

Figure S1: Relative abundance of viral species according to the season, sites, and genus of collected mosquitoes.

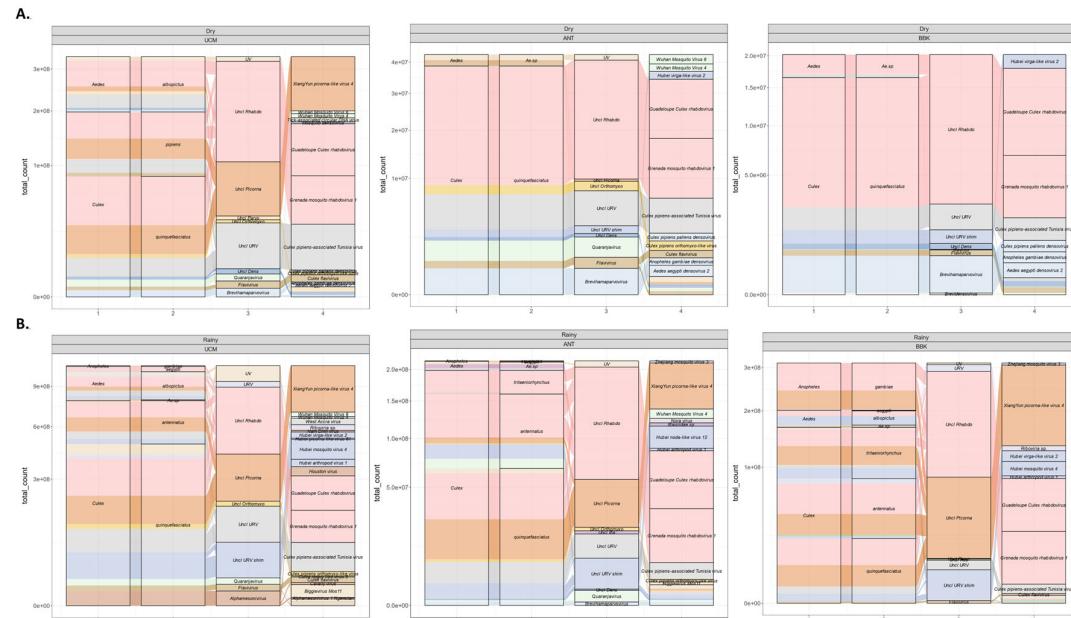


Figure S2: Alluvial plot showing the 62 viral species with >90% amino-acid identity to their known reference sequences, for all collection sites (UCM, ANT, and BBK) and the two seasons (A) dry and (B) rainy.

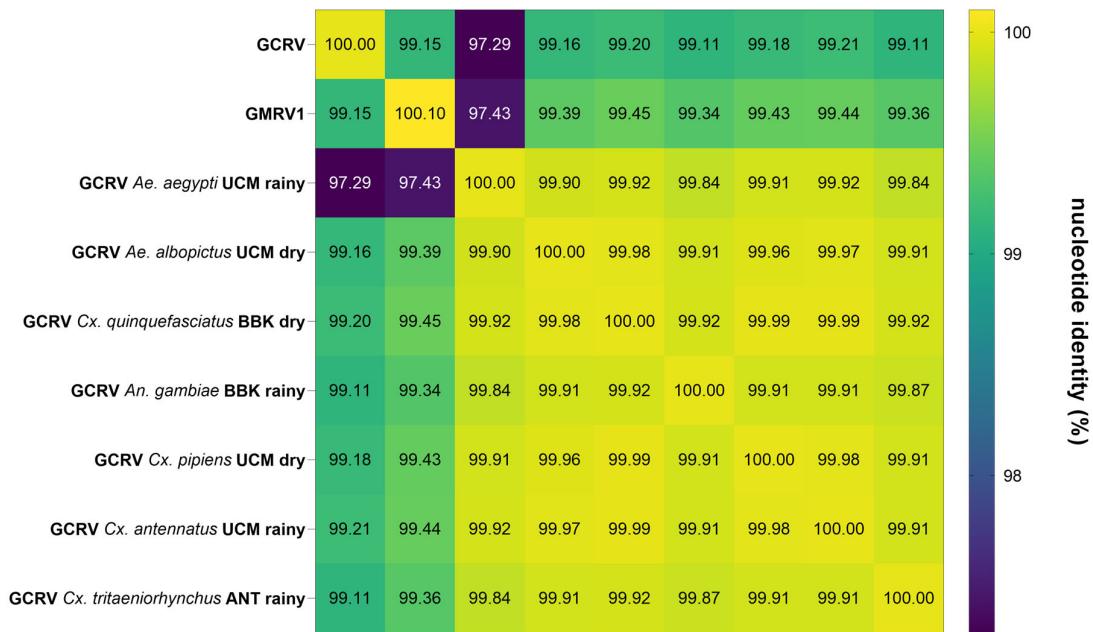


Figure S3: Pairwise nucleotide identity percentage across *Guadeloupe Culex rhabdovirus* from different seasons, sites, and mosquito host species of Madagascar.

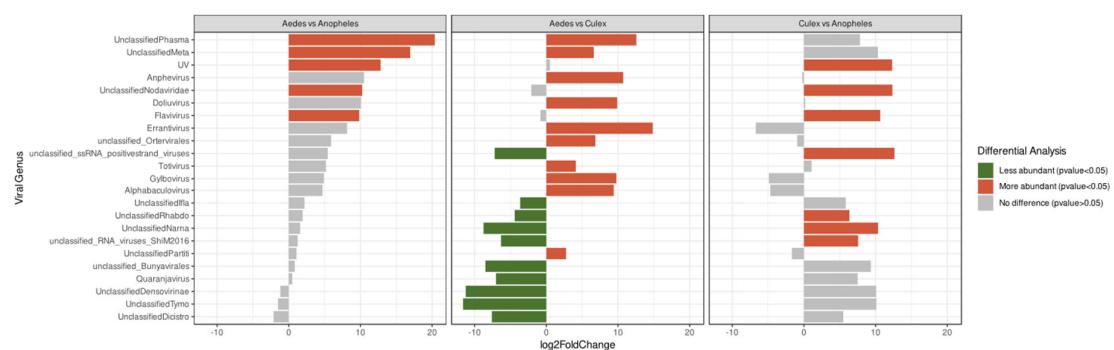


Figure S4: Log2 fold change for the comparisons of *Culex*, *Aedes*, and *Anopheles* in the differential analysis conducted. The color corresponds to significant viral genera.

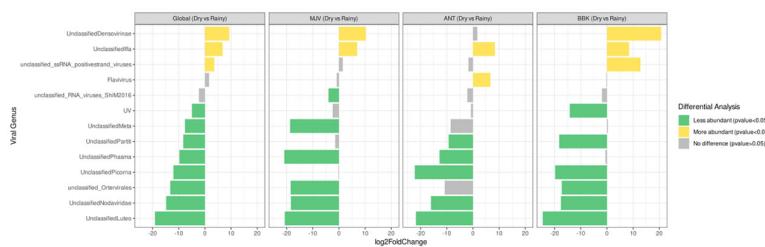


Figure S5: Log2 fold change for the comparisons of dry/rainy seasons in the differential analysis conducted on *Culex quinquefasciatus* mosquitoes. Each panel represents a different site studied. The color corresponds to significant viral genera.