

Table S1 Mosquito population assignment, molecular form, and 2La karyotype.

Table S1 is available for download as a Microsoft Excel spreadsheet at

<http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.112.004473/-/DC1>.

Each row in the spreadsheet corresponds to an individual mosquito. Columns indicate mosquito identifier, the malaria transmission season in which the mosquito was collected, the molecular form (see Methods), and karyotype of the 2La chromosomal inversion (see Methods).

Table S2 Fragment and PCR Oligo information.

Identifier	Gene	PCR		Fragment Length	Year Sampled	
		fragment	Forward oligo			Reverse oligo
AGAP005681	GPRNNA21	AmS010b	5'-GCATCATCATCGGTCACCG-3'	5'-CTGAGTCACCTGCAAACCG-3'	528	2007
AGAP005693	APL2	AmS011b	5'-CTATCCACCGTCCAGTTTG-3'	5'-GGTTCGGTGGAAATTCTAACC-3'	561	2007
AGAP005716	SCRB16	AmS013a	5'-TGCCGAAGATGAAACGTACG-3'	5'-CGTGCTAAAGATTGTCATCCG-3'	534	2007
AGAP005728	5728	AmS048b	5'-GAATTGCGCAAACAGTCCAG-3'	5'-CACGTTGCATATCTCGCTGA-3'	650	2007
AGAP005762	5762	AmS049b	5'-ATCGATGTCCTCGGCACTAC-3'	5'-GATGGTCAAAGCCAACGAAC-3'	525	2007
AGAP006102	PRS1	AmS052b	5'-CGAAAGTGATTCCGGACAAG-3'	5'-TTATCGCTCGCACAGCAC-3'	304	2007
AGAP006348	LRIM1	AmS059e	5'-CCTCGTACCGCTTGACGAT-3'	5'-GTGACCTGGATCAGTCTGC-3'	576	2007
AGAP006421	IRSP1	AmS053a	5'-ATGGCCATCTGGATAGCTTG-3'	5'-GATATTCGCTCCACCAGCTC-3'	563	2007
AGAP006974	TOLL9	AmS001b	5'-GCATCTCGAACTGACACCAG-3'	5'-TTCGGATATTCCGGAGGAG-3'	536	2007
AGAP007030	LRR(7030)	AmS002a	5'-AGAAACAACAGTCGCAAGCTC-3'	5'-ACATGCTGTGCACCATAAAGAA-3'	501	2007
AGAP007032	7032	AmS046a	5'-CGAAAGCAGCAGAAGAATCG-3'	5'-TGCTGCATCGTTGTGCACG-3'	601	2007
AGAP007033	APL1C	AmS003a	5'-CTTCTGAATAGTGTGCGGTAA-3'	5'-TGAGACAAACTTTGGAGGTCAG-3'	371	2007
AGAP007034	LRR(7034)	AmS047b	5'-CACAGATGCTCCAGCTTCG-3'	5'-CGTACTTGGTGGACCAACG-3'	738	2007
AGAP007035	APL1B	AmS036a	5'-AGATGGGTCTGTGTTGCTG-3'	5'-CGCACACCATTGATGTGGG-3'	833	2007-2008
AGAP007036	APL1A	AmS037d	5'-TGTGATTTAYMCAACTCATGC-3'	5'-TCAAAGTGCTCGATYTGTCG-3'	802	2007
AGAP007037	LRR(7037)	AmS038a	5'-CGTTGTCCAGTATCCACAG-3'	5'-CAACAACACGATCAAGCAGC-3'	580	2007
AGAP007041	FBN32	AmS004b	5'-GTACGATGGTACGGTCGATTC-3'	5'-GGTAGGAATGCTTCCGATTAG-3'	486	2007-2008

Table S2: Continued

Identifier	Gene	PCR		Reverse oligo	Fragment Length	Year Sampled
		fragment	Forward oligo			
AGAP007048	LRR(7048)	AmS005b	5'-TTTTTAAGCCTAGCCCGTCTG-3'	5'-CAGCTCGGTAAGCCGATTG-3'	491	2007-2008
AGAP007058	DLL	AmS007b	5'-GTACGTAGCCACCCATCTG-3'	5'-GTTAAGATCTGGTTTCAAATCG-3'	641	2007-2008
AGAP007059	LRR(7059)	AmS051b	5'-ACCAGGCGCTAGTTCTTTGA-3'	5'-TACCGCAACGGTCTTTAAC-3'	641	2007-2008
AGAP007060	LRR(7060)	AmS006b	5'-AGTAGCAGGCTCGTGAGTGAG-3'	5'-GAAGCACTTCCACTGGTGCT-3'	658	2007-2008
AGAP007061	LRR(7061)	AmS045b	5'-AGGAAAGATCAAGCAGCTCG-3'	5'-CTGGCGATCGTCAACAACG-3'	532	2007
H603flank	intergenic region	AmS050a	5'-CAAGGCAGCTTCTTCGTTCT-3'	5'-GTTACAGAGTTTGGTCTTGC-3'	522	2007-2008
AGAP001826	APOII/I	AmS056a	5'-CCGTTGACGTGGTACTTGG-3'	5'-ATGTGGCTGCCGATTTCTAC-3'	566	2007
AGAP002593	APOD	AmS057c	5'-GGTACGATCAACACTTCGAG-3'	5'-TGATGCGCATATCCTGTCG-3'	490	2007
AGAP010815	TEP1	AmS054c	5'-CGTATTTGGACGTCCGACG-3'	5'-CCATGCAATCAATGAGAACG-3'	579	2007
AGAP012352	AgMDL1	AmS055b	5'-CAGCAGGATTCAGTTCTC-3'	5'-ATCCATGAGGTTTCGATCTC-3'	486	2007
AGAP001081	WASP	AmS058b	5'-TTCGTCTCGGTAGCAAAG-3'	5'-TGGTGCAGCTGTACACGAC-3'	440	2007

Table S3 Sequenced fragment physical genomic locations

Identifier	Gene Name	Chromosome	Chromosomal		Chromosomal Strand
			Location ^a	Inside PRI?	
AGAP005681	GPRNNA21	2L	18693376	Yes	-
AGAP005693	APL2	2L	18785249	Yes	+
AGAP005716	SCRB16	2L	19542880	Yes	+
AGAP005728	5728	2L	19769635	Yes	-
AGAP005762	5762	2L	20339460	Yes	-
AGAP006102	PRS1	2L	26685850	No	+
AGAP006348	LRIM1	2L	30329656	No	-
AGAP006421	IRSP1	2L	31693742	No	+
AGAP006974	TOLL9	2L	40434581	Yes	-
AGAP007030	LRR(7030)	2L	41057548	Yes	-
AGAP007032	7032	2L	41245076	Yes	+
AGAP007033	APL1C	2L	41257877	Yes	-
AGAP007034	LRR(7034)	2L	41262272	Yes	-
AGAP007035	APL1B	2L	41266619	Yes	-
AGAP007036	APL1A	2L	41271509	Yes	-
AGAP007037	LRR(7037)	2L	41274607	Yes	-
AGAP007041	FBN32	2L	41381834	Yes	+
AGAP007048	LRR(7048)	2L	41648960	Yes	+
AGAP007058	Distalless	2L	42005592	Yes	-
AGAP007059	LRR(7059)	2L	42005592	Yes	+
AGAP007060	LRR(7060)	2L	42062331	Yes	-
AGAP007061	LRR(7061)	2L	42067616	Yes	-
	intergenic				
H603flank	region	2L	42071847	Yes	-
AGAP001826	APOII/I	2R	11201968	No	-
AGAP002593	APOD	2R	40909880	No	-
AGAP010815	TEP1	3L	11117128	No	-
AGAP012352	AgMDL1	3L	23677600	No	+
AGAP001081	WASP	X	23372448	No	-

^a Gene starting positions on chromosome 2 given according to locations in *A. gambiae* PEST genome sequence, which corresponds to the inverted 2La+ form of the 2La inversion.

Table S4 Population genetic summary statistics for all genes in each population.

Locus	Identifier	n^a	S_{syn}^b	D^c	H^d	EW^e	HEW^f
M form							
<i>Toll9</i>	AGAP006974	64	79	-0.6612	-0.3681	0.019	1
<i>LRR(7030)</i>	AGAP007030	64	34	-0.7755	-0.8827	0.062	0.0921
<i>APL1C</i>	AGAP007033	64	21	-0.546	-1.1648	0.2739	0.084
<i>FBN32</i>	AGAP007041	100	33	-1.0852	-0.7677	0.0864	0.0992
<i>LRR(7048)</i>	AGAP007048	100	68	-2.0115	-0.1663	0.046	0.1441
<i>LRR(7060)</i>	AGAP007060	100	42	-1.6659	0.084	0.0842	0.2152
<i>DLL</i>	AGAP007058	100	87	-2.0234	-0.6157	0.0208	0.1036
<i>GPRNNA21</i>	AGAP005681	64	16	-0.7143	0.1597	0.1201	0.2411
<i>APL2</i>	AGAP005693	64	27	-1.0359	0.6826	0.0459	0.7155
<i>SCRB16</i>	AGAP005716	64	47	-0.3479	-0.3037	0.0347	0.1326
<i>APL1B</i>	AGAP007035	100	88	-0.5362	-1.7003	0.0898	0.0294
<i>APL1A</i>	AGAP007036	62	110	-1.15	-2.5176	0.3002	0.014
<i>LRR(7037)</i>	AGAP007037	64	13	-1.682	-0.2348	0.5239	0.1441
<i>LRR(7061)</i>	AGAP007061	64	37	-0.8415	0.1359	0.0605	0.2283
<i>7032</i>	AGAP007032	64	73	-1.4061	0.5115	0.0181	1
<i>LRR(7034)</i>	AGAP007034	62	20	0.174	0.7383	0.1623	0.779
<i>5758</i>	AGAP005758	64	29	-1.5625	-0.1749	0.0815	0.1441
<i>5762</i>	AGAP005762	64	73	-1.6686	-0.2999	0.02	0.1326
<i>H603 flanking</i>	AGAP007058	100	54	-1.866	-0.4372	0.023	0.1326
<i>LRR(7059)</i>	AGAP007059	100	50	-1.8131	-1.6246	0.148	0.0302
<i>PRS1</i>	AGAP006102	64	16	-1.6028	-0.1924	0.1709	0.1441
<i>IRSP1</i>	AGAP006421	64	55	-1.4194	-2.4365	0.0557	0.014
<i>TEP1</i>	AGAP010815	64	10	-2.1817	-2.0996	0.7979	0.0233
<i>AgMDL2</i>	AGAP012352	64	66	-1.7729	0.0863	0.0249	0.2667
<i>APOII-I</i>	AGAP001826	64	23	-1.5496	-0.2477	0.1338	0.1441
<i>APOD</i>	AGAP002593	64	37	-0.8402	-0.9231	0.0454	0.4199
<i>WASP</i>	AGAP001081	64	42	-1.6375	-0.3393	0.0322	0.1326
<i>LRIM1</i>	AGAP006348	64	25	-0.1096	-2.4951	0.1221	0.0336
S form							
<i>Toll9</i>	AGAP006974	100	81	-0.6536	-0.4918	0.0118	0.1352
<i>LRR(7030)</i>	AGAP007030	100	59	-1.1477	-1.1961	0.0378	0.091
<i>APL1C</i>	AGAP007033	100	72	-1.3893	-0.885	0.126	0.0928
<i>FBN32</i>	AGAP007041	100	47	-1.7597	-0.7475	0.0454	0.1117
<i>LRR(7048)</i>	AGAP007048	100	79	-2.2608	-0.1704	0.0364	0.1473

<i>LRR(7060)</i>	AGAP007060	100	50	-2.0471	-1.4173	0.0684	0.091
<i>DLL</i>	AGAP007058	100	96	-1.9502	-1.2775	0.0146	0.091
<i>GPRNNA21</i>	AGAP005681	100	28	-1.7265	-0.4675	0.1156	0.1473
<i>APL2</i>	AGAP005693	100	43	-1.7926	0.4499	0.0434	0.3721
<i>SCRB16</i>	AGAP005716	100	58	-0.7949	-0.4554	0.026	0.1352
<i>APL1B</i>	AGAP007035	100	120	-0.7912	-1.5837	0.0172	0.091
<i>APL1A</i>	AGAP007036	100	147	-0.061	-1.4618	0.0158	0.1352
<i>LRR(7037)</i>	AGAP007037	100	49	-2.0094	-0.0114	0.0688	0.1535
<i>LRR(7061)</i>	AGAP007061	100	33	-0.9212	-0.1171	0.0894	0.1473
<i>7032</i>	AGAP007032	100	83	-1.7822	0.2356	0.0154	0.2135
<i>LRR(7034)</i>	AGAP007034	100	42	-1.9241	-0.099	0.0598	0.1473
<i>5758</i>	AGAP005758	100	37	-1.7718	-0.1192	0.0642	0.1473
<i>5762</i>	AGAP005762	100	100	-1.564	0.0407	0.0122	0.1535
<i>H603 flanking</i>	AGAP007058	100	83	-2.2543	-0.1461	0.0202	0.1473
<i>LRR(7059)</i>	AGAP007059	100	51	-0.986	-0.2439	0.042	0.1473
<i>PRS1</i>	AGAP006102	100	17	-1.4331	-0.2205	0.1842	0.1473
<i>IRSP1</i>	AGAP006421	100	61	-0.8321	-0.9617	0.017	0.0928
<i>TEP1</i>	AGAP010815	100	15	0.317	0.565	0.2096	0.5221
<i>AgMDL2</i>	AGAP012352	100	68	-1.4512	0.4507	0.0198	0.3682
<i>APOII-I</i>	AGAP001826	100	44	-2.0695	0.1091	0.0598	0.1926
<i>APOD</i>	AGAP002593	100	53	-1.819	-0.9022	0.065	0.0928
<i>WASP</i>	AGAP001081	100	77	-2.2284	-0.1177	0.0432	0.1473
<i>LRIM1</i>	AGAP006348	100	47	-0.5435	-0.0234	0.0228	0.1535

GOUNDRY

$2\text{La}^+/2\text{La}^+$

<i>ToII9</i>	AGAP006974	100	50	-0.1716	-3.0625	0.0868	0.0224
<i>LRR(7030)</i>	AGAP007030	100	23	-0.1144	0.5018	0.059	0.5892
<i>APL1C</i>	AGAP007033	100	22	-0.1767	-1.6356	0.2556	0.0999
<i>FBN32</i>	AGAP007041	100	23	0.2029	0.3183	0.2676	0.425
<i>LRR(7048)</i>	AGAP007048	100	14	1.5159	-0.1189	0.1616	0.3041
<i>LRR(7060)</i>	AGAP007060	100	10	0.0003	-0.5047	0.3704	0.425
<i>DLL</i>	AGAP007058	100	16	0.9977	-0.2242	0.211	0.3027
<i>GPRNNA21</i>	AGAP005681	100	11	-0.4812	0.0792	0.365	0.3683
<i>APL2</i>	AGAP005693	100	13	-1.0815	-0.5745	0.3712	0.2448
<i>SCRB16</i>	AGAP005716	100	21	1.0104	-1.0902	0.1456	0.2402
<i>APL1B</i>	AGAP007035	100	70	0.7992	-2.3727	0.336	0.0999
<i>APL1A</i>	AGAP007036	100	63	2.4401	-1.8712	0.1678	0.7745
<i>LRR(7037)</i>	AGAP007037	100	8	0.3655	0.6926	0.2866	0.7745

<i>LRR(7061)</i>	AGAP007061	100	8	2.4058	0.072	0.418	0.425
<i>7032</i>	AGAP007032	100	19	1.1648	-3.0339	0.328	0.2402
<i>LRR(7034)</i>	AGAP007034	100	6	0.8999	0.4665	0.4092	0.7579
<i>5758</i>	AGAP005758	100	2	2.3379	0.5497	0.4616	0.7745
<i>5762</i>	AGAP005762	100	20	1.0203	-0.4835	0.2026	0.2448
<i>H603 flanking</i>	AGAP007058	100	16	-1.469	0.3172	0.3162	0.425
<i>LRR(7059)</i>	AGAP007059	100	9	1.6054	-0.0451	0.3622	0.425
<i>PRS1</i>	AGAP006102	100	14	-1.6311	0.2602	0.3306	0.499
<i>IRSP1</i>	AGAP006421	100	10	-0.5248	-1.9277	0.1946	0.425
<i>TEP1</i>	AGAP010815	100	11	0.1881	0.0061	0.3224	0.7133
<i>AgMDL2</i>	AGAP012352	100	48	-0.423	0.6236	0.1192	0.7126
<i>APOII-I</i>	AGAP001826	100	8	1.1057	0.6108	0.2666	0.7186
<i>APOD</i>	AGAP002593	100	38	-0.57	0.1383	0.0688	0.4118
<i>WASP</i>	AGAP001081	100	13	-0.8877	0.1567	0.392	0.4439
<i>LRIM1</i>	AGAP006348	100	22	0.8458	-0.2961	0.2756	0.2863
<hr/>							
GOUNDRY							
<i>2La^a/2La^a</i>							
<i>Toll9</i>	AGAP006974	40	59	0.7813	-0.4603	0.0688	0.1255
<i>LRR(7030)</i>	AGAP007030	34	22	-1.3252	-1.5011	0.1211	0.0482
<i>APL1C</i>	AGAP007033	40	29	-0.1794	-0.6664	0.105	0.16
<i>FBN32</i>	AGAP007041	100	15	-1.2392	-1.6624	0.508	0.0482
<i>LRR(7048)</i>	AGAP007048	100	73	-1.6192	0.4025	0.1242	0.4164
<i>LRR(7060)</i>	AGAP007060	100	38	-2.0531	-2.2083	0.3992	0.028
<i>DLL</i>	AGAP007058	100	72	-2.3283	-2.5965	0.2512	0.0252
<i>GPRNNA21</i>	AGAP005681	40	9	-0.0237	-0.8588	0.3275	0.2329
<i>APL2</i>	AGAP005693	40	17	-1.4316	-0.7944	0.345	0.1101
<i>SCRB16</i>	AGAP005716	40	28	0.3575	-0.8282	0.1475	0.1033
<i>APL1B</i>	AGAP007035	100	70	0.2394	-2.4022	0.2408	0.0252
<i>APL1A</i>	AGAP007036	38	78	2.4679	-0.2821	0.2853	0.5291
<i>LRR(7037)</i>	AGAP007037	38	5	0.0936	-0.2734	0.4765	0.16
<i>LRR(7061)</i>	AGAP007061	40	19	-0.8833	-1.7333	0.2463	0.4164
<i>7032</i>	AGAP007032	40	36	-0.3302	0.3314	0.1038	0.3951
<i>LRR(7034)</i>	AGAP007034	40	10	1.2186	-1.045	0.4313	0.5291
<i>5758</i>	AGAP005758	38	9	1.173	0.9511	0.2175	0.931
<i>5762</i>	AGAP005762	38	25	-0.1673	0.4451	0.1177	0.4444
<i>H603 flanking</i>	AGAP007058	100	24	-1.312	-3.2452	0.1474	0.0994
<i>LRR(7059)</i>	AGAP007059	100	44	-0.924	-0.8104	0.1418	0.1033
<i>PRS1</i>	AGAP006102	40	8	0.5677	-1.2126	0.2888	0.1255

<i>IRSP1</i>	AGAP006421	40	34	-1.2448	-1.8962	0.22	0.1255
<i>TEP1</i>	AGAP010815	40	11	0.2615	0.3394	0.345	0.5291
<i>AgMDL2</i>	AGAP012352	40	44	-0.7708	0.7287	0.185	0.6782
<i>APOII-I</i>	AGAP001826	40	8	0.6999	0.5657	0.275	0.5291
<i>APOD</i>	AGAP002593	40	38	-1.0434	0.0154	0.08	0.2317
<i>WASP</i>	AGAP001081	38	16	-1.3667	0.3246	0.3213	0.4164
<i>LRIM1</i>	AGAP006348	38	17	2.1208	0.2522	0.3269	0.3668

a- Number of chromosomes in the sample. Loci with $n=100$ had more than 100 in the original sample, but were down-sampled to 100 for this analysis.

b- Number of synonymous segregating sites.

c- Tajima's D calculated using only synonymous sites.

d- Normalized Fay and Wu's H calculated using only synonymous sites.

e- Ewens-Watterson's haplotype homozygosity statistic calculated using only synonymous sites.

f- HEW p -value with Benjamini and Hochberg correction for multiple tests.

Statistical significance of HEW was evaluated by comparison to 10^5 neutral coalescent simulations of each sample (see Methods).

Table S5 Results from *post-hoc* evaluation of haploype reconstruction for genes with significant *HEW* result.

Gene	Confidence Rank ^a	Mean Probability (<1) ^b	Proportion Imputed Rank ^c	Proportion Phased Rank ^d
M form				
<i>LRIM1</i>	50	0.82	55	26
<i>TEP1</i>	20	0.76	90	100
<i>APL1A</i>	86	0.74	33	12
<i>APL1B</i>	76	0.81	36	19
<i>LRR (7059)</i>	40	0.78	70	72
<i>IRSP1</i>	24	0.73	35	32
GOUNDRY				
2La ^a /2La ^a				
<i>DLL</i>	53	0.73	27	70
<i>APL1B</i>	94	0.86	39	7
<i>LRR (7030)</i>	2	0.78	24	58
<i>LRR (7060)</i>	64	0.76	37	83
<i>FBN32</i>	74	0.77	62	88
GOUNDRY				
2La ⁺ /2La ⁺				
<i>TOLL9</i>	63	0.78	29	24

Haplotype reconstruction and imputation was conducted for each gene in each population separately. For GOUNDRY, genes inside the 2La inversion were treated separately according to 2La homokaryotype, while genes outside of the inversion were treated as one group. In total, this resulted in 102 runs of the program PHASE (Stephens, Smith, and Donnelly 2001). When a heterozygous site is phased, it is given a statistical confidence probability ranging from 0.5 to 1, where 0.5 is low confidence or complete ambiguity and 1 being the highest level of confidence.

^a Genes ranked based on the proportion of phased sites that were given a confidence probability less than 1, with 1 indicating the gene with the most

^b Mean probability calculated for each gene for sites with probabilities less than 1.

^c Genes ranked based on the proportion of sequenced sites that were imputed, with 1 representing gene with the most imputed sites.

^d Genes ranked based on the proportion of sequenced sites that were phased, with 1 representing the gene with the most statistically phased sites.