

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

Table S2 - Percentage of genome occupied by main TE superfamilies in studied species of the *Anopheles* genus.

	<i>An darlingi</i>	<i>An gambiae</i>	<i>An arabiensis</i>	<i>An quadriannulatus</i>	<i>An melas</i>	<i>An merus</i>	<i>An christyi</i>	<i>An epiroticus</i>	<i>An dirus</i>	<i>An stephensi</i>	<i>An funestus</i>	<i>An albimanus</i>
LTR	1.40	3.94	1.29	0.77	0.66	2.56	0.08	1.22	0.65	0.21	0.50	0.15
Pao-Bel	0.06	1.60	0.57	0.29	0.24	0.97	0.01	0.65	0.23	0.05	0.12	0.01
Copia	0.74	0.40	0.18	0.15	0.12	0.28		0.07	0.06	0.04	0.13	
Gypsy	0.75	1.41	0.54	0.31	0.30	1.26	0.01	0.39	0.32	0.11	0.14	0.11
Non-LTR	1.25	3.48	1.72	1.35	1.31	2.16	0.38	1.34	1.07	1.52	0.64	0.25
LINE	0.15	1.67	0.63	0.49	0.78	0.85	0.01	0.16	0.57	0.12	0.03	0.03
Jockey	0.35	0.48	0.33	0.26	0.27	0.33		0.04	0.02	0.03	0.01	0.01
R1	0.37	0.24	0.01	0.08	0.08	0.15		0.06	0.06		0.08	0.08
SINE	0.11	0.43	0.51	0.45	0.47	0.21	0.39		0.08	1.34	0.36	
DNA-transposons	2.44	1.21	0.73	0.39	0.42	0.90	0.10	0.32	0.26	0.13	0.14	0.40
Tc1-mariner	1.06	0.59	0.48	0.21	0.22	0.29	0.03	0.22	0.12	0.10	0.06	0.28
P	0.02	0.01			0.01	0.02		0.01				
hAT	0.41	0.02	0.02	0.01	0.01	0.02	0.05		0.01	0.03	0.01	
pyggyBac	0.02	0.01			0.01							
helitron	0.11	0.05		0.01	0.01							
Total TE	5.67	17.78	9.38	7.69	7.29	11.61	2.81	6.27	5.09	5.04	4.03	1.98

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. Observation: Some families were joined into superfamilies

²This study.