

Gene	VectorBase ID	CA/SC	Location
Plugin	AGAP009368*	3R (–)	31,812,524 – 31,814,708
AGAP009098	AGAP009098*	3R (–)	25,583,824 – 25,586,349
AGAP009099	AGAP009099*	3R (+)	25,588,861 – 25,591,488
AGAP009100	AGAP009100	3R (+)	25,596,779 – 25,599,732
AEDES 1	AAEL006978*	1.230	224,090 – 229,150
AEDES 2	AAEL006978*	1.230	180,069 – 184,614
CULEX 1	CPIJ003524	3.48	900,874 - 903,335
CULEX 2	CPIJ003523*	3.48	886,757 – 889,084

Supplementary Table 2. Genomic locations of Plugin and TGase gene predictions.

VectorBase IDs that refer to incomplete or otherwise incorrect gene predictions are indicated by an asterisk. The genomic positions of our corrected predictions are indicated by the chromosome arm (CA, orientation in parentheses) or the super contig (SC) number, as well as the specific location. Only Plugin and AGAP009099 were fully sequenced. The reported locations of other genes refer only to *ab initio* predictions. *Ab initio* predictions for mosquito TGase genes were determined using BLAST searches using known TGases from other species and scanning the resulting genomic regions with *ab initio* gene prediction software (Fgenesh, Genescan, and Augustus). Each consensus sequence was analyzed for conserved domains using PFAM 22.0 and SMART 5.1 to ensure it contained the three canonical TGase domains.