Supplementary Material S1

Chloroplast structural variants

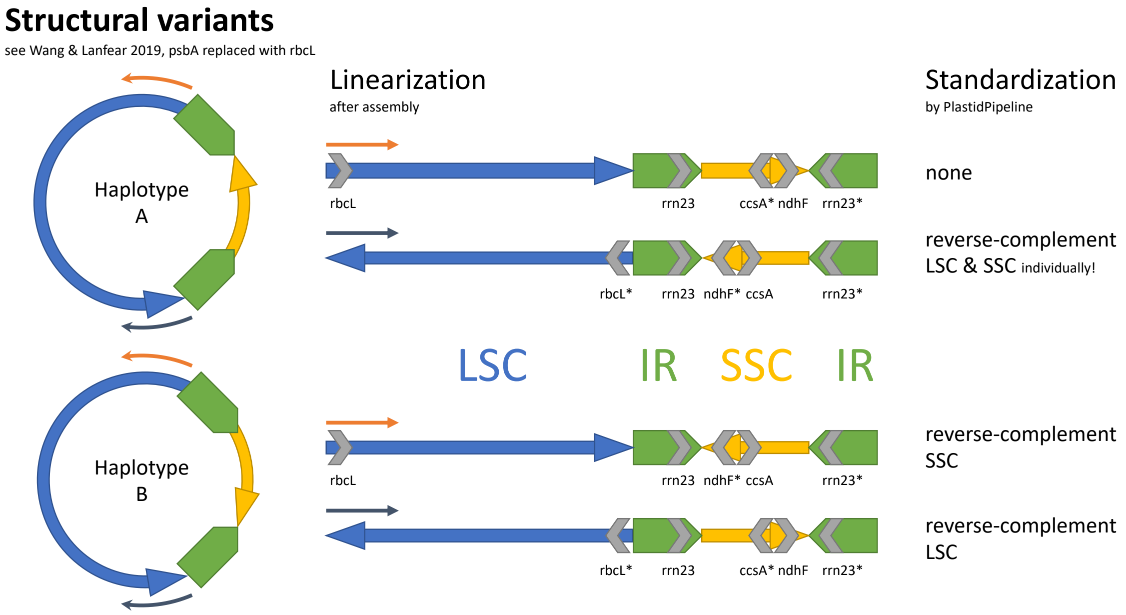

Figure S1.1 Schematic overview of structural variants, their linearizations and the respective structural standardization operations performed by the PlastidPipeline. Blue: Long Single Copy (LSC) region – yellow: Short Single Copy (SSC) region – green: Inverted Repeat (IR) regions – grey: genes. Orange and dark blue arrows: Possible directions for linearization of the circular plastome into the format LSC-IR-SSC-IR, e.g. as output by GetOrganelle. Note that all four linear conformations correspond to naturally occurring plastome structures.

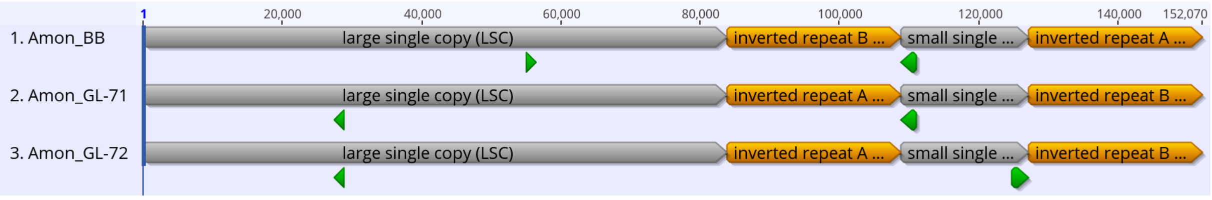

Figure S1.2 Examples for alternative linear plastome conformations before structural standardization (Geneious screenshot). Raw output from GetOrganelle with preliminary GeSeq annotation, filtered for structural features (grey – LSC, SSC, orange – IRA, IRB) and the two genes (green – *rbcL, ndhA*) used by default for standardization in the PlastidPipeline.

Figure S1.3 Examples of automatically standardized, fully annotated plastomes output by the PlastidPipeline (Geneious screenshot). Structural annotations and standardization genes (incl. CDS, exons, intron) highlighted.

Additional phylogenetic trees

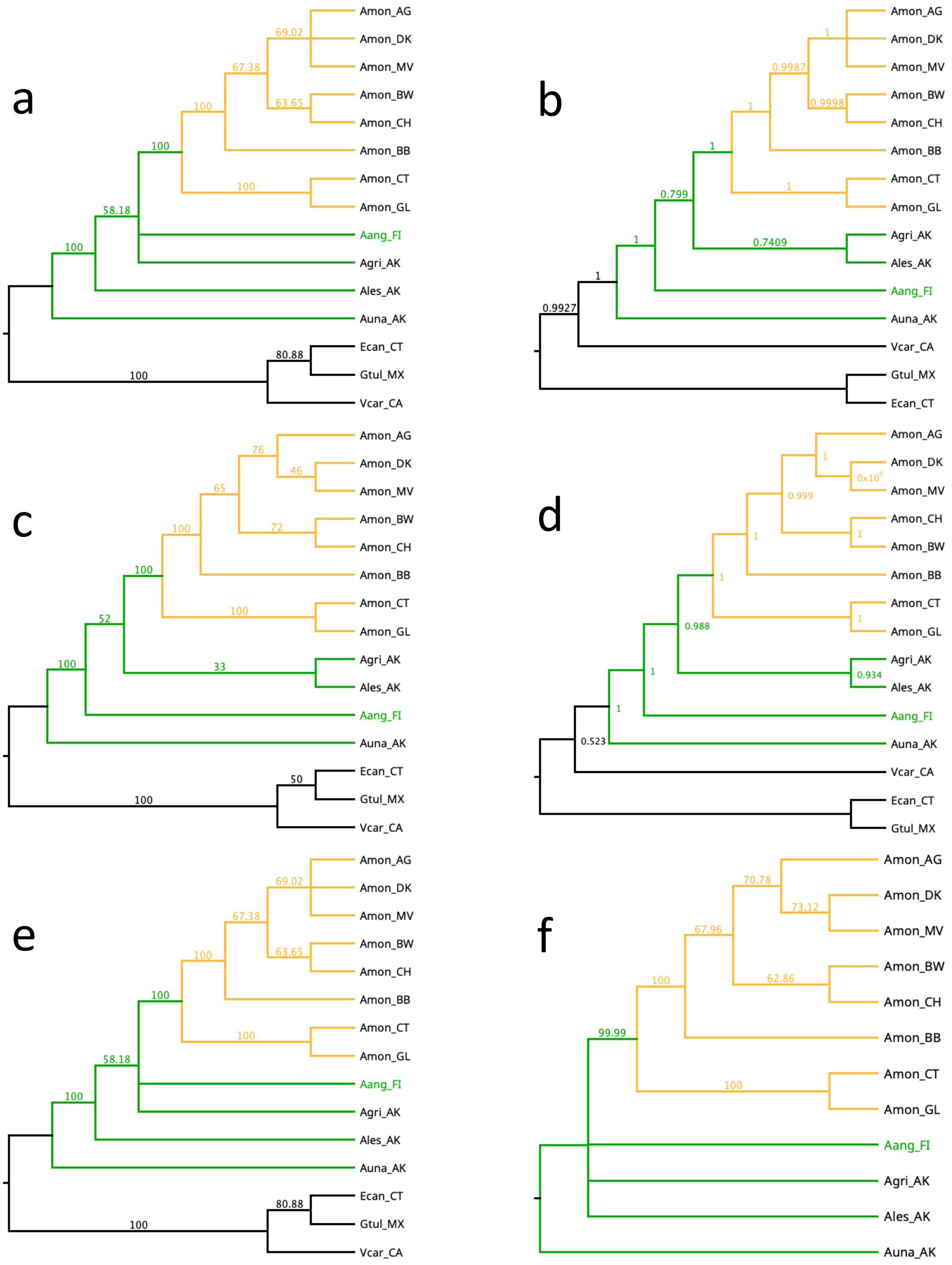

Figure S1.4 Additional phylogenetic trees based on all samples (AS alignment with non-*Arnica* species as outgroup, based on SNPs, a-e) or all genus *Arnica* samples (AA alignment with *A. unalaschcensis* as outgroup, based on SNPs + 2-state indels, f). *A. angustifolia* sample highlighted for comparison. a. PAUP* Parsimony tree with bootstrap support values (10 000 replicates). b. MrBayes tree with posterior probabilities. c. RAxML Maximum Likelihood tree with bootstrap values (10 000 replicates). d. PhyML Maximum Likelihood tree with Chi2-based branch support values. e. PAUP* Neighbor-Joining tree with bootstrap support values (10 000 replicates, support < 50% shown as polytomy). f. PAUP* Neighbor-Joining tree with bootstrap support values (10 000 replicates, support < 50% shown as polytomy – compare with Fig. 2C in the main text inferred from the same data).

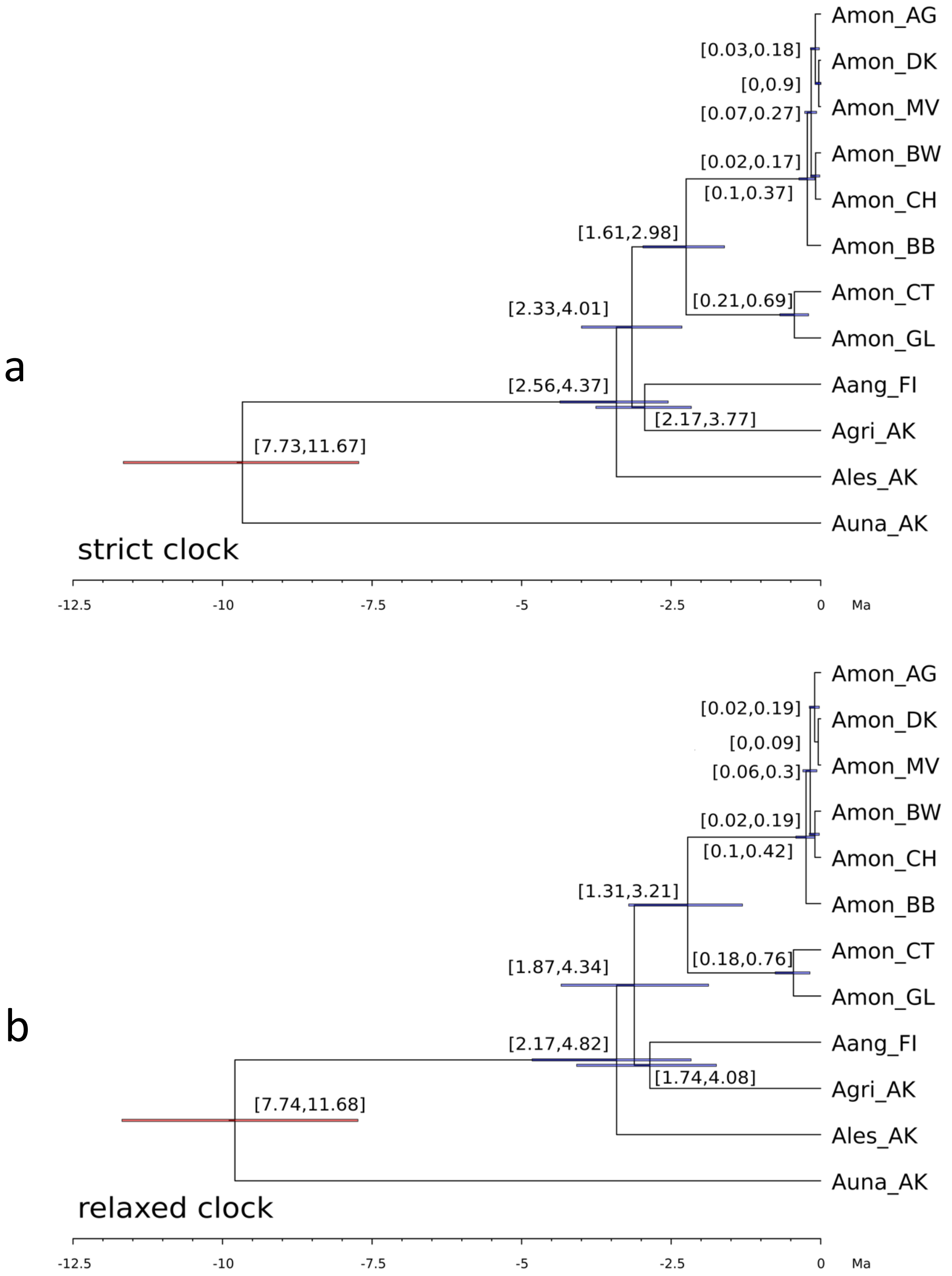

Figure S1.5 Time-calibrated phylogeny assuming a strict (a) or a relaxed (b) molecular clock. BEAST 2.7.7. analysis of the unpartitioned AA alignment, using the extremes of the four date suggestions [7.73, 11.92] Ma for the *A. montana / A. chamissonis* split in Zhang et al. 2024 as uniform prior range for the secondary calibration of the root of the tree (red age bar). Node age bars: age range, node age intervals: 95% confidence interval.