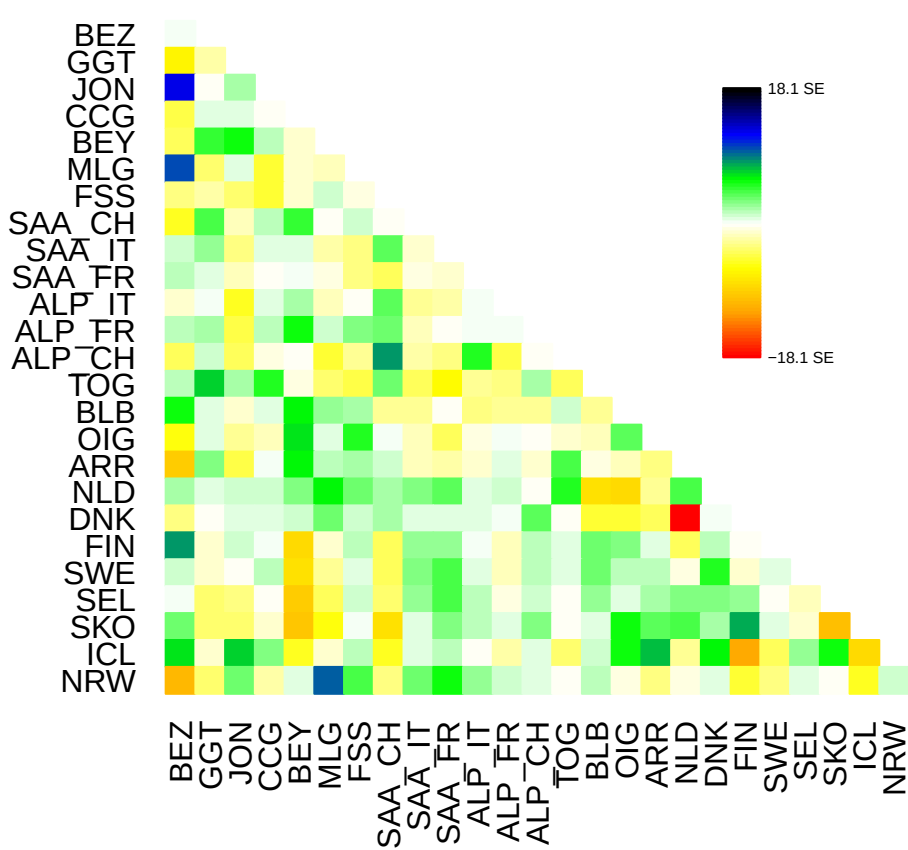
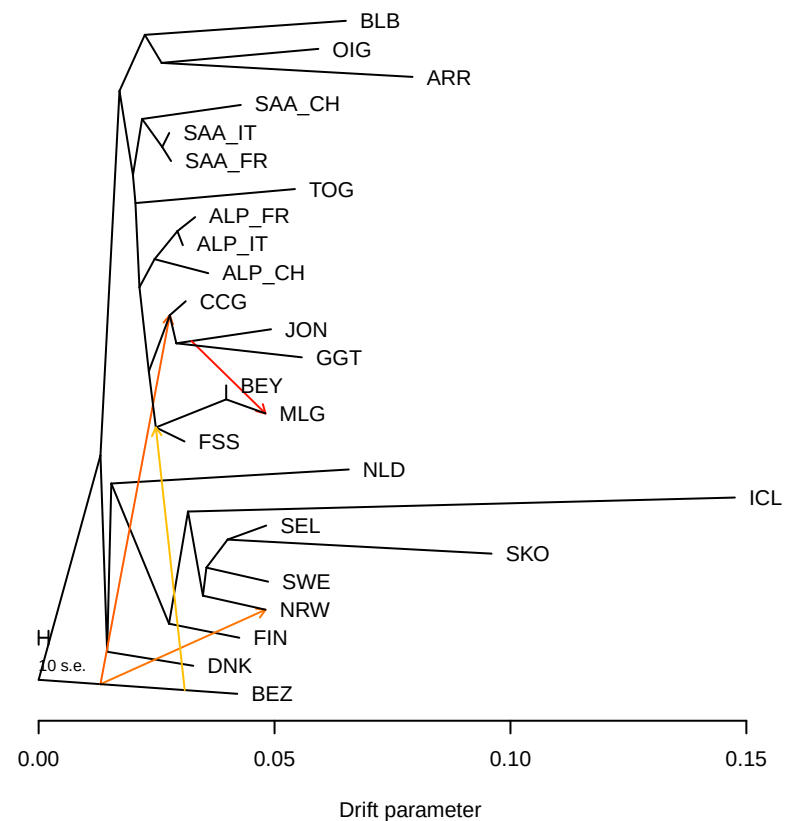
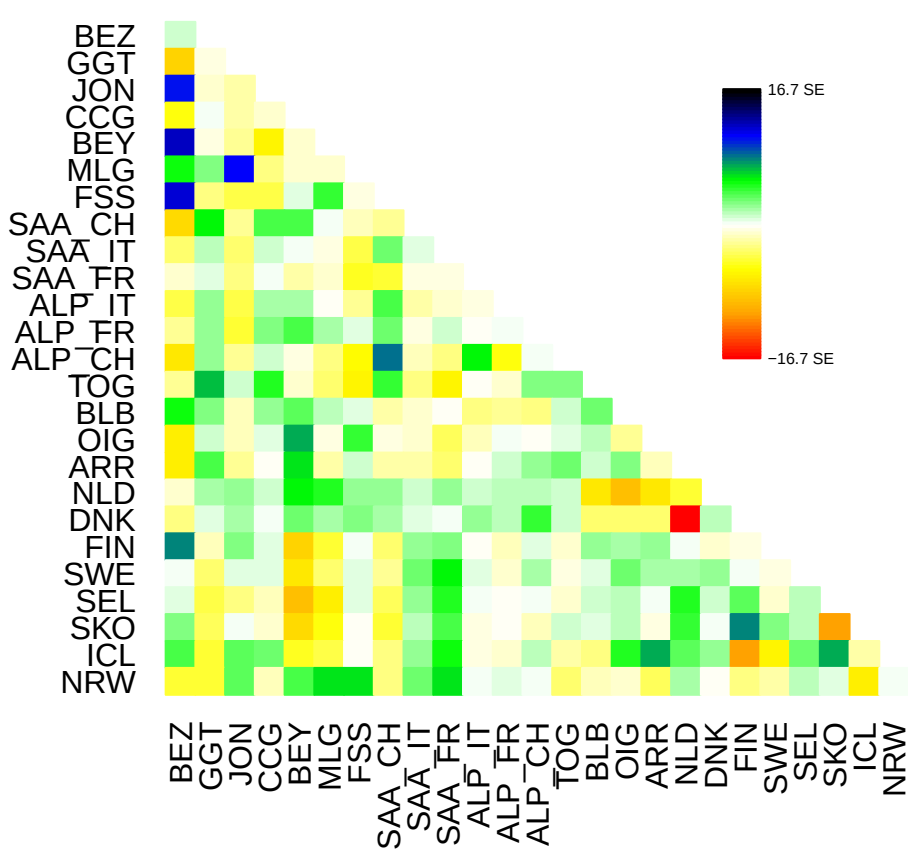
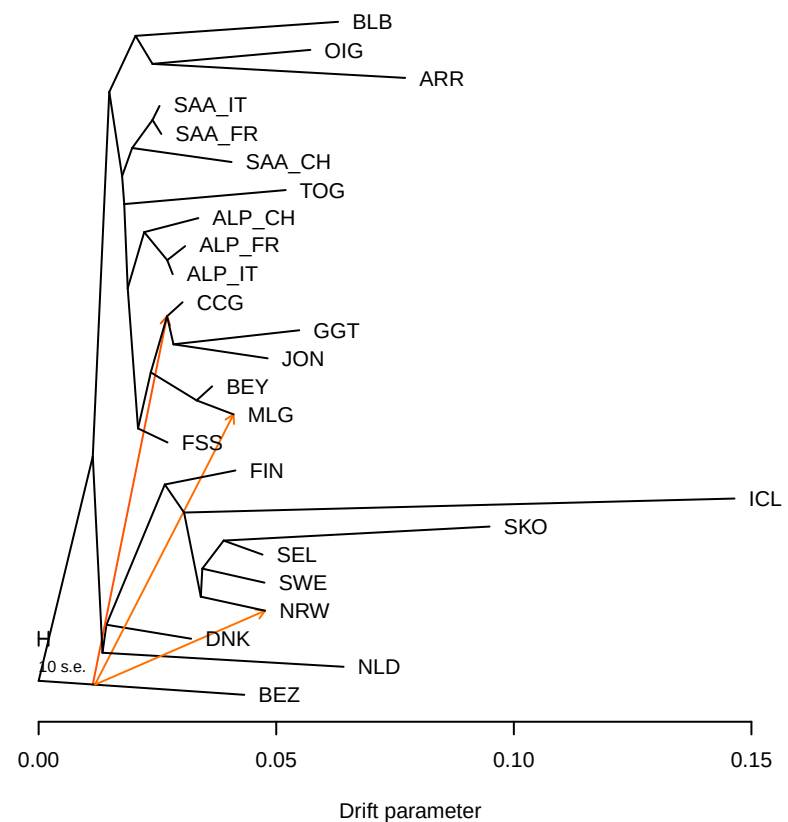
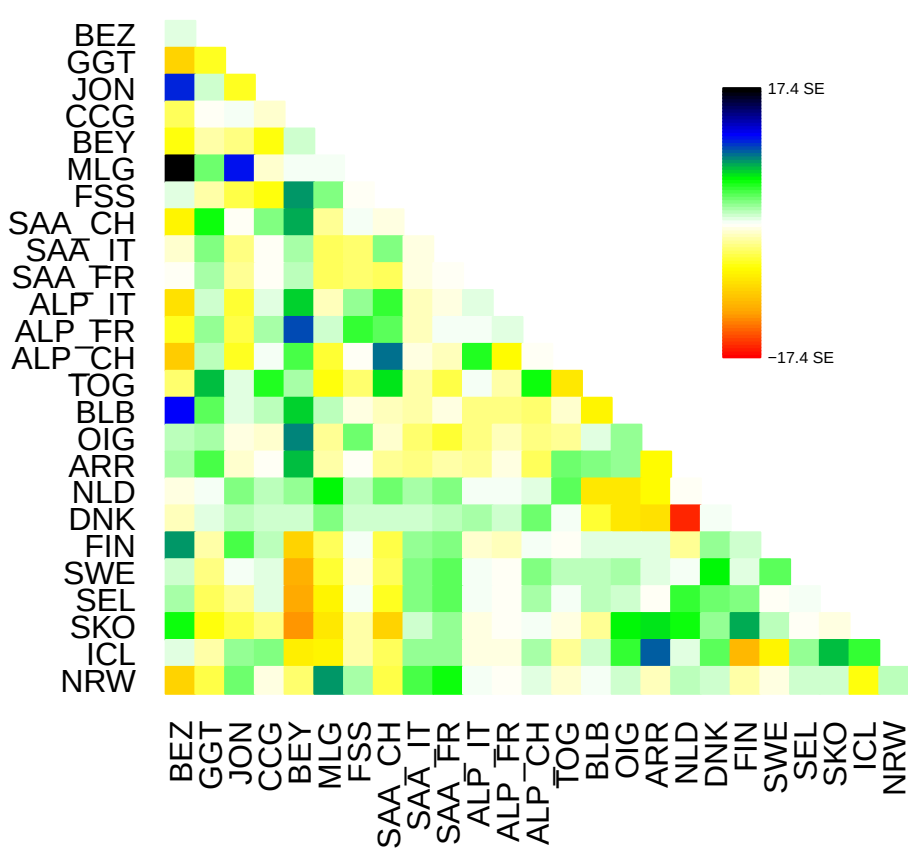
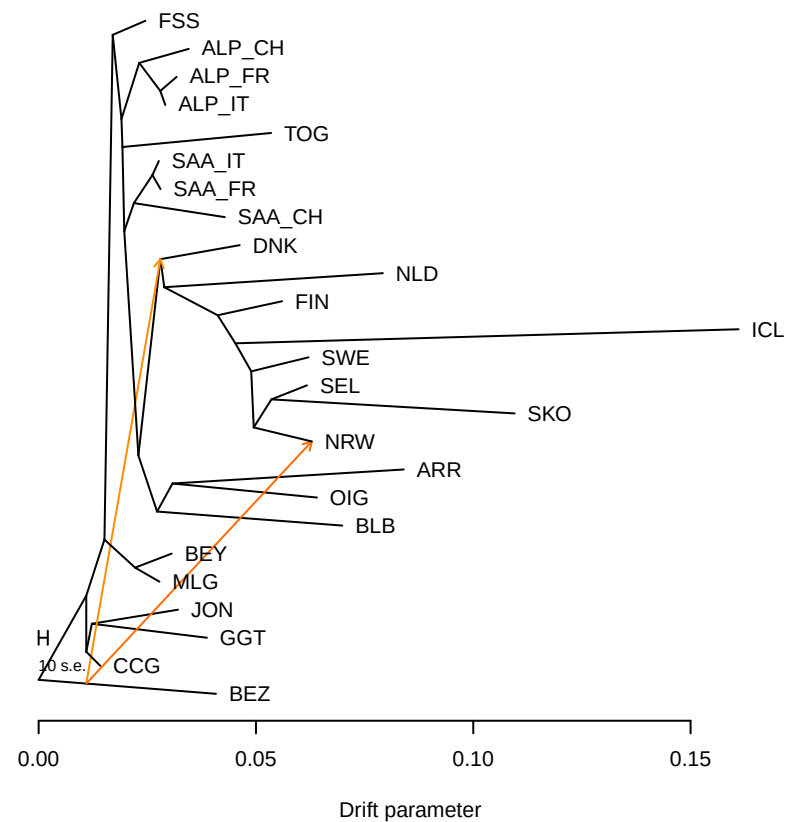
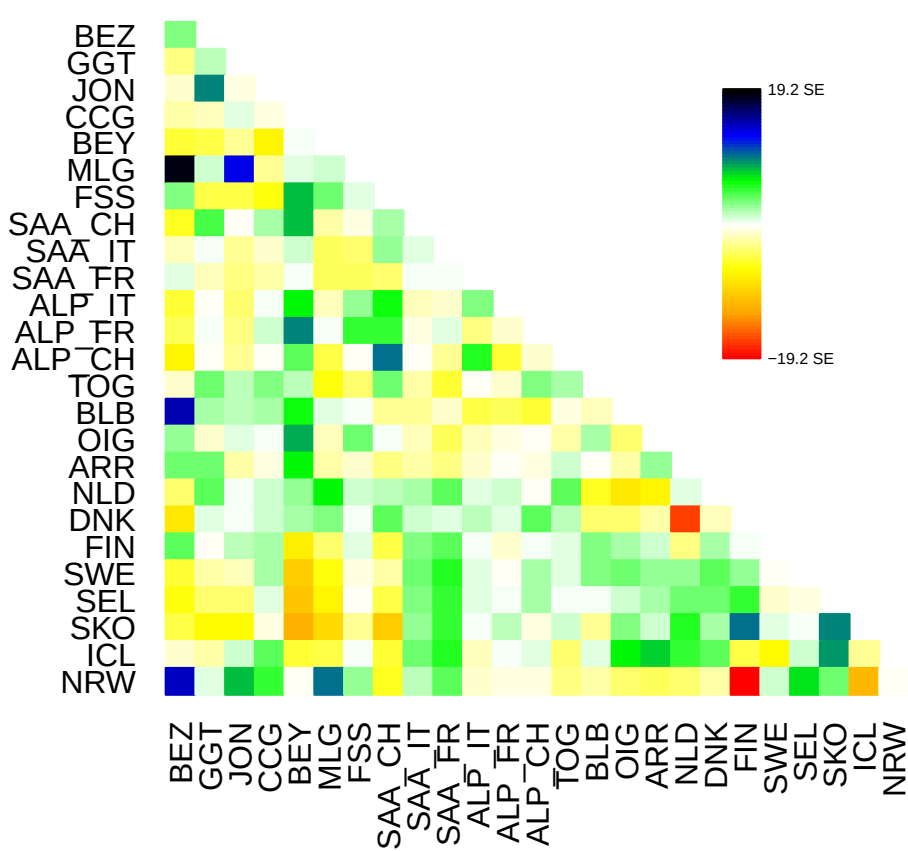
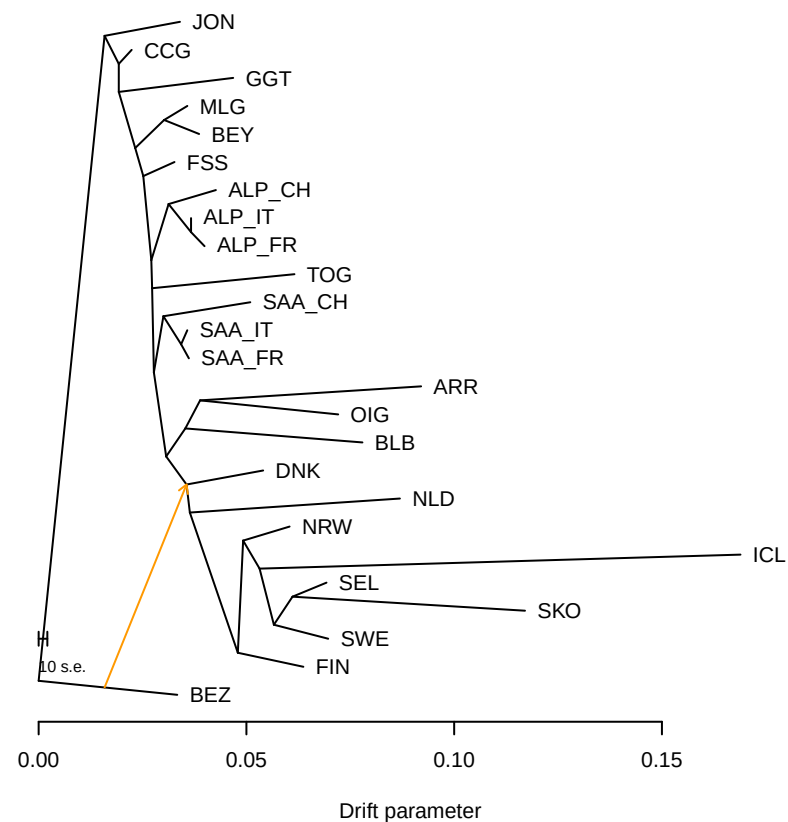
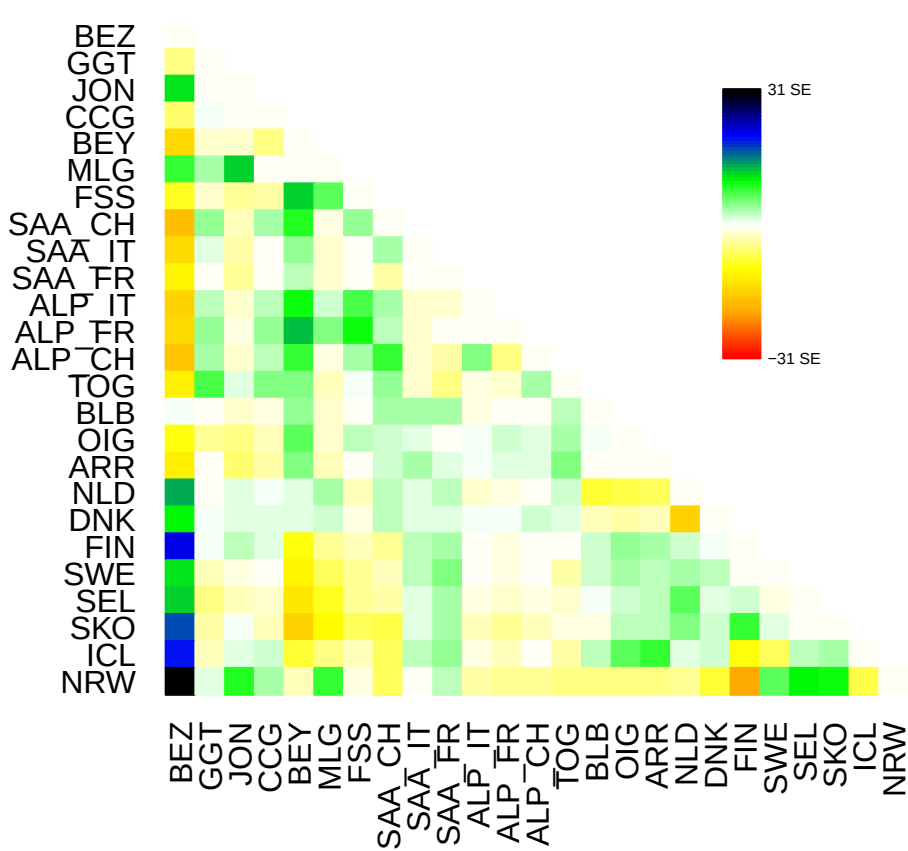
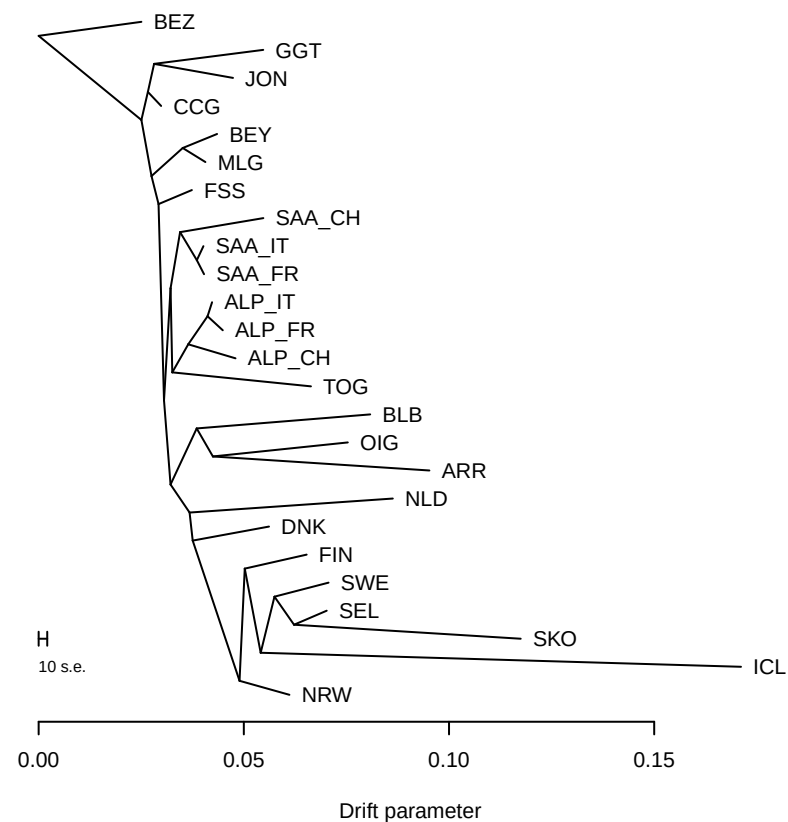
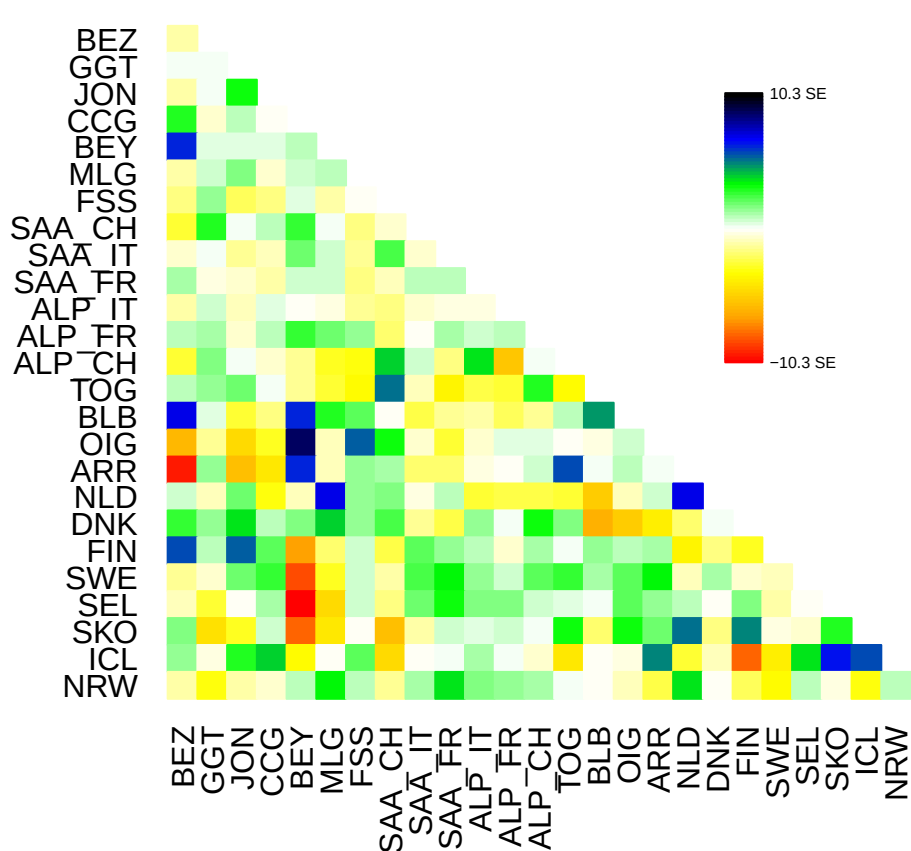
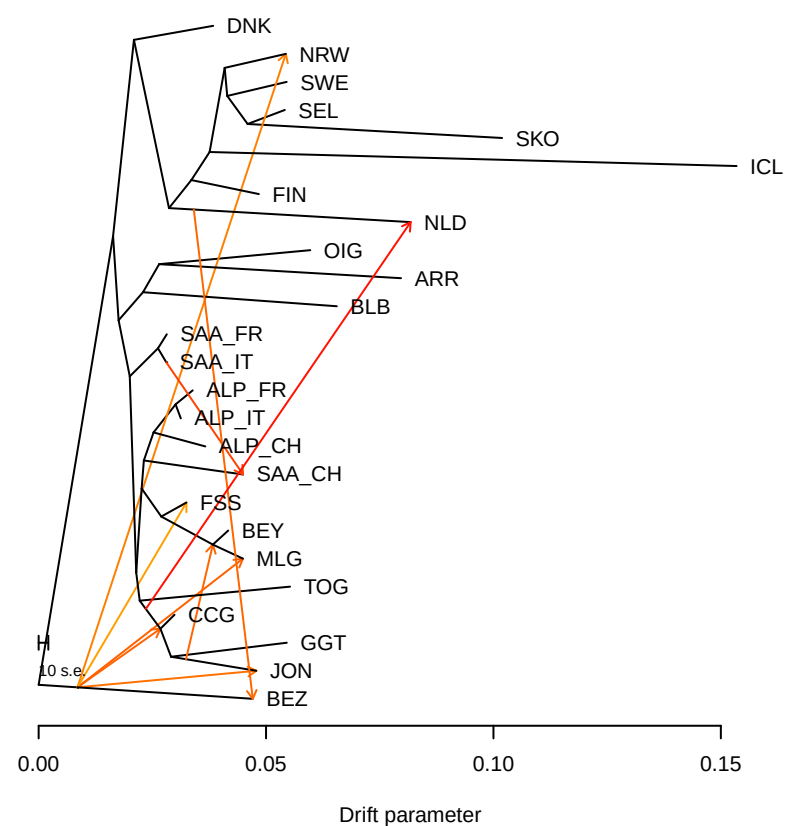
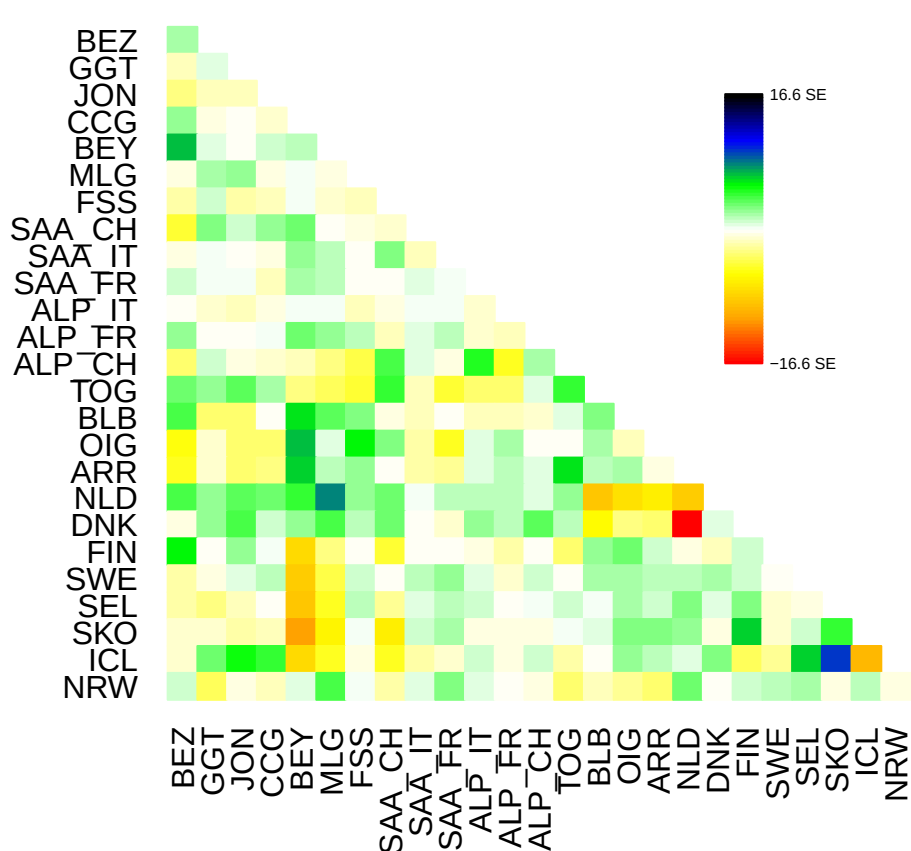
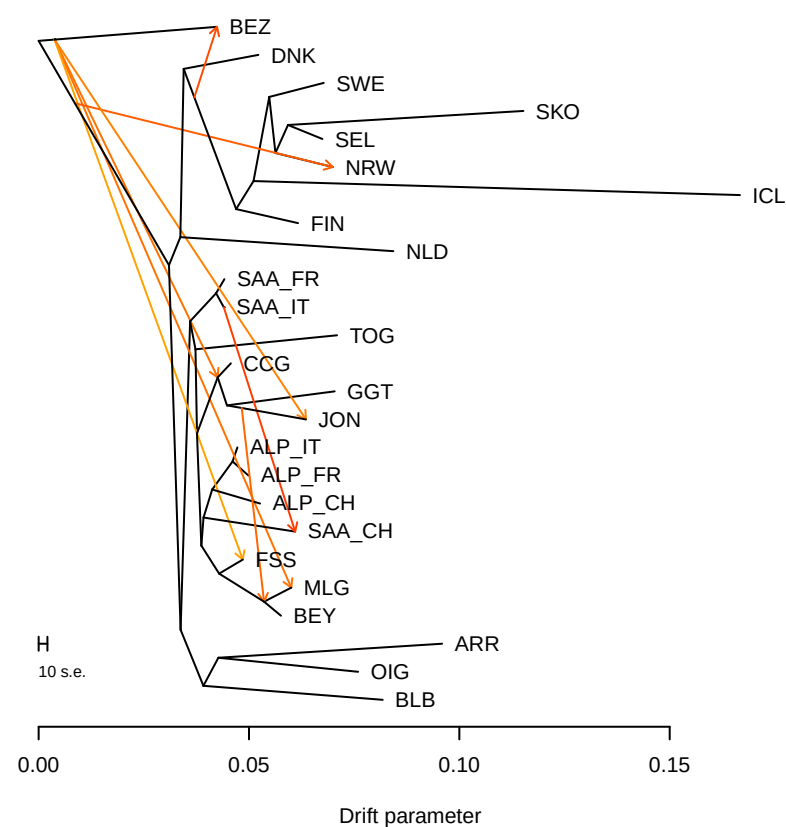
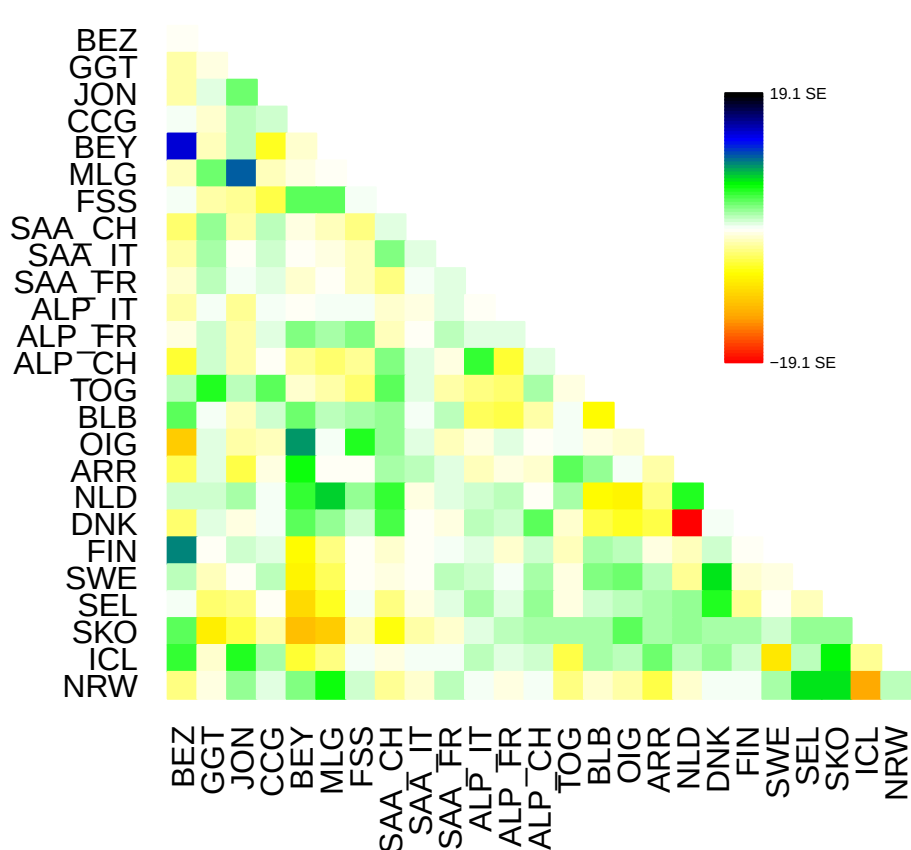
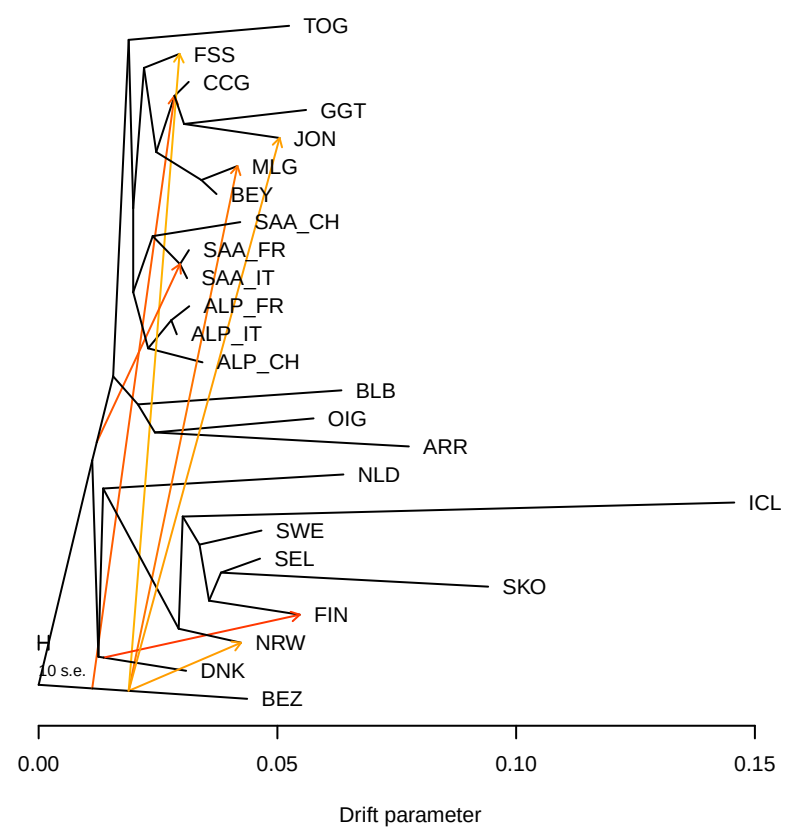
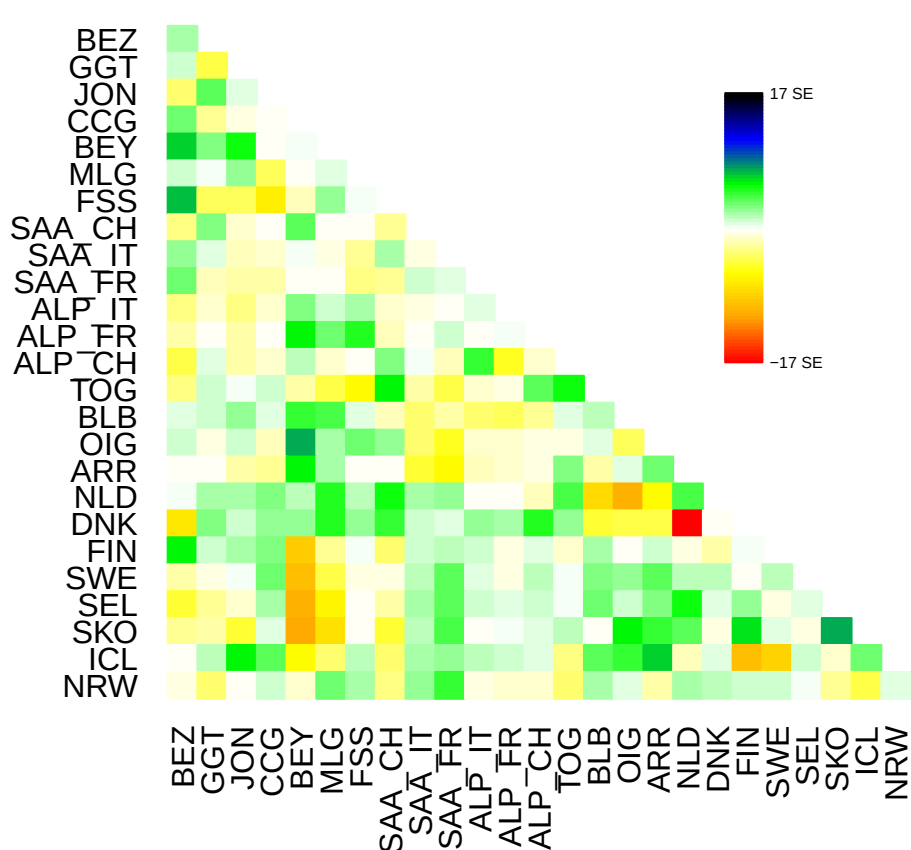
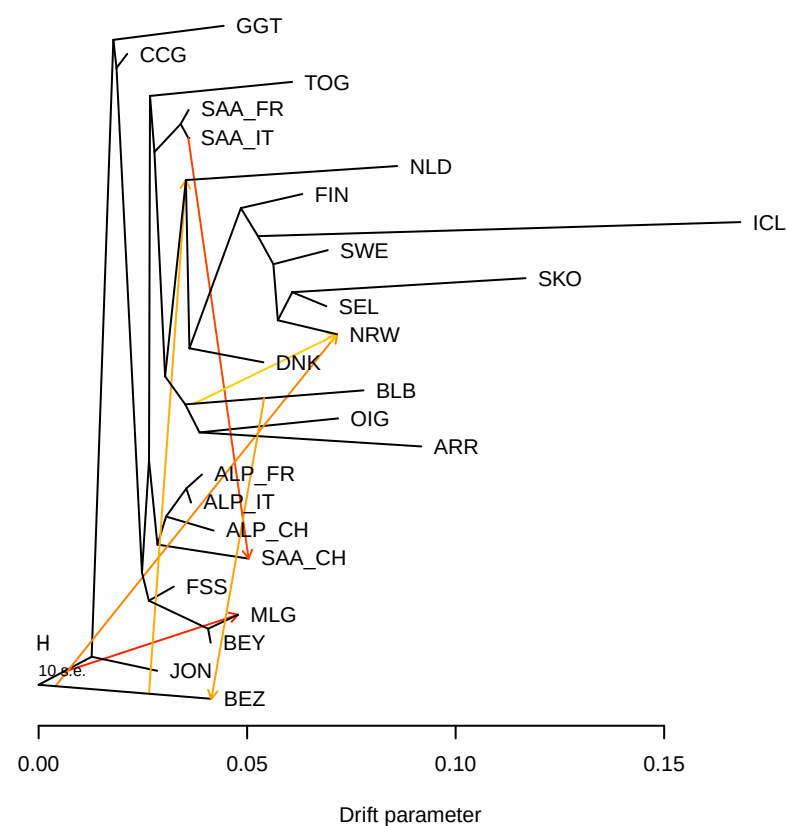
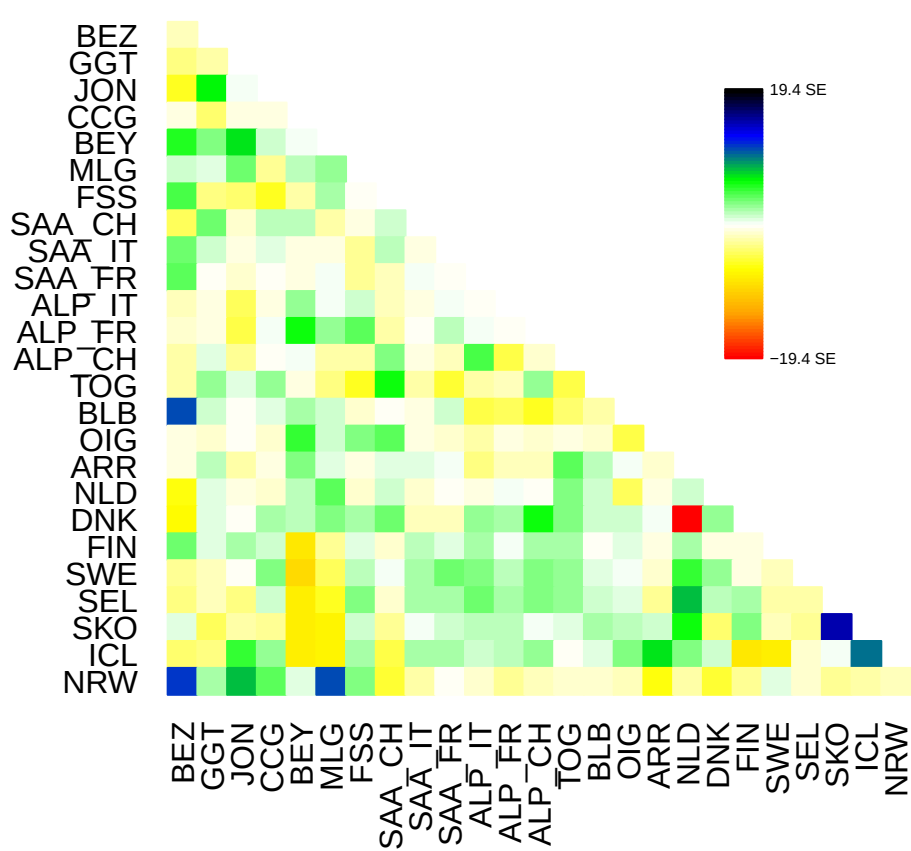
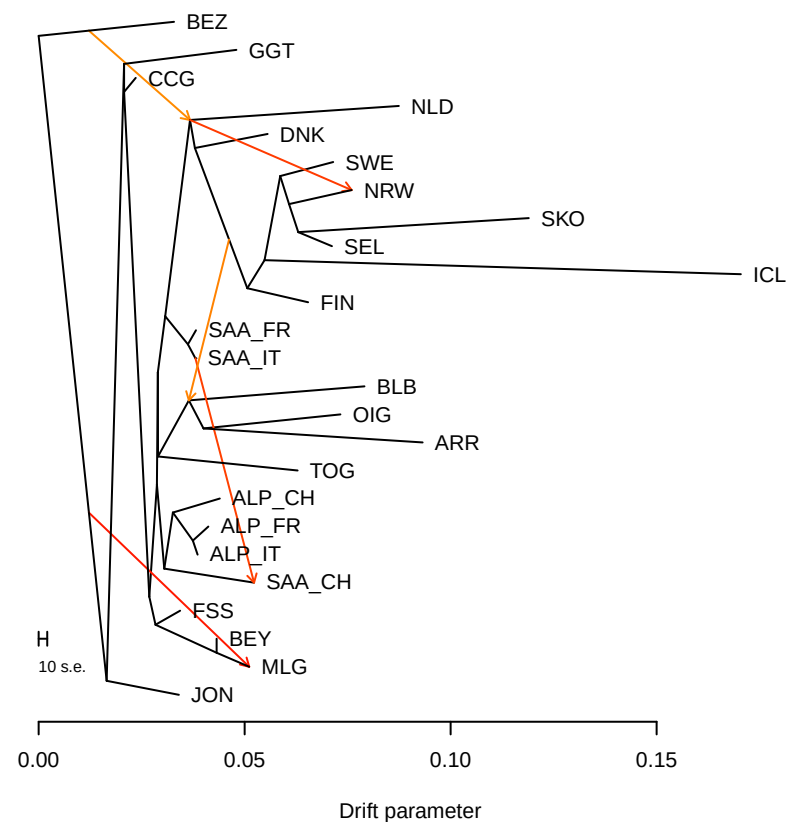
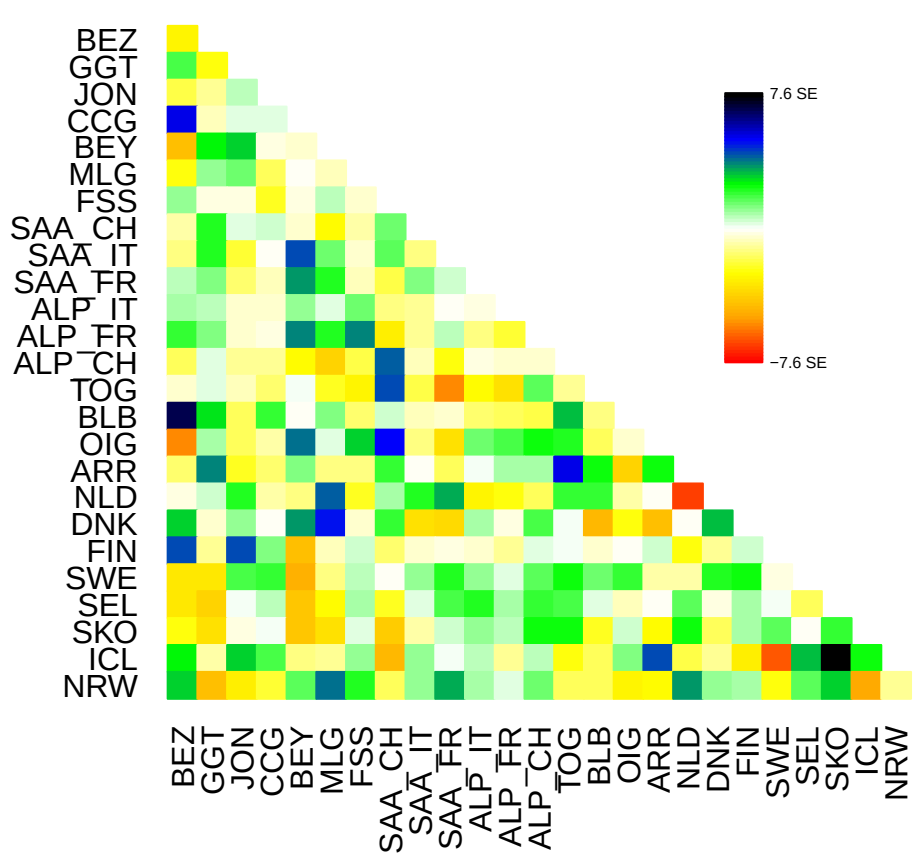
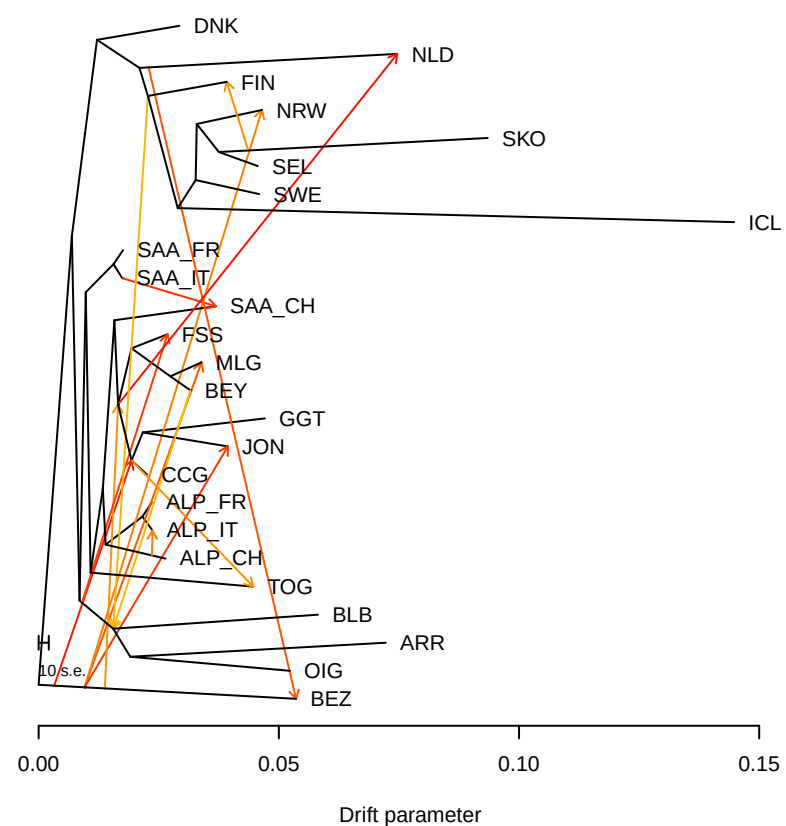
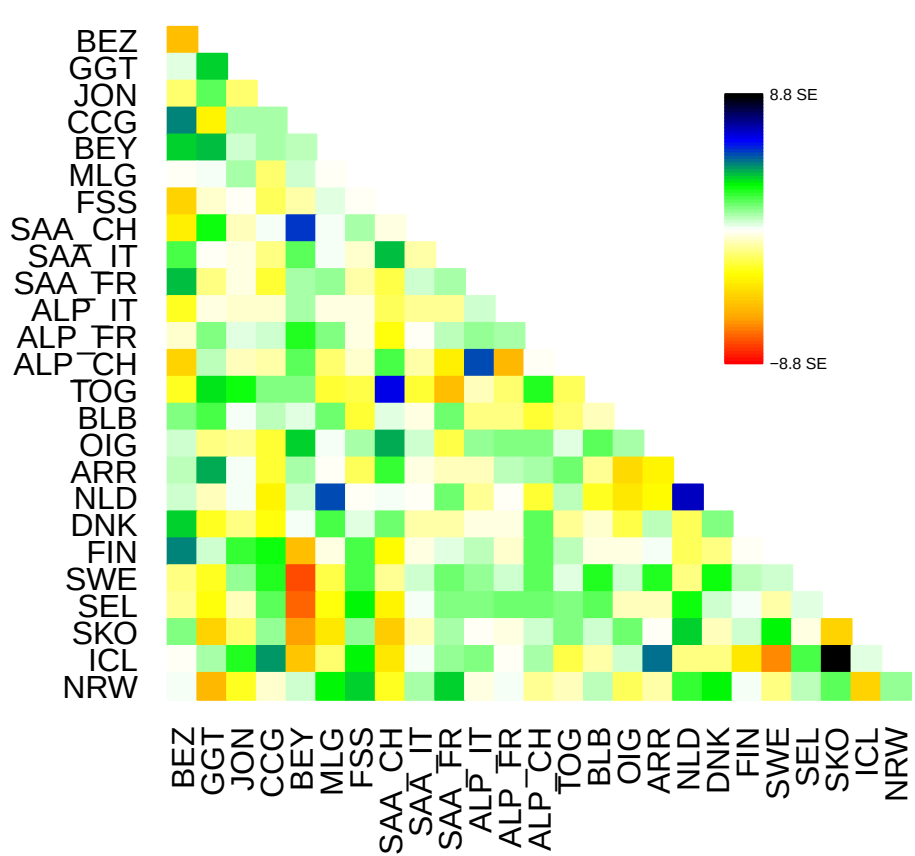
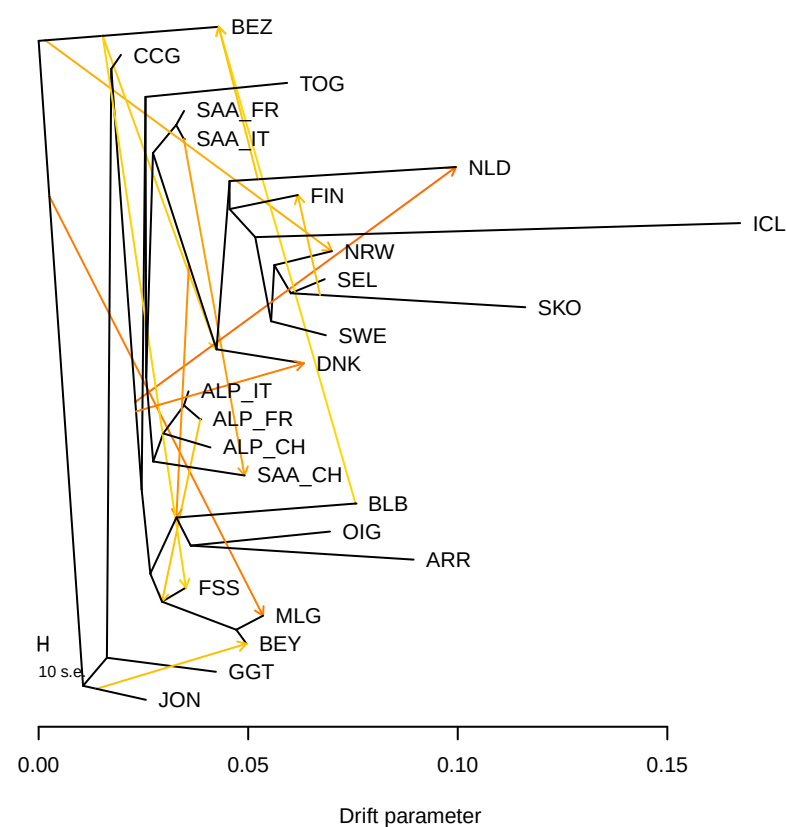
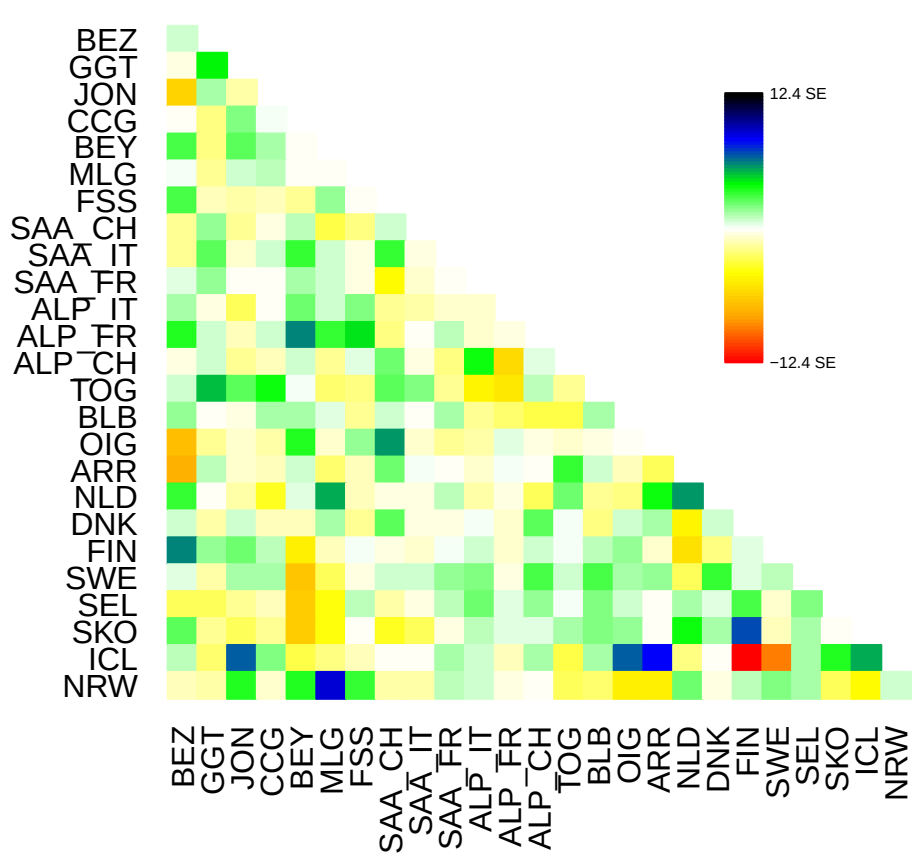
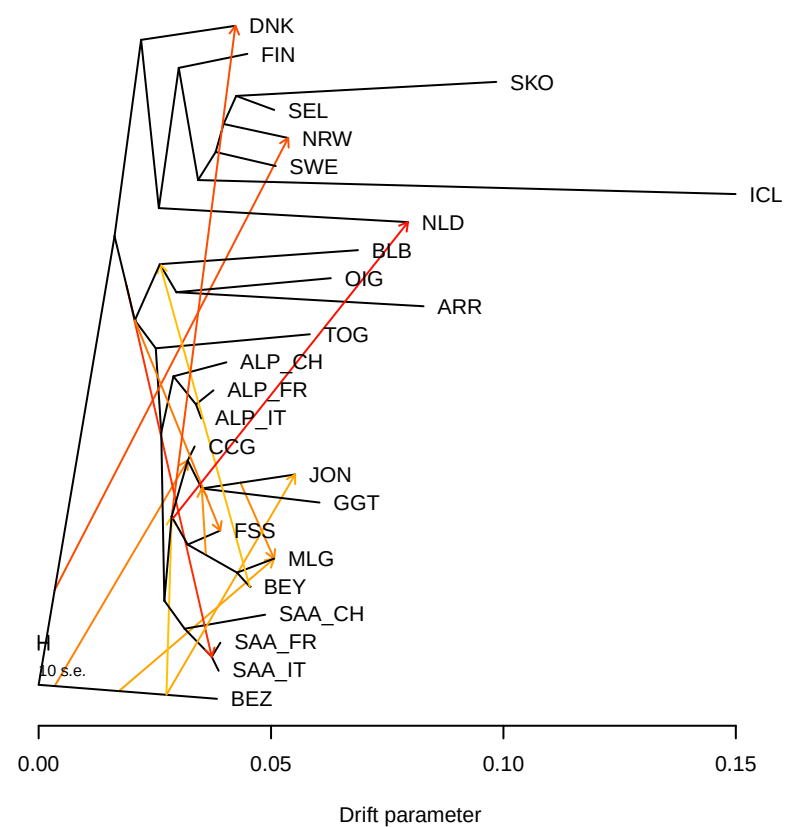
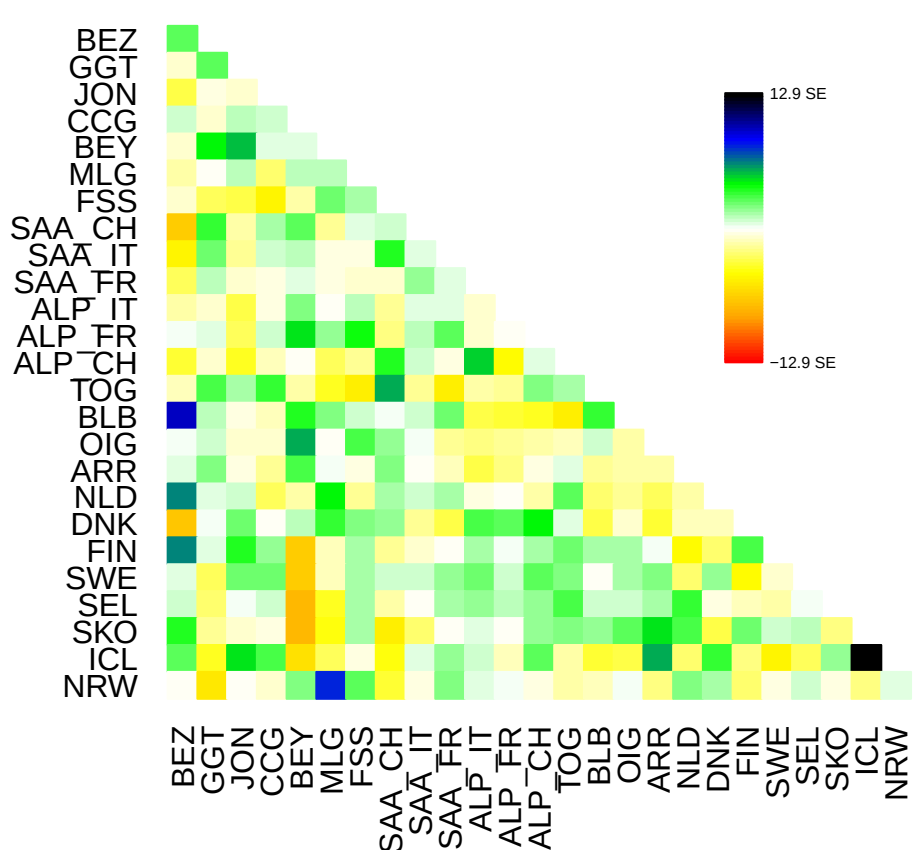
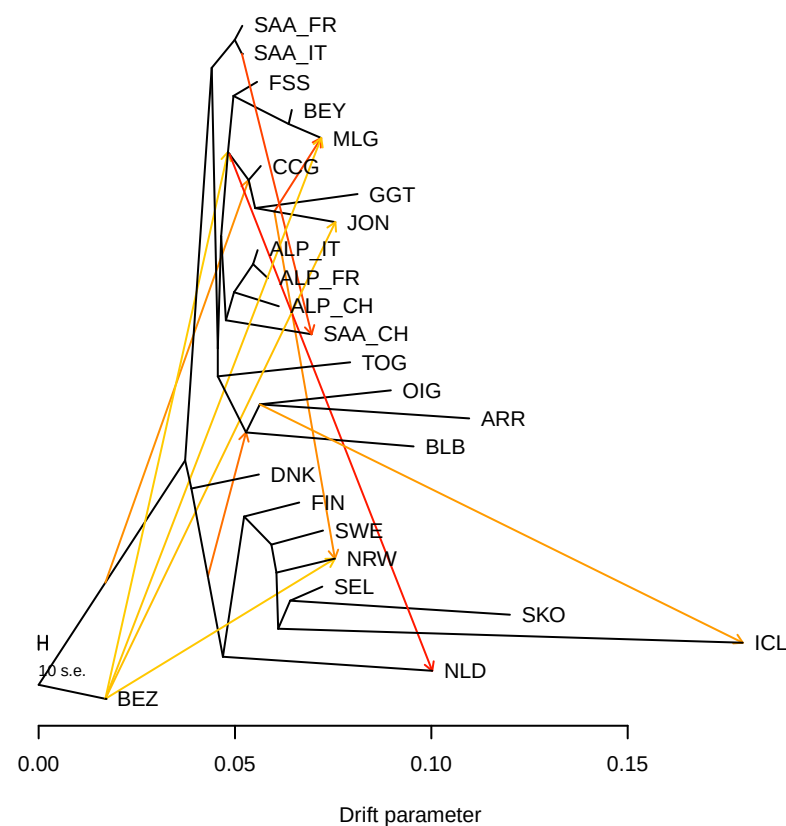
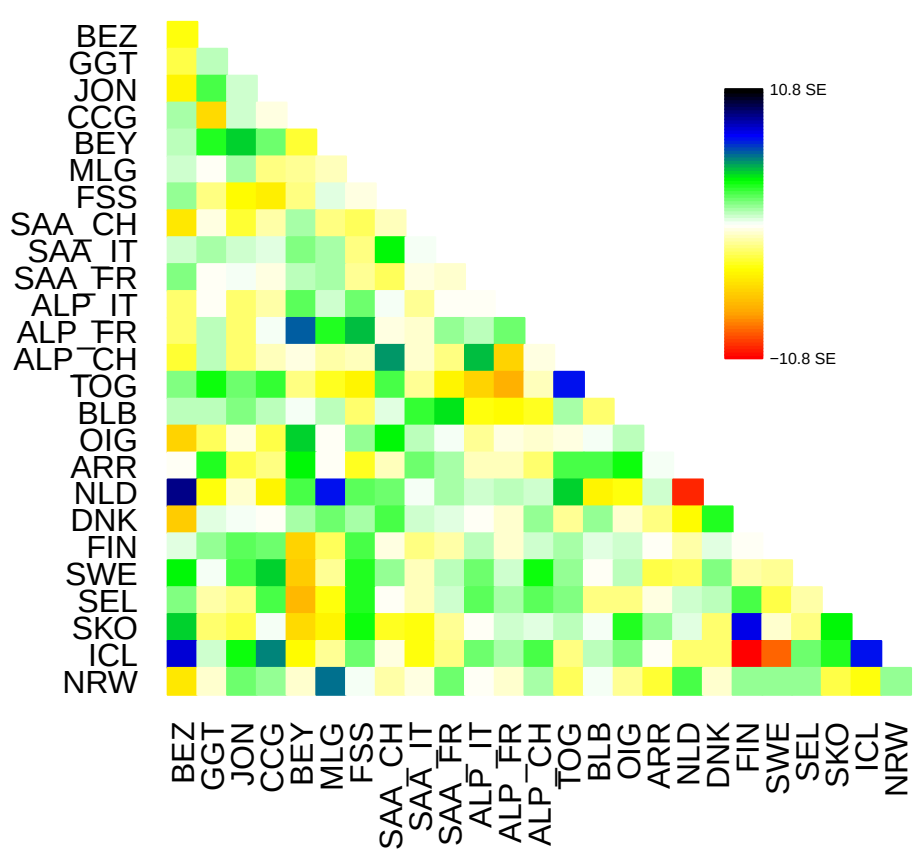
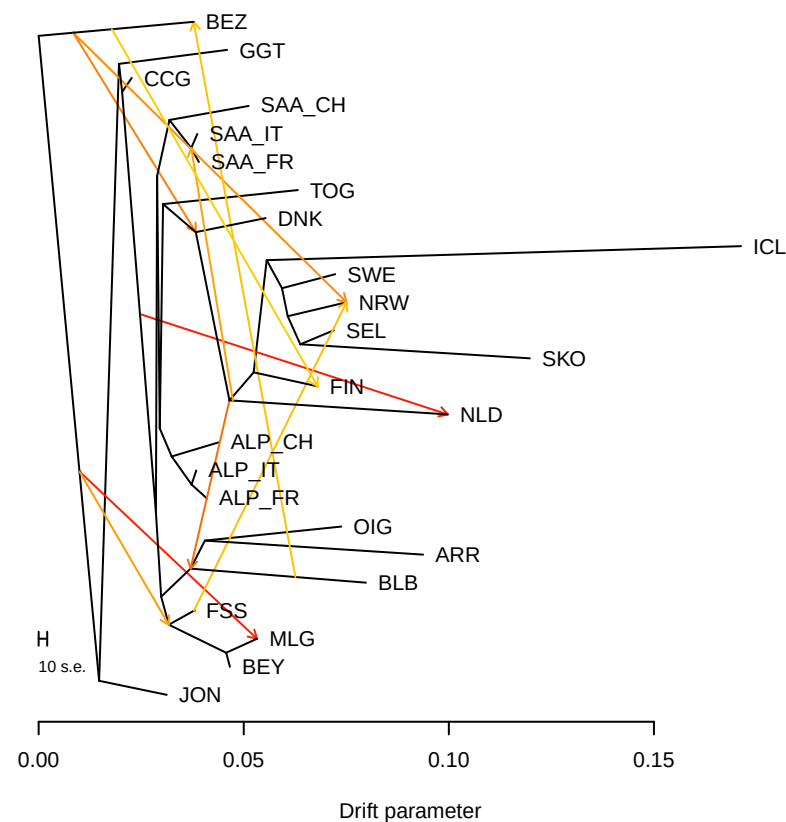
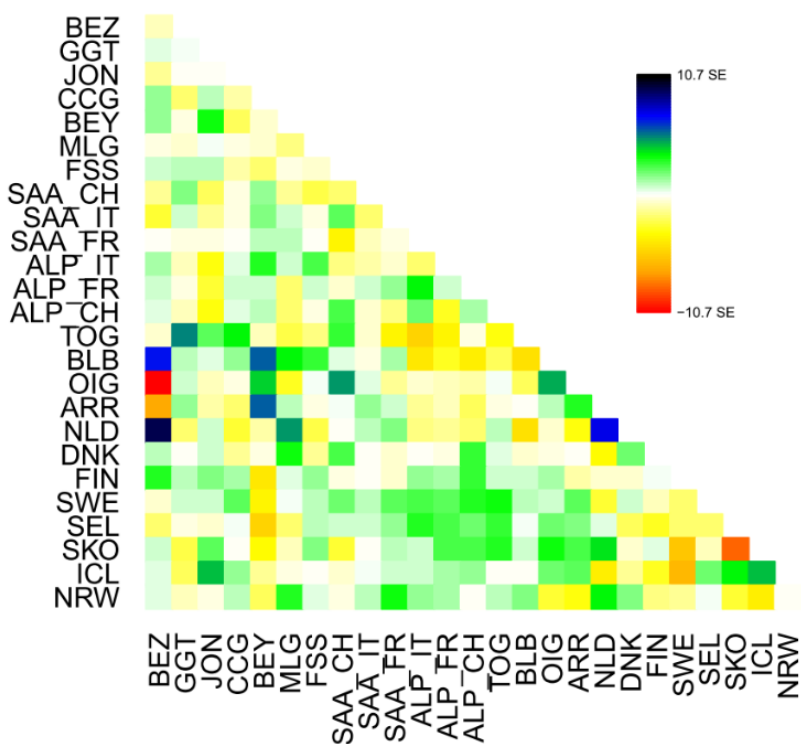
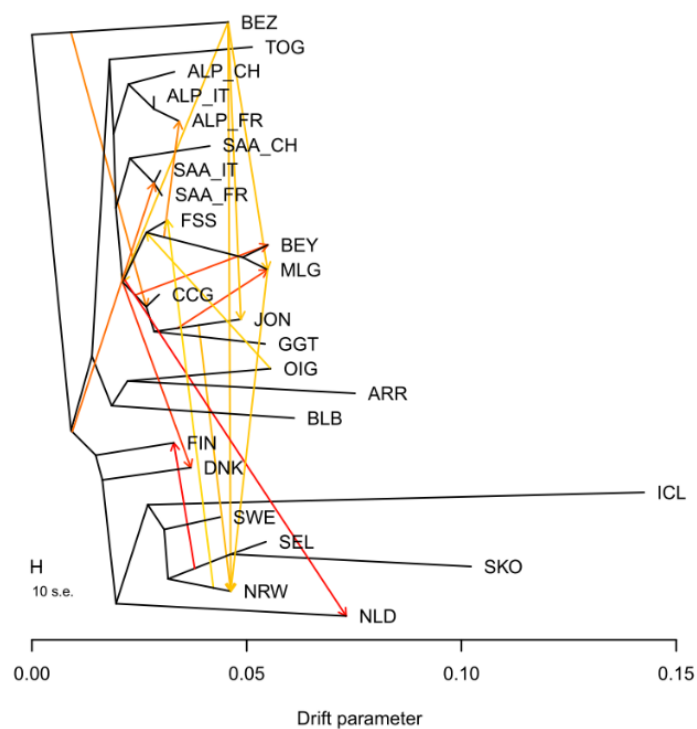
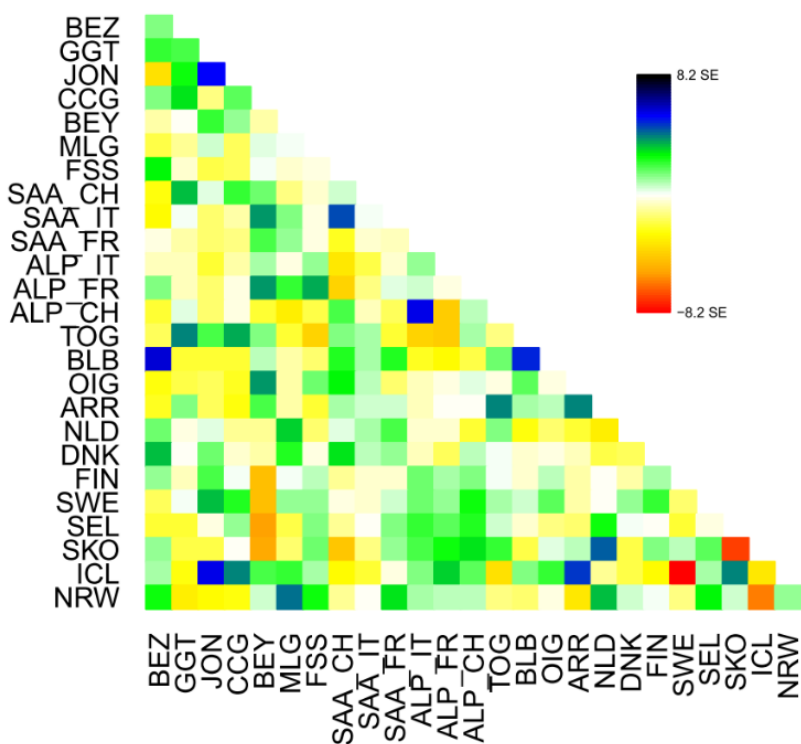
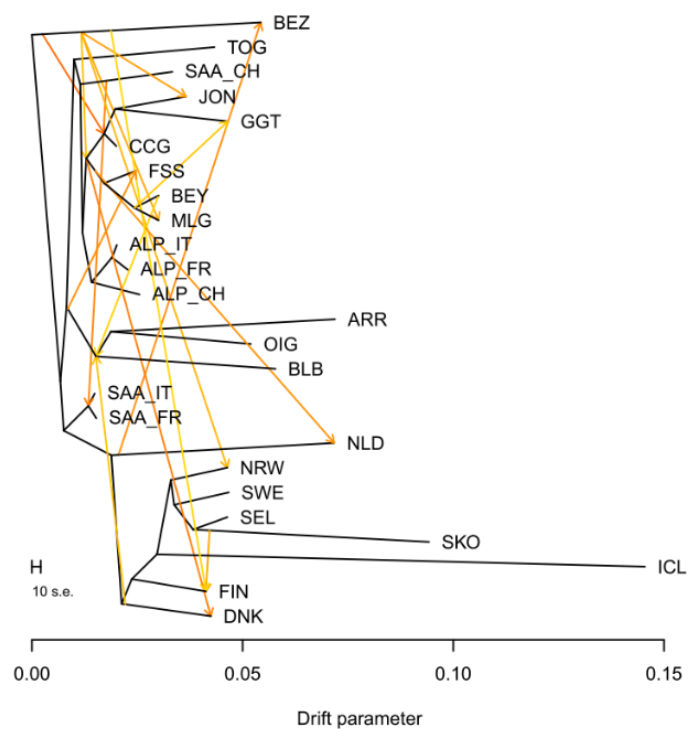
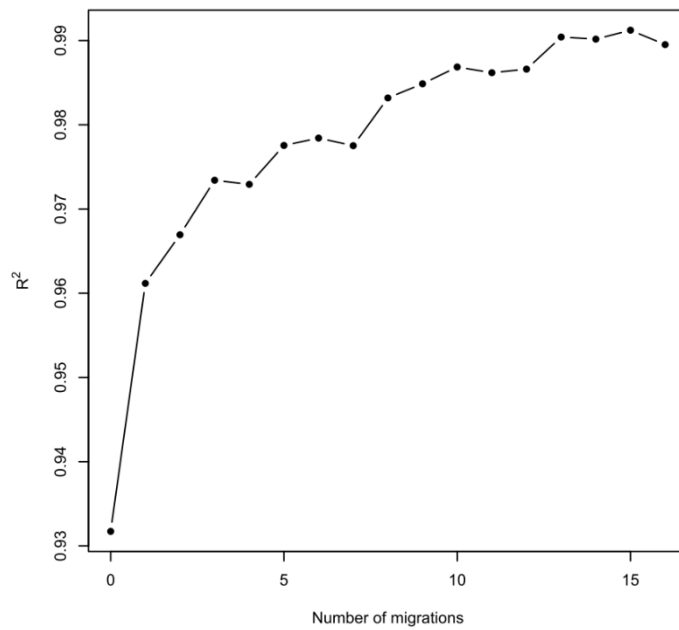












Supplementary Figure 5 A. Population graphs inferred by TREEMIX program using both datasets. The Maximum Likelihood trees inferred from the allele frequencies show the evolutionary relationships across breeds (nodes), where the branches' length s proportional to the evolutionary changes. Breeds are labelled with the same IDs code. The inferred admixture events range from 1 to 15 and are showed with arrows whose the colour is and indicator of the weight of the migration event that is the ancestry received from the source population (from yellow - 0 - to red - 0.5). Scaled residuals from the fit of the model to the data are displayed at the right side of each tree. The scale bar represents ten times the average standard error (SE) of the values in the sample covariance matrix.