Supplementary Table 1 Comparison of the pilot version of ZWA (ZWA1) against the evolved ZWA2 version in terms of software features as well as virus mapping and de novo assembly performance based on the *Anopheles sacharovi* mosquito RNA-seq sample (SRA accession number SRR13449040), its 28S and 18S rRNAs given as reference (GenBank accession numbers MT808434 & MT808462), and Xanthi rhabdovirus (GenBank MW520377) genome used for testing.

		Software features						Virus mapping performance			de novo assembly performance		
	Implementation	Input file type	Prerequisites	Alignment software	*De novo* assembly	User adjustability	Execution time (seconds)	Virus mapped reads (n)	Virus coverage (%)	Mean depth of virus mapped reads (n)	Average query covbases (nucleotides)	Max query covbases (nucleotides)	UG₁₀% (%)
ZWA1	Bash script	FASTQ, FASTA	7 (BIOAWK, BLAST, BLAST+, BBMAP reformat.sh, faSomeRecords, BWA, samtools, Trinity)	BWA & BLASTn	Mandatory (Trinity required)	None	1006344.582	1299	99.8039	12.9743	1251.88	2520	11.77
ZWA2	Bash script	FASTQ, FASTA, BAM	2 (BWA, samtools)	BWA only	Optional (MEGAHIT recommended)	Alignment stringency	228.838	1359	99.902	13.2237	1430.86	3554	24.21