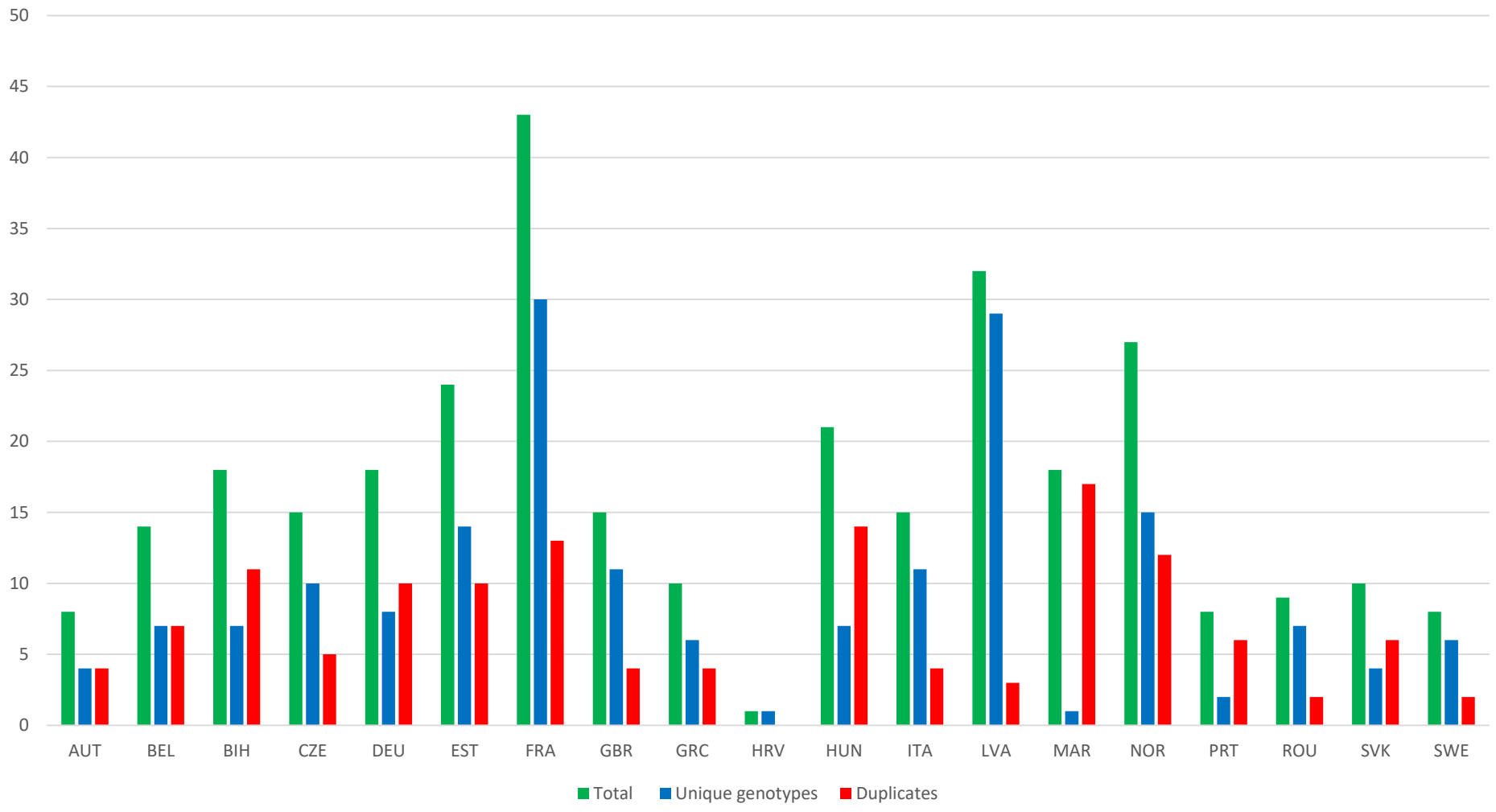


Figure S1: Distribution of type of accessions (unique or duplicate genotype) according to the country maintaining the collection

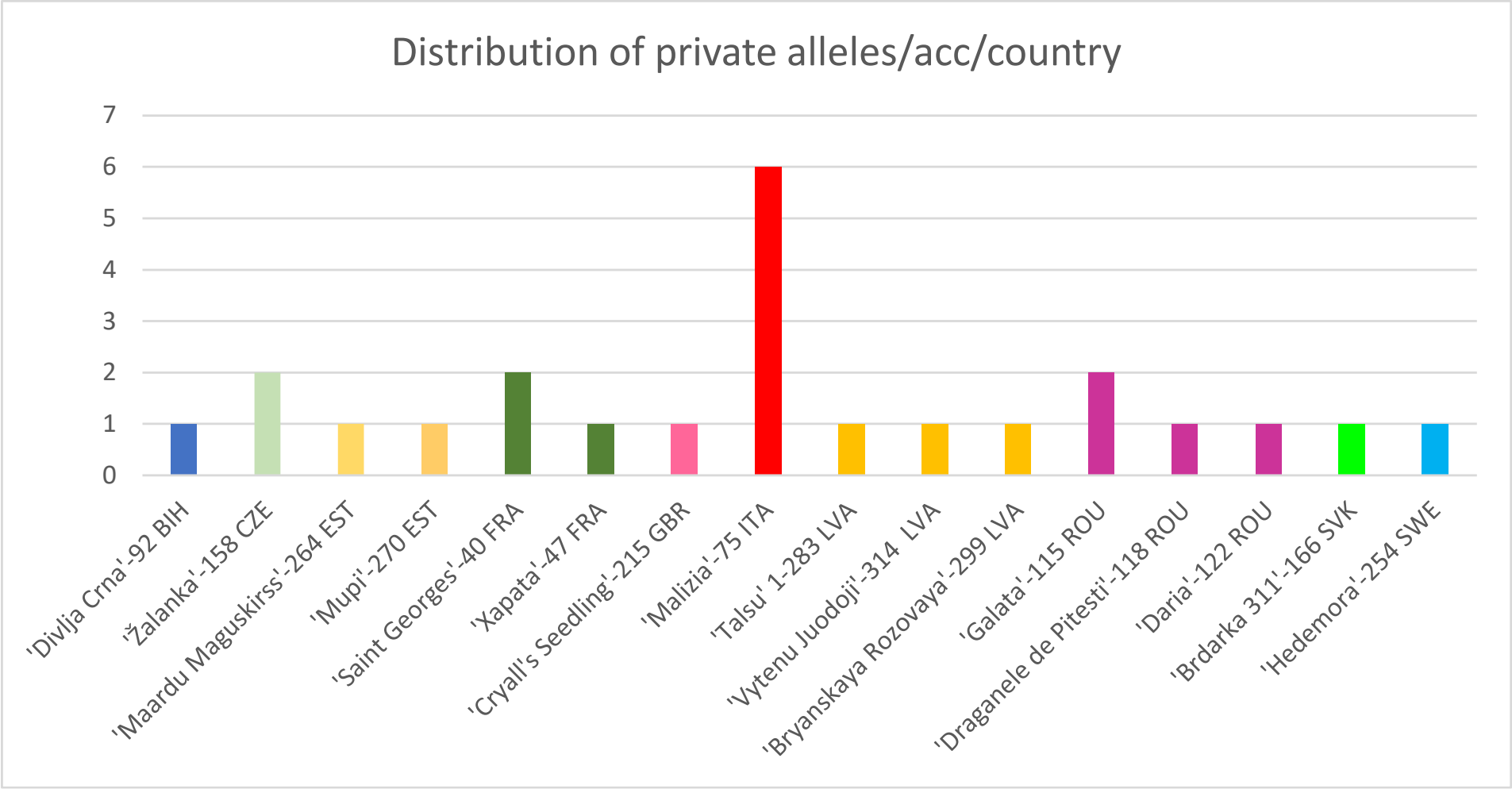
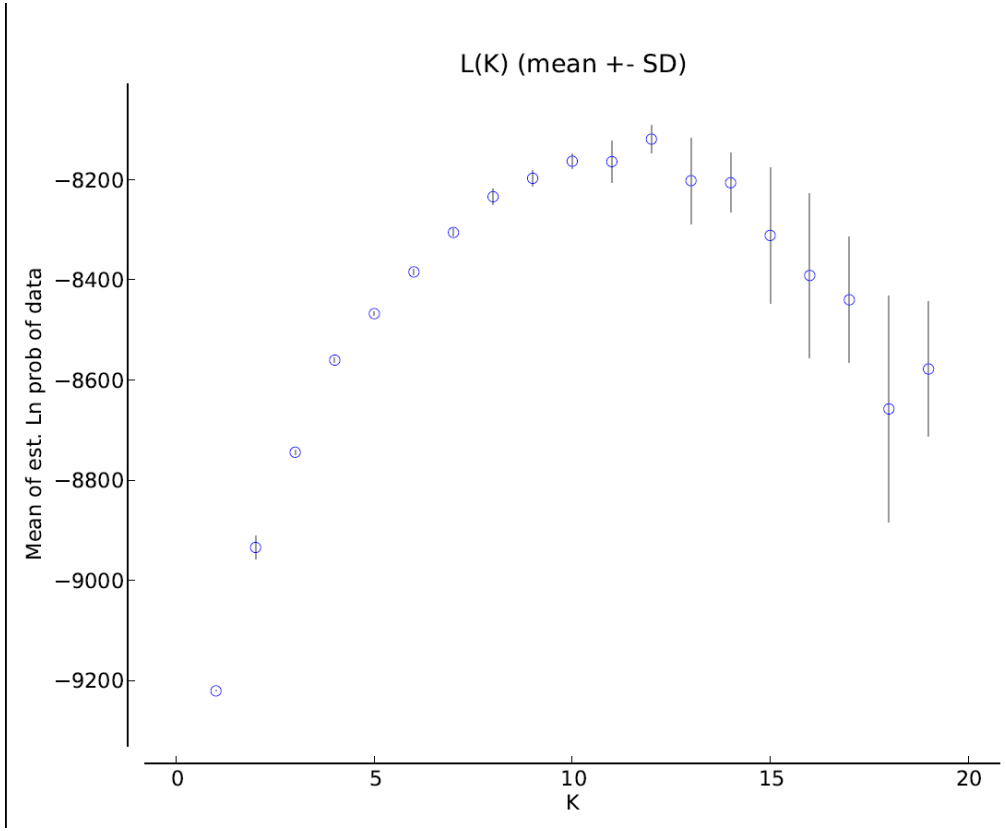
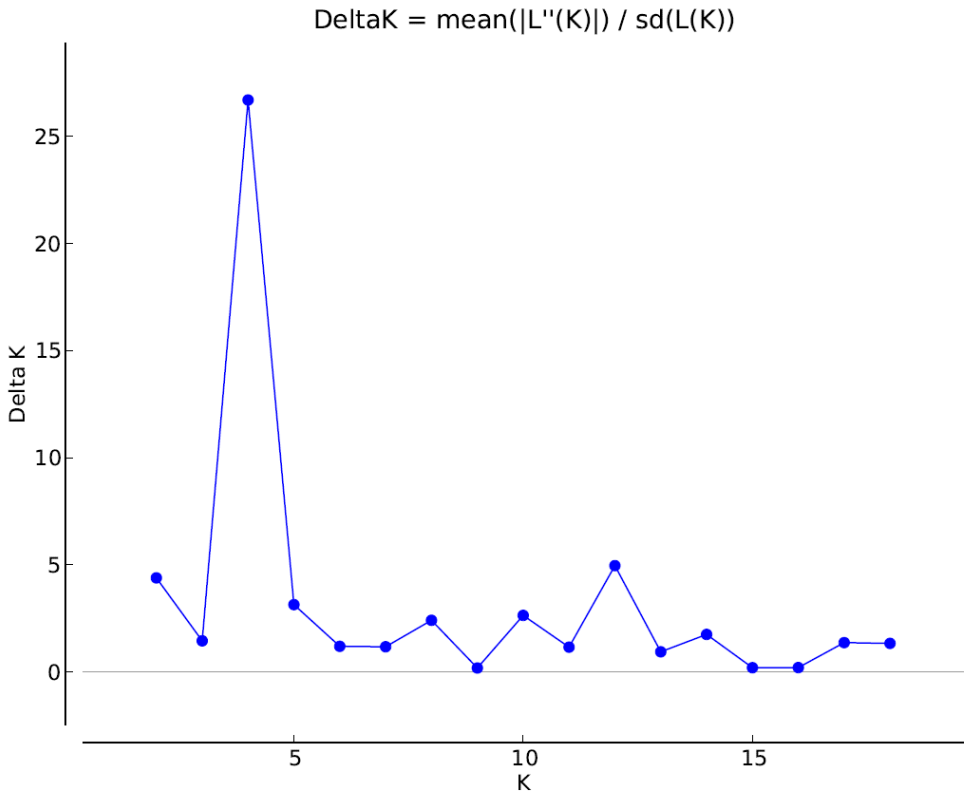


Figure S2: Distribution of private alleles/accessions/collection



a



b

Figure S3: Graphical method (as in [48]) allowing the detection of the number of groups K using:
(a) the rate of change of the likelihood distribution (Mean log-likelihood values) and (b) the ΔK

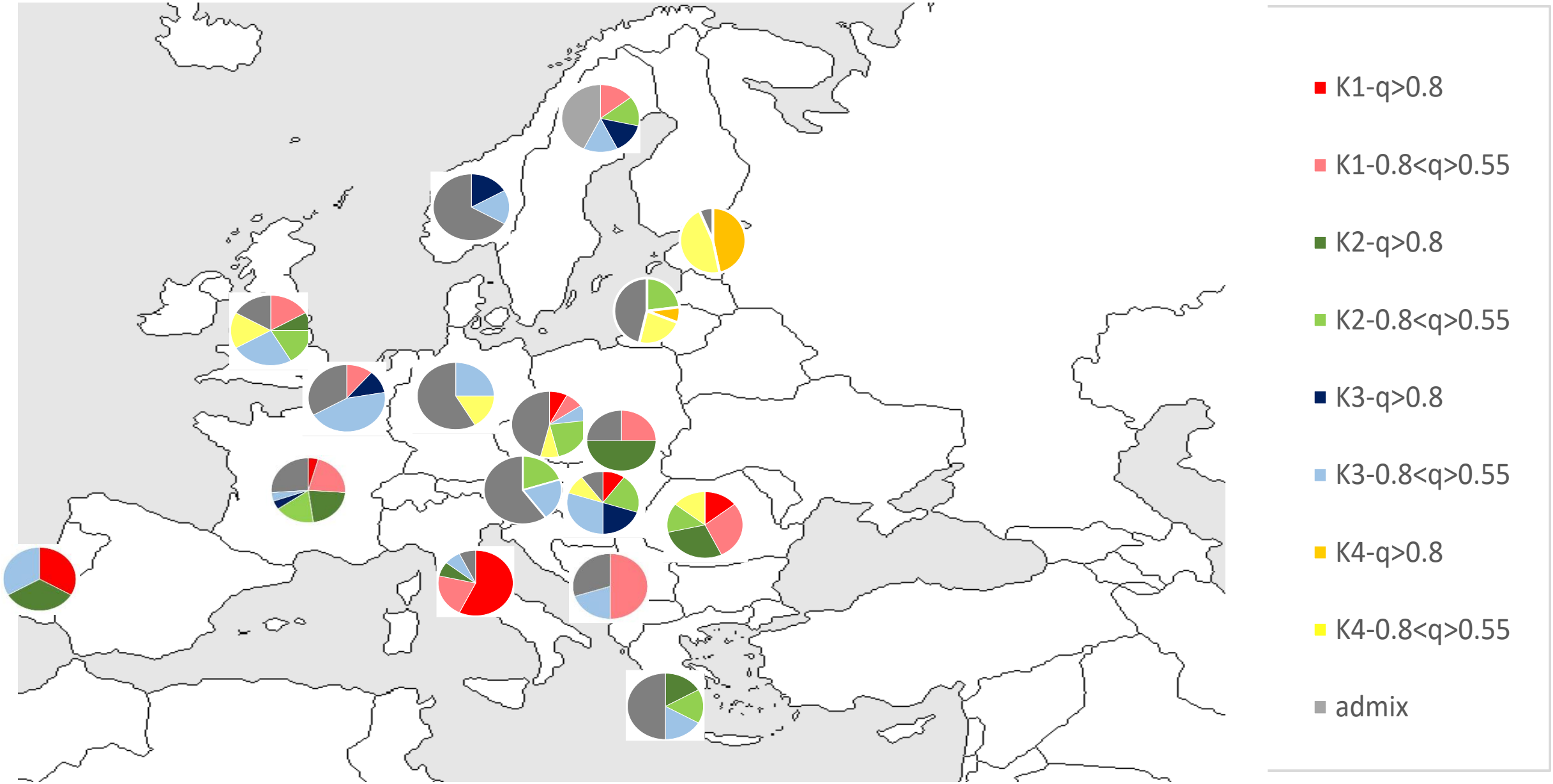


Figure S4: Genetic composition of the national collections according to the K= 4 populations inferred by STRUCTURE.