

Supplementary Material “A re-annotation of the *Anopheles darlingi* mobilome”

Table S1 - Comparison of genome size and TEs contents in *Anopheles* genus

Species	genome size	% of TEs	source
<i>A. albimanus</i>	170.5	1.98	1
<i>A. arabiensis</i>	246.6	9.38	1
<i>A. christyi</i>	172.7	2.81	1
<i>A. darlingi</i>	173.9	2.29 / 5.61*	2/ *3
<i>A. dirus</i>	216.3	5.09	1
<i>A. epiroticus</i>	223.5	6.27	1
<i>A. funestus</i>	225.2	4.03	1
<i>A. gambiae</i>	273.1 / 236.4	17.78	1
<i>A. quadriannulatos</i>	283.8	7.69	1
<i>A. melas</i>	227.4 / 224.2	7.29	1
<i>A. merus</i>	251.8 / 288.0	11.43	1
<i>A. stephensis</i>	221.3 / 225.4	5.04	1

Sources:

¹Neafsey DE, Waterhouse RM, Abai MR, Aganezov SS, Alekseyev MA, Allen JE, Amon J, Arcá B, Arensburger P *et al.* (2015) Highly evolvable malaria vectors: The genomes of 16 *Anopheles* mosquitoes. *Science* 347:1258522.

²Marinotti O, Cerqueira GC, de Almeida LG, Ferro MI, Loreto EL, Zaha A, Teixeira SM, Wespiser AR, Almeida E, Silva A, Schlindwein AD, *et al.* (2013) The Genome of *Anopheles darlingi*, the main Neotropical malaria vector. *Nucleic Acids Res* 41:7387-7400.

³This study.