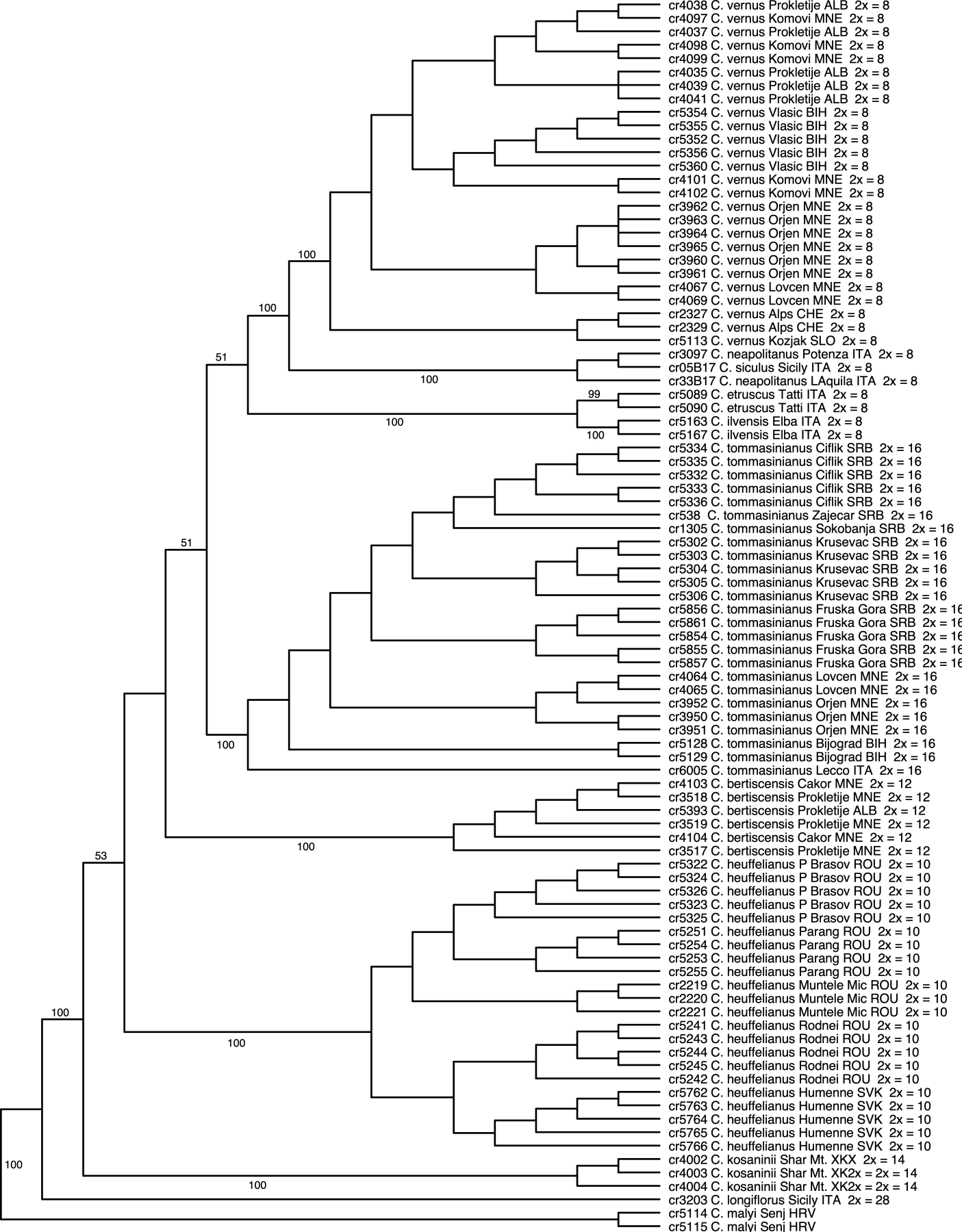
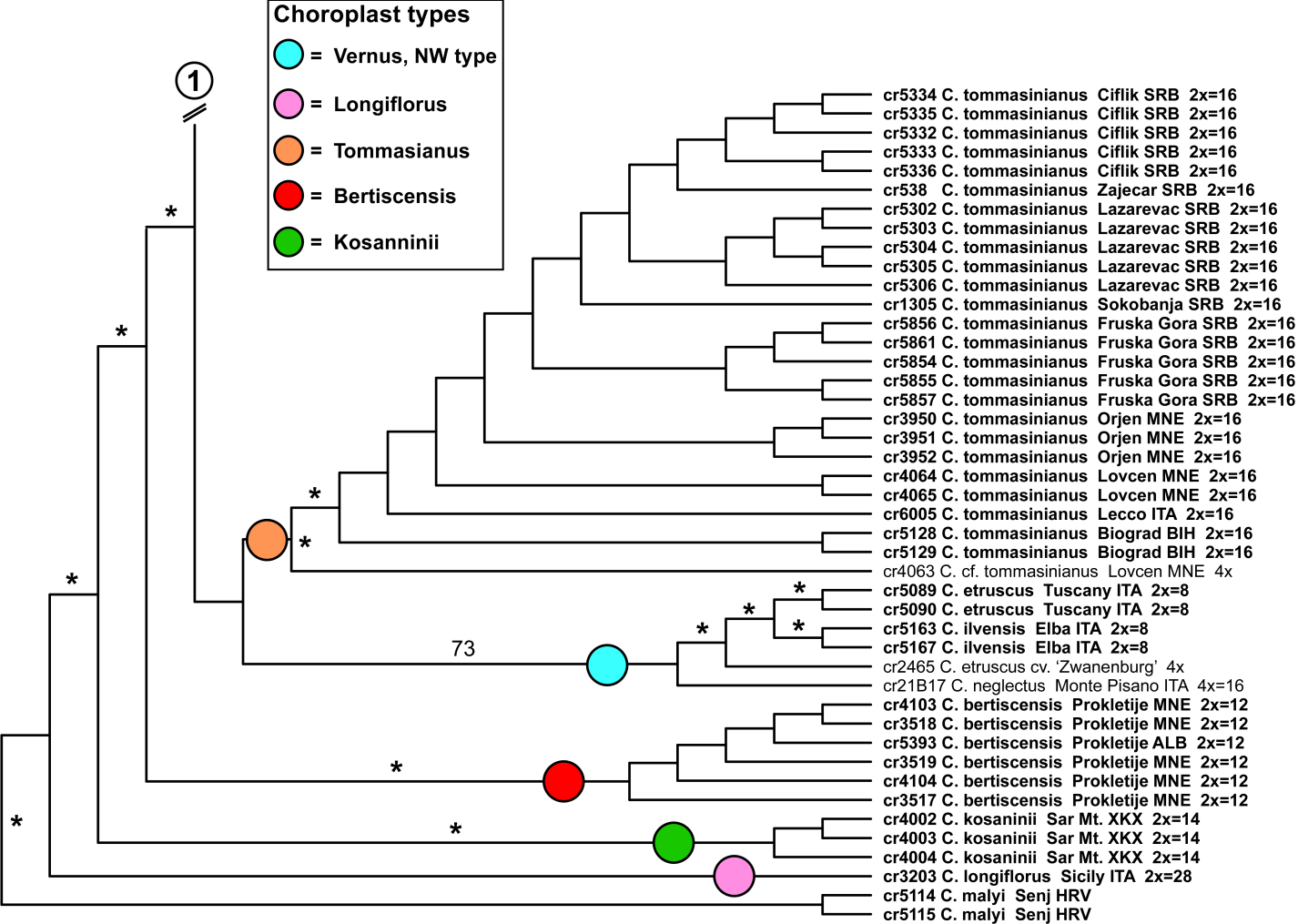


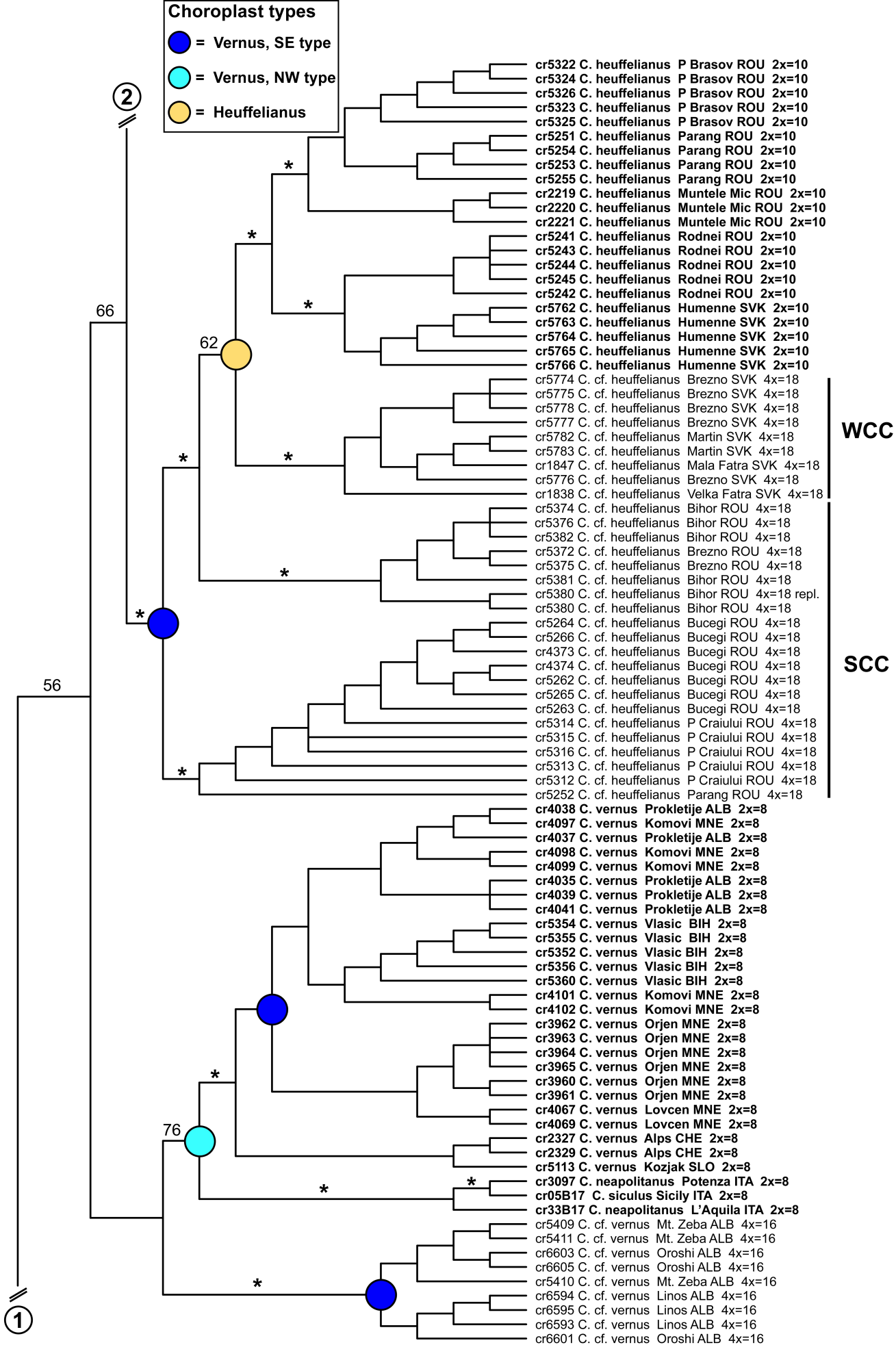
**Figure S1.** Chromosome counts for diploid *C. vernus* and *C. heuffelianus* (A and B), tetraploid *C. cf. vernus* (C), and tetraploid *C. cf. heuffelianus* (D-F). Asterisks show relatively shorter chromosomes. G) The chromosome number and genome size in diploid and tetraploid *C. ser. Verni* taxa show a general negative relationship, which was only significant when *C. longiflorus* was included.



**Figure S2.** Strict consensus MP tree based on 2009 GBS loci including only diploid accessions of *Crocus* ser. *Verni* taxa.

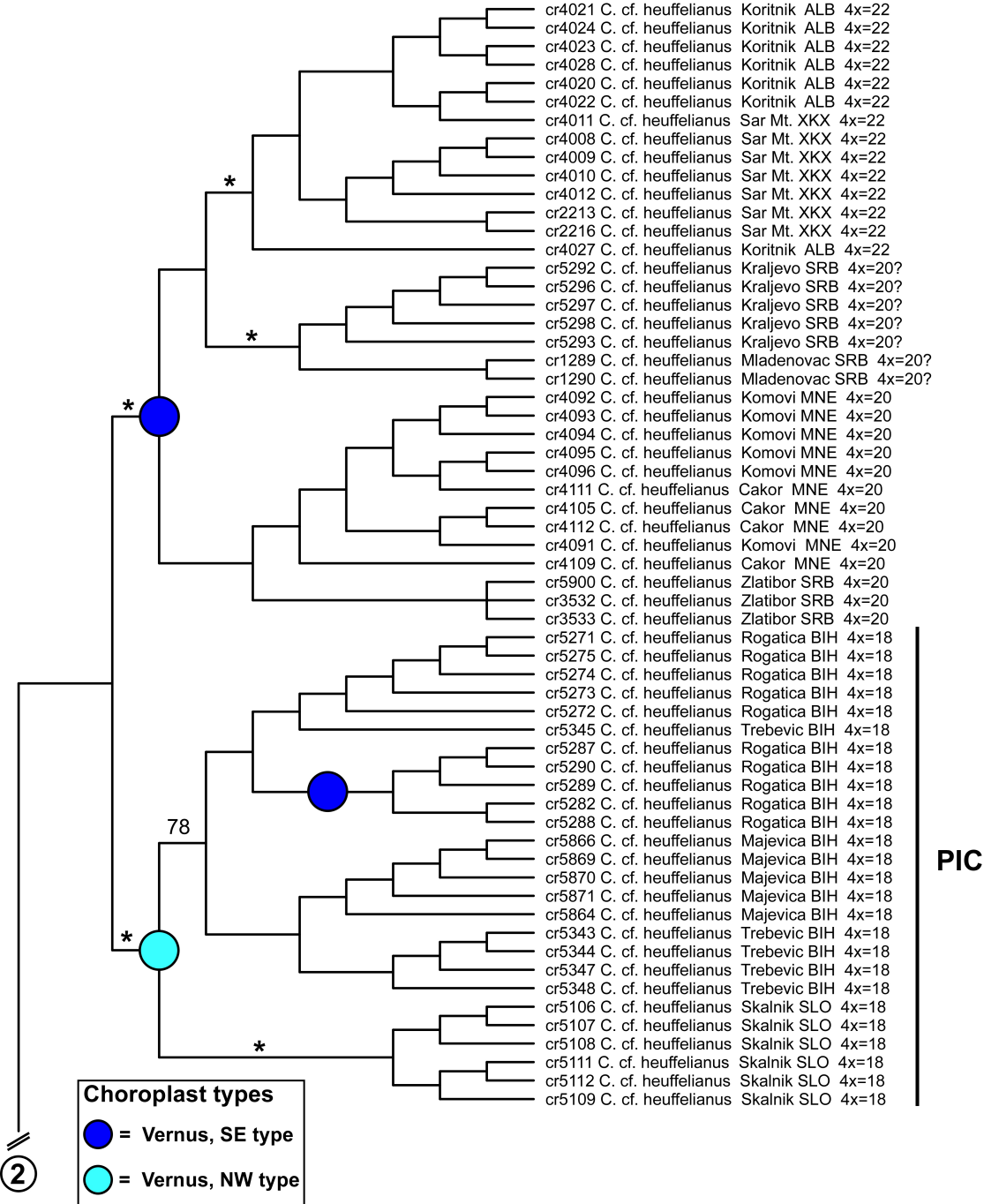


**Figure S3.** Strict consensus of 4500 most parsimonius phylogenetic trees derived from an analysis of the GBS dataset including di- and tetraploid cytotypes of *Crocus* ser. *Verni* taxa. Numbers along the backbone branches provide bootstrap values ( $\geq 50\%$ ) with asterisks indicating support values  $> 80\%$ . Colors in the circles refer to the chloroplast types present in the respective clades. Bold face indicate diploid individuals. *Crocus malyi* was defined as outgroup in the analysis.

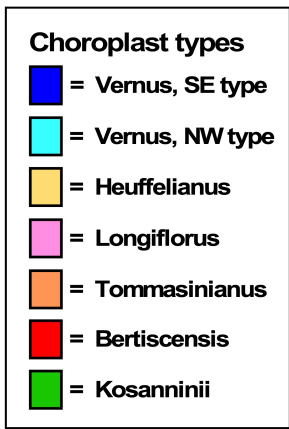


**Figure S3.** Continued.

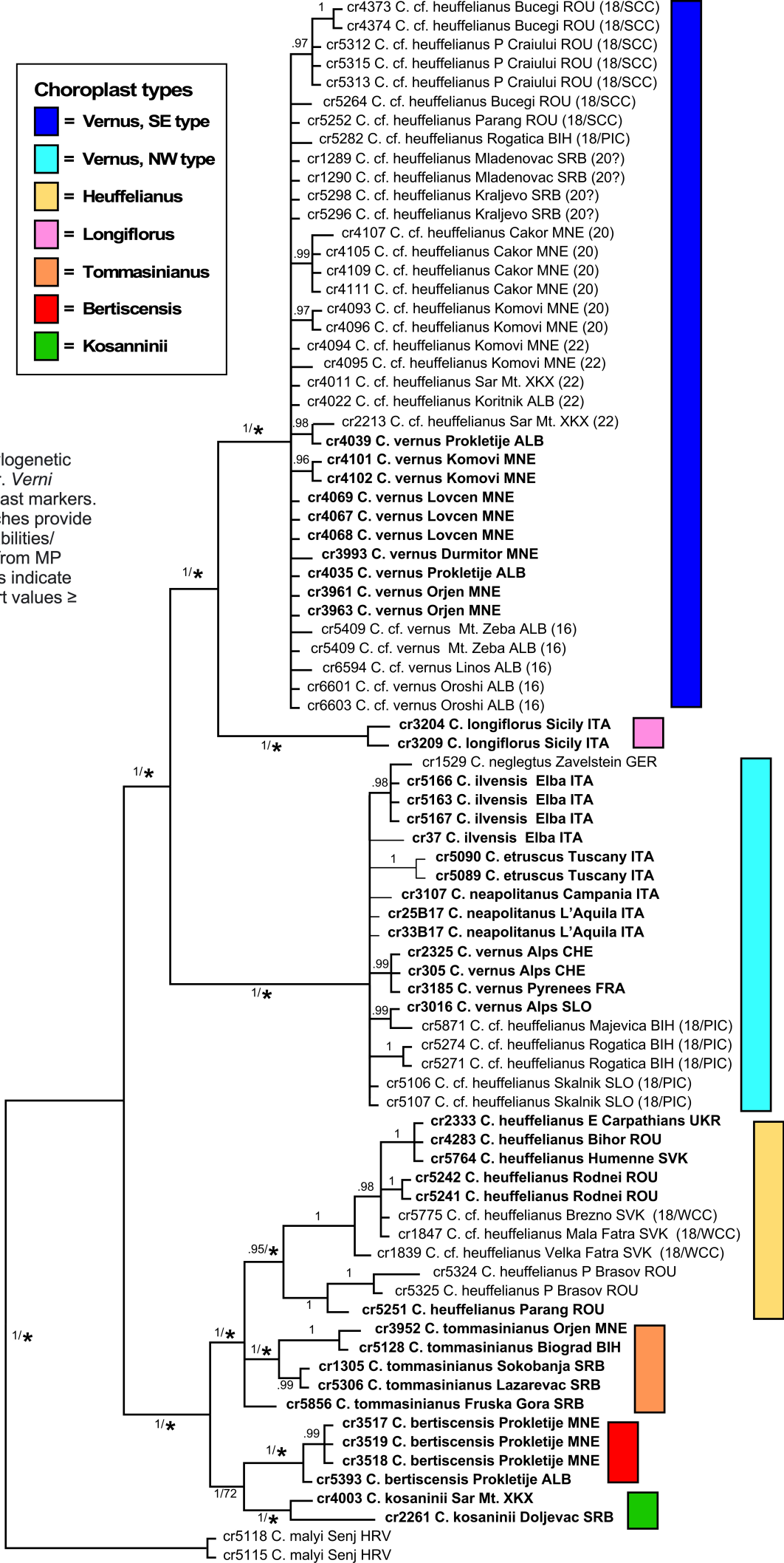


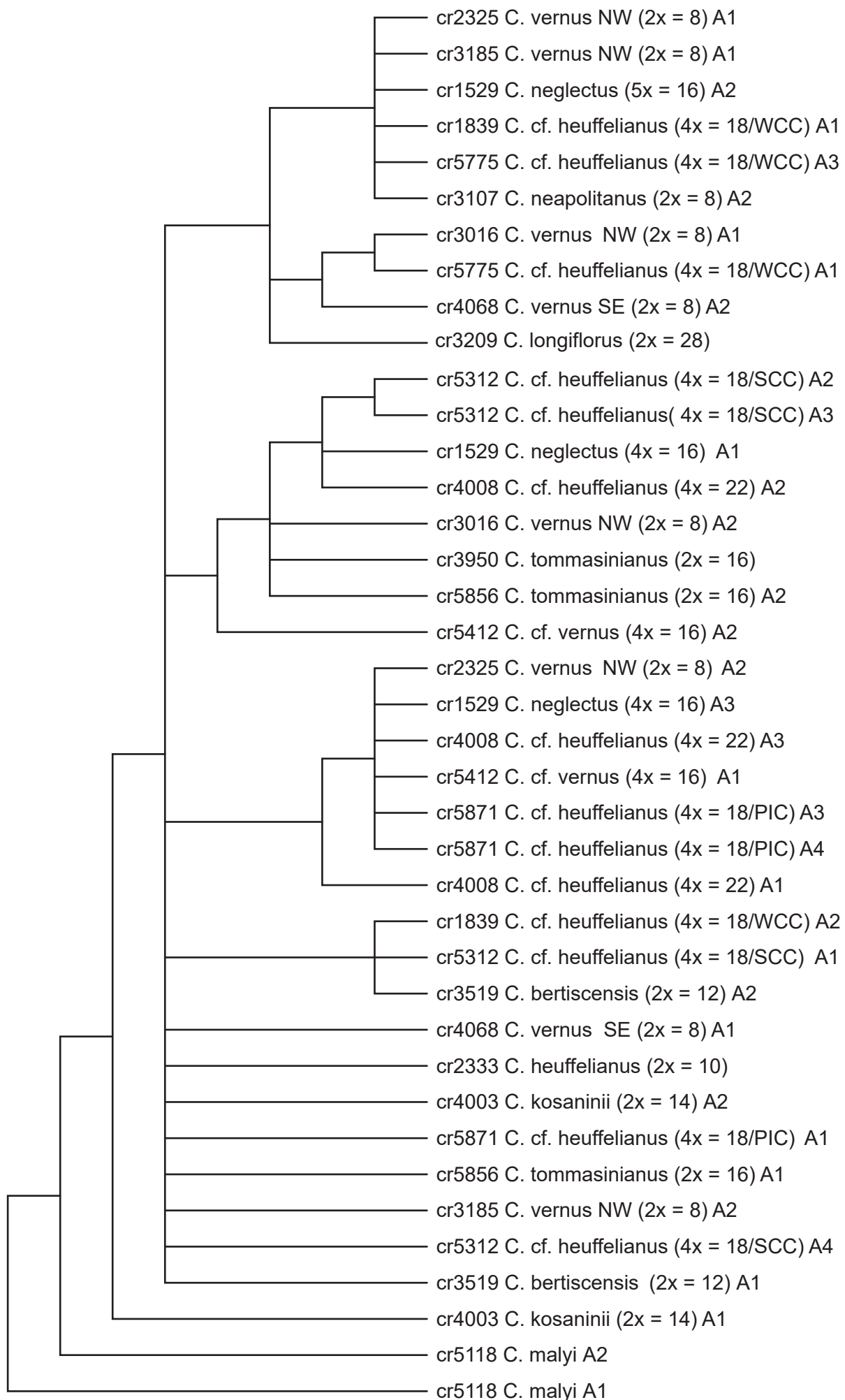


**Figure S3.** Continued.

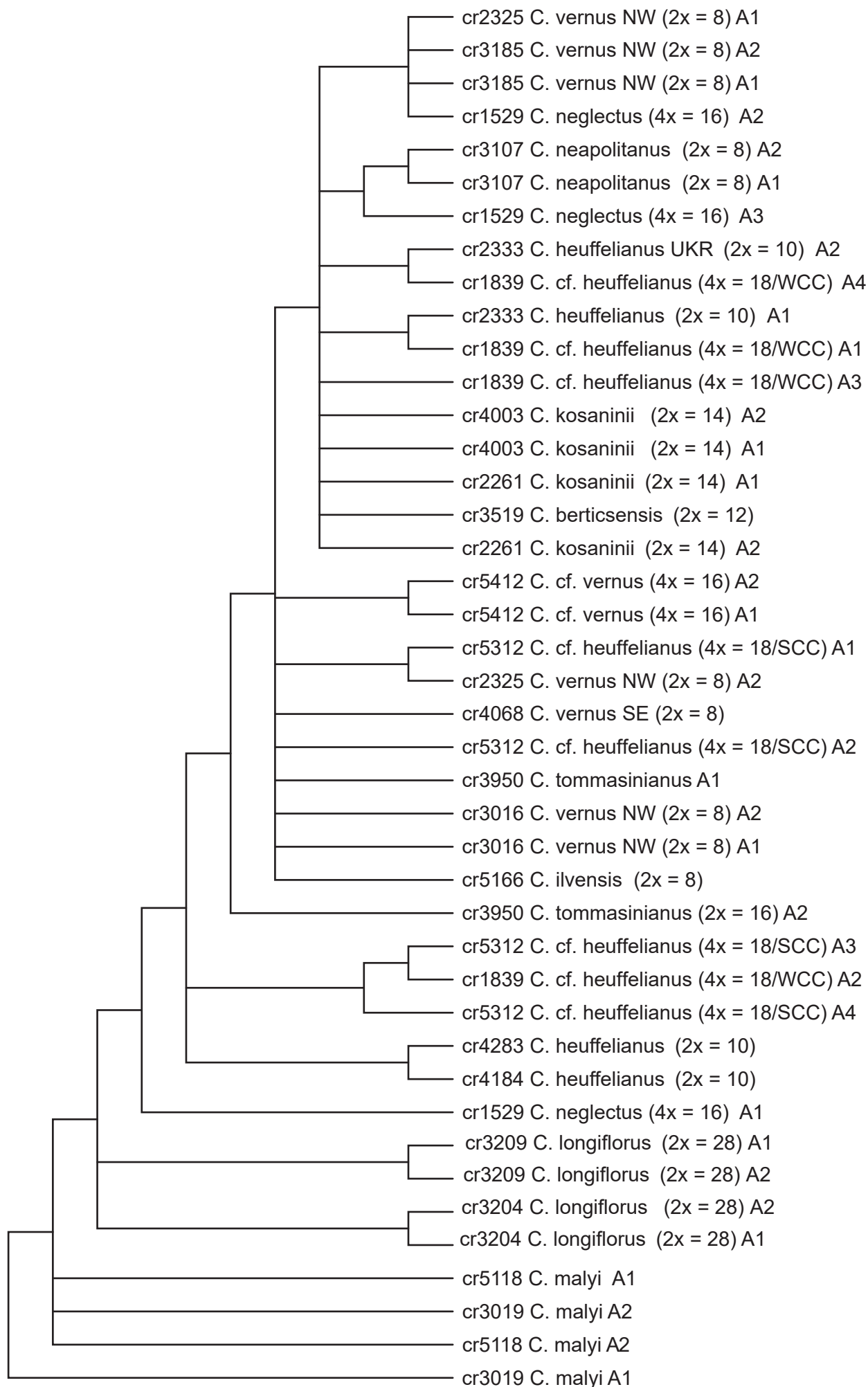


**Figure S4.** BI phylogenetic tree of *Crocus* ser. *Verni* based on chloroplast markers. Numbers at branches provide BI posterior probabilities/ bootstrap values from MP analysis. Asterisks indicate bootstrap support values  $\geq 80\%$ .

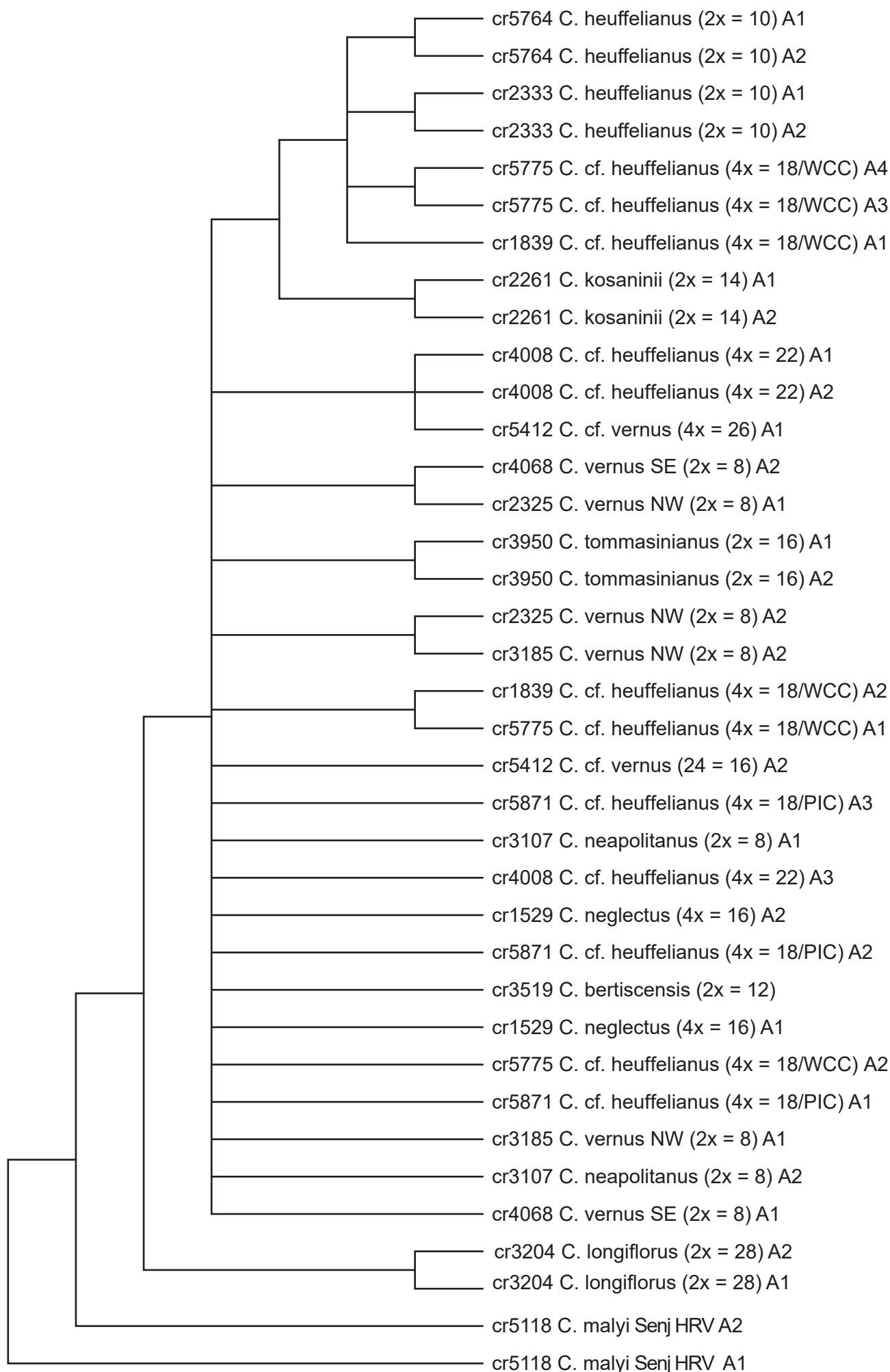




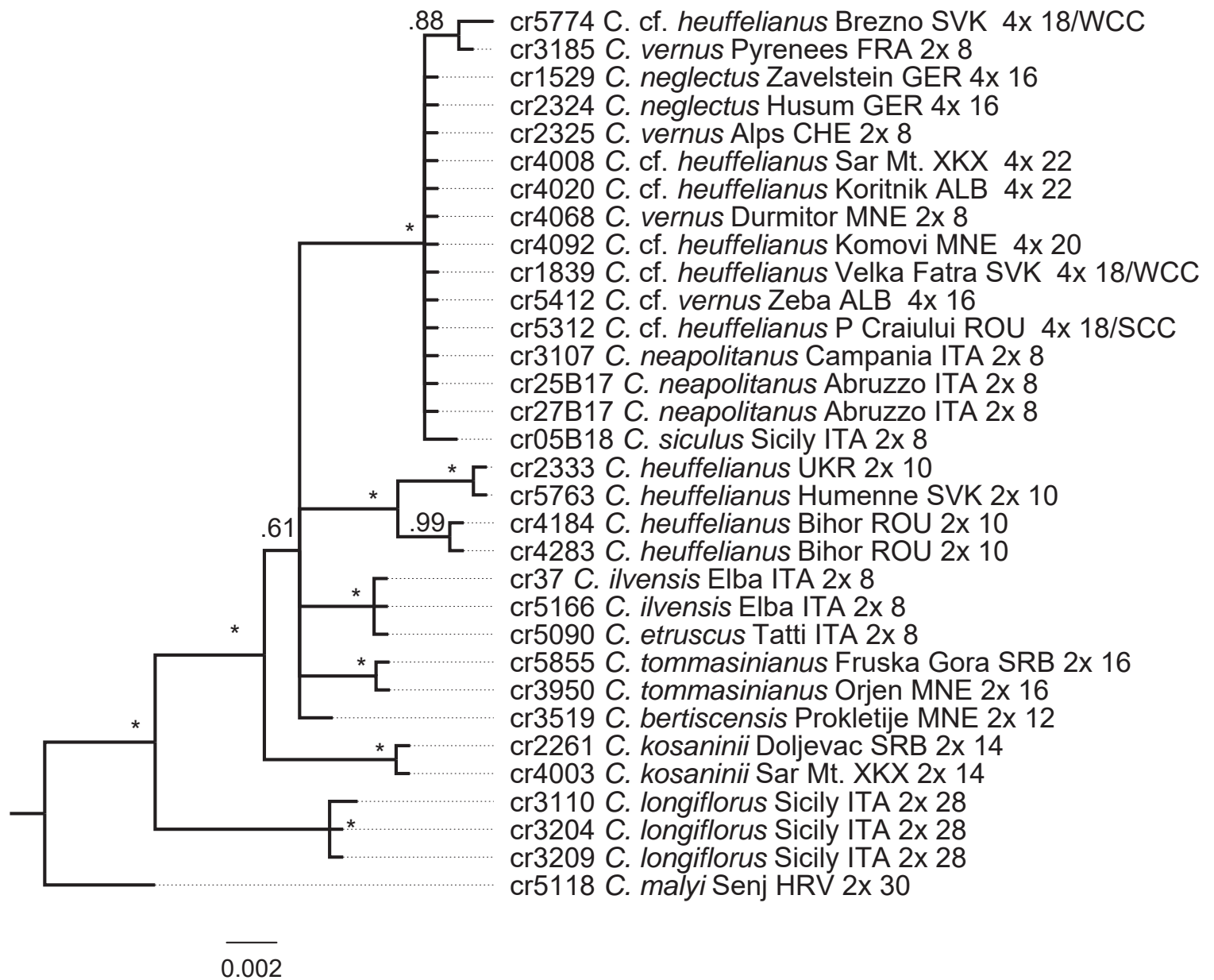
**Figure S5.** Strict consensus MP tree of *topo6*. Allelic differences (A1–A4) in these markers were used to track the bi-parental contributions of diploids to allotetraploids.



**Figure S6.** Strict consensus MP tree *rcf2*. Allelic differences (A1–A4) in these markers were used to track the bi-parental contributions of diploids to allotetraploids.

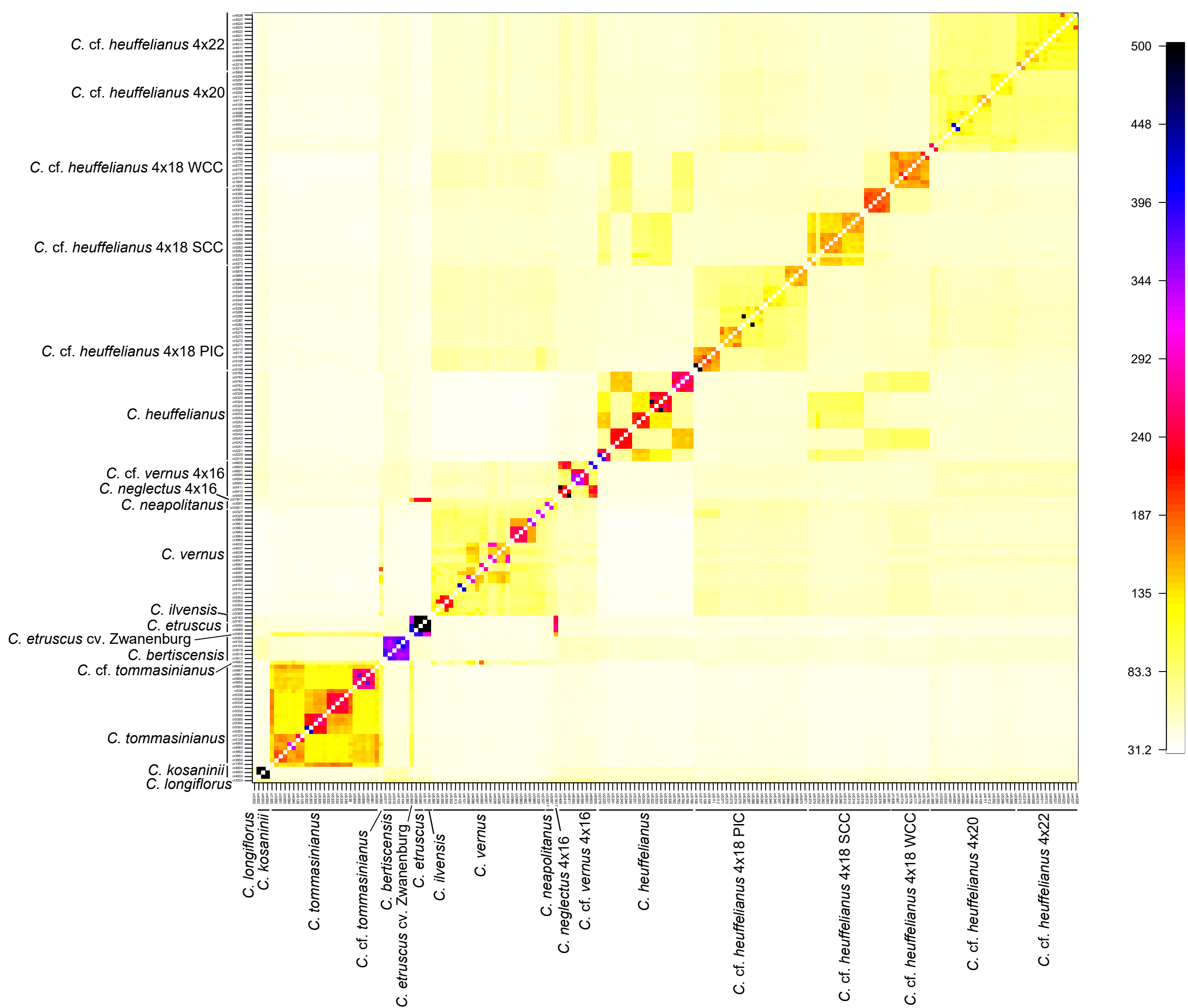


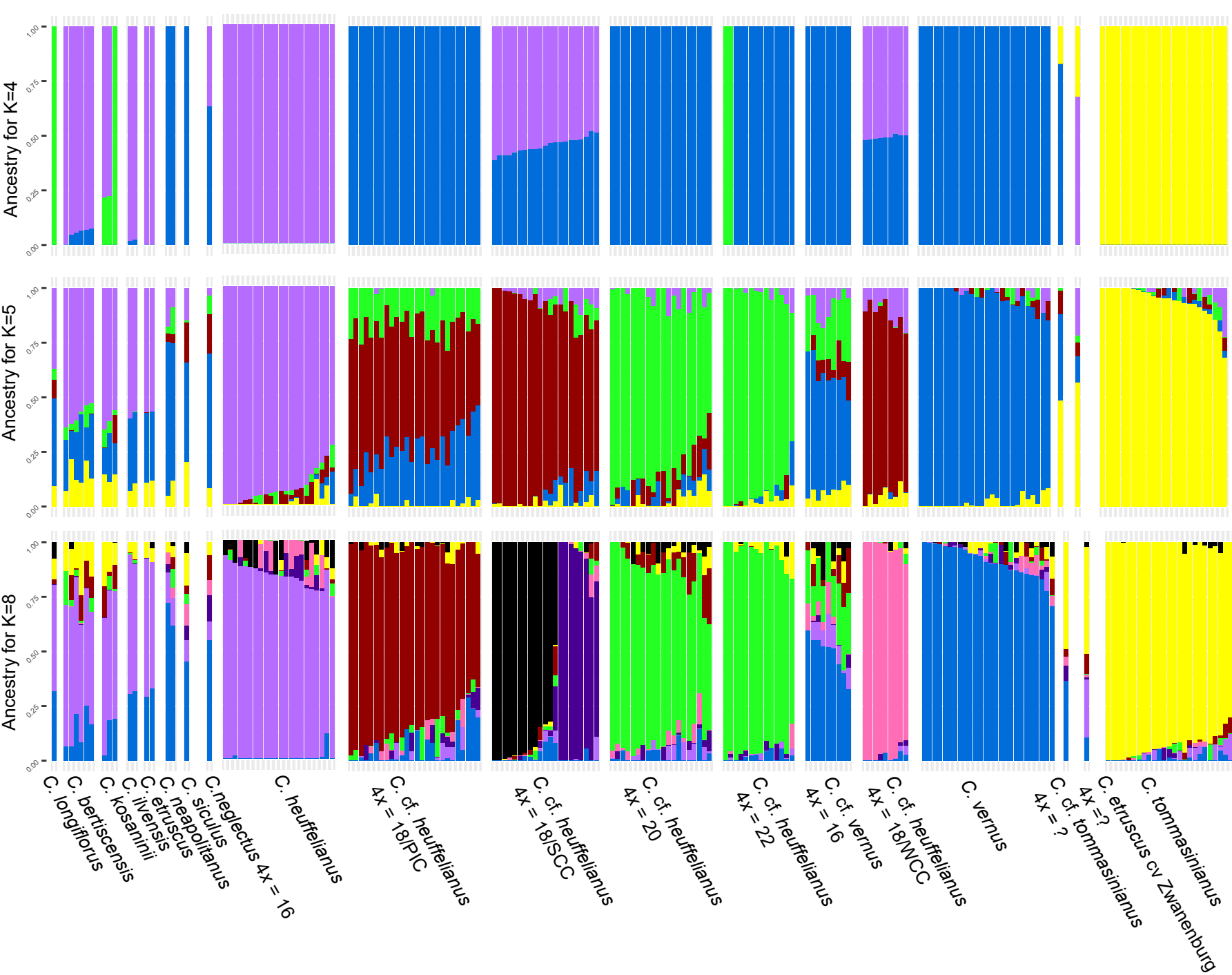
**Figure S7.** Strict consensus MP tree *orcp*. Allelic differences (A1–A4) in these markers were used to track the bi-parental contributions of diploids to allotetraploids.



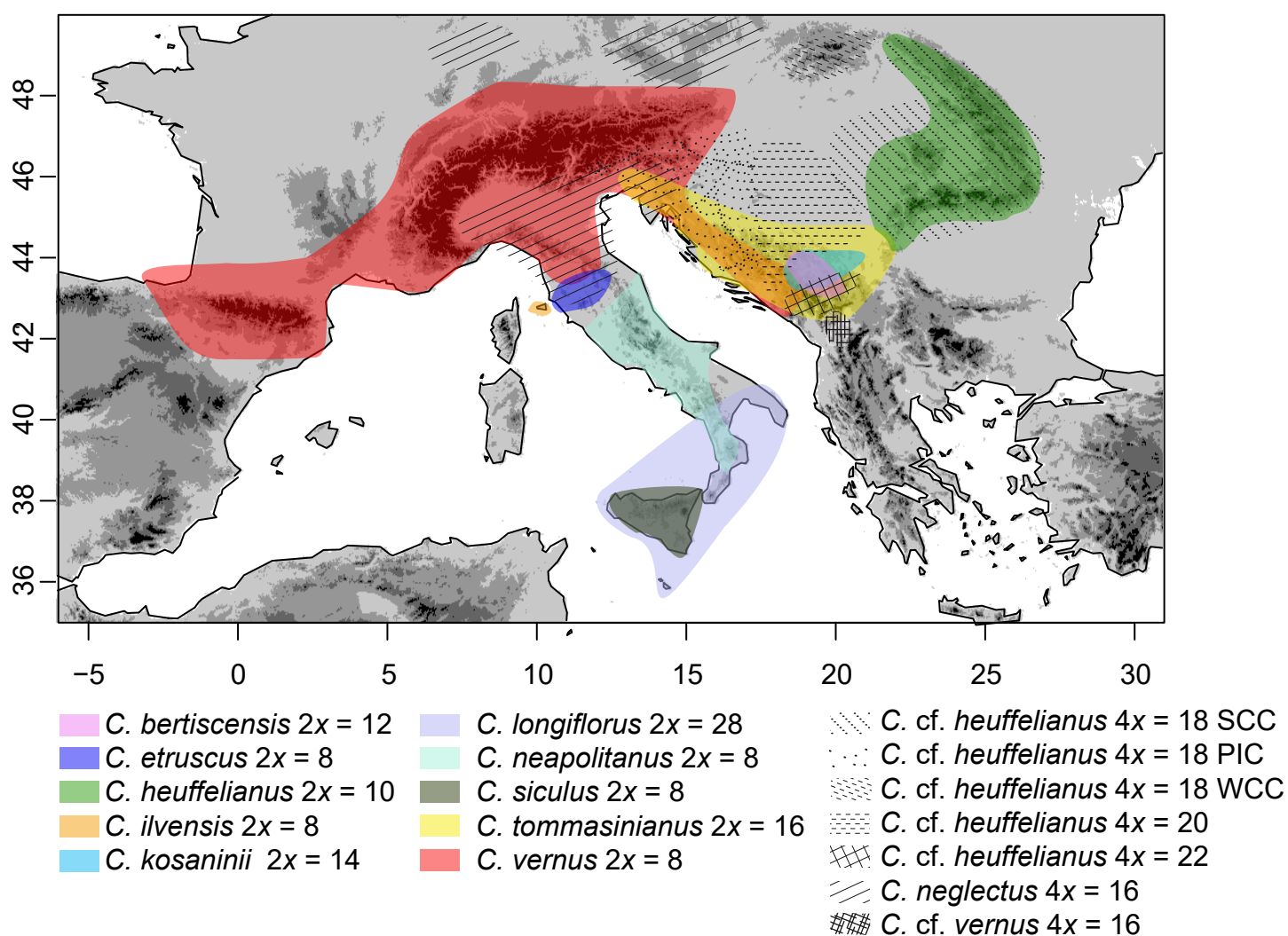
**Figure S8.** Phylogenetic trees obtained through Bayesian phylogenetic inference based on rDNA ITS sequences. Numbers along branches indicate BI posterior probabilities (pp), pp supports of 1.0 are indicated by asterisks.







**Figure S10.** Population structure analysis based on 2207 GBS loci using fastSTRUCTURE at K = 4 (30661 SNPs) and LEA K = 5 and 8 (2172 unlinked SNPs). Each vertical line represents one individual, while each color shows the genetic composition that is assigned into a distinct genetic cluster.



**Figure S11.** Map with the approximate distributions of species in *Crocus* ser. *Verni*. Distribution areas of different species are indicated by different colors or shapes (see legend).