

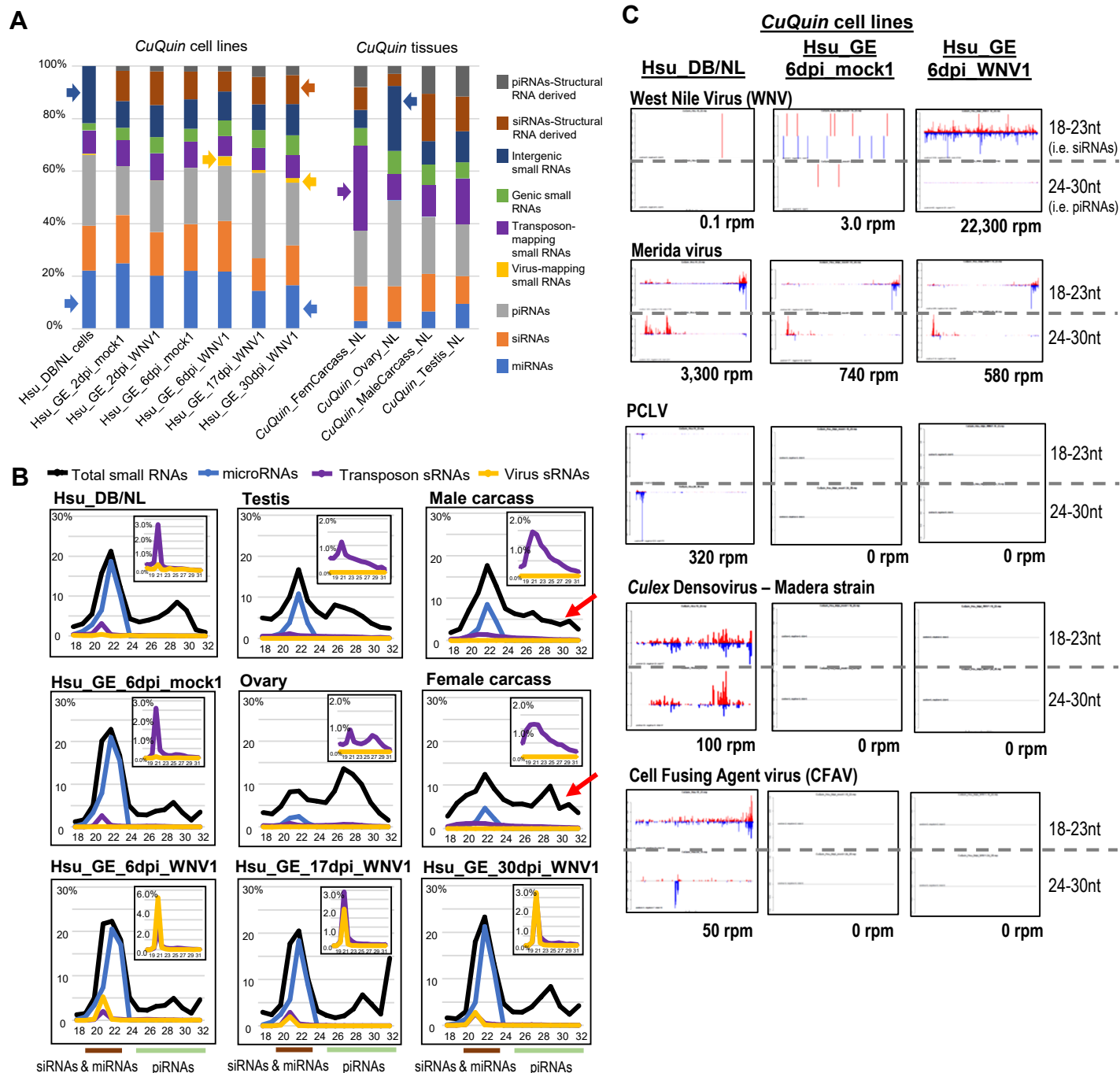


Figure S3. *Culex quinquefasciatus* (*CuQuin*) small RNA profiles full analysis gallery.

(A) Functional compositions of small RNAs in *CuQuin* cells and tissues. Colored arrows point to notable portions of miRNAs, transposon-mapping small RNAs, and viral small RNAs. (B) Small RNA size distributions from *CuQuin* cells and tissues, with colored lines marking the siRNAs and miRNAs ranging between 19-23nt, while piRNAs are between 24-30nt. The inset charts magnify the distribution of transposon and virus sRNAs under a different Y-axis range, and the red arrow points to low levels of somatic piRNAs. (C) Profiles of virus small RNAs in *CuQuin* cell culture lines. 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.

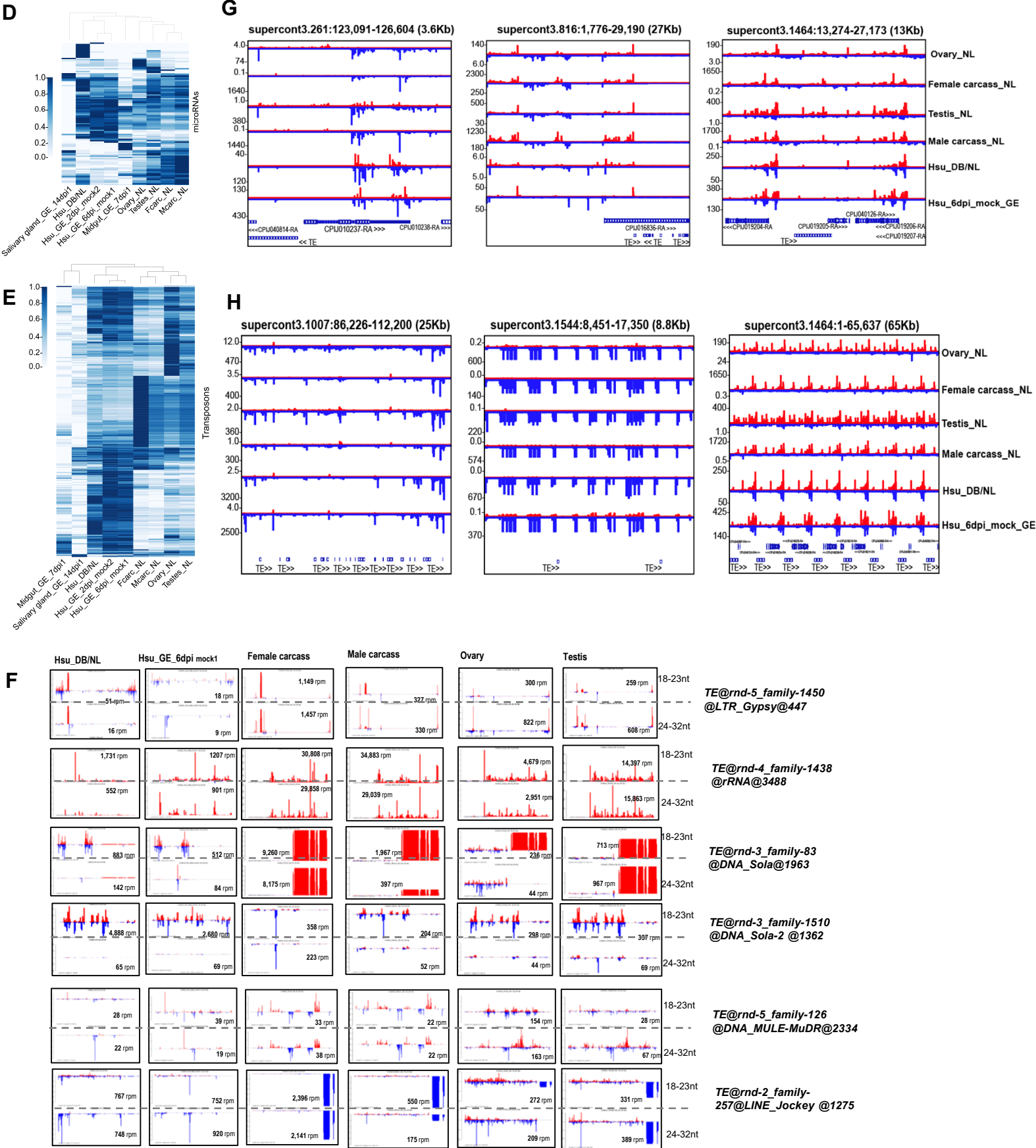


Figure S3. *Culex quinquefasciatus* (*CuQuin*) small RNA profiles full analysis gallery.
Hierarchical clustering of (D) miRNAs and (E) transposon-mapping small RNA patterns for the cell lines versus the mosquito tissues. (F) Profiles of the *CuQuin* transposons with most abundant small RNAs both in cell cultures and *CuQuin* tissues. (G) Genome browser views of notable genic piRNA Cluster Loci (piRCL) in *CuQuin*. (H) Genome browser views of notable intergenic piRCLs in *CuQuin*.