

	Software features							Virus mapping performance			<i>de novo</i> assembly performance		
	Implementation	Input file type	Prerequisites	Alignment software	<i>De novo</i> assembly	User adjustability	Execution time (seconds)	Virus mapped reads (n)	Virus coverage (%)	Meandepth of virus mapped reads (n)	Average query covbases (nucleotides)	Max query covbases (nucleotides)	UG ₅₀ % (%)
ZWA1	Bash script	FASTQ, FASTA	7 (BIOAWK, 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