Figure S2 Analysis of *G. affinis* and *G. holbrooki* pooled-sequencing reads aligned to the genome of *X. maculatus*.

Male/female F_{ST} was computed in non-overlapping 10 kb windows from *G. affinis* (A) and *G. holbrooki* (B) pooled-sequencing reads aligned to *X. maculatus* genome. The number of female-specific SNPs (FSS, in red) and male-specific SNPs (MSS, in blue) was similarly computed, and results are shown for LG1 for *G. affinis* (C) and LG16 for *G. holbrooki* (D). For details see Figure 3.