ONLINE FIGURES

Figure S1. Simulation results from model 4, a model similar to model 3, but in which instead of being neutral, the two derived substitutions were considered to be universally favored across the two populations (i.e. universally beneficial). Shown is the difference in allele frequency between populations at locus B (frequency diff.) as a function of the number of generations since secondary contact between populations, for different epistasis (ep) and migration regimes (*m*). In each panel, allele frequencies differences are contrasted between scenarios where the two loci reside in genomic regions with no recombination between loci (r = 0.0 = inversion with no recombination), low recombination between loci (r = 10^{-8} = inversion with low recombination) and free recombination between loci (r = 0.5 = collinear genomic region). In this model, genetic differences upon secondary contact were maintained in all genomic regions when migration was low or modest or tended to be lost in all genomic regions when migration was high (exception being *m* = 0.1 and ep = 0.50). In some cases, the results for two of the three recombination rates were essentially identical, denoted by the small 'X' in the relevant panels.

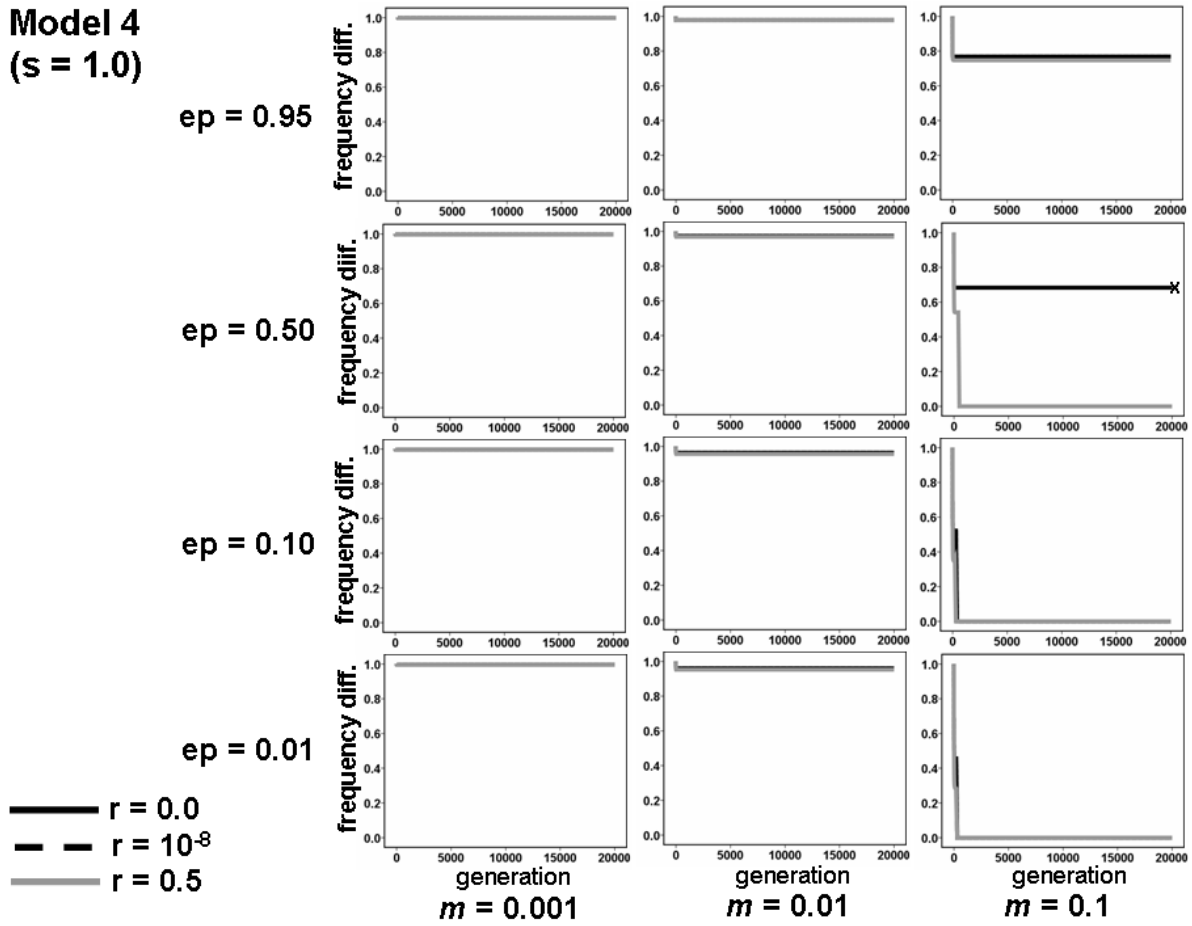

Figure S2. Simulation results from model 4, a model similar to model 3, but in which instead of being neutral, the two derived substitutions were considered to be universally favored across the two populations (i.e. universally beneficial). Shown is the difference in allele frequency between populations at locus B (frequency diff.) as a function of the number of generations since secondary contact between populations, for different epistasis (ep) and migration (*m*) regimes. In each panel, allele frequencies differences are contrasted between scenarios where the two loci reside in genomic regions with no recombination between loci (r = 0.0 = inversion with no recombination), low recombination between loci (r = 10^{-8} = inversion with low recombination) and free recombination between loci (r = 0.5 = collinear genomic region). In this model, genetic differentiation could be maintained under some conditions in regions with no recombination, but pronounced differences in the maintenance of genetic divergence between regions of low versus free recombination did not occur (but some slight differences appear to persist when migration is low = 0.001). In some cases, the results for two of the three recombination rates were essentially identical, denoted by the small 'X' in the relevant panels.

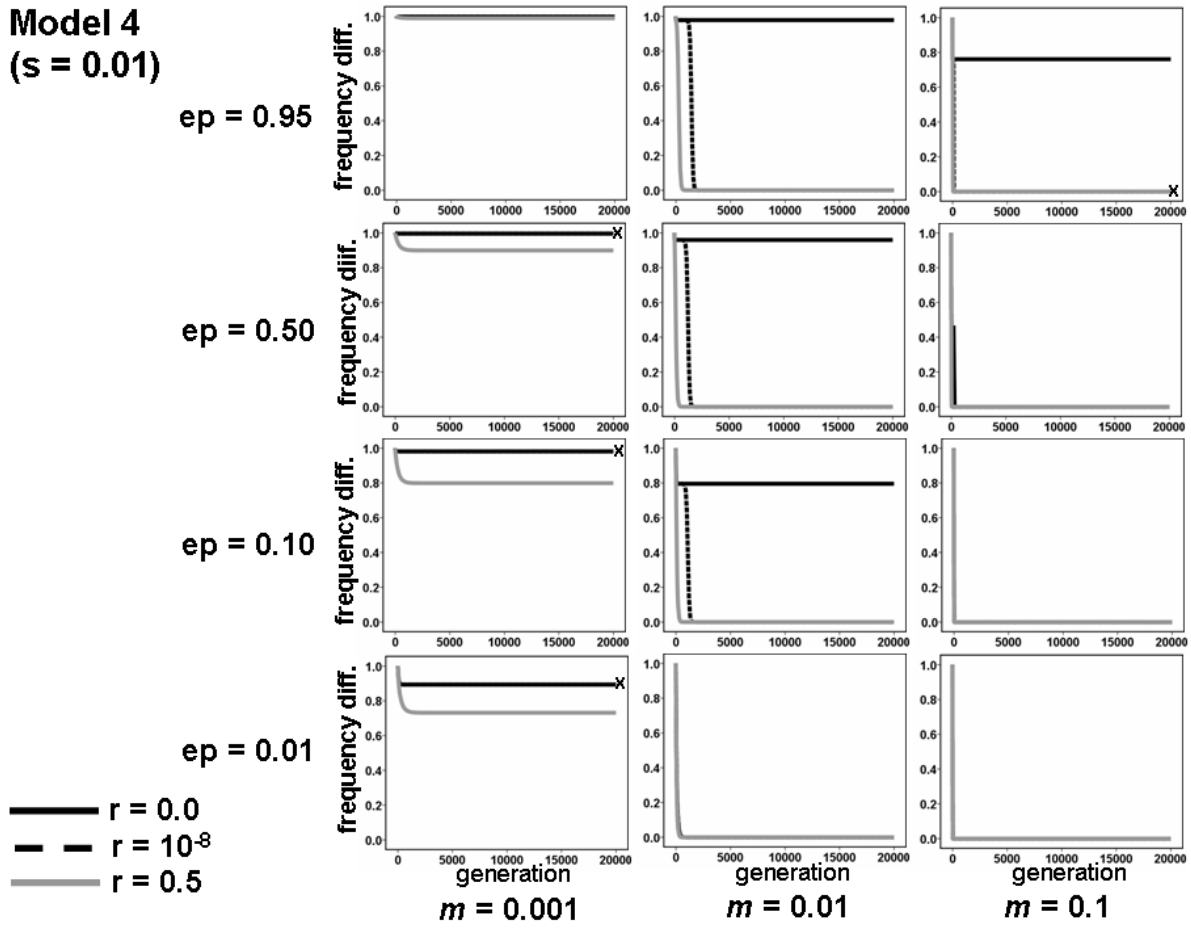

Figure S3. Simulation results from model 5, which examined the consequences of negative interactions between derived and ancestral allelic states. In this case, derived and universally favored substitutions were envisioned to first fix at locus A, and then at locus B, in population 1.. Shown is the difference in allele frequency between populations at locus B (frequency diff.) as a function of the number of generations since secondary contact between populations, for different epistasis and migration regimes. In each panel, allele frequencies differences are contrasted between scenarios where the two loci reside in genomic regions with no recombination between loci (r = 0.0 = inversion with no recombination), low recombination between loci ($r = 10^{-8}$ = inversion with low recombination) and free recombination between loci (r = 0.5 = collinear genomic region). In this model, genetic differences were maintained only in regions of no recombination, and only when epistasis was strong or very strong (ep = 0.50 or 0.95) and migration low or modest (m = 0.001 or 0.01). Thus, differences in levels of genetic divergence maintained in regions with low versus free recombination are not expected. In some cases, the results for two of the three recombination rates were essentially identical, denoted by the small 'X' in the relevant panels.

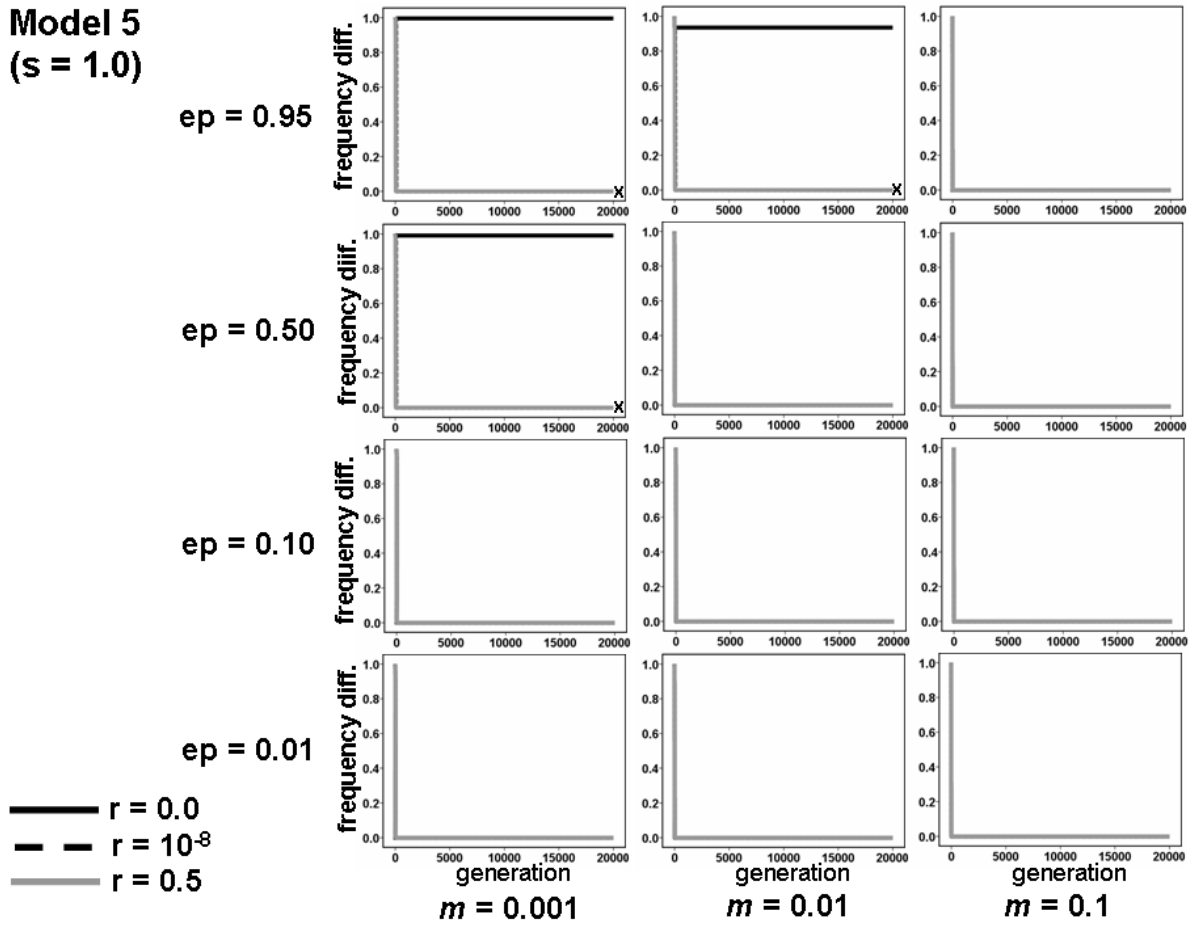

Figure S4. Simulation results from model 5, which examined the consequences of negative interactions between derived and ancestral allelic states. In this case, derived and universally favored substitutions were envisioned to first fix at locus A, and then at locus B, in population 1. Shown is the difference in allele frequency between populations at locus B (frequency diff.) as a function of the number of generations since secondary contact been populations, for different epistasis and migration regimes. In each panel, allele frequencies differences are contrasted between scenarios where the two loci reside in genomic regions with no recombination between loci (r = 0.0 = inversion with no recombination), low recombination between loci (r = 10^{-8} = inversion with low recombination) and free recombination between loci (r = 0.5 = collinear genomic region). In this model, genetic differences were maintained only in regions of no recombination, and only when epistasis was very strong relative to migration. Thus, differences in the level of genetic divergence maintained in regions with low versus free recombination are not expected (except perhaps for a short time period upon very recent secondary contact, but even then only if migration is low, m = 0.001). In some cases, the results for two of the three recombination rates were essentially identical, denoted by the small 'X' in the relevant panels.

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