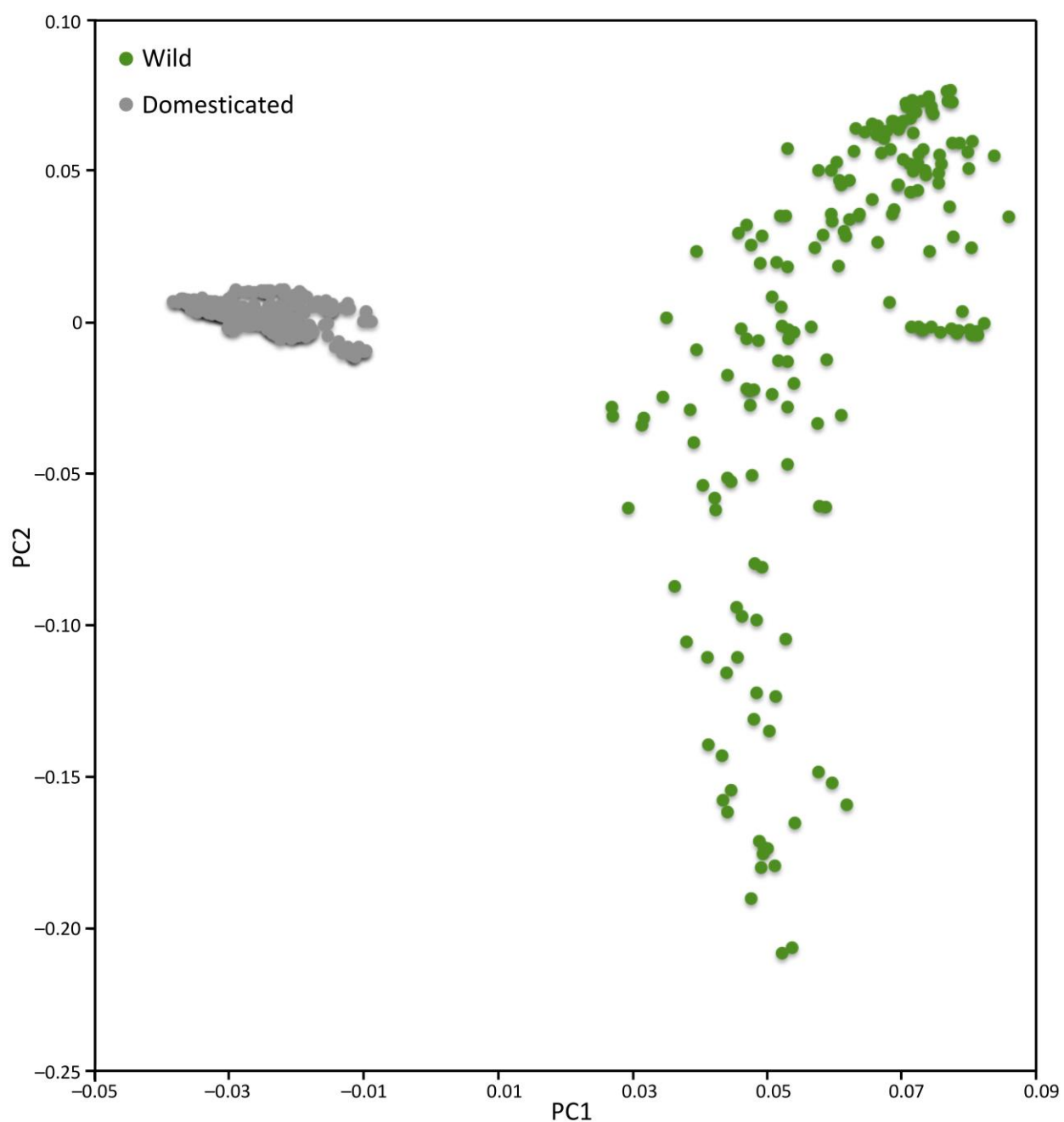
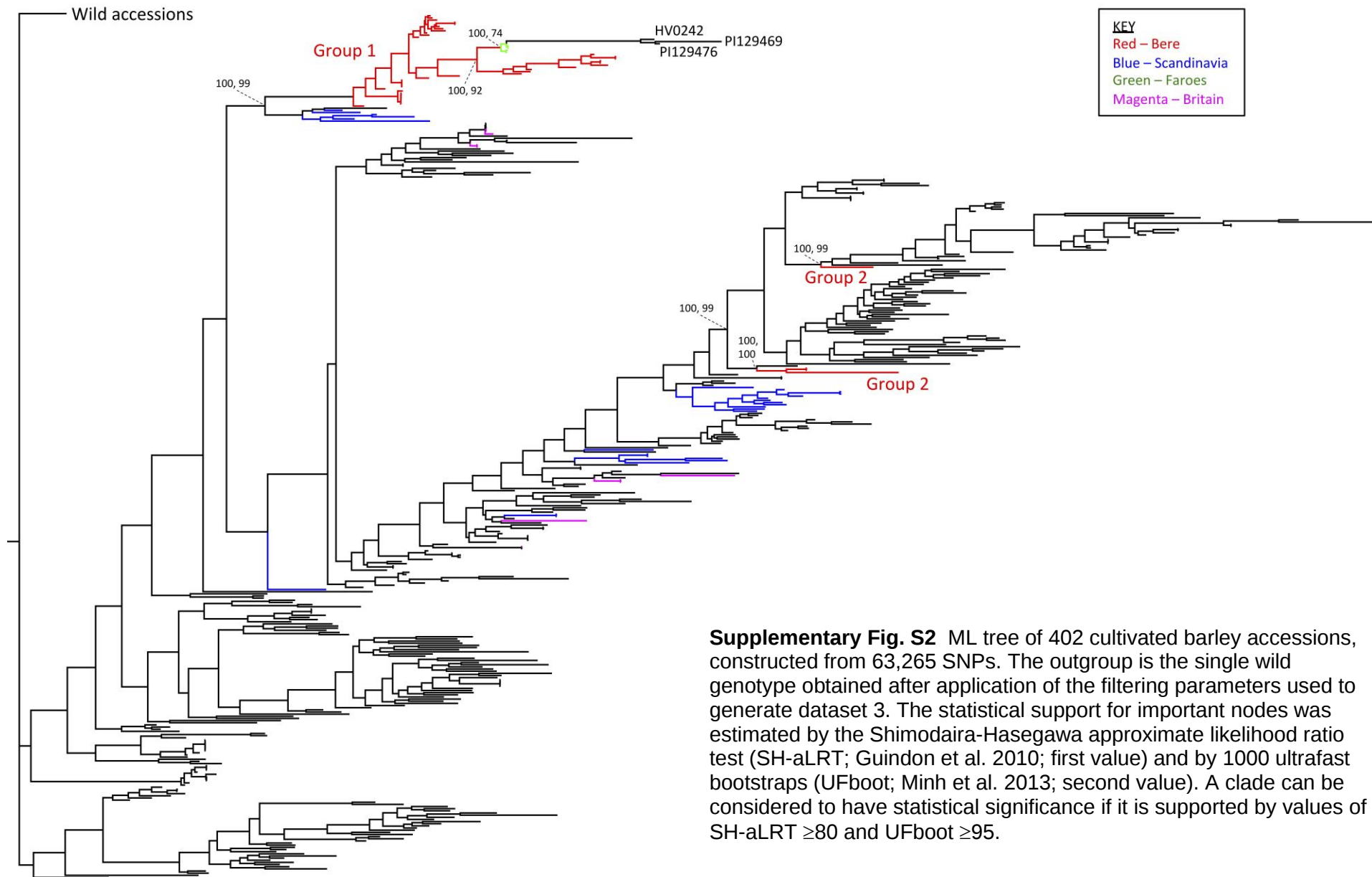
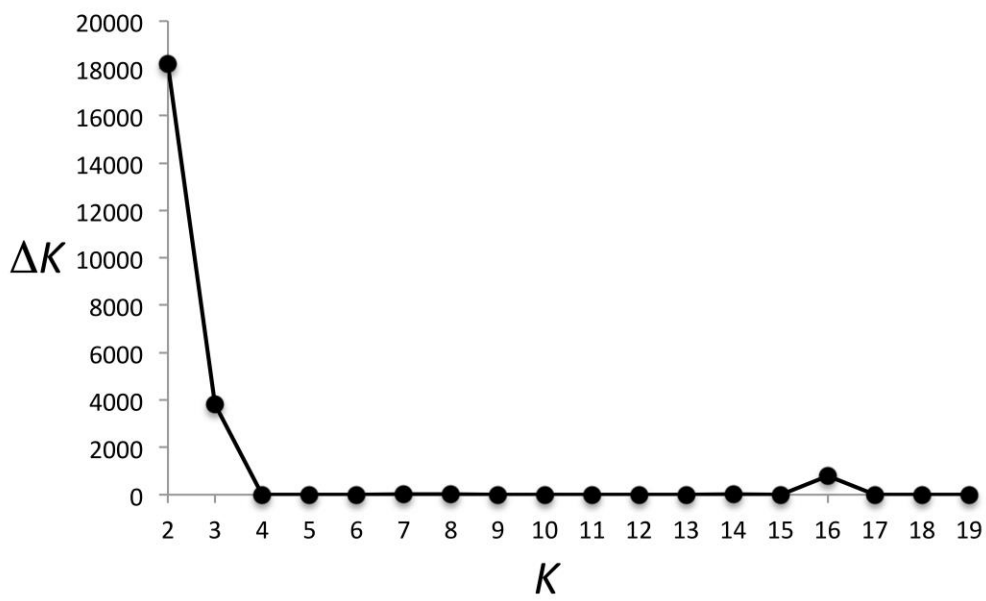




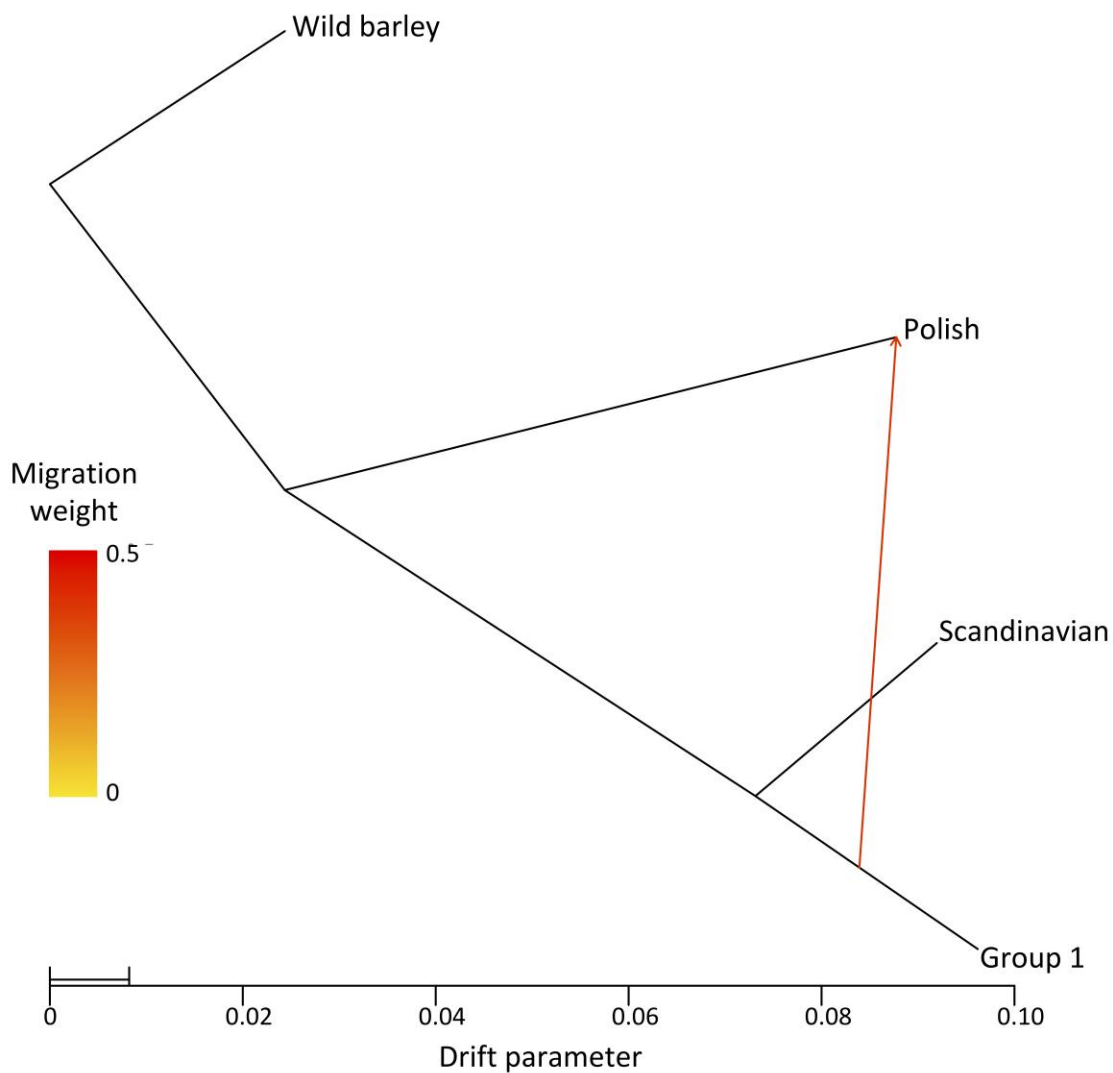
Supplementary Fig. S1 PCA of 584 wild and cultivated barley accessions, generated from dataset 1 (1,946,469 SNPs filtered for <70% missing data, a probability of excess heterozygosity of <0.5 and minor allele count of ≥ 9).



Supplementary Fig. S2 ML tree of 402 cultivated barley accessions, constructed from 63,265 SNPs. The outgroup is the single wild genotype obtained after application of the filtering parameters used to generate dataset 3. The statistical support for important nodes was estimated by the Shimodaira-Hasegawa approximate likelihood ratio test (SH-aLRT; Guindon et al. 2010; first value) and by 1000 ultrafast bootstraps (UFboot; Minh et al. 2013; second value). A clade can be considered to have statistical significance if it is supported by values of SH-aLRT ≥ 80 and UFboot ≥ 95 .



Supplementary Fig. S3 Evanno plot (Evanno et al. 2005) for K values of 1–20 from STRUCTURE analysis of 9719 SNPs.



Supplementary Fig. S4 Treemix population graph (Pickrell and Pritchard 2012) modeling a single admixture event. Admixture is indicated by the arrow which is coloured according to the inferred relative genetic contribution ('migration weight'). The population graph with one admixture event improves the fit of the graph to the data with high significance ($p = 9.80441e-06$). After the addition of one migration edge, the residual covariance is zero and modeling further admixture events does not improve the fit to the data.