

Figure S1: The joint allele frequency spectrum (JAFS) obtained from empirical data (upper left panel of each panel) and predicted under the best model (upper right), the Poisson residuals between model and data represented on the spectrum (lower left) and the distribution of residuals (lower right). Blue cells (negative residuals) represent model under-predictions and red cells (positive residuals) model over-predictions. Panels corresponds to A) Témiscouata Lake, B) East Lake, C) Indian Lake and D) Cliff Lake.

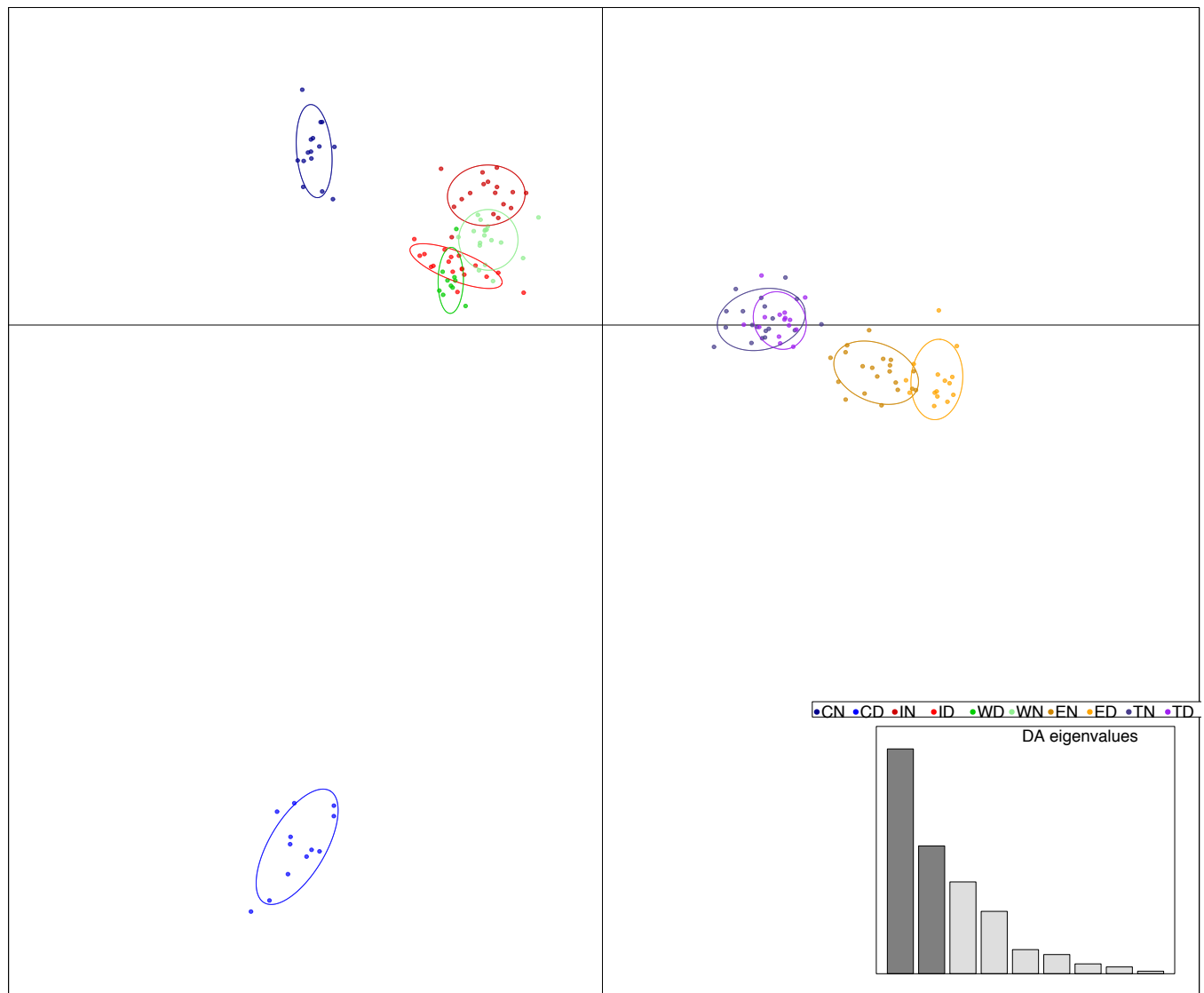


Figure S2: Discriminant analysis of principal components (dAPC) of the different lakes (Cliff, Indian, Webster, East, Témiscouata) for either Dwarf or Normal whitefish (D or N), representing relationships between populations. The first (horizontal) axis (LD1-39.5% of the total variance), clustering of populations by lakes, captures the geographical distribution of the lakes. The second (vertical) axis LD2 (22.5%) mostly separates dwarf and normal whitefish populations from Cliff Lake.

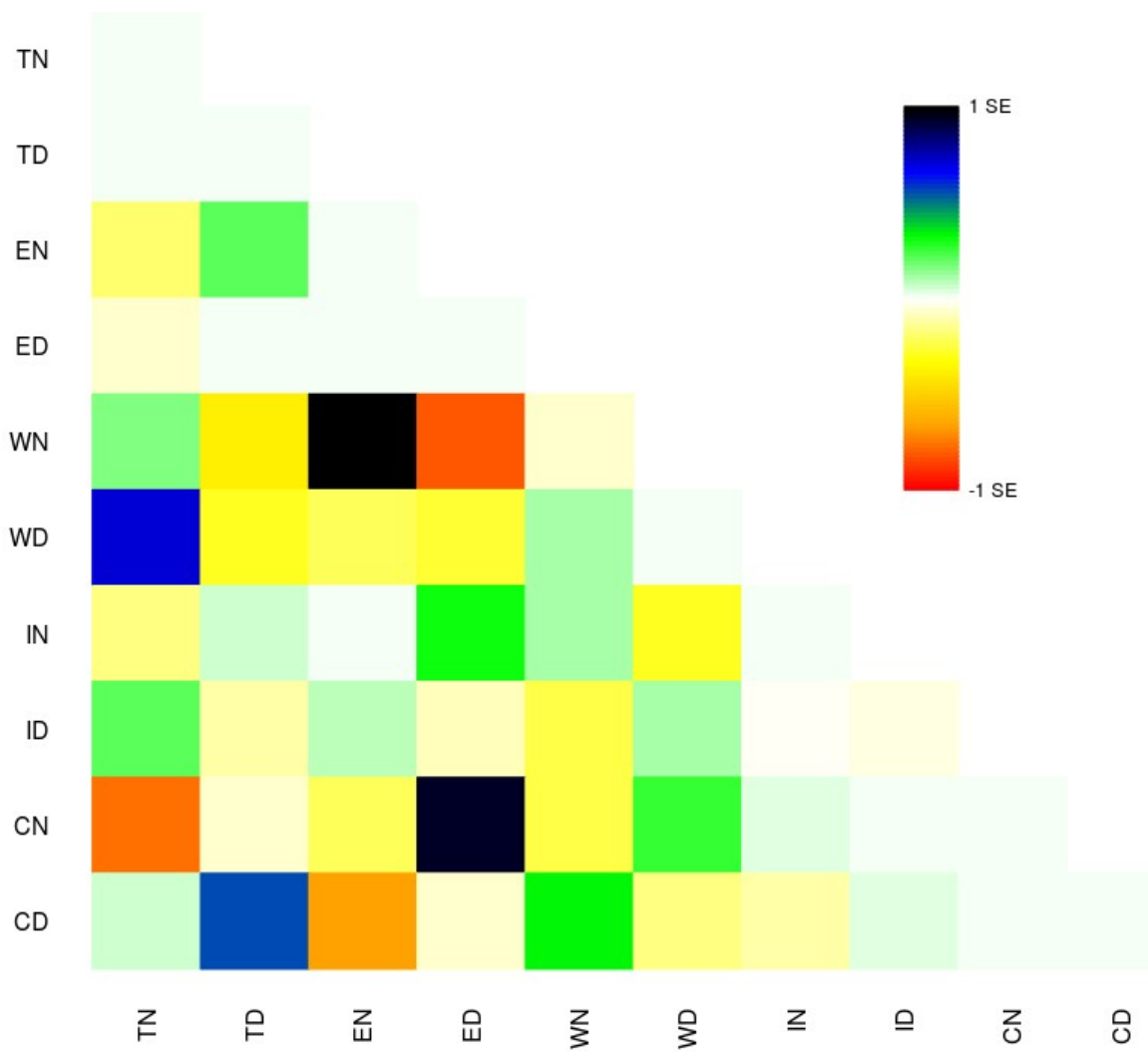


Figure S3: Residual fit from the maximum likelihood tree plotted in Figure 7. The residual covariance between each pair of populations was divided by the average standard error across all pairs. Green blue and dark colors indicate population pairs that are more closely related.