



Fig S5. Results from forward simulations showing the effect of (A-B) the symmetric migration rate, (C) the population size, and (D) the mutation rate for new S-alleles on the proportion of migrants per population observed in time frames of 1000 generations following the speciation event. The filled circles indicate values for the S-linked loci and the empty circles the values for the neutral loci. The default parameter values used in the simulations were: population size = 1000, symmetrical migration rate = 1×10^{-7} , mutation rate for S-alleles = 1×10^{-6} . Each point represents the mean value from 5000 independent simulations.