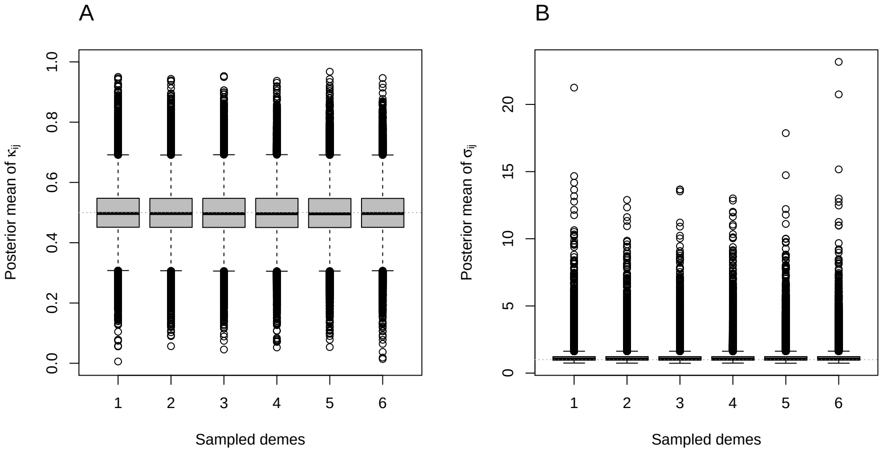

Figure S19 Analysis of the allele count data from a simulation of 50,000 neutral markers. The simulation was performed according to an island model with n_d = 50 ''uncolored'' demes, each made of N = 250 diploid individuals (500 genes). Samples were collected in six demes (50 individuals per deme). The migration rate was chosen to achieve the expected value of F_{ST} = 0.15, using equation 6 in Rousset (1996). The realized value was F_{ST} = 0.153 (multilocus estimate). (A) Boxplot representation of the posterior means of the parameters κ_{ij} (that indicate which allele is selected for) for the 50,000 neutral markers in ''uncolored'' demes (1–6). (B) Boxplot representation of the posterior means of the selection coefficients σ_{ij} for the 50,000 neutral markers (unconditional on κ_{ij}). The horizontal dotted line indicates the prior mean σ_{ij} = 1