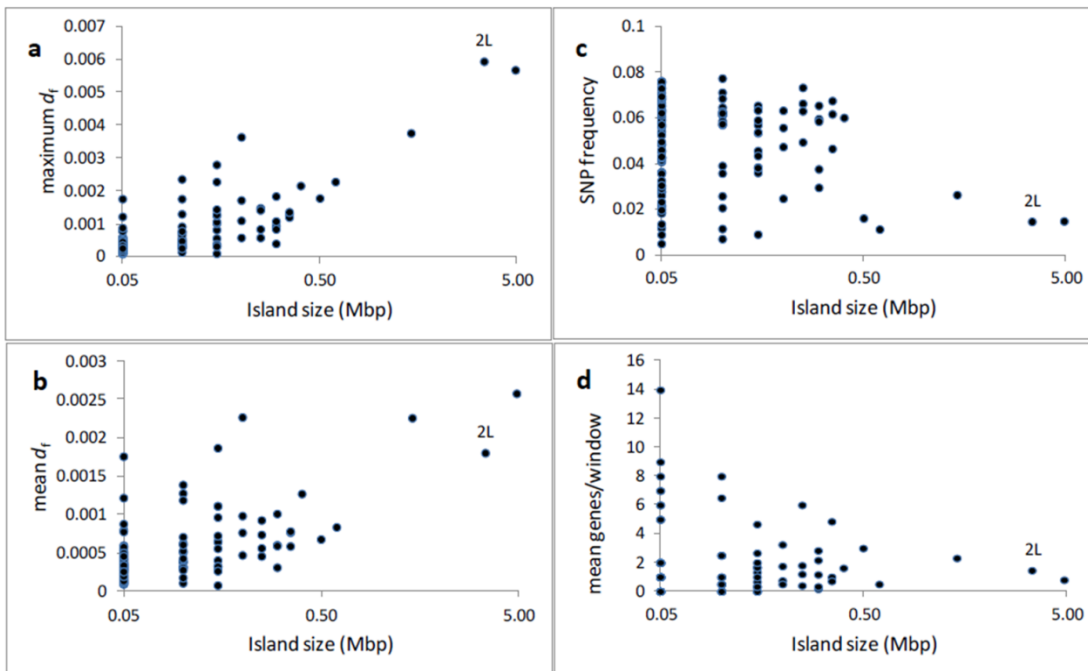
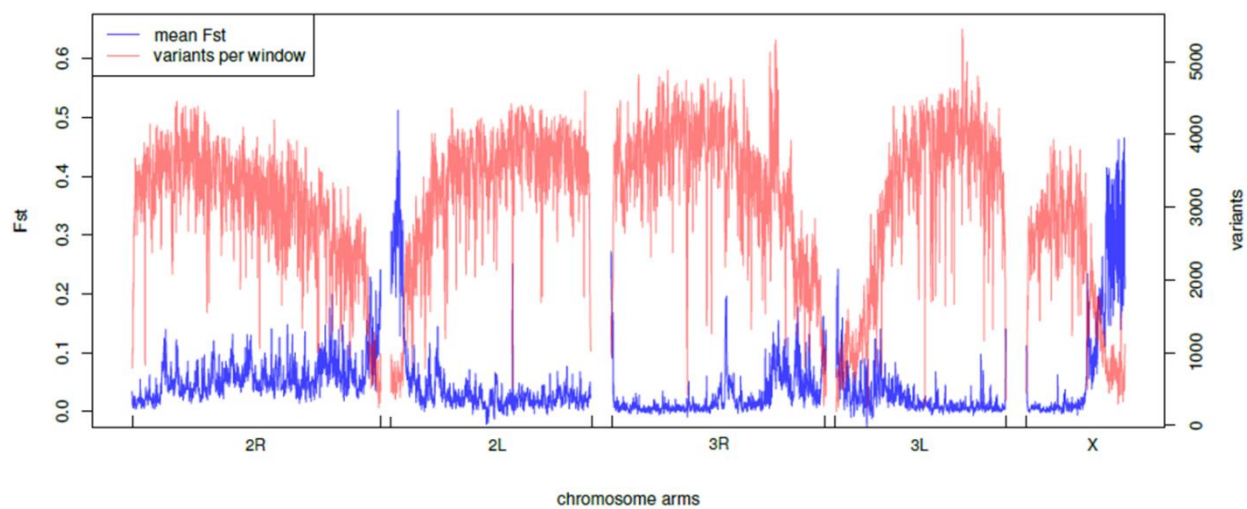


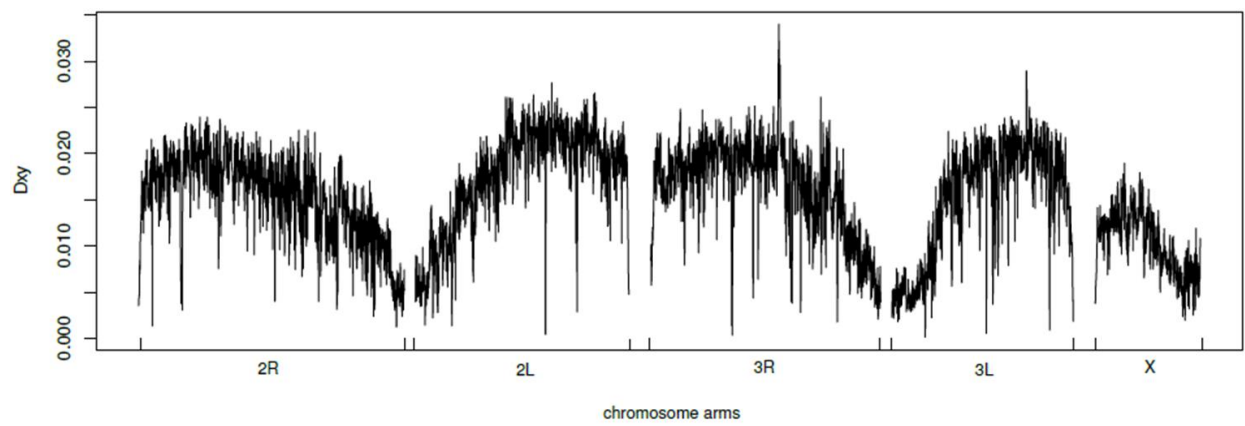
Supplementary figure 1 | Analysis of recombination beyond the 2L genomic island. Lines show proportionate M form ancestry for each individual in the *M-kdr* group based on ancestry informative markers (fully diagnostic of M and S) on the centromere proximate 5Mb of the 2R chromosome arm.



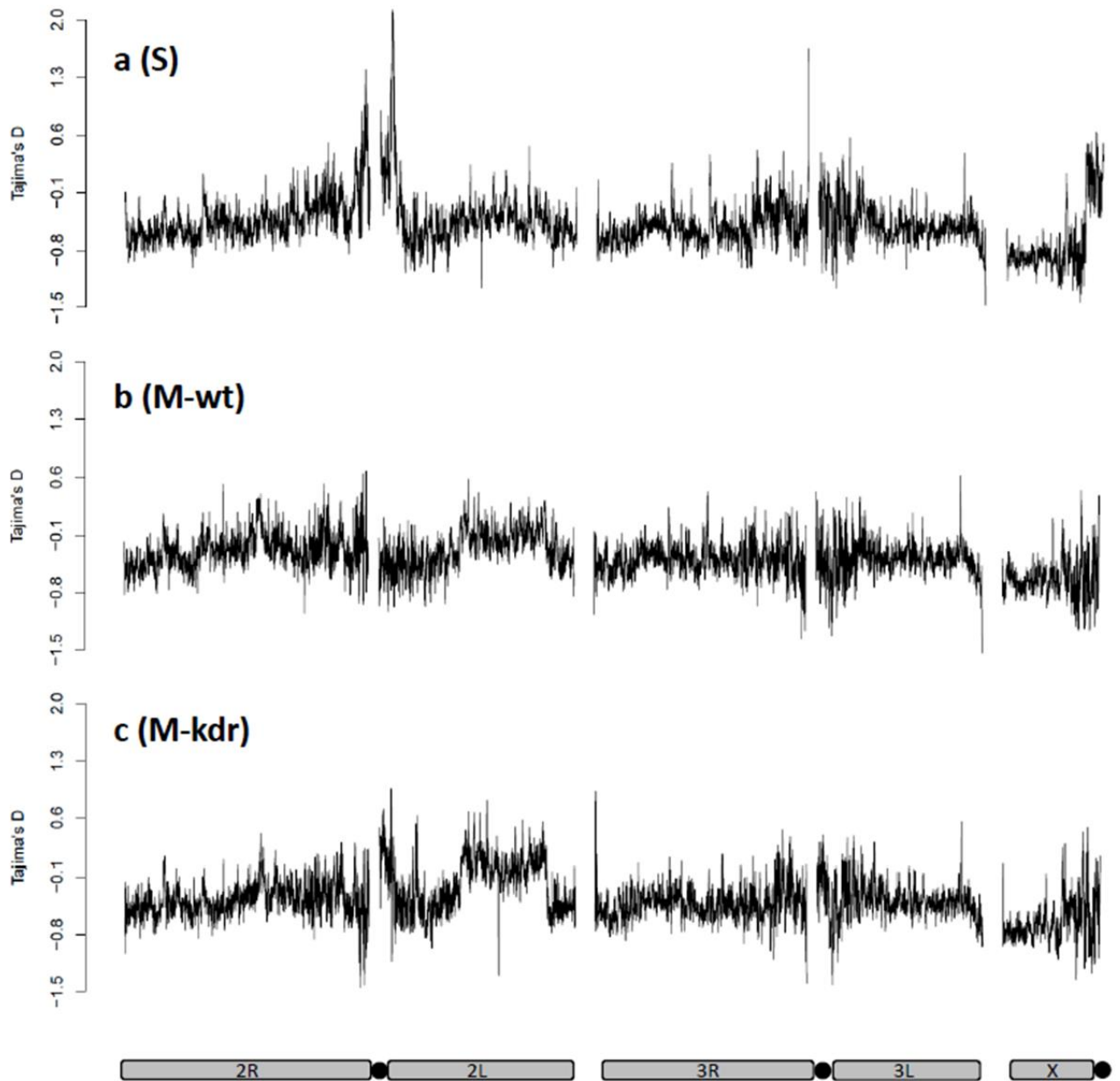
Supplementary figure 2 | Scatterplots showing the relationships between the size of divergent genomic islands and descriptive statistics for diversity and differentiation. Plots demonstrate the relationship between island size and **(a)** Maximum d_f , **(b)** Mean d_f , **(c)** SNP frequency within islands and **(d)** the mean number of genes per window. Points in each plot points are islands (total N=117). Owing to heterogeneity in island size a log scale is used in each plot; the major 2L genomic island is indicated.



Supplementary figure 3 | F_{ST} -based pairwise divergence between M-wt and S *A. gambiae* with number of variants per window. The plot describes mean F_{ST} (blue) and the number of variants (red) in 100 SNP stepping windows across the whole genome (all chromosome arms) for M-wt vs. S.



Supplementary figure 4 | Dxy-based pairwise divergence between M-wt and S *A. gambiae*. Dxy calculated between M-wt and S *A. gambiae* across the genome (all chromosome arms) in 50kb stepping windows.



Supplementary figure 5 | Whole genome Tajima's D for the three groupings of *A. gambiae*. Plots are based on Tajima's D calculated in 50kb stepping windows for (a) S form, (b) M-wt and (c) M-kdr. Chromosomes are shown by solid grey bars and centromere positions by black circles.

Supplementary Table 1 Statistics associated with kernel plots of chromosomal differentiation					
	2L	2R	3L	3R	X
Mean F_{ST}	0.0294	0.0545	0.0171	0.0225	0.0453
F_{ST} 95% CI \pm	0.0006	0.0004	0.0004	0.0004	0.0018
Sample Skewness (G1)	4.362	1.367	2.440	2.495	2.870
Standard Error Skewness (SES)	0.014	0.013	0.015	0.013	0.024
Skew Zg1 (test stat) = G1/SES	316.9	106.5	158.3	192.3	118.6
Skew inference $\alpha=0.05$	positive	positive	positive	positive	positive
Level of skewness inference	high	high	high	high	high
Sample Excess Kurtosis (G2)	32.7	3.4	11.5	9.7	8.8
Standard Error Kurtosis (SEK)	0.028	0.026	0.031	0.026	0.048
Kurtosis Zg2 (test stat) = G2/SEK	1186.5	132.0	374.0	372.6	181.6
Excess Kurtosis Inference $\alpha=0.05$	positive	positive	positive	positive	positive
Direction	leptokurtic	leptokurtic	leptokurtic	leptokurtic	leptokurtic

Supplementary Table 2 Relationships between island descriptive statistics					
	size	d_f _mean	d_f _max	SNPs/window	genes/window
size		<<0.001	<<0.001	0.823	0.648
d_f _mean	0.564		<<0.001	0.001	0.833
d_f _max	0.656	0.983		0.004	0.674
SNPs/window	-0.021	0.300	0.266		0.343
genes/window	0.043	-0.020	-0.039	-0.088	

Supplementary Table 3 DAVID annotation term clustering results												
Annotation Cluster 1	Enrichment Score: 2.67 (>1.3 regarded as significant)											
Category	Term	Count	%	P-Value	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0008061~chitin binding	5	7.04	6.34E-04	AGAP000986, AGAP000987, AGAP000988, AGAP000989, AGAP001006	29	78	5399	11.93413	0.04466	0.022585	0.658317
GOTERM_MF_FAT	GO:0030247~polysaccharide binding	5	7.04	7.32E-04	AGAP000986, AGAP000987, AGAP000988, AGAP000989, AGAP001006	29	81	5399	11.49212	0.051359	0.017421	0.759325
GOTERM_MF_FAT	GO:0001871~pattern binding	5	7.04	7.32E-04	AGAP000986, AGAP000987, AGAP000988, AGAP000989, AGAP001006	29	81	5399	11.49212	0.051359	0.017421	0.759325
INTERPRO	IPR002557:Chitin binding protein, peritrophin-A	5	7.04	8.10E-04	AGAP000986, AGAP000987, AGAP000988, AGAP000989, AGAP001006	52	78	9418	11.60996	0.091181	0.091181	0.922999
SMART	SM00494:ChtBD2	5	7.04	0.0010	AGAP000986, AGAP000987, AGAP000988, AGAP000989, AGAP001006	27	78	4403	10.45347	0.028976	0.028976	0.852445
GOTERM_BP_FAT	GO:0006030~chitin	5	7.04	0.0015	AGAP000986,	25	93	4335	9.322581	0.322225	0.322225	1.961577

	metabolic process				AGAP000987, AGAP000988, AGAP000989, AGAP001006							
GOTERM_BP_FAT	GO:0006022~aminoglycan metabolic process	5	7.04	0.0025	AGAP000986, AGAP000987, AGAP000988, AGAP000989, AGAP001006	25	107	4335	8.102804	0.479508	0.278549	3.271269
GOTERM_BP_FAT	GO:0005976~polysaccharide metabolic process	5	7.04	0.0035	AGAP000986, AGAP000987, AGAP000988, AGAP000989, AGAP001006	25	117	4335	7.410256	0.595188	0.260251	4.50176
GOTERM_CC_FAT	GO:0005576~extracellular region	5	7.04	0.2330	AGAP000986, AGAP000987, AGAP000988, AGAP000989, AGAP001006	24	227	2096	1.923642	0.999995	0.997763	91.85548
Annotation Cluster 2	Enrichment Score: 0.44											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0046872~metal ion binding	10	14.0 8	0.3232	AGAP000958, AGAP001015, AGAP000954, AGAP000952, AGAP000974, AGAP000971, AGAP000983, AGAP000996, AGAP000984,	29	1444	5399	1.289283	1	0.996379	98.28042

					AGAP000946							
GOTERM_MF_FAT	GO:0043167~ion binding	10	14.08	0.3765	AGAP000958, AGAP001015, AGAP000954, AGAP000952, AGAP000974, AGAP000971, AGAP000983, AGAP000996, AGAP000984, AGAP000946	29	1508	5399	1.234565	1	0.99655	99.26827
GOTERM_MF_FAT	GO:0043169~cation binding	10	14.08	0.3765	AGAP000958, AGAP001015, AGAP000954, AGAP000952, AGAP000974, AGAP000971, AGAP000983, AGAP000996, AGAP000984, AGAP000946	29	1508	5399	1.234565	1	0.99655	99.26827

Supplementary Table 4 Samples used for whole genome sequencing						
origin	location	date	latitude	longitude	form	<i>Vgsc L1014F</i>
Ghana	Dawhenya	summer 2007	5.556	-0.19631	M	FF
Ghana	Okyereko	summer 2010	5.417	-0.600	M	FF
Ghana	Okyereko	summer 2010	5.417	-0.600	M	FF
Ghana	Okyereko	summer 2010	5.417	-0.600	M	FF
Ghana	Okyereko	summer 2010	5.417	-0.600	M	FF
Ghana	Dawhenya	summer 2007	5.556	-0.19631	M	LL
Ghana	Dawhenya	summer 2007	5.556	-0.19631	M	LL
Ghana	Kwamekyer	summer 2007	5.575	-0.6461	M	LL
Ghana	Kwamekyer	summer 2007	5.575	-0.6461	M	LL
Ghana	Kwamekyer	summer 2007	5.575	-0.6461	M	LL
Ghana	Awomberew	summer 2007	5.565	-0.6527	S	FF
Ghana	Awomberew	summer 2007	5.565	-0.6527	S	FF
Ghana	Gomoa, Onyadzi	summer 2007	5.359	-0.7061	S	FF
Ghana	Odumasi	summer 2007	5.907	-0.0833	S	FF
Ghana	Odumasi	summer 2007	5.907	-0.0833	S	FF