

reads mapped against contigs				NCBI blastn of contigs				
^a contig	# reads mapped	sequence length	mean coverage	top BLAST hit	query cover	percent identity	accession	pathogen taxonomic family
2	3451	4695	103	Yeltsovka tombus-like_virus putative capsid	90%	80%	MW251332.1	<i>Tombusviridae</i>
3	3367	3837	127	PCLV isolate Rio segment M	99%	100%	NC_038261.1	<i>Bunyavirales</i>
1	2613	6781	55	PCLV isolate Rio segment L	99%	100%	NC_038262.1	<i>Bunyavirales</i>
4	2503	3089	115	Guadeloupe mosquito virus segment RNA1	100%	100%	MW434816.1	unclassified
11	1877	1341	202	PCLV isolate Rio segment S	100%	100%	NC_038263.1	<i>Bunyavirales</i>
5	1037	1632	85	Guadeloupe mosquito virus segment RNA2	100%	99%	MW434807.1	unclassified
13	779	1278	88	n.d.	-	-	-	-
9	344	1423	35	Chap-like virus isolate CLv.PozaRica20 ORF gene	99%	100%	MT742176.1	<i>Partitiviridae</i>
10	311	1348	33	<i>Aedes aegypti</i> leucine-rich repeat transmembrane neuronal protein 3	4%	95%	XM_001659114.2	-
6	251	1585	22	Elizabethkingia anophelis strain 2-8 chromosome	99%	100%	CP071530.1	<i>Weeksellaceae</i>
8	197	1454	19	Verdadero virus isolate Vv.PozaRica20 putative capsid	99%	100%	MT742175.1	<i>Partitiviridae</i>
7	144	1455	13	Elizabethkingia anophelis JUNP 353 DNA	100%	100%	AP022313.1	<i>Weeksellaceae</i>

^acontigs derived from Spades assembly of remaining reads when filtered against *Aedes aegypti* genome (GCA_002204515.1)
PCLV = Phasi Charoen-like virus
n.d. = no hits returned for BLAST of contig