

# Supplementary Info

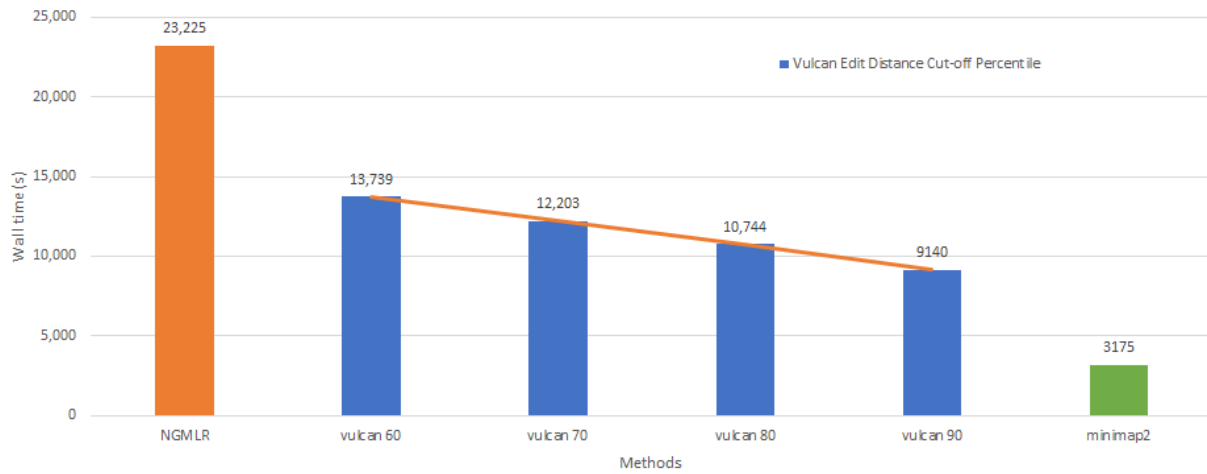
**Supplementary Table 1: Programs, program versions, and parameters used in this study.**

Program	Version	Usage	Parameters
Vulcan	1.0.2	read mapping	vulcan [] -t threads
minimap2	2.17-r941	simulated ONT read mapping	minimap2 --MD -x map-ont -a
minimap2	2.17-r941	Human ONT read mapping	minimap2 --MD -x map-ont -a -z 600,200
minimap2	2.17-r941	Human PacBio HiFi read mapping	minimap2 --MD -a -k 19 -O 5,56 -E 4,1 -B 5 -z 400,50 -r 2k -eqx --secondary=no
minimap2	2.17-r941	Human Pacbio CLR read mapping	minimap2 --MD -x map-pb -a -eqx -L -O 5,56 -E 4,1 -B 5 --secondary=no -z 400,50 -r 2k -Y
NGMLR	0.2.7	read mapping	NGMLR -x [ont   pacbio] -bam-fix
Sniffles	1.0.12	SV calling	sniffles -s 2
bcftools	1.7	VCF filtering	bcftools view -i (INFO/SVLEN>=50 INFO/SVLEN<=-50 INFO/SVLEN=0 INFO/SVLEN=1)&(INFO/RE={read_num})
Truvari	v2.0.0-dev	SV benchmarking	truvari bench -b {GIAB_vcf} -c {sorted_gzipped_vcf} -f {reference_genome} -passonly-giabreport -pctsim=0 -multimatch -includebed {GIAB_bed} -o {benchmarking_output}
SURVIVOR	1.0.7	SV simulation	SURVIVOR simSV {reference_genome} {parameter_file} 0.01 0 {output_prefix}

**Supplementary Table 2: Accuracy, Precision and F1 score of simulated data.**

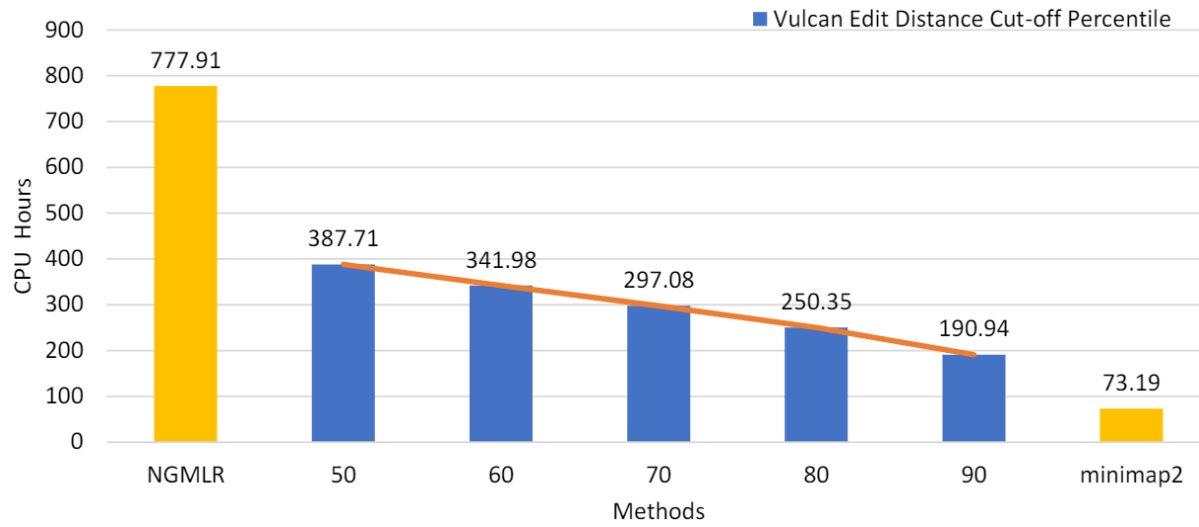
<b>Nanopore Simulated 10X</b>	<b>Recall</b>	<b>Precision</b>	<b>F1</b>
minimap2	81%	62%	70.24%
NGMLR	92%	62%	74.24%
Vulcan 80%	<b>95%</b>	<b>74%</b>	<b>83.13%</b>

### Supplementary Figure 1: Wall time benchmarking of Vulcan, NGMLR and minimap2 on Nanopore 10X datasets



A wall time benchmarking has been performed to compare the performance of three different methods. From the chart we can infer that Vulcan takes less than 2/5 time than NGMLR. The experiment was performed on a Nanopore 10X submaple real dataset from the GIAB project.

**Supplementary Figure 2: CPU time benchmarking of Vulcan, NGMLR and minimap2 on PacBio 20X datasets**



Vulcan achieves an approximately linear acceleration with the increase of the cut-off percentile. With a 90% percentile cut-off, Vulcan only takes about 1/4 of NGMLR's runtime. The experiment was performed on a PacBio CLR 20X subsampled real dataset from the GIAB project.