



**Supplemental Figure S1. Size Distribution of *Anopheles albimanus* Assembled Contigs Using RNA-Seq.** The x-axis represents 100 bp bins of contig sizes while the y-axis is the number of contigs. Our multiple k-mer de novo transcriptome assembly produced 15,764 contigs. The average and median contig lengths were 988 bp and 634 bp, respectively, with the largest contig being 7,435 bp. The total length of all contigs was ~15.6 Mb, which is approximately 80% the length of the *Anopheles gambiae* transcriptome (~19.3 Mb).