**Supplemental Fig 1.** **Differential gene expression in *Culex tarsalis.***

Heat map of 10 fold upregulated salivary gland transcripts when compared to carcasses in adult male and female *Culex tarsalis*. The Z score transformed data of RPKM for each library is shown. The left-sided dendogram shows two main branches, one associated with female and the other with male overexpressed salivary transcripts.

**A close up of a logo  Description generated with very high confidence**

**Supplemental Figure 2: Phylogram of the apyrase/5’-nucleotidase protein family in mosquitoes.** The numbers on the tree nodes represent the percent bootstrap support in 1,000 trials of the phylogeny reconstruction using the UPGMA method (Tamura et al., 2013). The bar at the bottom indicates amino acid divergence. The *Culex tarsalis* sequences are marked with a red symbol. The apyrase gene from *Aedes aegypti* is marked with a blue symbol. The 5’-ncucleotidase protein of the same mosquito is marked with a green symbol. The sequences are named in six letters followed by an alpha-numeric format where the 3 first letters represent the 3 first letters of the genus, followed by the first 3 letters of the species binomial name. The following alphanumeric string represents the NCBI accession code. For more details, see text.



**Supplemental Figure 3: Phylogram of the 16.7 kDa/WRP family of mosquitoes.** The numbers on the tree nodes represent the percent bootstrap support in 1,000 trials of the phylogeny reconstruction using the UPGMA method (Tamura et al., 2013). The bar at the bottom indicates amino acid divergence. The *Culex tarsalis* sequences are marked with a red symbol. *C. quinquefasciatus* and *C. pipiens* sequences are marked with a green symbol. The *Corethrella appendiculata* sequences are marked with a blue symbol. The sequences are named in six letters followed by an alpha-numeric format where the 3 first letters represent the 3 first letters of the genus, followed by the first 3 letters of the species binomial name. The following alphanumeric string represents the NCBI accession code. For more details, see text.



**Supplemental Figure 4: Phylogram of the 34/62 kDa family of mosquitoes.** The numbers on the tree nodes represent the percent bootstrap support in 1,000 trials of the phylogeny reconstruction using the UPGMA method (Tamura et al., 2013). The bar at the bottom indicates amino acid divergence. The *Culex tarsalis* sequences are marked with a red symbol. The sequences are named in six letters followed by an alpha-numeric format where the 3 first letters represent the 3 first letters of the genus, followed by the first 3 letters of the species binomial name. The following alphanumeric string represents the NCBI accession code. For more details, see text.



Tamura, K., Stecher, G., Peterson, D., Filipski, A., Kumar, S., 2013. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular biology and evolution 30, 2725-2729.