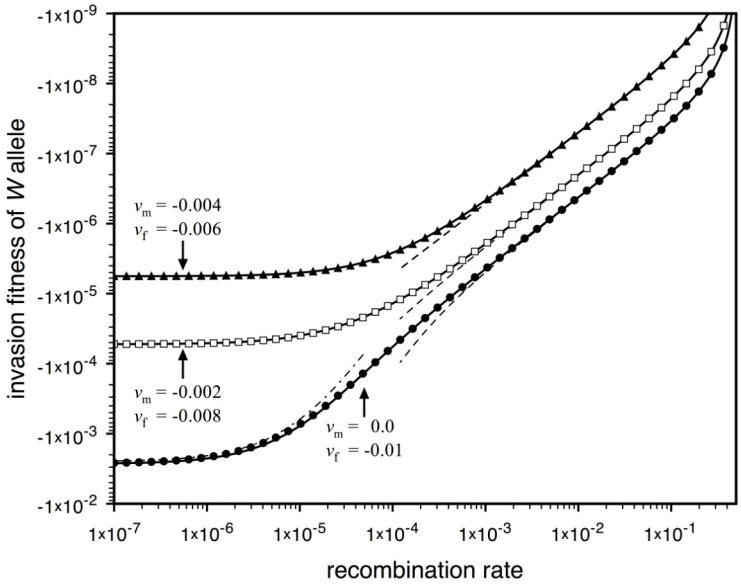

FIGURE S2. – Deleterious alleles on the ancestral y-chromosome oppose the invasion of *W*. One quarter of the mutant population is homozygous for *Y* when the *W* allele is rare. Within that subpopulation, recessive deleterious alleles on the ancestral y-chromosome are expressed, reducing the fitness of the *W* allele. The figure shows the magnitude of the fitness reduction as a function of the rate of recombination between the locus with deleterious alleles and the ancestral sex-determination locus, for three different values of sex-specific deleterious fitness effects (symbols indicate invasion-fitness values calculated by iterating the exact population-genetic recursions). The curves show analytical predictions (for tight linkage (solid), loose linkage (dashed), and the explicit solution assuming mutation-selection balance (equation 11 in the main text; dot-dashed)). Other parameters are: $r' = 0.5$, $h_f = h_m = 0.0$, $\bar{\mu} = 1.0 \cdot 10^{-5}$, $\bar{\mu} = 0.0$.