

Figure S1

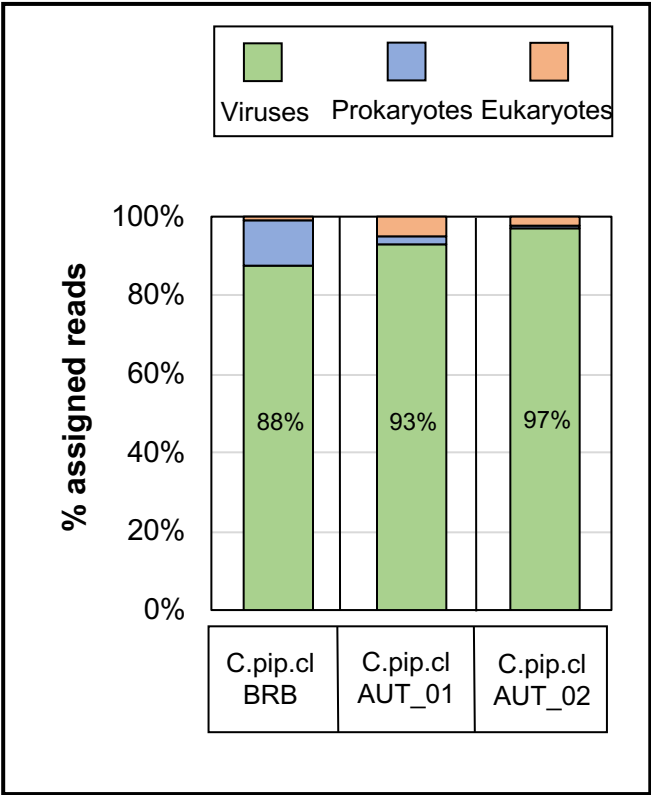


Figure S1 Fraction of reads mapping on contigs classified as viruses, prokaryotes and eukaryotes.

Figure S2

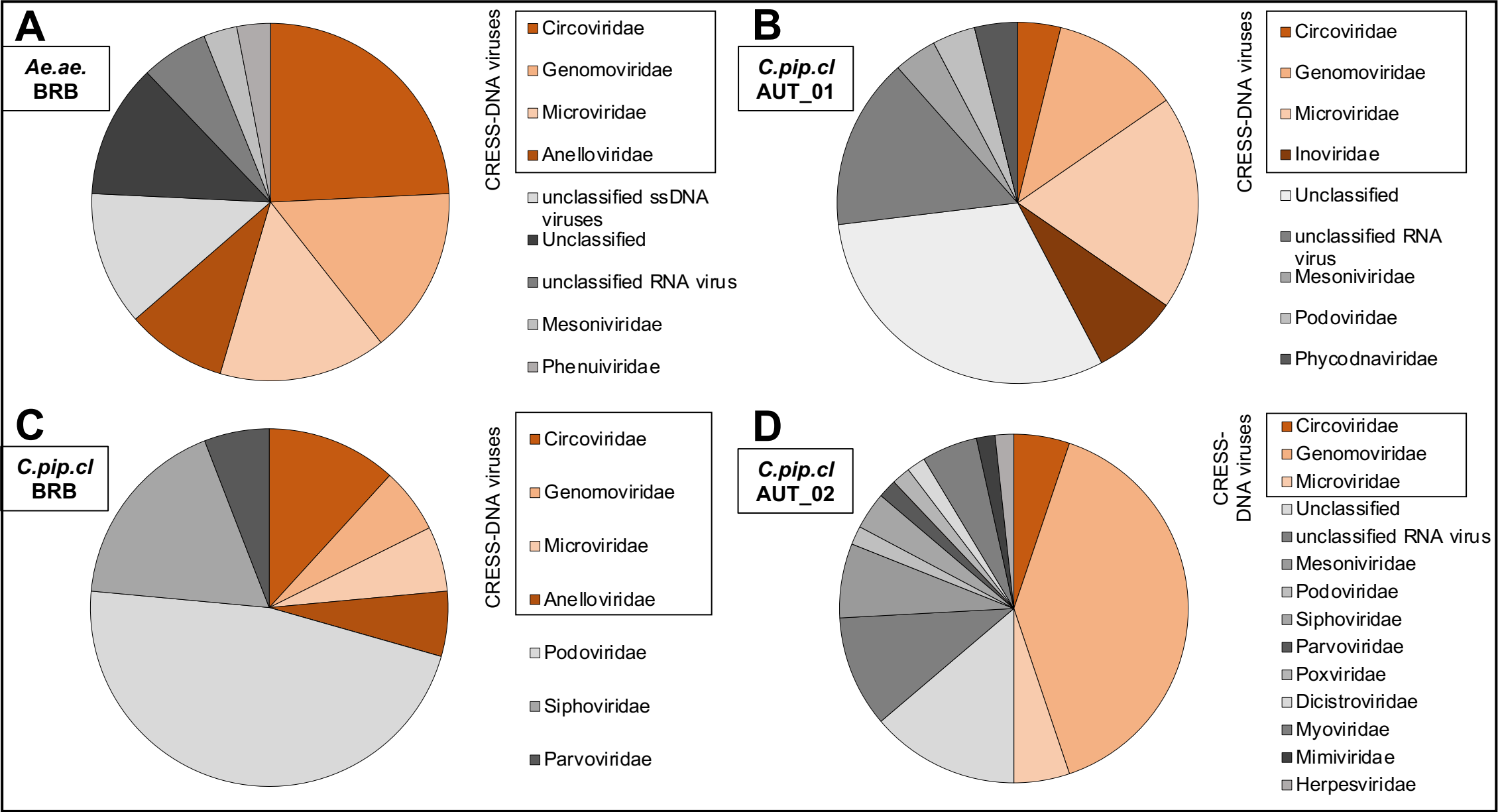


Figure S2 Virome composition on taxonomic family level as number of hits to indicated clade; families of the group of circular rep encoding single stranded (CRESS)- DNA viruses are marked in shades of red;

Figure S3

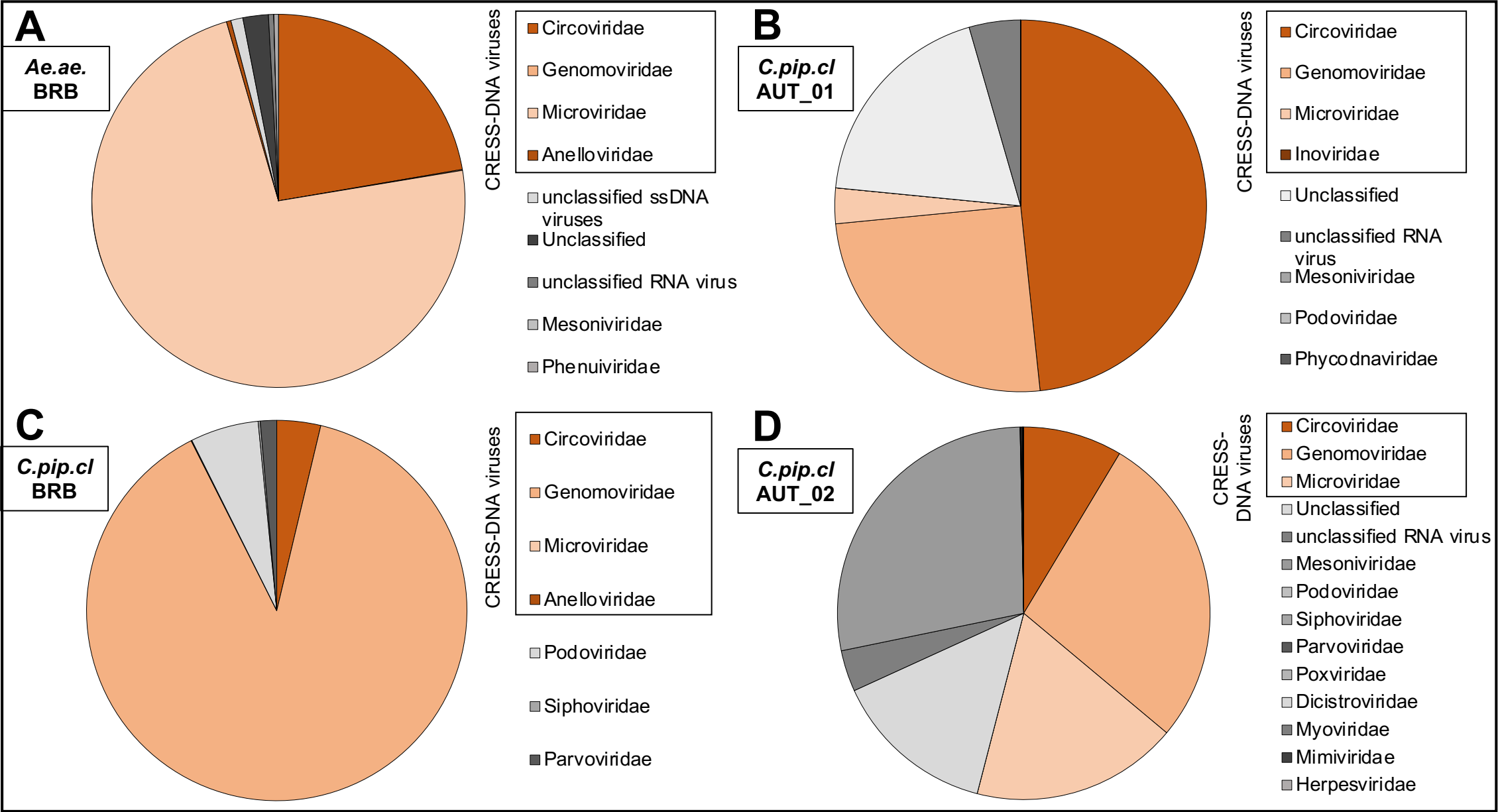


Figure S3 Relative abundance of viral hits on taxonomic family level in RPKM; families of the group of circular rep encoding single stranded (CRESS)- DNA viruses are marked in shades of red;

Figure S4

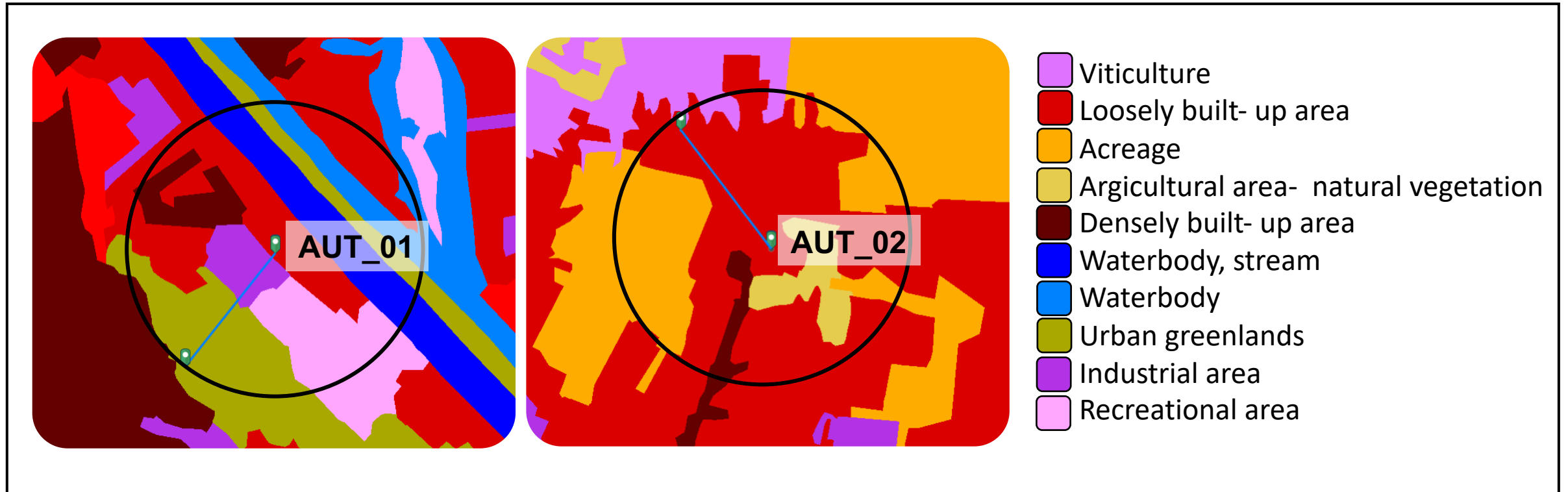


Figure S4 Land coverage of Austrian collection spots AUT_1 and AUT_2; circle represents area covered by mean flight distance of 1.3 km from point of collection of *C.pipiens* complex mosquitoes (approx 1.33 km)

Figure S5

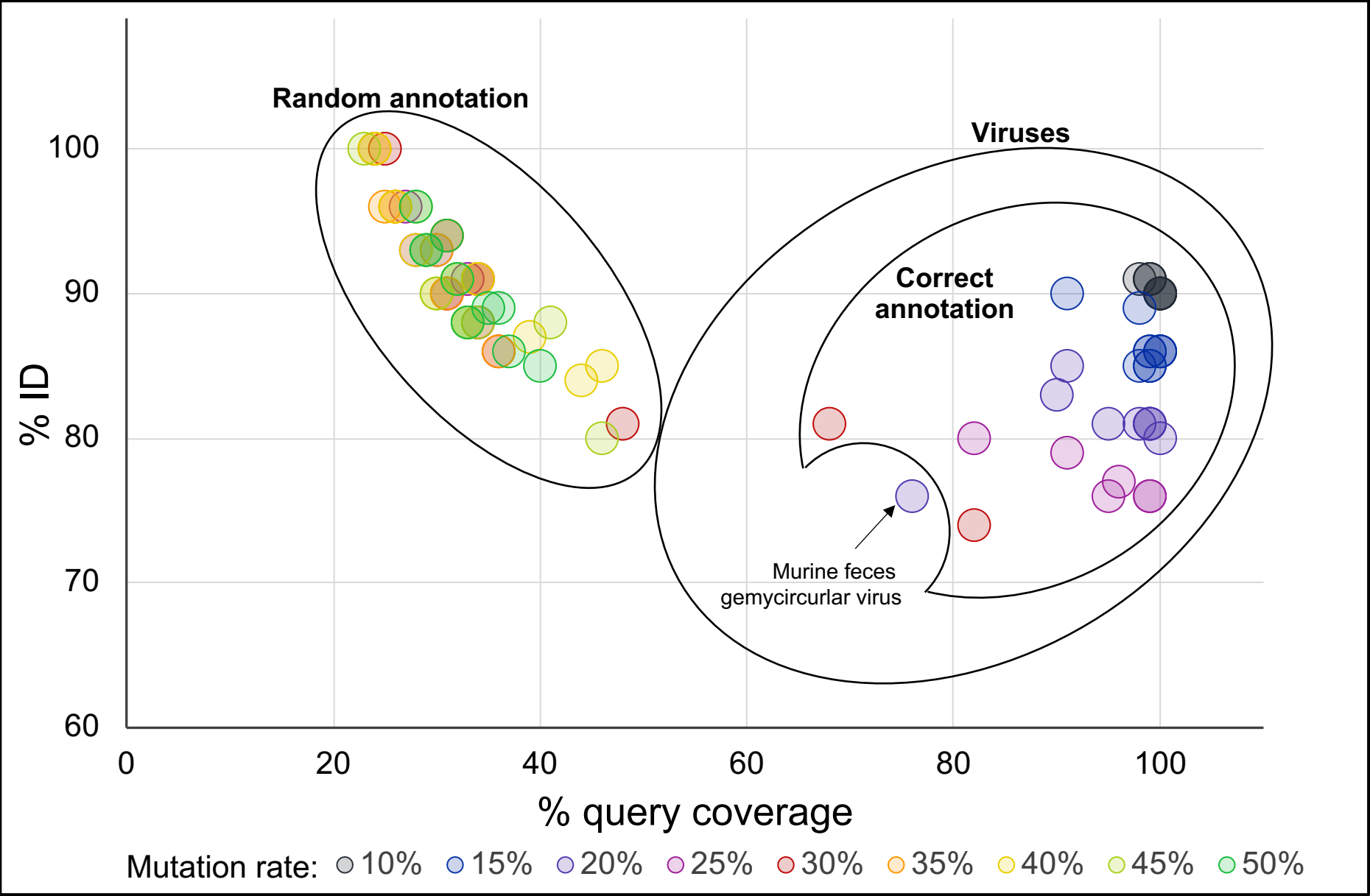


Figure S5 Goodness of alignment- fit of best BLAST N hits for for mutated model sequences

Figure S6

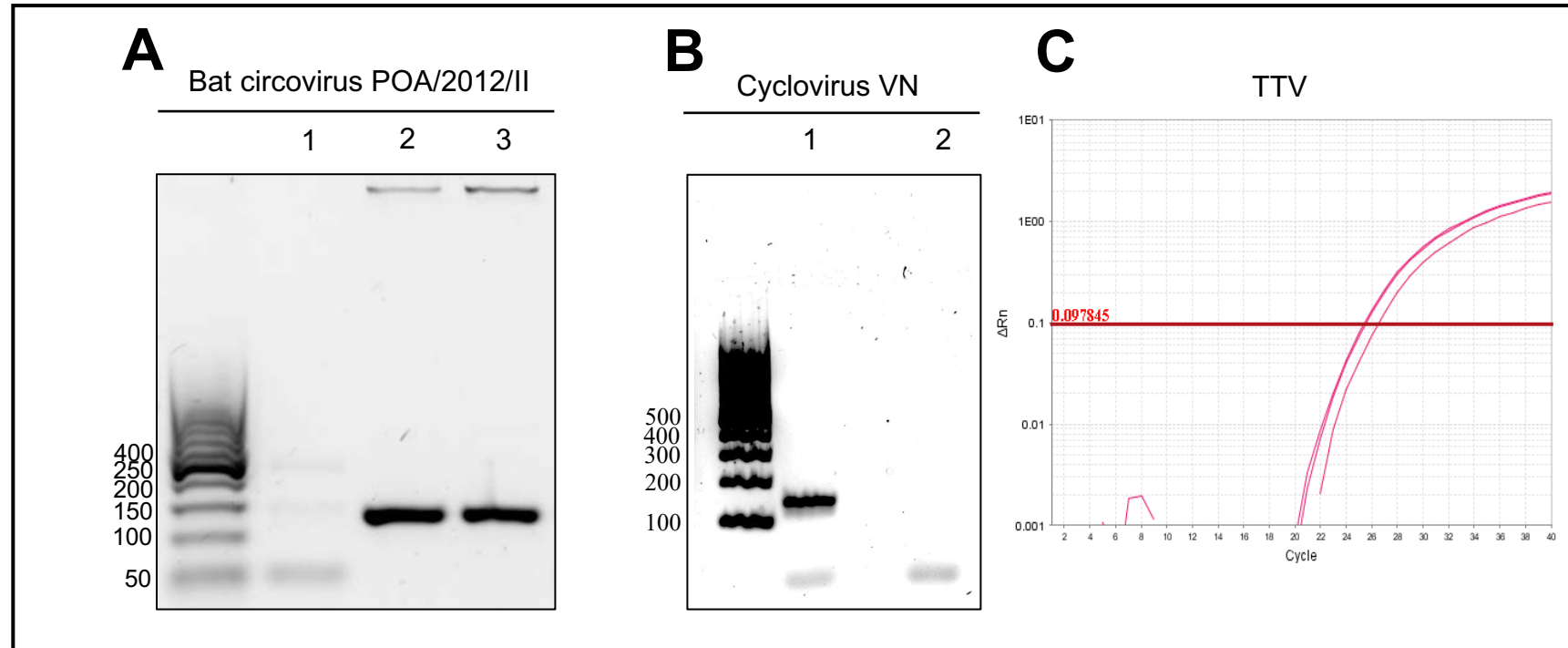


Figure S6 Verification of metagenomic hits by **(A)** specific PCR assay designed to target a 132bp sequence (pos 965-1096) of Bat circovirus POA/2012/II (NC_025791); lane 1: negative control; lane 2: *Ae.ae.* BRB; lane 3: *C.pip.cl.* BRB; **(B)** specific PCR assay designed to target a 160bp sequence (pos 574-714) of Cyclovirus VN isolate hcf1 (NC_021707); lane 1: *Ae.ae.* BRB; lane 2: negative control; **(C)** specific taqMan rtPCR assay designed to target a conserved 63 bp sequence among human infecting TTV genome sequences

Figure S7

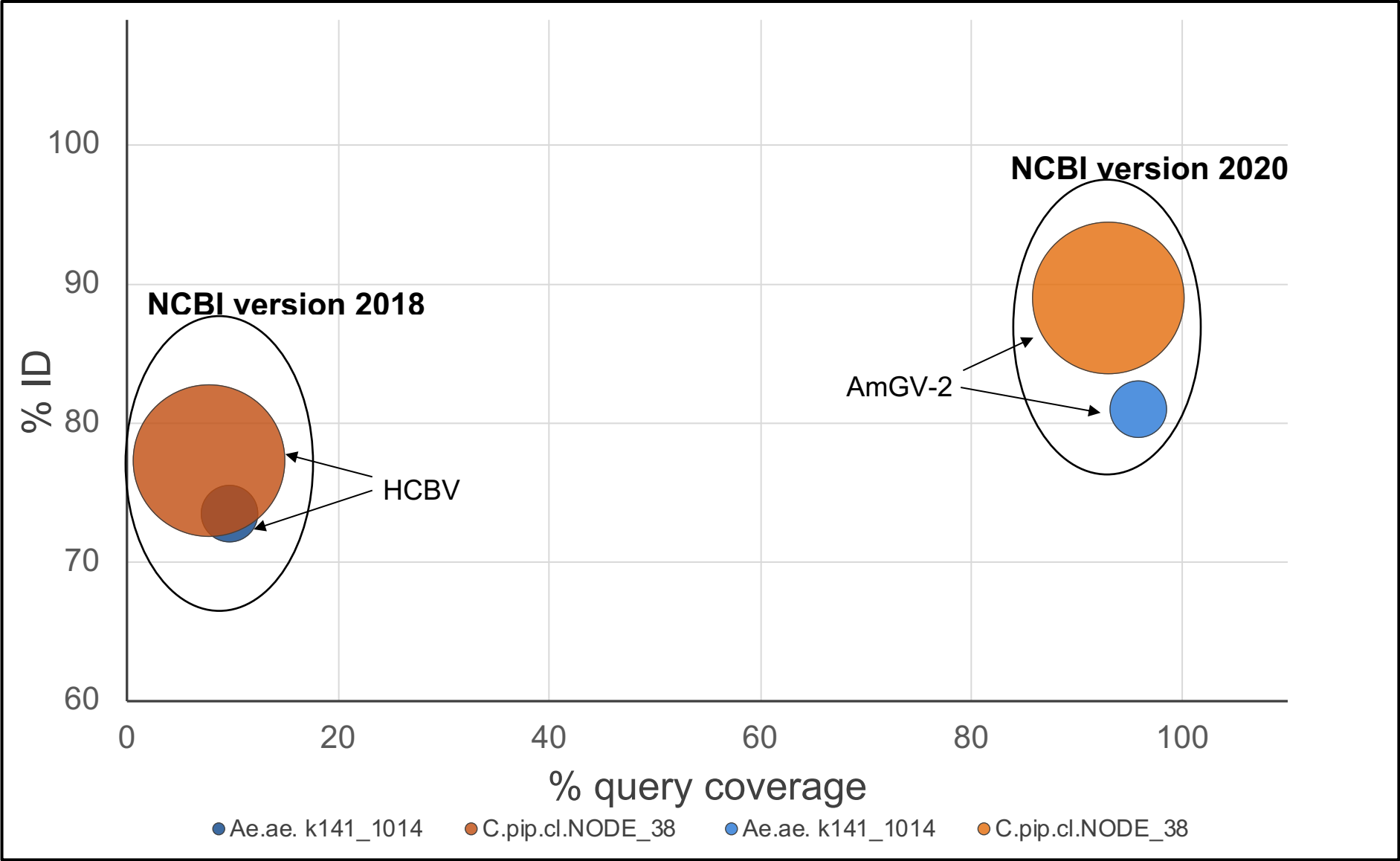


Figure S7 Goodness of assignment- fit for best BLAST N hit of contig sequence k141_1014 from *Aedes aegypti* (*Ae.ae.*) metagenome and contig sequence NODE_38 from *Culex pipiens* complex (*C.pip.cl.*) Barbados (BRB) using NCBI database version 2018 and updated database version 2020;

Figure S8

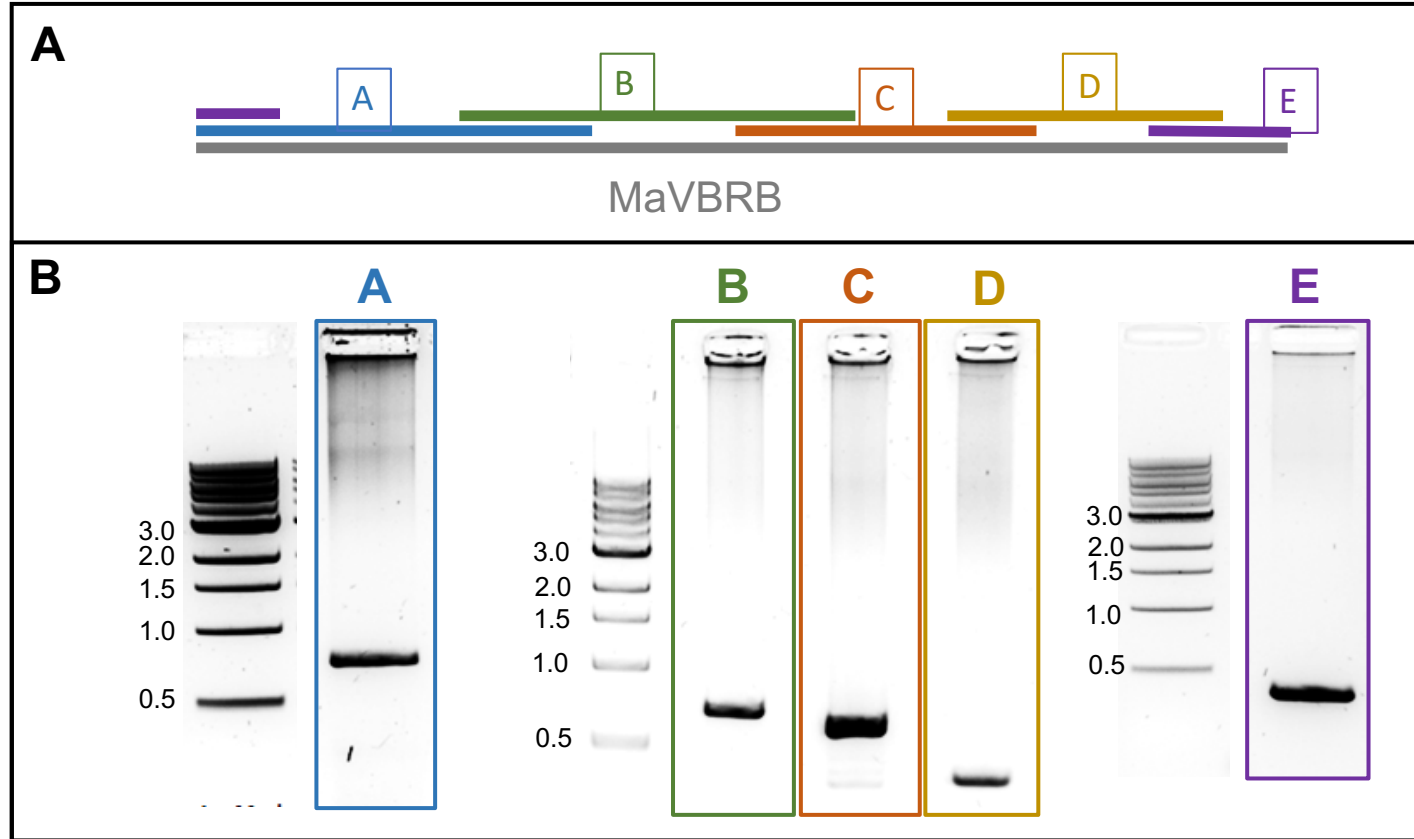


Figure S8 Verification of metagenomic assembled *mosquito associated virus Barbados* (MaVBRB) genome sequences by abutting primer PCR reactions; **(A)** position of PCRs on genomic virus sequence and **(B)** gel separation of PCR products