**Supplementary Figure 1**. Scatterplots of hybrid zone data for each marker used. To superimpose the data from the two transects, the average cline center from the 6-parameter cline models (Supplementary Table 3) was set to 0 km in each transect, and transect distances were recalculated as positive or negative distances from this center point. Points shown represent the average of all individuals at a given collecting locality, and genotypes are averaged over all 41 markers scored.













































































