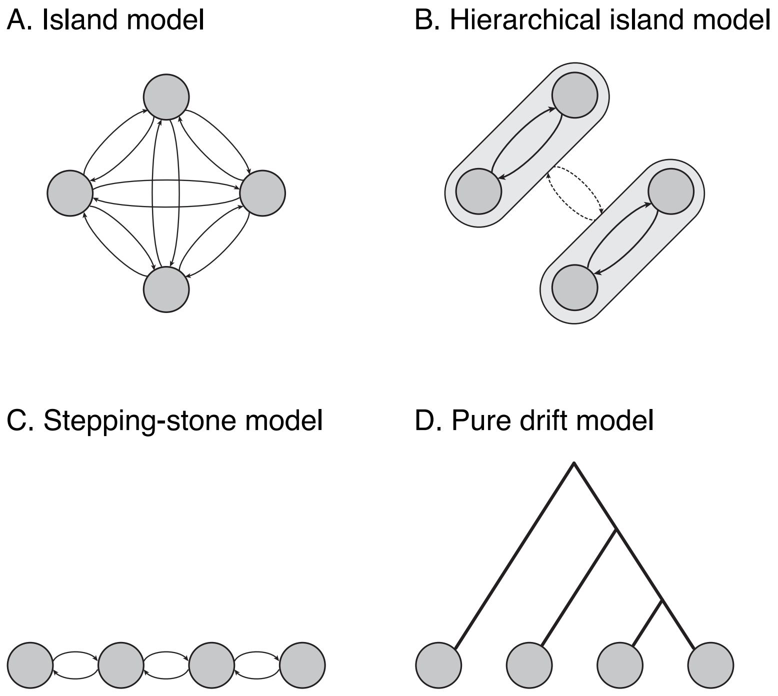

Figure S1 (A) Schematic representation of an island model. The actual data were simulated with n_{d} = 100 demes, each made of *N* = 250 diploid individuals (500 genes). Fifty diploid individuals (100 genes) were sampled per deme, in 9 demes. The migration rate (*m* = 0.003, plain arrows) was fixed to achieve the desired value of F_{ST} = 0.24, using equation 6 in Rousset (1996). (B) Schematic representation of a hierarchical island model. The actual data were simulated with 10 groups of 10 demes, each made of *N* = 250 diploid individuals (500 genes). Fifty diploid individuals (100 genes) were sampled per deme, in 3 groups of 3 demes. The migration rate within (*m* = 0.017, plain arrows) and among groups (*m* = 0.0003, dashed arrows) were fixed to achieve the desired values of F_{SC} = 0.05, F_{CT} = 0.05 and F_{ST} = 0.24, using equations A8–A10 in Excoffier *et al.* (2009). (C) Schematic representation of a stepping-stone model. The actual data were simulated with n_{d} = 100 demes, each made of *N* = 250 diploid individuals (500 genes). Fifty diploid individuals (100 genes) were sampled per deme, in 9 demes.The migration rate was fixed (*m* = 0.028, plain arrows), by trial and error, to achieve the desired value of F_{ST} = 0.24. (D) Schematic representation of a pure drift model. The actual data were simulated with 9 demes, diverging sequentially as depicted. The sample characteristics (number of individuals, number of sampled demes) were the same as in (A–C), and the divergence time (24 generations) between any two successive splits was tuned in order to achieve an overall F_{ST} of ≈ 0.24. In (A–D) 10,000 neutral markers were simulated.