Table S2 Observed values and simulated values of four summary statistics of nucleotide diversity and LD (π, δ_{ST}, Z_{nS}, and Z_g) for three classes of loci: selected loci (SL), intergenic loci (IL), and flanking loci (FL).

			Median values from simulations		
	Locus	Empirical values	Equilibrium model	Isolation-with-migration model 4*Nm*=0	Isolation-with-migration model 4*Nm*=1
π	SL	0.020	0.032	0.016	0.018
	IL	0.021	0.013	0.012	0.012
	FL	0.005	0.012	0.013	0.012
δ_{ST}	SL	0.011	0.013	0.019	0.022
	IL	0.010	0.002	0.014	0.015
	FL	0.002	0.001	0.015	0.013
Z_{nS}	SL	0.159	0.158	0.060	0.064
	IL	0.185	0.112	0.057	0.057
	FL	0.108	0.099	0.055	0.053
Z_g	SL	0.102	0.096	0.008	0.009
	IL	0.088	0.021	0.007	0.007
	FL	0.064	0.009	0.005	0.005

The empirical measures of diversity and LD for the ‘selected loci’ are an average value for the two *HBB* paralogs, measures for the intergenic loci are an average value for *F4* and *F5*, and measures for the flanking loci are an average value for *HBG* and *OlfR67*; see Fig. 1). Median values for the ‘equilibrium’ model of population structure are graphically depicted in Figure 6B. Median values for the ‘isolation-with-migration’ models of population structure were paramterized with results of the IMa analyses (see text for details). For the isolation-with-migration simulations, the ancestral population size was 200 and the total descendant population size was 1670; the ratio of these values was derived from the IMa analysis. The number of generations since population divergence was 0.15 times the contemporary N_e for the total population. Simulation results for two different isolation-with-migration models are presented, the first with no gene flow since population divergence and the second with 4*Nm*=1.