

GENETICS

Supporting Information

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The Population Genomics of Trans-Specific Inversion Polymorphisms in *Anopheles gambiae*

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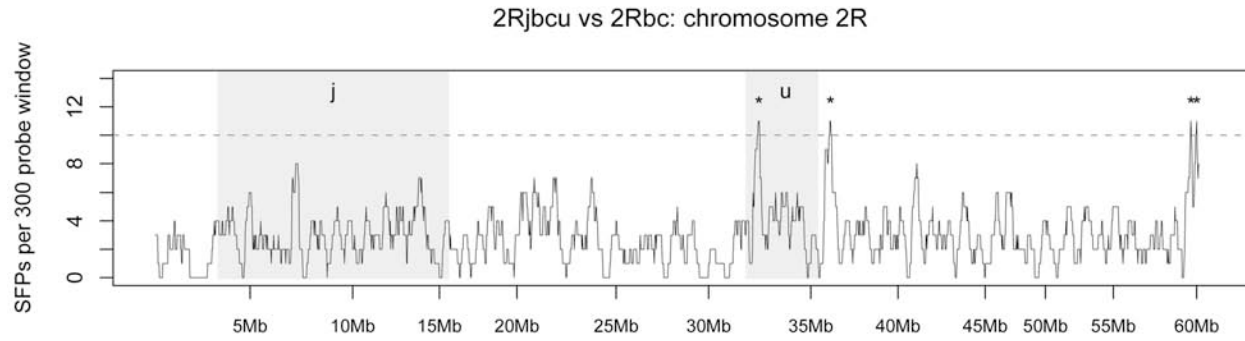


FIGURE S1.—Sliding window analysis of divergence between alternative arrangements across the 2R chromosome between karyotypes 2Rjbcu and 2Rbc, measured in terms of the proportion of SFPs per 300 probe window. Chromosome 2R is shown from telomere (left) to centromere (right). Shaded areas represent chromosomal inversions. Horizontal dashed line is the significance threshold at 12 SFPs per window. Asterisks denote significantly diverged regions.

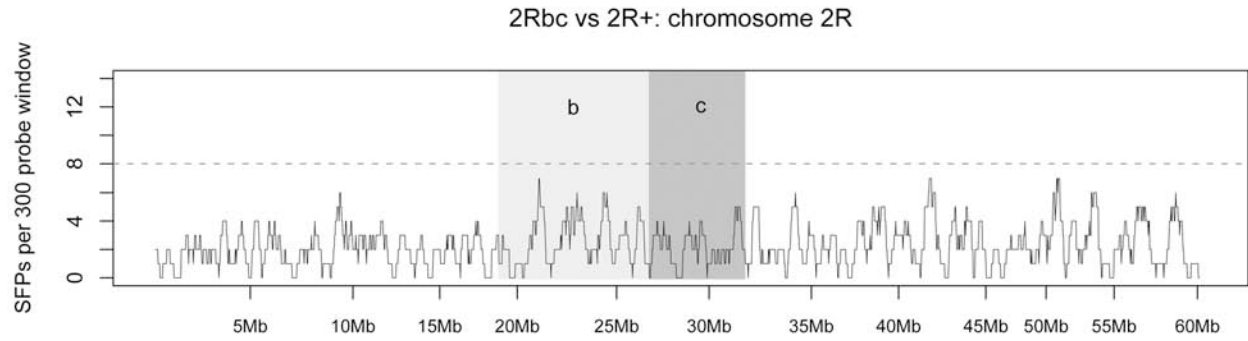


FIGURE S2.—Sliding window analysis of divergence between alternative arrangements across the 2R chromosome between karyotypes 2Rbc and 2R+, measured in terms of the proportion of SFPs per 300 probe window. Chromosome 2R is shown from telomere (left) to centromere (right). Shaded areas represent chromosomal inversions. Horizontal dashed line is the significance threshold at 12 SFPs per window. In this contrast, no significant differentiation was detected.

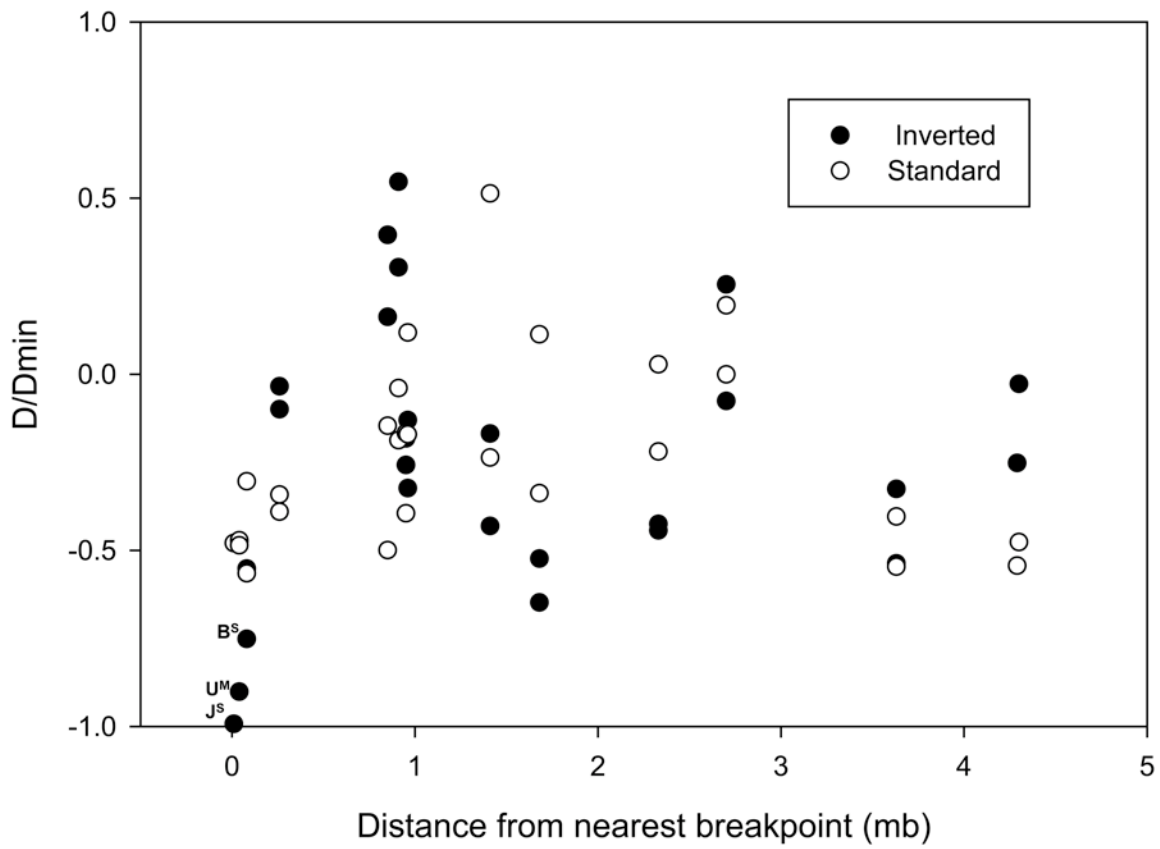


FIGURE S3.—Plot of the ratio of Tajima's D to the theoretical minimum of Tajima's D (D_{\min}) for all genes sequenced in each *Anopheles gambiae* molecular form and gene arrangement. Breakpoint loci are labeled by inversion and molecular form (in superscript).

TABLE S1**Genes and primers used for sequence determination on chromosome 2R in Malian populations of *An. gambiae***

Gene	Gene ID	Primer Sequences (5'-3')	Chromosomal Position (AgamP3.4)
<i>hex2</i>	AGAP001659	F: CGTTCCTGGAGAAGCAGAAG	7552268-7552287
		R: AGCCGTTGTGGTAGTTTTTCG	7553116-7553097
<i>clk-6</i>	AGAP001856	F: CGTACCGGTTTCTGGTGAAC	11454087-11454068
		R: CGTTGCTTTCGGAGCTAAAA	11453386-11453405
<i>Sema</i>	AGAP002424	F: ATCGCCGTCACCAACTGTA	21200436-21200454
		R: ACTCGAGCTTCTCGCAGGT	21201153-21201135
2576	AGAP002576	F: TCGCTCGACATCGAGATACA	23117991-23117972
		R: GCCCCAGATGAGATTCGTTA	23117214-23117233
2751	AGAP002751	F: GAAGGTGCTCTGCCTCAAAG	26667813-26667832
		R: GTATGTTTCGGGAACGAGTGC	26668540-26668521
2775	AGAP002775	F: TCACCAGAGGCTATGTGCTG	27041004-27040985
		R: CGAAAACTGCTCCGACTTC	27040213-27040232
<i>dcr</i>	AGAP002836	F: GCGGAAATATGCAACCATCT	28196955-28196974
		R: TTTCGTTTCGACCATGTACCA	28197702-28197683
<i>med</i>	AGAP002902	F: CAGCCTTCATCACAGTCCAA	29118353-29118372
		R: ACGGATCCACATACCCATC	29119145-29119127
<i>gpr45</i>	AGAP003053	F: GTGTACGGTGCTGATCGAAA	31519286-31519305
		R: TATAAACACCCGACCCATGA	31520044-31520025
3085	AGAP003085	F: AACAAAGTTCGCCGACATACC	32330467-32330486
		R: CCTTCACCTTGTCCCACAGT	32331310-32331291
<i>e2-230k</i>	AGAP003090	F: AGGAAAACGACAATGCGAAC	32389332-32389351
		R: CATTACGCTCAGCAAGTCCA	32390014-32389995
<i>gpr23</i>	AGAP003098	F: AAGCTGCTGATCGTGTTCCT	32427925-32427906

		R: GATGTGAGCAGTTCCTCGATT	32427264-32427283
<i>3106</i>	AGAP003106	F: CGACGAGAACATTGTGCAGT R: GCTCCGGATCGAGTATGAAG	32441688-32441669 32440901-32440920
<i>3205</i>	AGAP003205	F: GGGCTTTTGCTTCATCTACG R: GCCTAGAGCCGTGTCTTGAG	33827546-33827527 33826780-33826799
<i>4112</i>	AGAP004112	F: AATATCGGCCCCATACTTCC R: TCTCCATCCTCCACATCCTC	50099114-50099095 50098407-50098426
<i>mcm2</i>	AGAP004275	F: AACCGATATTGTGCGGTTTC R: AACAGTTCGCTTTCGAGGAA	53568163-53568182 53568871-53568852

TABLE S2**Predicted genes in a significantly diverged region of the *An. gambiae* 2Ru rearrangement**

Gene ID	Description	Affy Plasmodium Anopheles probe set	Gene Start (bp)	Gene End (bp)	Number of SFPs	
					2R _{jb} cu vs 2R+	2R _{bc} cu vs 2R _{bc}
AGAP003079		Ag.2R.2722.0_CDS_at	32254248	32256017	2	0
AGAP003080			32273374	32288370	0	0
AGAP003081		Ag.2R.1721.0_CDS_at	32297951	32300052	1	0
AGAP003082		Ag.2R.3351.0_CDS_s_at	32301727	32302947	0	0
AGAP003083		Ag.2R.3351.0_CDS_s_at, Ag.2R.1722.0_CDS_at	32303704	32308399	0	0
AGAP003084		Ag.2R.1723.0_CDS_at, Ag.UNKN.568.0_CDS_s_at	32320490	32325718	0	0
<u>AGAP003085</u>		Ag.2R.1936.0_CDS_at	32329882	32331426	0	0
AGAP003086		Ag.2R.2723.0_CDS_at, Ag.2R.338.0_CDS_at	32378725	32379968	0	0
AGAP003086			32378725	32379968		
AGAP003087		Ag.2R.386.0_CDS_a_at, Ag.2R.719.0_CDS_s_at, Ag.2R.719.1_s_at	32380097	32381431	1	0
AGAP003088		Ag.2R.719.1_s_at, Ag.2R.386.0_CDS_a_at, Ag.2R.719.0_CDS_s_at	32381681	32383151	0	0
AGAP003089		Ag.2R.720.0_CDS_at	32383651	32385665	0	0
AGAP003090		Ag.2R.1114.0_CDS_a_at	32386739	32390959	0	1
<u>ENSANGEST00000008826</u>		Ag.2R.1114.1_at, Ag.2R.3684.0_at	32389514	32394038	4	4
AGAP003091		Ag.2R.1043.0_CDS_at	32394345	32395223	0	0
AGAP003092		Ag.2R.504.0_CDS_at, Ag.2R.889.0_CDS_a_at	32404897	32414429	0	0
AGAP003093		Ag.2R.504.0_CDS_at, Ag.2R.1415.0_CDS_at	32415560	32416806	0	0
AGAP003094		Ag.2R.504.0_CDS_at	32416873	32417819	1	2
AGAP003094		Ag.2R.1415.0_CDS_at	32416873	32417819		
AGAP003095	Dopachrome conversion enzyme	Ag.2R.25.1_CDS_a_at	32419121	32421544	0	0
AGAP003096		Ag.2R.989.0_CDS_at	32423179	32424670	0	0
AGAP003097		Ag.2R.989.0_CDS_at,	32425204	32426891	1	1

		Ag.2R.237.0_CDS_at				
<u>AGAP003098</u>	gustatory receptor gpr23	Ag.2R.989.0_CDS_at, Ag.2R.237.0_CDS_at	32427076	32428603	1	0
AGAP003099		Ag.2R.237.0_CDS_at, Ag.2R.844.0_CDS_at	32428675	32430131	1	1
AGAP003100	tRNA-Gly	Ag.2R.237.0_CDS_at, Ag.2R.844.0_CDS_at	32429430	32429500	0	0
AGAP003101	tRNA-Ile		32431955	32432028	0	0
AGAP003102	tRNA-Ile		32433892	32433965	0	0
AGAP003103	tRNA-Lys		32434922	32434994	0	0
AGAP003104	tRNA-Gly		32435182	32435252	0	0
AGAP003105	tRNA-Met		32435821	32435892	0	0
<u>AGAP003106</u>		Ag.2R.1724.0_CDS_at	32440110	32442980	1	0
AGAP003107	tRNA-Glu		32444715	32444786	0	0
AGAP003108		Ag.2R.1937.1_CDS_a_at	32497091	32500709	1	0

Underlined genes were re-sequenced in this study; see Table 2.