



Figure S1. F_{ST} versus heterozygosity estimates, obtained using Arlequin, version 3.5, assuming a hierarchical model of migration.

Dashed blue line, 95% confidence interval; dashed red line, 99% confidence interval; solid grey line, median; filled blue circles, loci significant at the 5% level; red filled circles, loci significant at the 1% level; empty circles, putatively neutral loci.