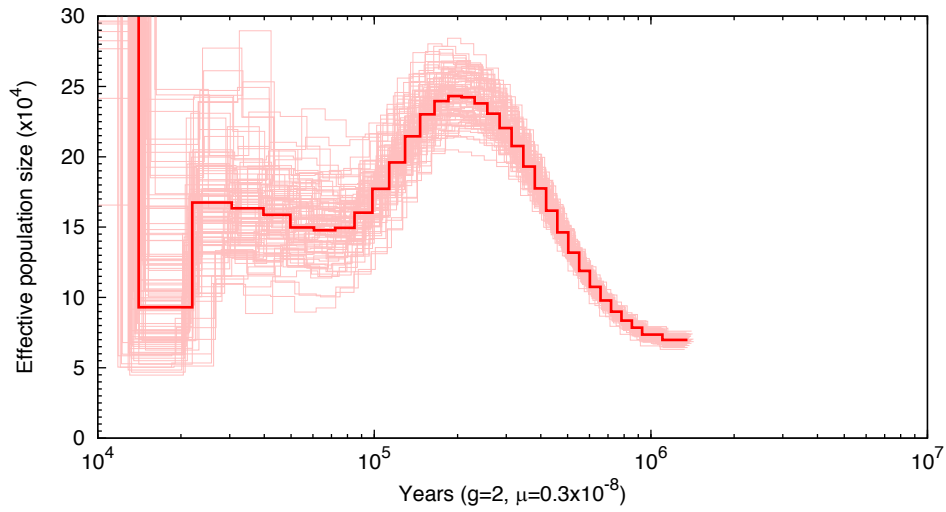
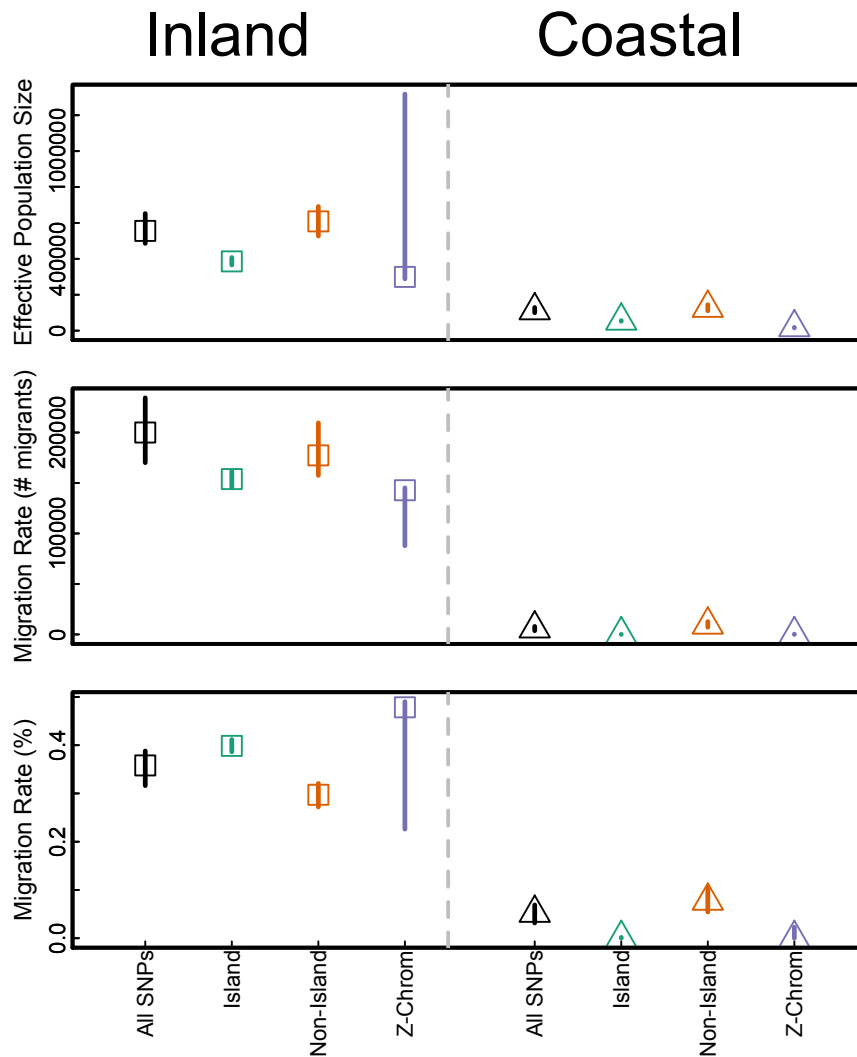


Supplementary Figure 1. Site frequency spectra (SFS) for inland and coastal subspecies of Swainson's thrush. SFS are shown for four sets of SNPs: 1) All SNPs, 2) Autosomal SNPs in islands of divergence, 3) Autosomal SNPs not in islands of divergence, and 4) SNPs on the Z chromosome. Color reflects the number of SNPs with a given combination of allele frequencies in the two populations.



Supplementary Figure 2. PSMC analysis of historical population size using whole genome resequencing data from a single *Catharus ustulatus* individual (Delmore et al. 2015). Shifts in population size likely represent both true expansions and declines and changes in connectivity between the two subspecies.



Supplementary Figure 3. Simulations based on subsamples of 5000 SNPs.

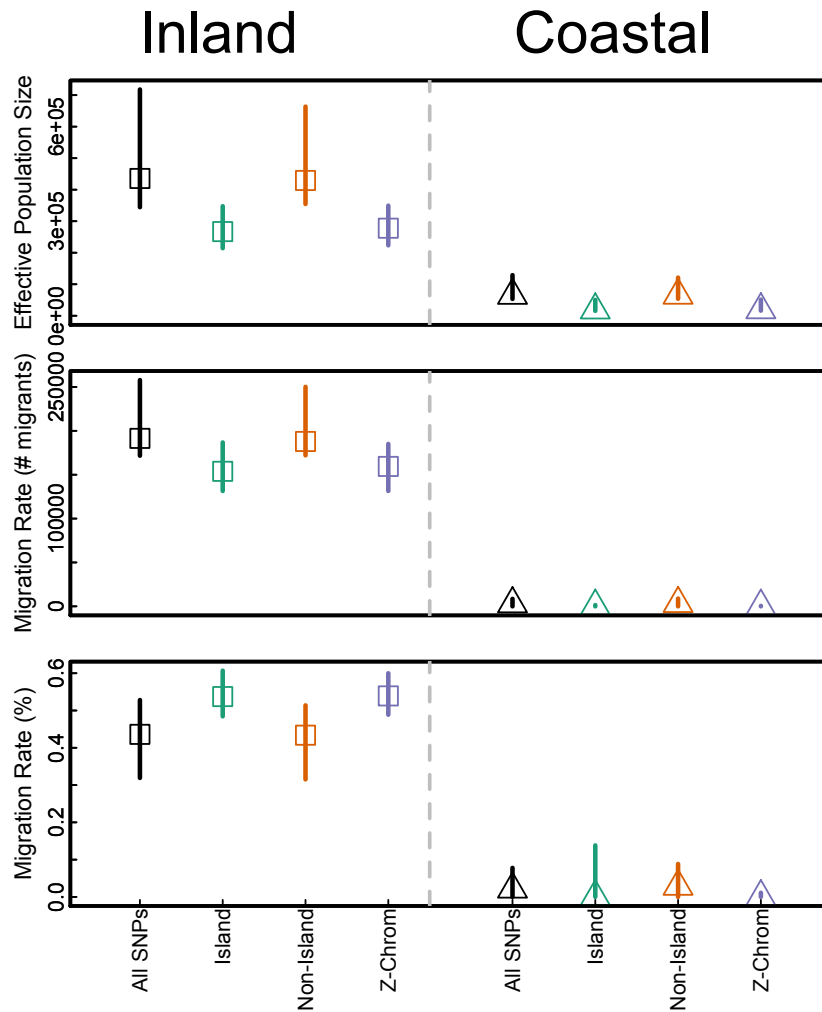
Estimates of effective population size and migration rate for four subsets of SNPs.

Points represent median values and error bars reflect 95% confidence intervals.

Migration rates on the left side of the dashed line represent migration from the

inland to the coastal subspecies while migration rates on the right represent

migration from coastal to inland.



Supplementary Figure 4. Simulations based on subsamples of 1000 SNPs

Estimates of effective population size and migration rate for four subsets of SNPs.

Here, points represent 75% confidence intervals because sampling error present in 95% confidence intervals obscured patterns between median values. Points represent median values and error bars reflect 95% confidence intervals. Migration rates on the left side of the dashed line represent migration from the inland to the coastal subspecies while migration rates on the right represent migration from coastal to inland.

