Supplementary Data 4. Heatmaps for the most highly differentiated SNPs at all 28 loci. Per species average allele frequencies for the SNPs reaching statistical significance in the ground finch admixture mapping are presented. The frequencies of the major allele defined in the small ground finch (*G. fuliginosa*) are shown for 18 species of Darwin's finches, two outgroup species and birds of the Big Bird lineage. The data are summarized in **Fig. 2**.

A reasonable assumption is that most of the present genetic diversity among Darwin's finches evolved subsequent to colonization of Galápagos. This is supported by the fact that the outgroups appear to be fixed for one or the other allele at most, but not all, of the highly differentiated loci. Therefore, average delta allele frequencies in the two outgroup species (*L. noctis* and *T. bicolor*) reflect the proportion of derived alleles present on *G. magnirostris* haplotypes, because we use the major alleles in this species as reference. There is some bias towards a higher proportion of derived alleles in G. magnirostris haplotypes in this set of SNPs. This is probably because of selective sweeps and possibly genetic drift that has occurred in *G. magnirostris* or its ancestor as indicated by the significantly lower nucleotide diversity at the 28 loci in this species (Fig. **1b**) Species/locus combinations that show a more extreme bias towards higher delta allele frequencies than that observed in the outgroups indicate that the haplotype blocks were established prior to the split between the species compared. Thus, the divergence of most haplotype blocks, if not all, predates the divergence between Geospiza and Camarhynchus, and many diverged prior to the basal split between warbler finches and other finches.























































