

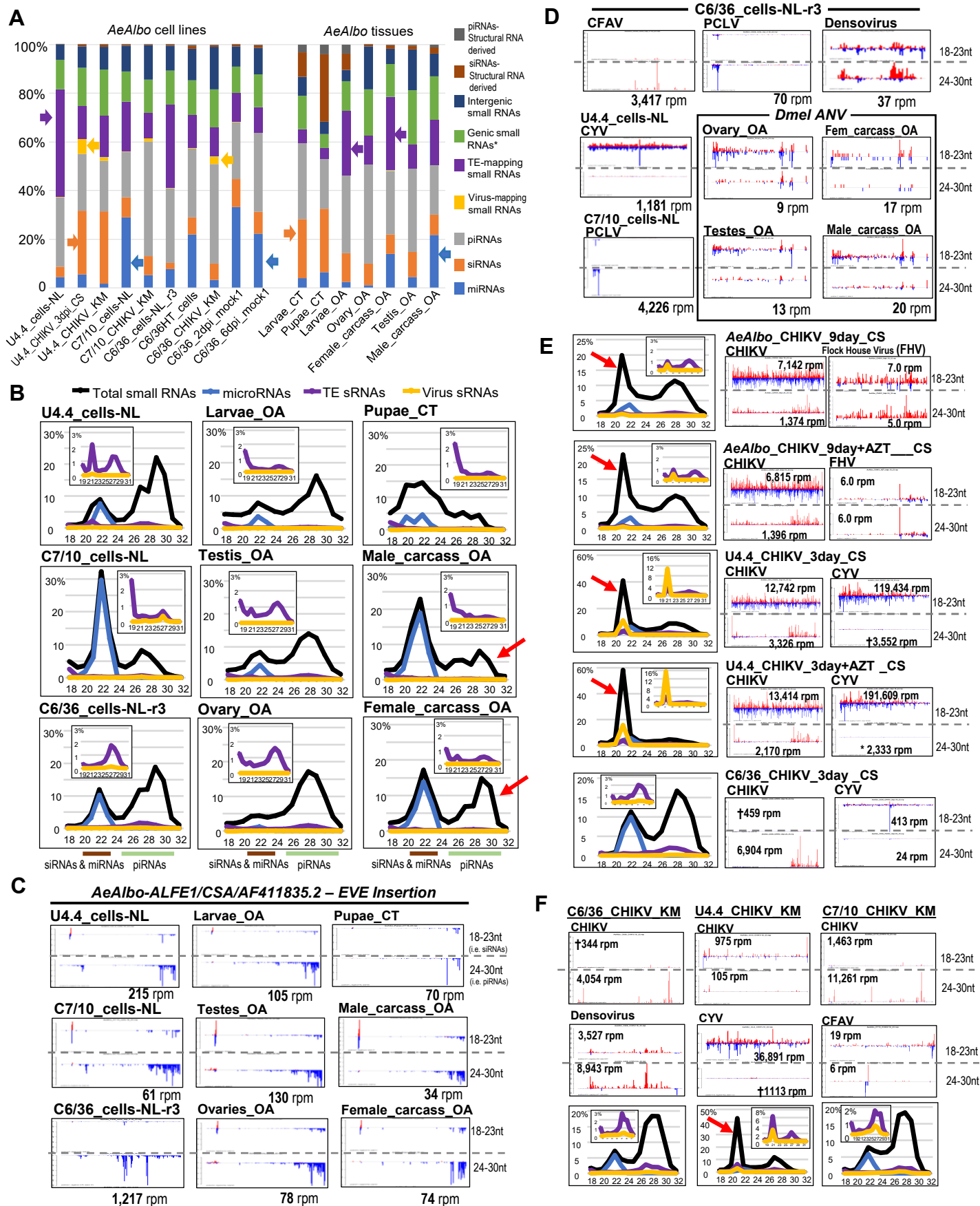


Figure S5. *Aedes albopictus* (*AeAlbo*) small RNA profiles full analysis gallery.

(A) Functional compositions of small RNAs in *AeAlbo* cells and tissues. Arrows point to notable portions of miRNAs, TE-mapping small RNAs, and viral small RNAs. (B) Small RNA size distributions from *AeAlbo* cells and tissues, with brackets highlighting siRNAs and miRNAs between 19-23nt, while piRNAs are between 24-30nt. The inset charts magnify the distribution of TE and virus sRNAs under a different Y-axis range. (C) Gallery of small RNAs from an Endogenous Viral Element in the *AeAlbo* genome, with homolog to capsid and NS5 proteins of flaviviruses like CFAV. Reads per million (rpm) numbers are totals of the siRNA-length and piRNA-length small RNAs that come from the plus strand in red and minus strand in blue. (D) Inherent viral small RNAs within the libraries sequenced in this study. (E) Small RNA size distributions and profiles and counts of *AeAlbo* mosquitoes and cells infected with CHIKV from the Carla Saleh lab (*_CS); (F) and for comparison *AeAlbo* cells infected with CHIKV from the Kevin Myles lab (*_KM). A top persisting arbovirus generating the most viral small RNAs is shown next to CHIKV, whereas red arrows point to the massive proportion of siRNAs in *AeAlbo* mosquitoes and U4.4 cells from the Saleh and Myles labs. † marks small RNA reads that appear to be squashed by the Y-axis of the other plot in that diagram.

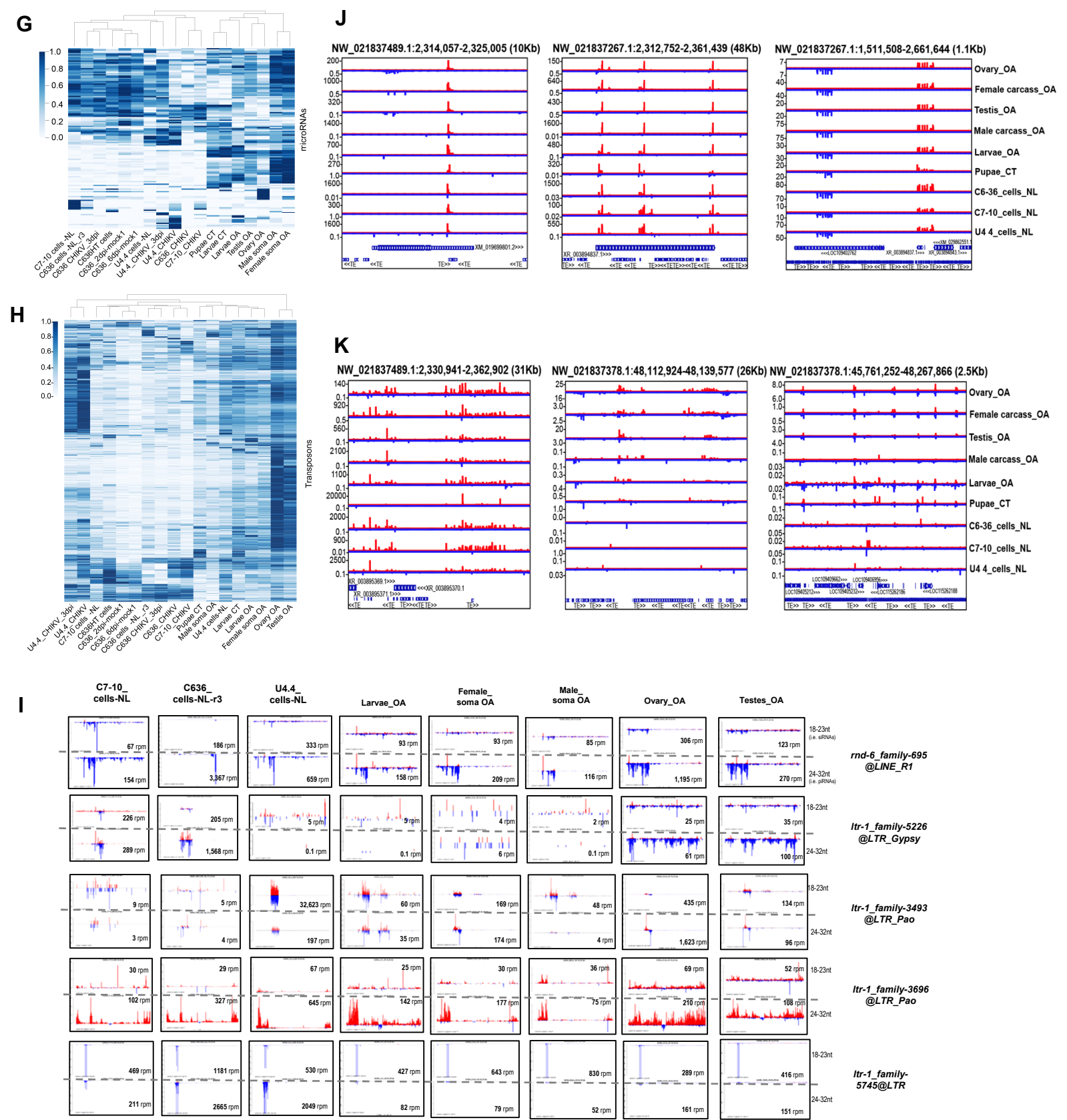


Figure S5. *Aedes albopictus* (*AeAlbo*) small RNA profiles full analysis gallery. Hierarchical clustering of (G) miRNAs and (H) transposon-mapping small RNA patterns for the cell lines versus the mosquito tissues. (I) Profiles of the *AeAlbo* transposons with most abundant small RNAs both in cell cultures and *AeAlbo* tissues. (J) Genome browser views of notable genic piRNA Cluster Loci (piRCL) in *AeAlbo*. (K) Genome browser views of notable intergenic piRCLs in *AeAlbo*.