FIGURE S3. – Homologous transitions depend on the details of sex-antagonistic selection. The two panels show analytical invasion-fitness estimates for homologous transitions (solid curves) and numerical results based on the exact population genetic recursions (symbols) across a range of sex-antagonistic selection coefficients and for different combinations of dominance parameters. Overall, higher male-beneficial allele frequencies (right on the horizontal axes) favor homologous transitions to ZW sex-determination, since female heterogamety allows rare female-beneficial alleles to accumulate on the w-chromosome without being exposed to selection in males. (A) A feminizing mutation at the ancestral sex-determination locus is more likely to spread, if male-beneficial alleles at nearby loci are recessive and female-beneficial alleles are dominant, since this increases the expression of favorable effects in both the homogametic and heterogametic sex. (B) Sex-specific differences in the dominance coefficients influence the scope for the maintenance of variation at sex-antagonistic loci. Stronger support of sex-antagonistic variation by sex-specific dominance ($h_m > h_f$) allows for heterogamety transitions over a wider range of selection coefficients, but is also associated with a smaller changes in sex-antagonistic allele frequencies during a heterogamety transition, reducing the maximal strength of indirect selection on the W allele. Other parameters: $r = r' = 0.01$, $\bar{\mu} = \bar{\mu} = 1.0 \cdot 10^{-5}$.