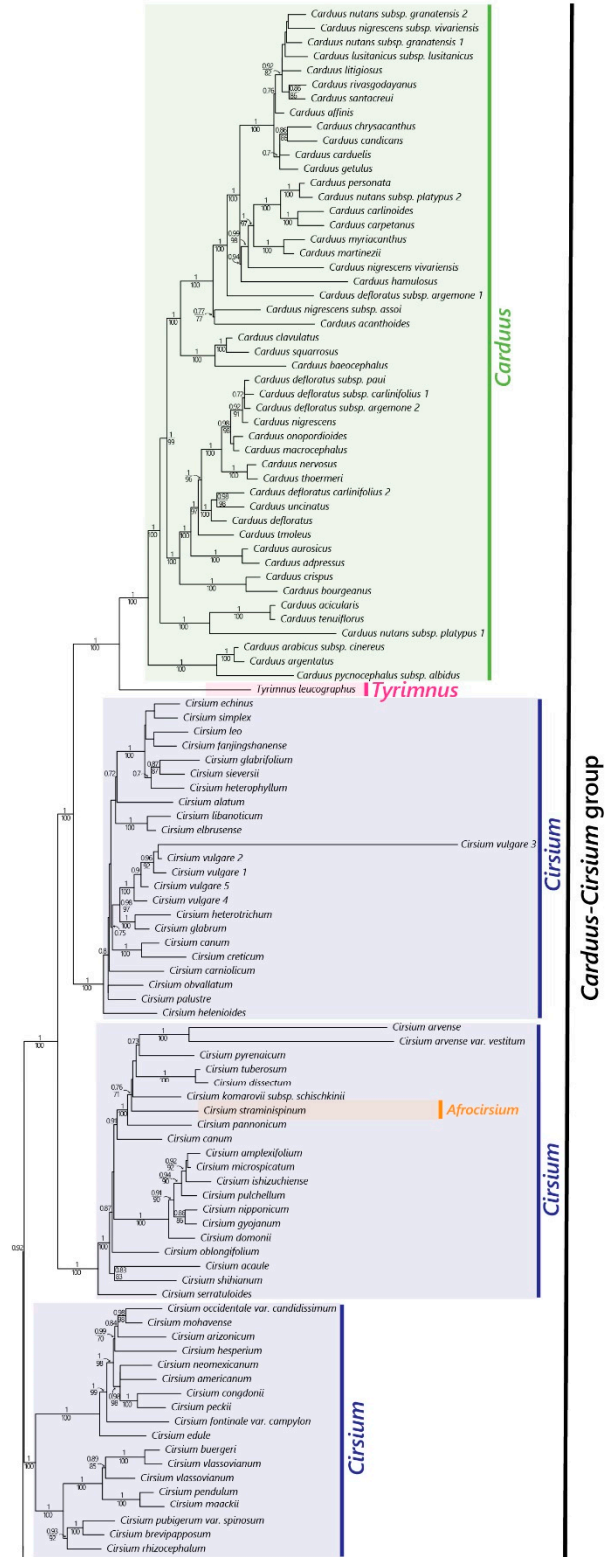


Figure S1. Pairwise distance histogram generated with ParalogWizard. The distribution of pairwise distances between exonic contigs for each locus is shown; distances are given as divergence percentage values (8.63-22.6%). The position of the first and second peak is indicated. The mean divergence and the standard deviation (plus and minus sigma) for each peak are marked by dashed lines; values are provided in the legend.

A



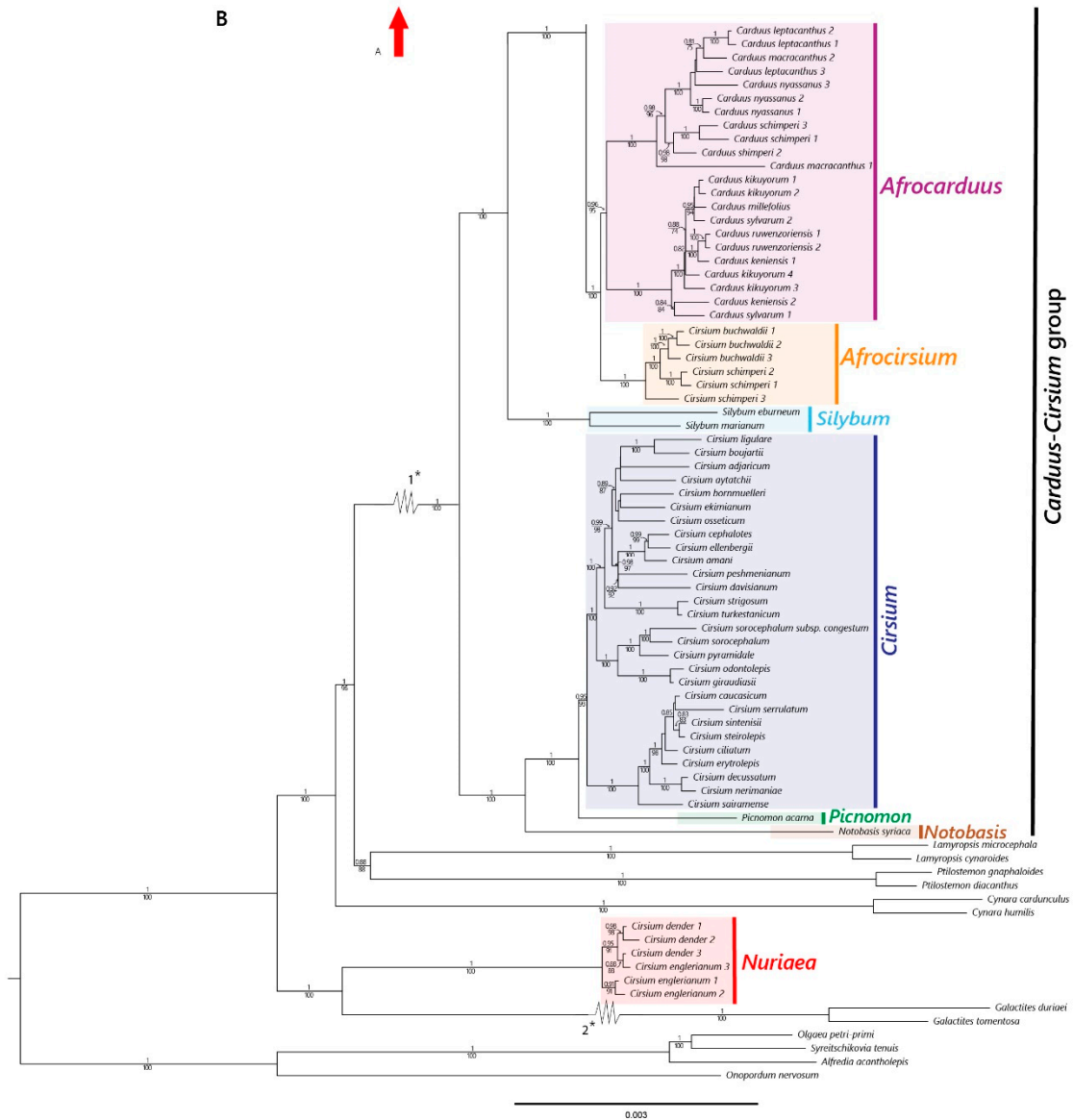


Figure S2. A) Maximum likelihood phylogenetic reconstruction for the subtribe Carduinae obtained with the chloroplast dataset. Values above branches indicate Transfer Expected Bootstrap (TBE) and those below branches indicate Felsenstein's bootstrap (BS); only values above 70% are shown. B) Maximum likelihood phylogenetic reconstruction for the subtribe Carduinae obtained with the chloroplast dataset. Values above branches indicate Transfer Expected Bootstrap (TBE) and those below branches indicate Felsenstein's bootstrap (BS); only values above 70% are shown. Branches shortened for fit are indicated on the phylogeny as 1* (50% of reduction) and 2* (30% of reduction).