

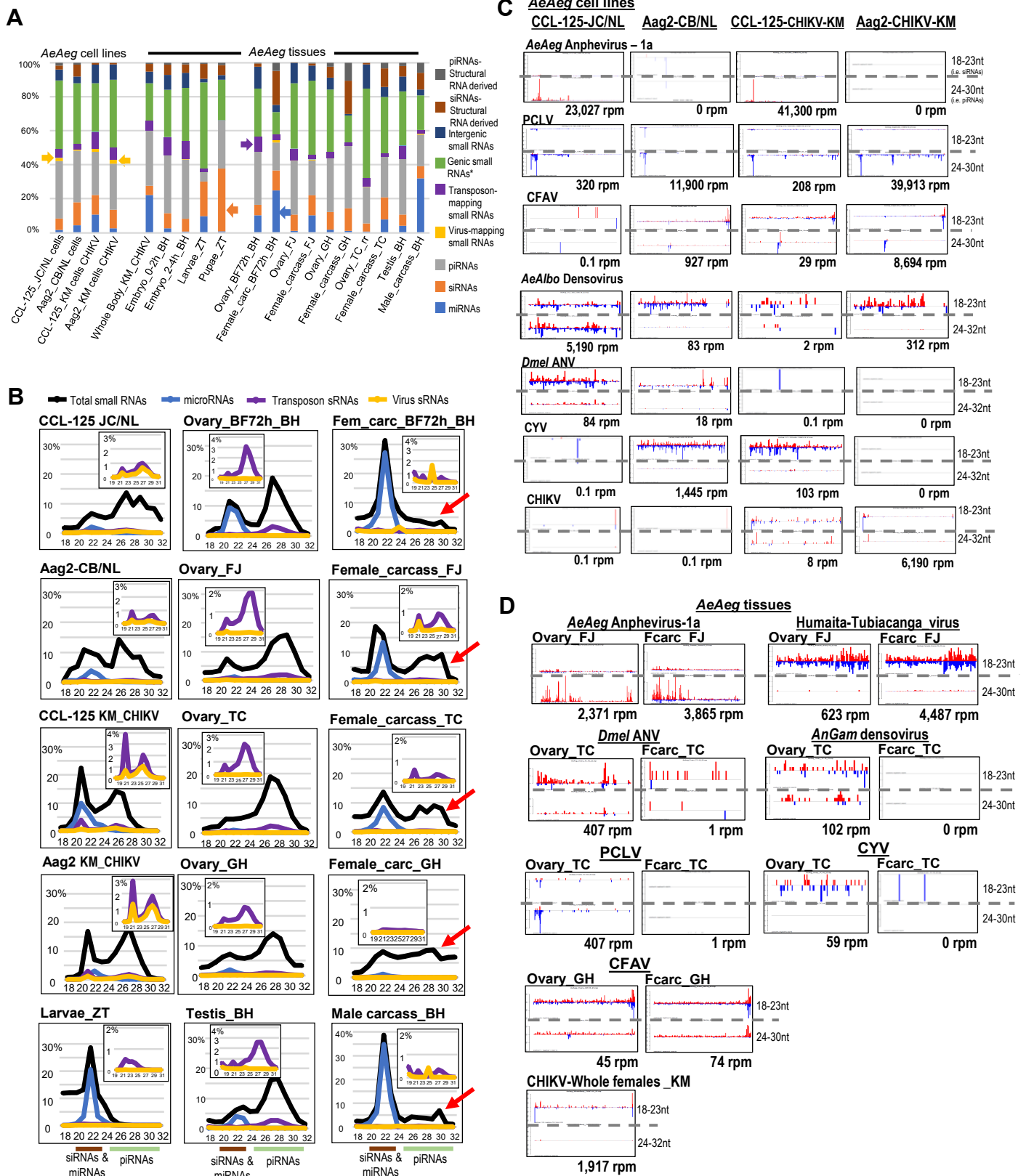


Figure S4. *Aedes aegypti* (AeAeg) small RNA profiles full analysis gallery.

(A) Proportions of small RNA functional annotations. Arrows point to notable portions of miRNAs, transposon-mapping small RNAs, and viral small RNAs. (B) Length distributions of small RNAs as a percentage of the library. Inset graphs zoom in on the proportions of transposon and virus sRNAs. Red arrows highlight data points of significant somatic piRNAs. (C) Mapping patterns and counts of notable viruses generating small RNAs in mosquito cells. (D) Persistent viral piRNAs in certain AeAeg strains that also exhibit greater amounts of somatic piRNAs, whereas the AeAeg strain from the Akbari et al (BH) study lacks inherent viral piRNAs and low amounts of somatic piRNAs. (E) Profiles and counts of mainly antisense piRNAs from the Endogenous Virus Element (EVE) AEFE1 / AY347953.2 that has homology to the NS5 gene of flaviviruses like CFAV.

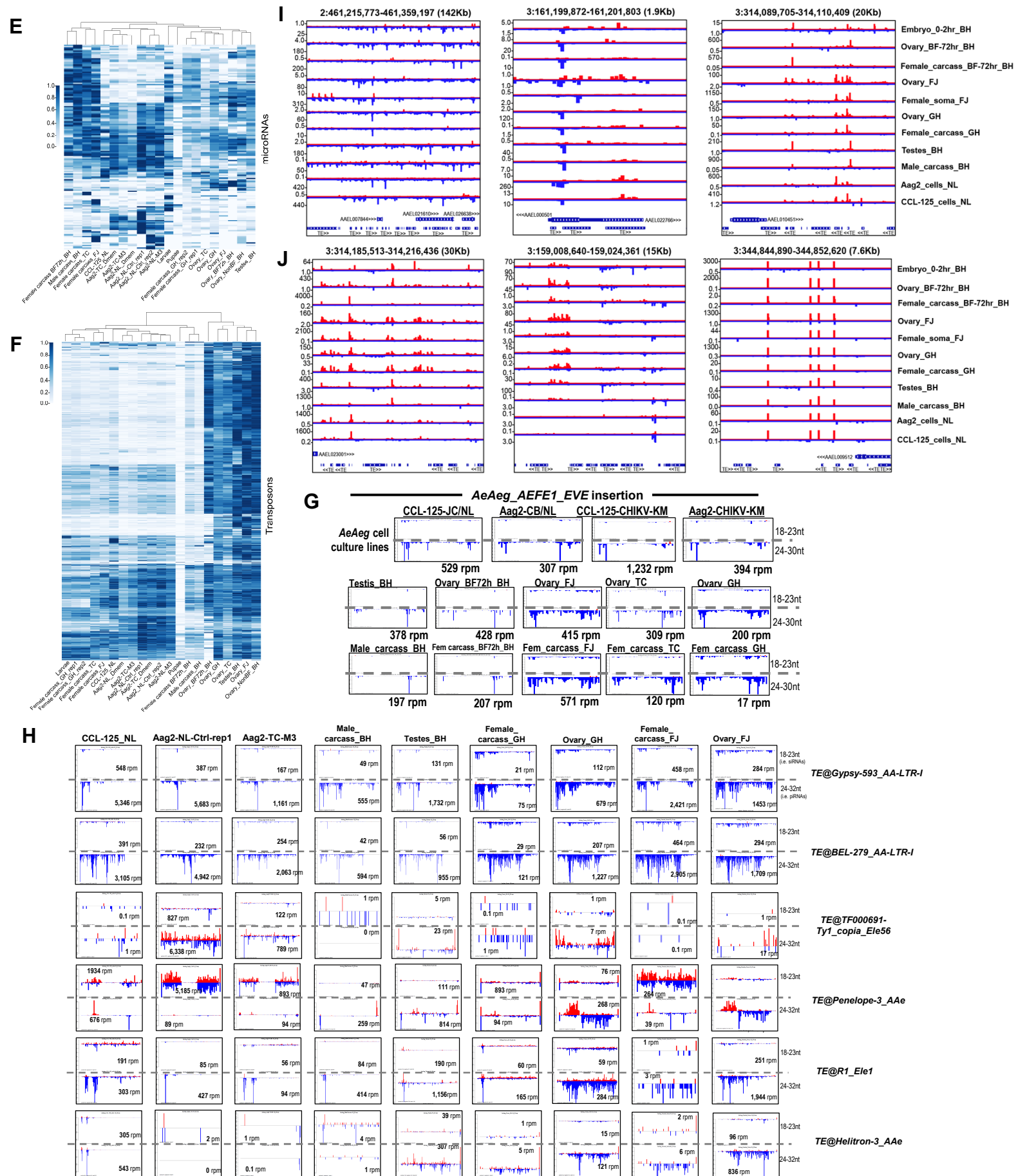


Figure S4. *Aedes aegypti* (AeAeg) small RNA profiles full analysis gallery.

Hierarchical clustering of (E) miRNAs and (F) transposon-mapping small RNA patterns for the cell lines versus the mosquito tissues. (G) Profiles of small RNAs mapping to the prominent EVE insertion AEFE1 in mosquito cell cultures and tissues. (H) Profiles of the other *AeAeg* transposons with most abundant small RNAs both in cell cultures and *AeAeg* tissues. (I) Genome browser views of notable genic piRNA Cluster Loci (piRCL) in *AeAeg*. (J) Genome browser views of notable intergenic piRCLs in *AeAeg*.