

Supplementary information

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

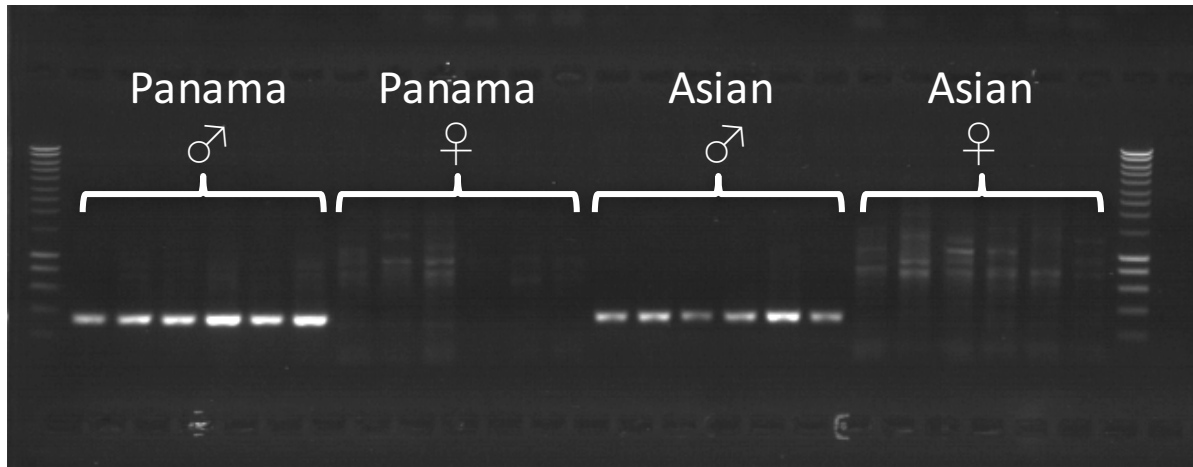


Figure S1: PCR screening of the M locus gene *Nix* in male and female DNA of wild type *Aedes aegypti* strains. Primers used were Nix1F (3'-TTGAGTCTGAAAAGTCTATGCAA-5') and Nix1R (3'-TCGCTCTTCCGTGGCATTGA-5'), targeting *Nix* exon 1.

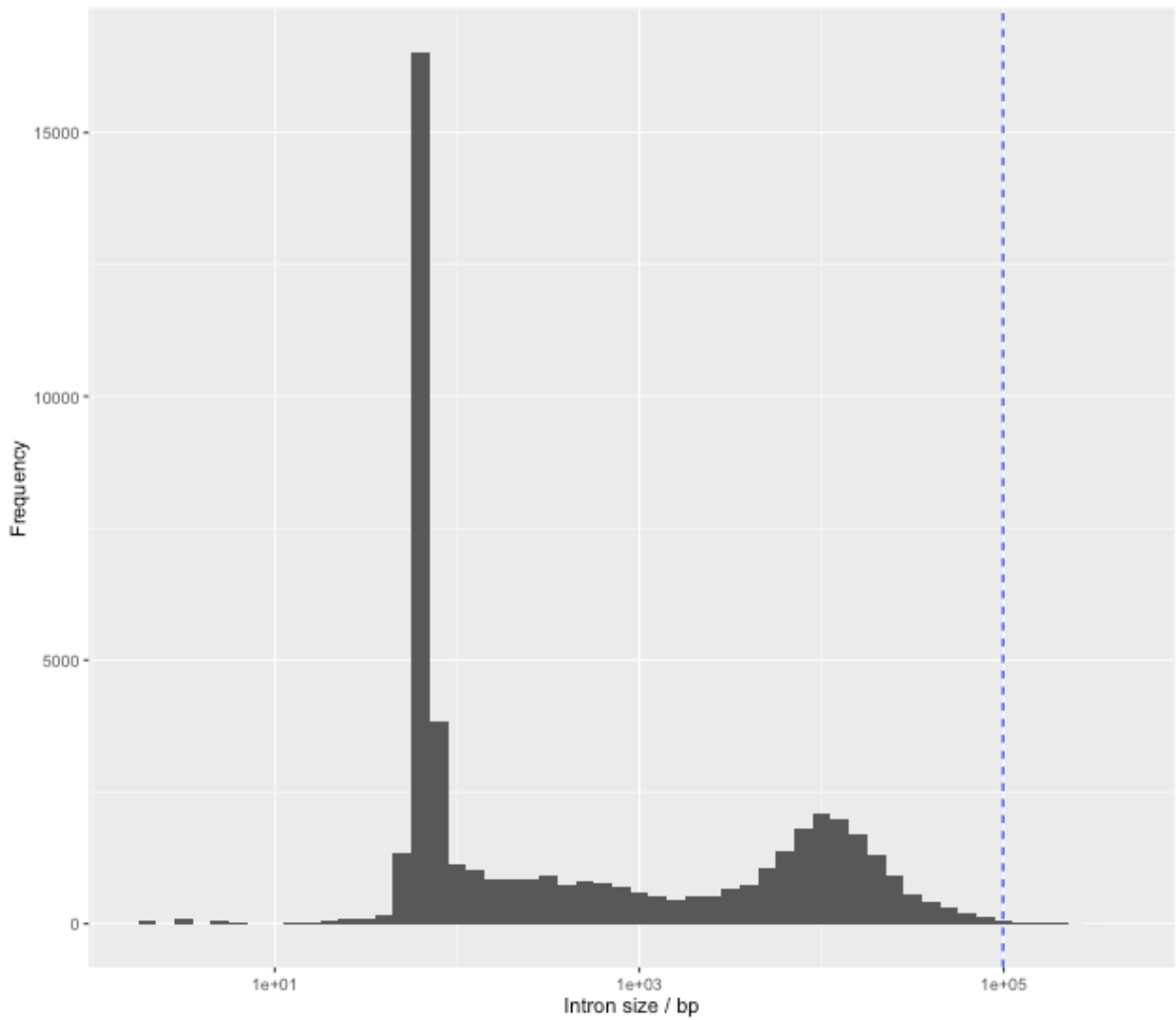


Figure S2: Intron size distribution in *Aedes aegypti* Liverpool reference genome AaegL3. Blue dashed line indicates the size of the *Nix* intron relative other introns. X axis is transformed by \log_{10} .

Table S1: Types and abundance of repeats in the 207kb assembled M locus region and 99kb *Nix* intron, identified by RepeatMasker using the *Aedes aegypti* repeat library.

Repeat Type	Entire region		<i>Nix</i> intron region	
	Number of elements	Percentage of sequence	Number of elements	Percentage of sequence
Retroelements	105	42.1%	49	51.0%
SINEs	8	0.81%	5	1.11%
Penelope	3	0.08%	2	0.20%
LINEs	24	5.43%	6	6.85%
L2/CR1/Rex	4	0.13%	0	0%
R1/L0A/Jockey	13	3.87%	3	6.60%
RTE/Bov-B	3	1.33%	0	0%
L1/CIN4	1	0.02%	1	0.05%
LTR Elements	73	35.8%	38	43.0%
BEL/Pao	9	0.71%	3	0.87%
Ty1/Copia	16	11.3%	14	19.2%
Gypsy/DIRS1	48	23.8%	21	23.0%
DNA transposons	97	11.7%	69	20.1%
Tc1-IS630-Pogo	11	3.87%	11	9.04%
Other (Mirage, P-element, Transib)	1	0.06%	0	0%
Unclassified	6	0.48%	3	0.22%
Small RNA	8	0.81%	5	1.11%
Satellites	1	0.75%	0	0%
Simple repeats	19	0.34%	7	0.24%
Low complexity	3	0.07%	1	0.04%
Total repeats		55.4%		71.6%