Supporting Table S1: Population genetic parameter estimates for M and S form mosquitoes at the three *APL1* paralogs.

Collection	n[1]	bp[2]	π_{tot}[3]	θ_{tot}[4]	TajD[5]	π_{syn}[6]	π_{non}[7]
APL1A							
M form	20	1669	0.018	0.032	– 1.784	0.034	0.016
S form	28	1537	0.081	0.069	0.703	0.116	0.064
APL1B							
M form	26	2005	0.016	0.021	– 0.816	0.021	0.017
S form	33	1966	0.039	0.048	– 0.691	0.070	0.034
APL1C							
M form	20	2587	0.009	0.012	– 1.037	0.015	0.007
S form	33	2393	0.031	0.028	0.272	0.060	0.022

[1] number of alleles sequenced
[2] locus size, in base pairs, excluding insertions and deletions
[3] average number of differences per pair of alleles, per nucleotide
[4] Watterson's estimator of the population genetic parameter $4N_e\mu$
[5] Tajima's *D* test statistic
[6] average number of difference per pair of alleles, per nucleotide, synonymous sites only
[7] average number of difference per pair of alleles, per nucleotide, nonsynonymous sites only