Supplemental Data S1
Read mapping coverage of male and female aabys sequences to house fly genes.

Supplemental Data S2
Read mapping coverage of male and female aabys sequences to house fly genes.

Supplemental Data S3
Read mapping coverage of male and female aabys sequences to house fly genes.

Supplemental Data S4
Information on blastx hits to male scaffolds with highest percent unmatched by female sequencing reads, and >5kb male scaffolds with >50% unmatched by female reads.

Supplemental Data S5
Sequences of male scaffolds with the highest percent unmatched by female sequencing reads

Supplemental Data S6
Sequences of male scaffolds that are >5kb and >50% unmatched by female reads.

Supplemental Data S7
Information about the 214 1kb windows that are 2-fold enriched in coverage in males vs females or in females vs males.

Supplemental Methods S1
Example pipeline for the YGS approach to identify male-specific contigs/scaffolds.

Supplemental Methods S2
Script used as part of YGS.sh pipeline.

Supplemental Methods S3
Example pipeline for SNP calling.