

Supporting Figure S1: Alignment of amino acid haplotypes observed in the PANGGL regions of *APL1C* and *APL1A*² alleles. Period symbols (.) indicate identity with the residue indicated in the first row. Dashes (-) indicate deleted sequence. The repeated motif TNFGGQ is highlighted in red. The repeated motif PANGGL and related sequences are highlighted in blue. The numbers in the first four columns indicate the number of times each haplotype was observed in the Bancoumana dry, Bancoumana rainy, Toumani-Oulena and Makouchetoum collections, respectively. The 33 S form mosquitoes carry 19 distinct haplotypes in this protein region, while the 18 M form mosquitoes carry only 3 haplotypes. The fifth column indicates the molecular form each haplotype was found in. There were no haplotypes found in both molecular forms, and we found no *APL1A*² alleles in *A. arabiensis*, *A. quadriannulatus*, or *A. merus*.

APL1C

[illegible]

A. arabiensis
A. quadriannulatus
A. merus

APL1A²

[illegible]

B	B	T	M	f
C	C	M	K	o
d	r			r
r	a			m
y	i			
	n			
	y			