

Additional file 1

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The sequence of a male-specific genome region containing the sex determination switch in *Aedes aegypti*.

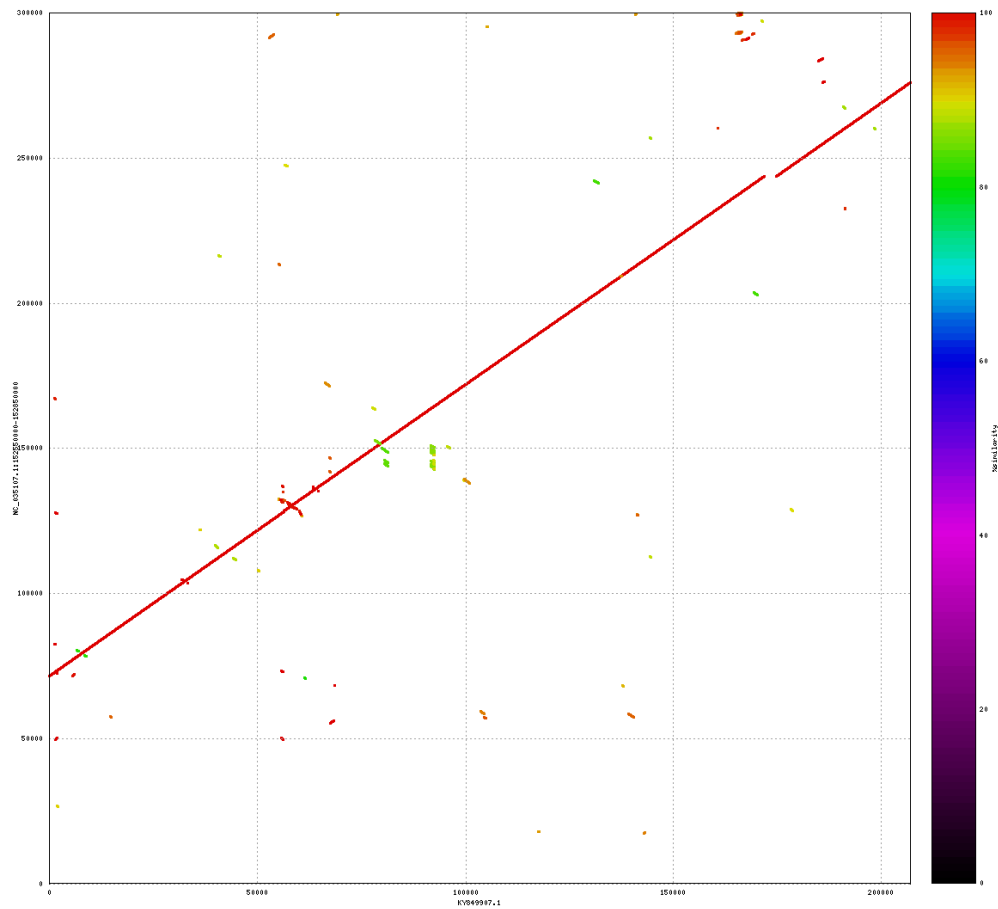


Figure S1: Alignment of the 207 kb BAC region to the corresponding region in the AaegL5 male reference assembly. The query BAC sequence is on the x axis (KY849907.1) and the reverse complement of the reference genome sequence is on the y axis (NC_035107.1:152550000-152850000, indicating coordinates 152,550,000-152,850,000 on chromosome 1). Plot lines are coloured by percentage similarity. Alignment and plot generated using MUMMER 4.0.0 [1].

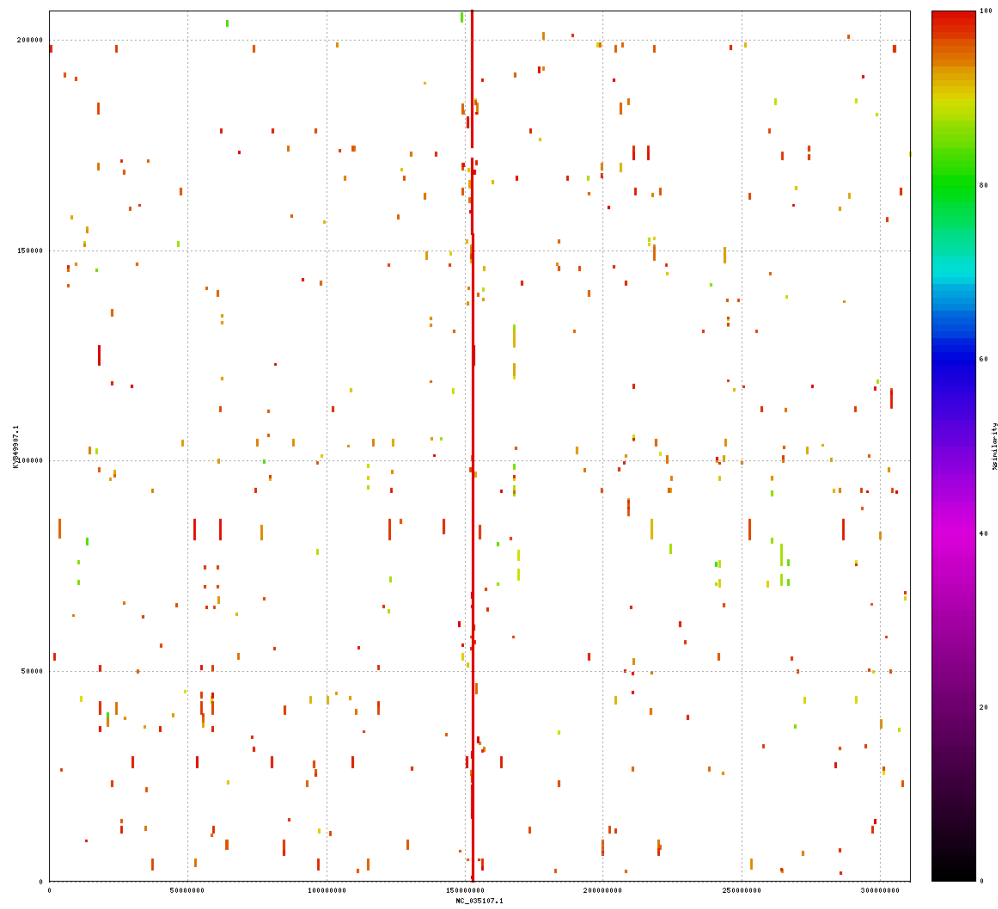


Figure S2: Alignment of the 207 kb BAC region to chromosome 1 of the AegL5 male reference assembly. The query BAC sequence is on the y axis (KY849907.1) and the reverse complement of the reference genome sequence is on the x axis (NC_035107.1). Plot lines are coloured by percentage similarity. Alignment and plot generated using MUMMER 4.0.0 [1].

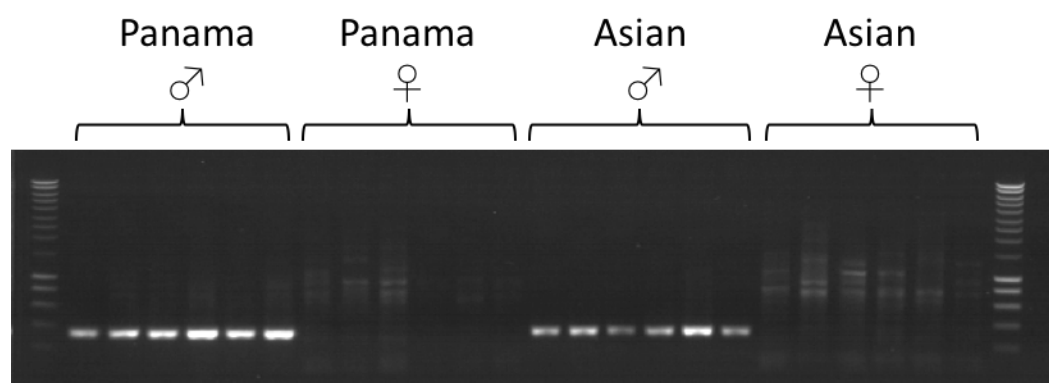


Figure S3: PCR screening of the M locus gene *Nix* in male and female DNA of wild type *Aedes aegypti* strains. Primers used were Nix1F (3'-TTGAGTCTGAAAAGTCTATGCAA-5') and Nix1R (3'-TCGCTCTTCCGTGGCATTGA-5'), targeting *Nix* exon 1.

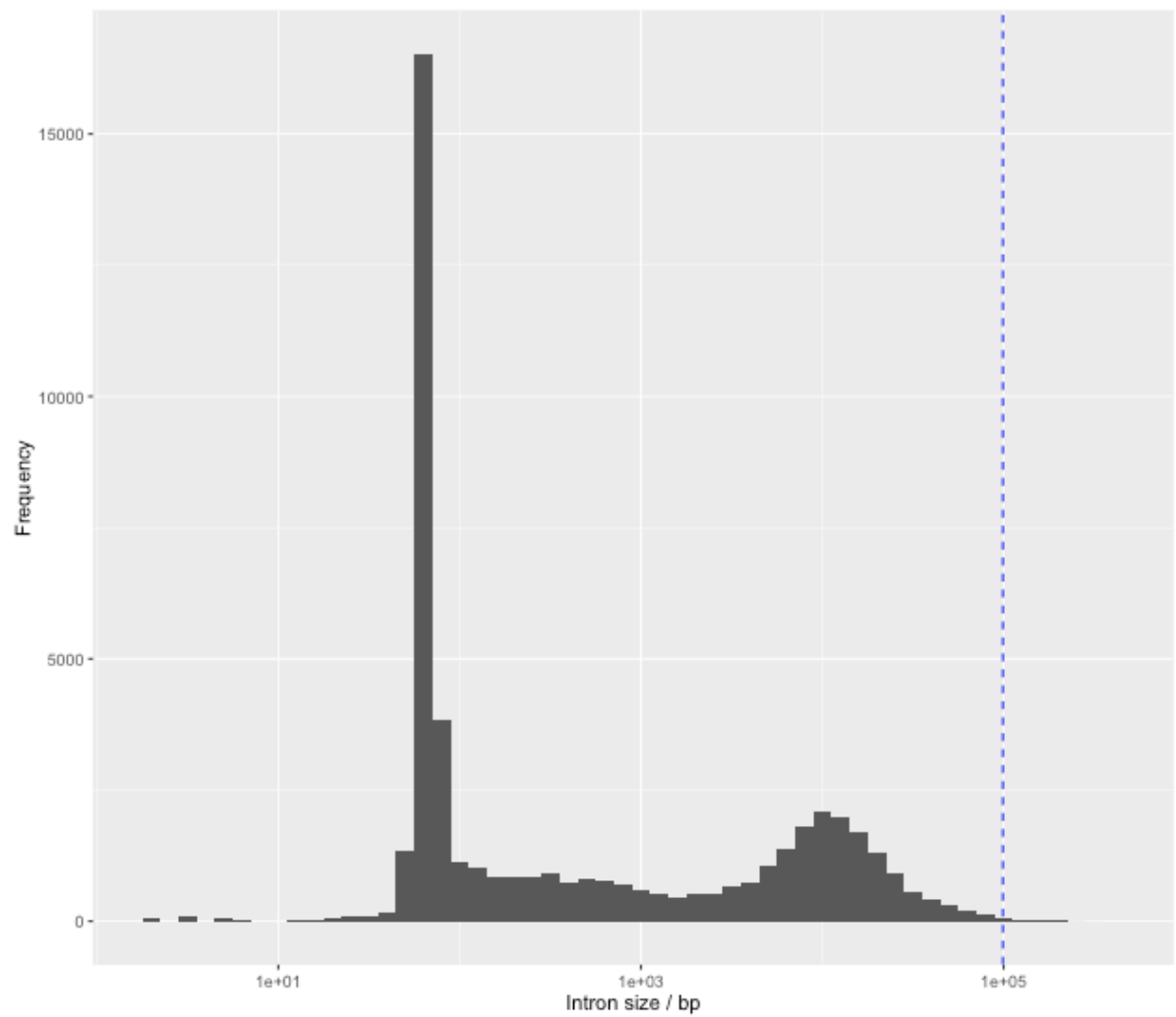


Figure S4: Intron size distribution in *Aedes aegypti* Liverpool reference genome AaegL3. Blue dashed line indicates the size of the *Nix* intron relative other introns. X axis is transformed by $\log_{10}$.

References

1. Kurtz S, Phillippy A, Delcher AL, Smoot M, Shumway M, Antonescu C, et al. Versatile and open software for comparing large genomes. *Genome Biol.* 2004;5:R12.