

Figure S1

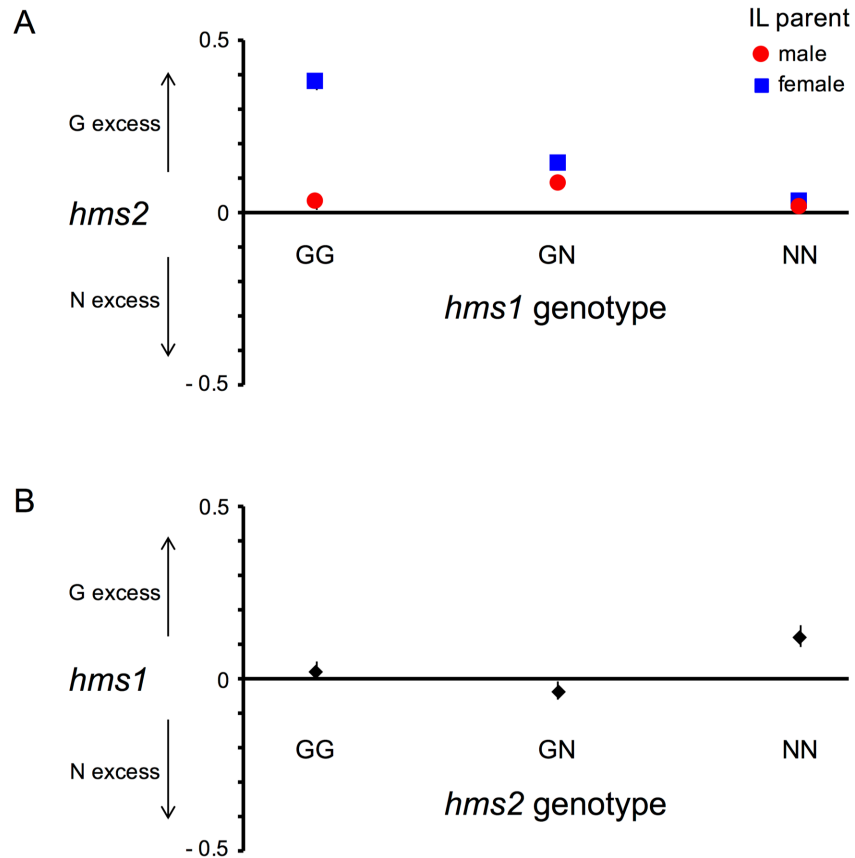


Figure S1. Transmission ratio distortion at *hms1* and *hms2* in IL-backcross progeny. The vertical position of each symbol shows the magnitude and direction of the deviation of allelic transmission from the Mendelian expectation (0.5). *M. guttatus* deviations are graphed directly [deviation = $f(N - 0.5)$], and the *M. nasutus* deviations are graphed as negative [deviation = $- (f(N-0.25))$]. Thus, values above zero indicate excess of *M. guttatus* alleles and values below zero indicate excess of *M. nasutus* alleles. G = *M. guttatus* allele, N = *M. nasutus* allele. A) Allelic transmission of *hms2* in the progeny of IL-backcrosses is significantly affected by IL parental genotype at *hms1* ($F = 37.6919$, $P < 0.0001$), cross direction ($F = 72.3339$, $P < 0.0001$), and their interaction ($F = 31.8353$, $P < 0.0001$). B) Allelic transmission of *hms1* in the progeny of IL-backcrosses is significantly affected by IL parental genotype at *hms1* ($F = 7.7977$, $P = 0.0043$).