

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 13:04:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975283.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR975283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975283_1.fastq.gz SRR975283_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 13:04:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975283.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	52,525,372
Mapped reads	52,255,052 / 99.49%
Unmapped reads	270,320 / 0.51%
Mapped paired reads	52,255,052 / 99.49%
Mapped reads, first in pair	26,208,266 / 49.9%
Mapped reads, second in pair	26,046,786 / 49.59%
Mapped reads, both in pair	52,035,726 / 99.07%
Mapped reads, singletons	219,326 / 0.42%
Secondary alignments	0
Supplementary alignments	129,791 / 0.25%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	36,227,599 / 68.97%
Duplication rate	59.1%
Clipped reads	30,405,948 / 57.89%

2.2. ACGT Content

Number/percentage of A's	1,316,983,066 / 26.57%
Number/percentage of C's	1,123,797,308 / 22.68%
Number/percentage of T's	1,336,049,073 / 26.96%
Number/percentage of G's	1,177,951,879 / 23.77%
Number/percentage of N's	1,046,498 / 0.02%

GC Percentage	46.45%
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2.3. Coverage

Mean	1.6015
Standard Deviation	27.2698

2.4. Mapping Quality

Mean Mapping Quality	56.21
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2.5. Insert size

Mean	114,270.53
Standard Deviation	3,330,953.3
P25/Median/P75	191 / 233 / 283

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	41,548,043
Insertions	608,329
Mapped reads with at least one insertion	1.15%
Deletions	1,257,724
Mapped reads with at least one deletion	2.37%
Homopolymer indels	45.17%

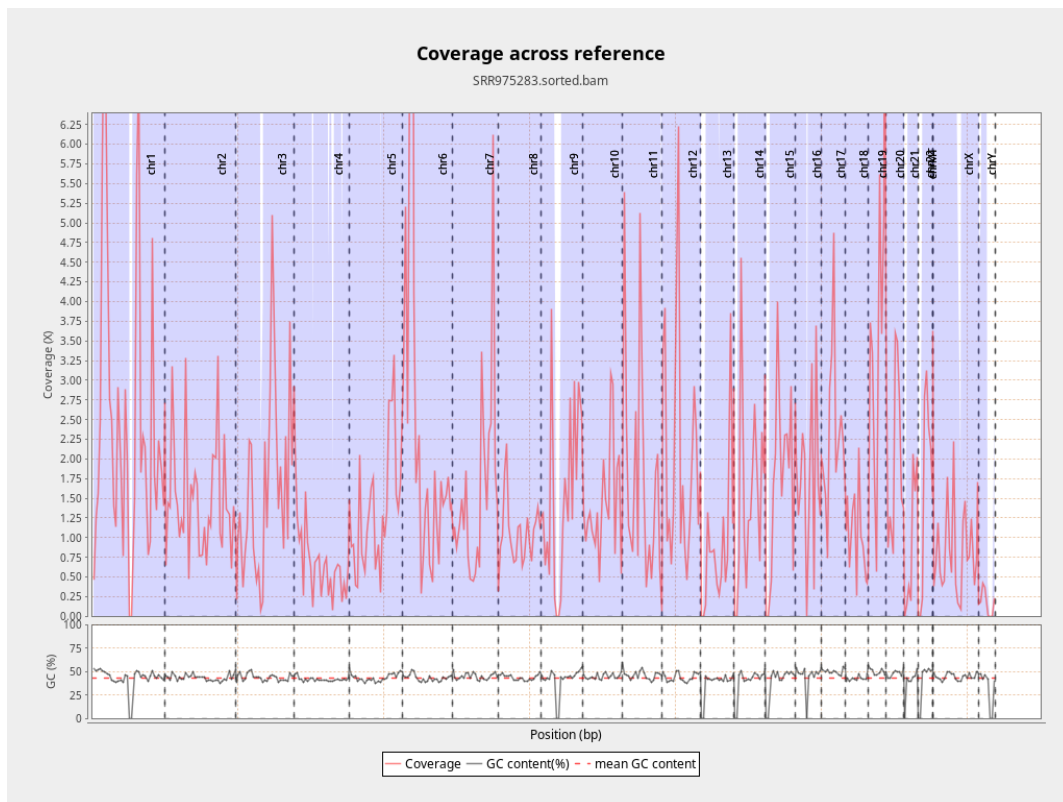
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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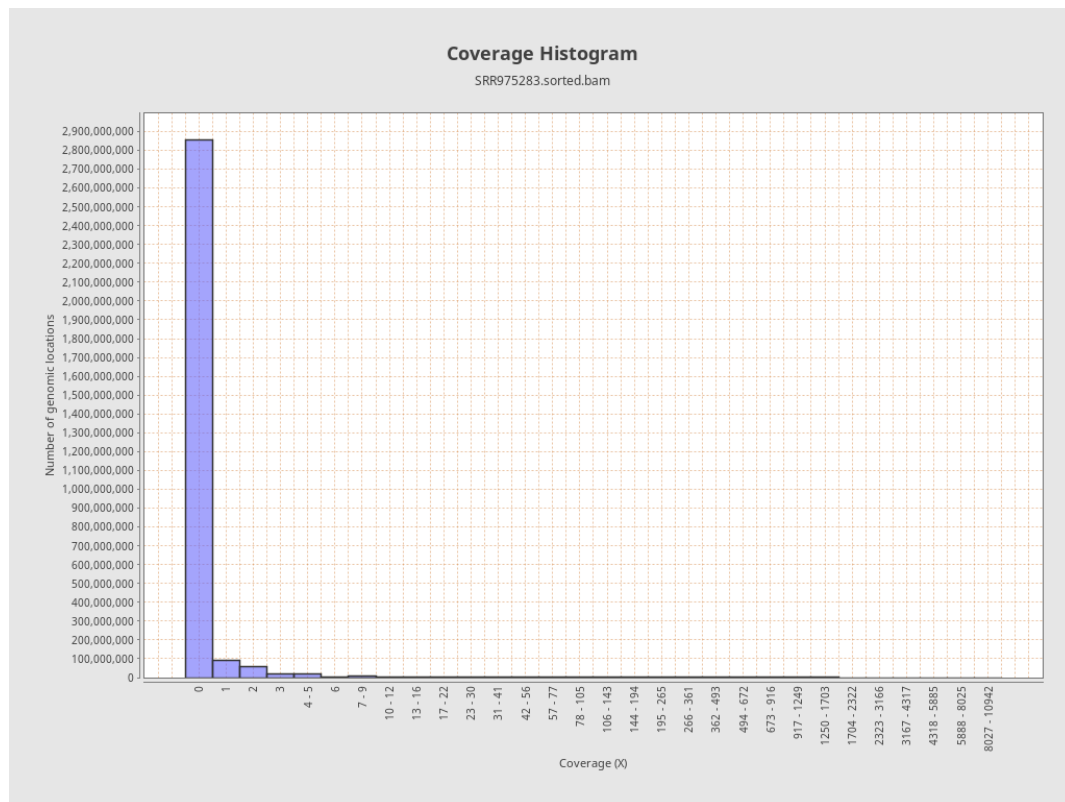
		bases	coverage	deviation
chr1	249250621	609812845	2.4466	34.7036
chr2	243199373	355413330	1.4614	23.1219
chr3	198022430	327412893	1.6534	25.9007
chr4	191154276	127129333	0.6651	13.2613
chr5	180915260	243306927	1.3449	23.6331
chr6	171115067	468889168	2.7402	46.8942
chr7	159138663	255760230	1.6072	26.8423
chr8	146364022	160028264	1.0934	18.9606
chr9	141213431	205560429	1.4557	24.6767
chr10	135534747	196973682	1.4533	21.1743
chr11	135006516	244363450	1.81	26.6811
chr12	133851895	278381544	2.0798	33.4896
chr13	115169878	103324799	0.8972	22.5547
chr14	107349540	159109803	1.4822	23.703
chr15	102531392	180622306	1.7616	27.8338
chr16	90354753	155208598	1.7178	24.748
chr17	81195210	193096806	2.3782	31.9949
chr18	78077248	82203121	1.0528	18.0186
chr19	59128983	205791623	3.4804	47.6122
chr20	63025520	136377529	2.1638	32.4767
chr21	48129895	43837648	0.9108	15.662
chr22	51304566	85942717	1.6751	26.5603
chrMT	16571	60063	3.6246	8.2778
chrX	155270560	129014540	0.8309	18.5105

chrY	59373566	10046111	0.1692	6.7351
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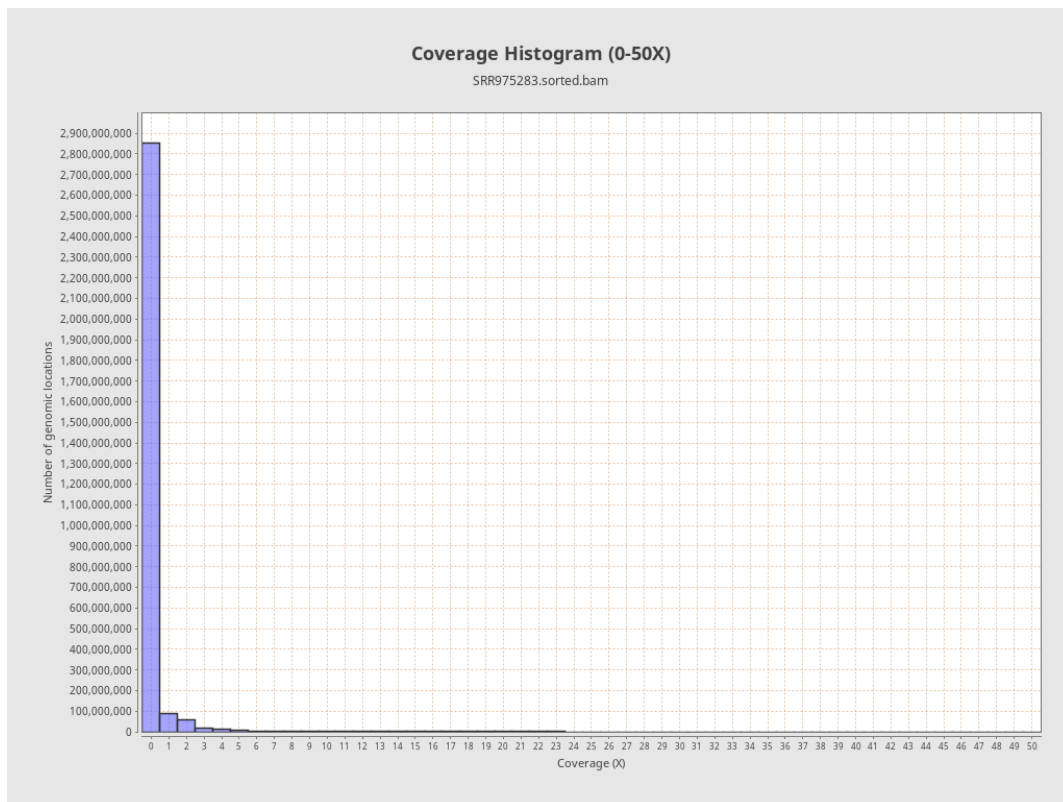
3. Results : Coverage across reference



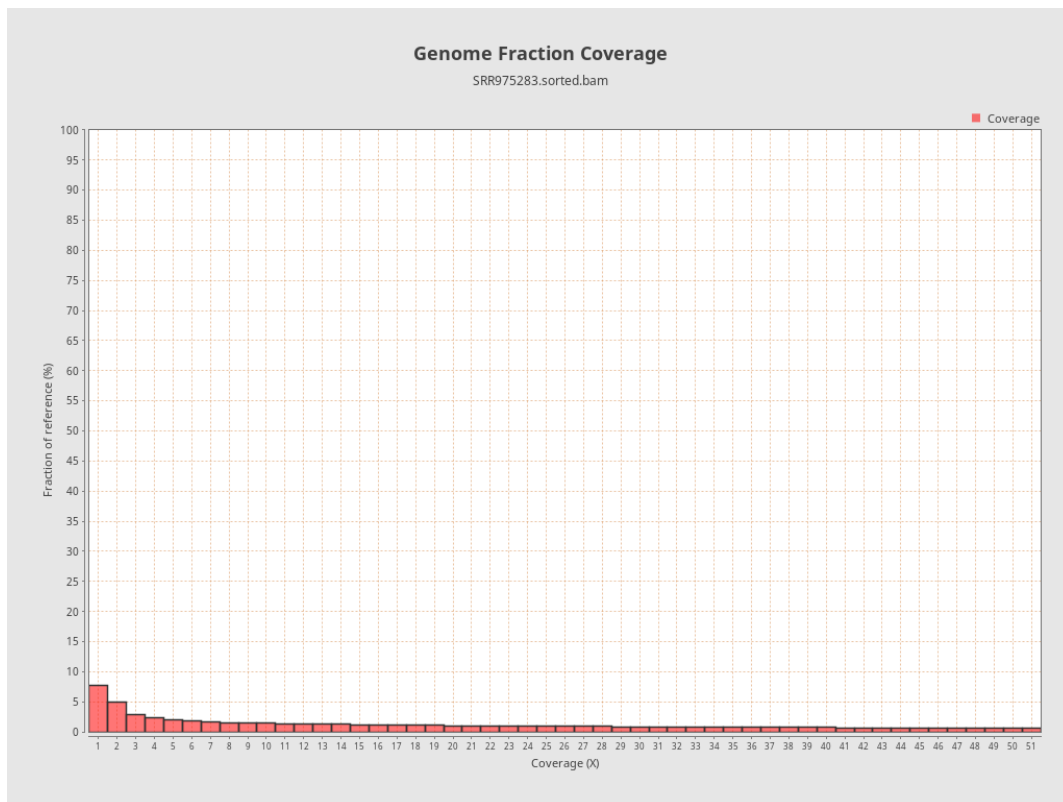
4. Results : Coverage Histogram



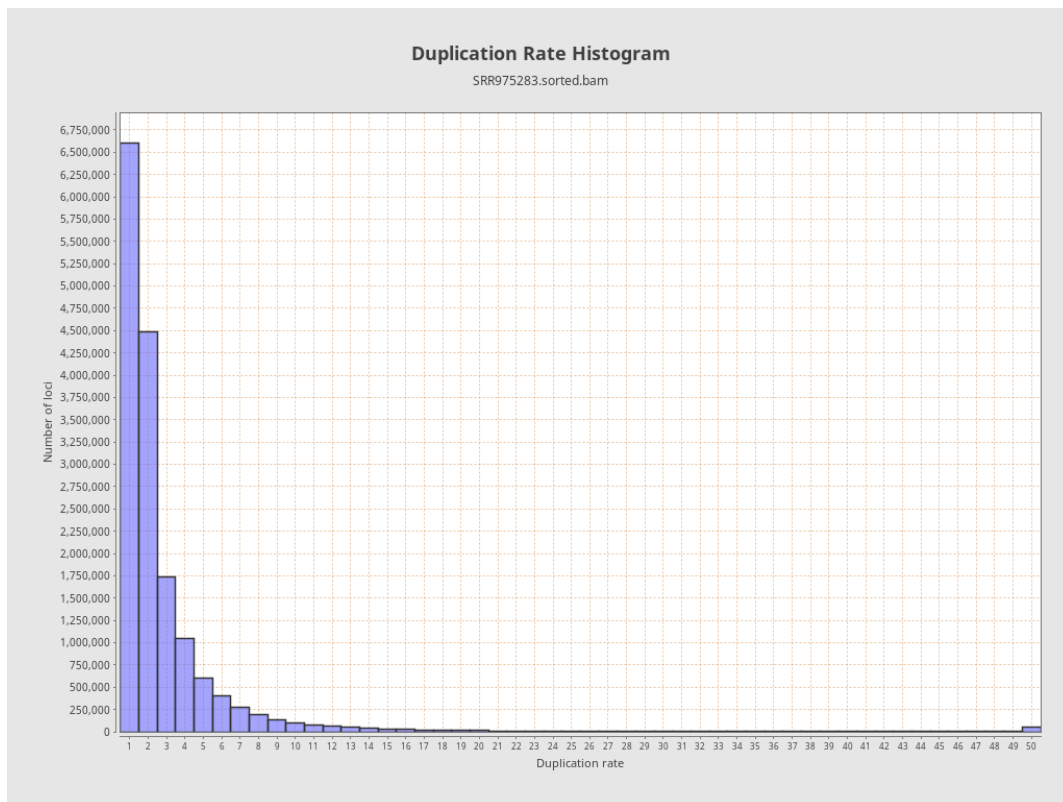
5. Results : Coverage Histogram (0-50X)



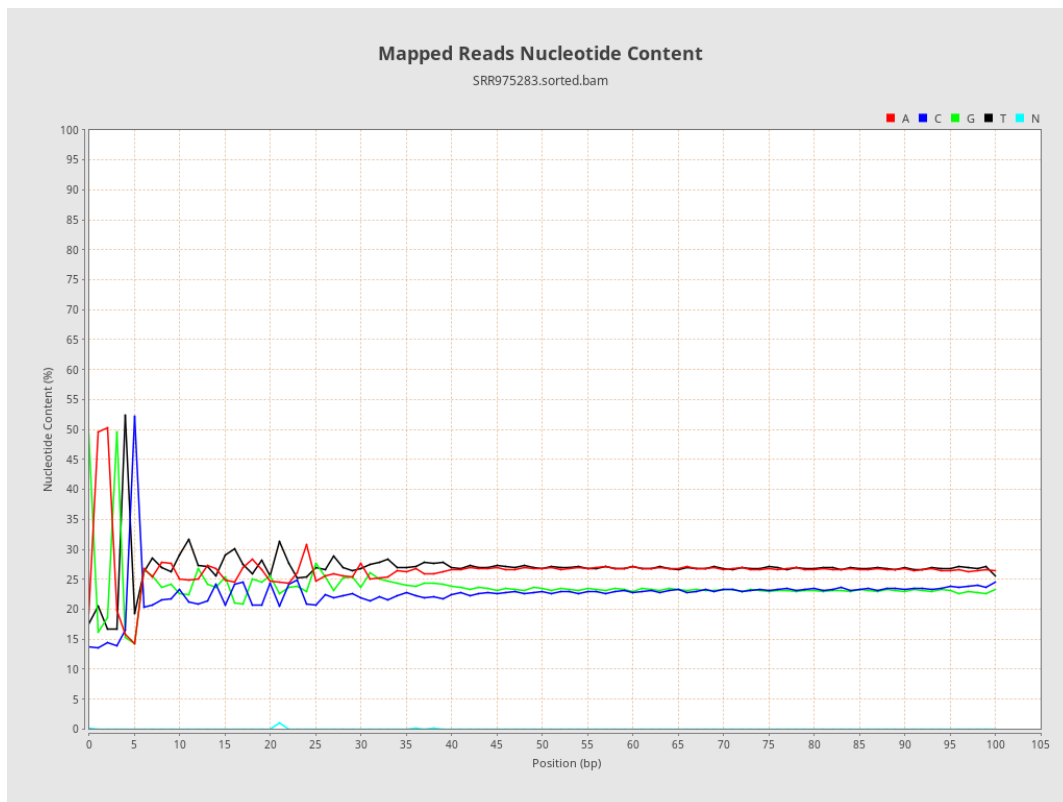
6. Results : Genome Fraction Coverage



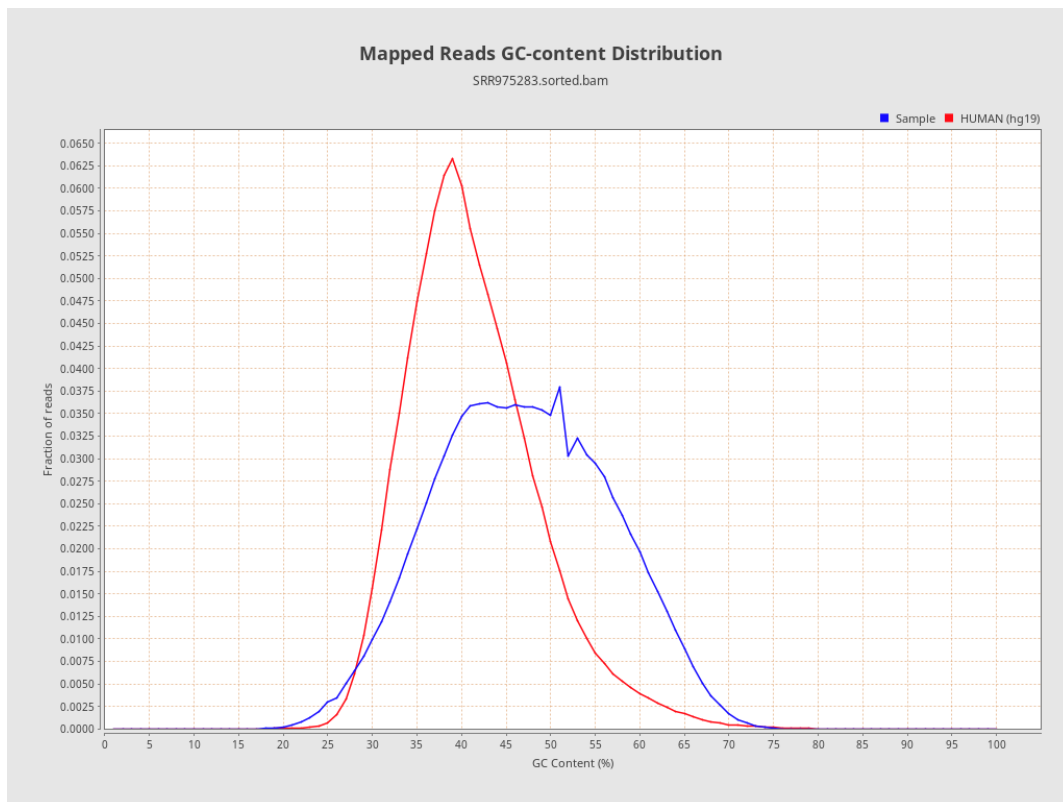
7. Results : Duplication Rate Histogram



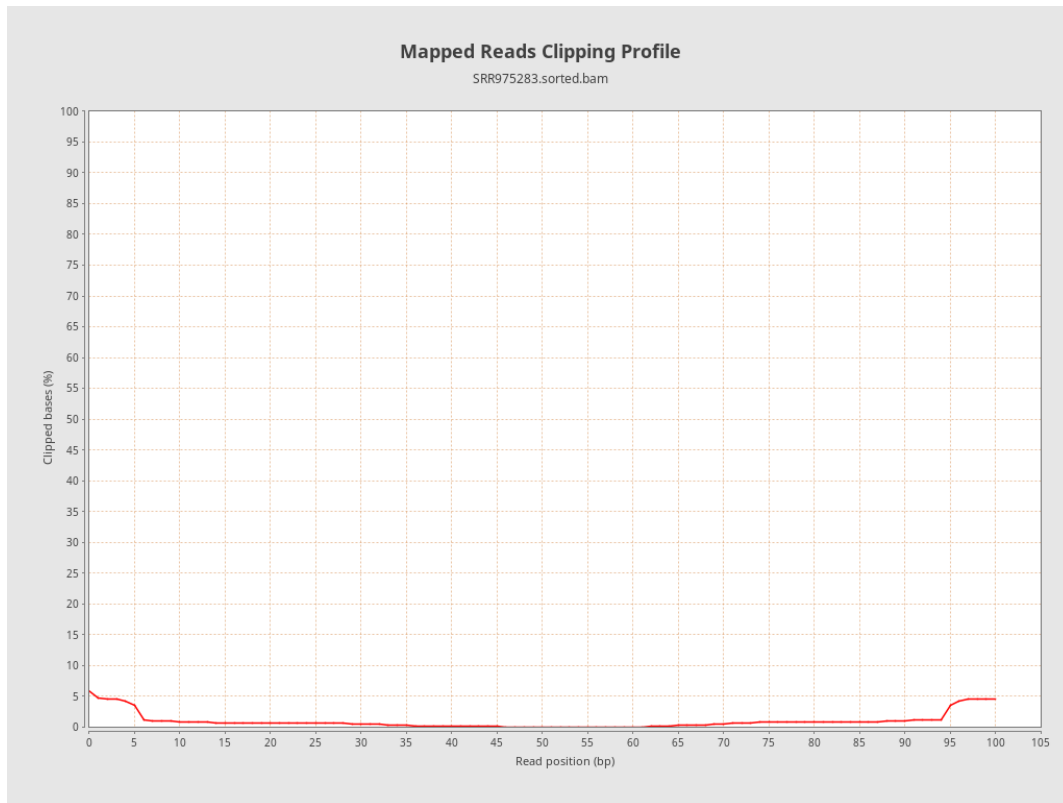
8. Results : Mapped Reads Nucleotide Content



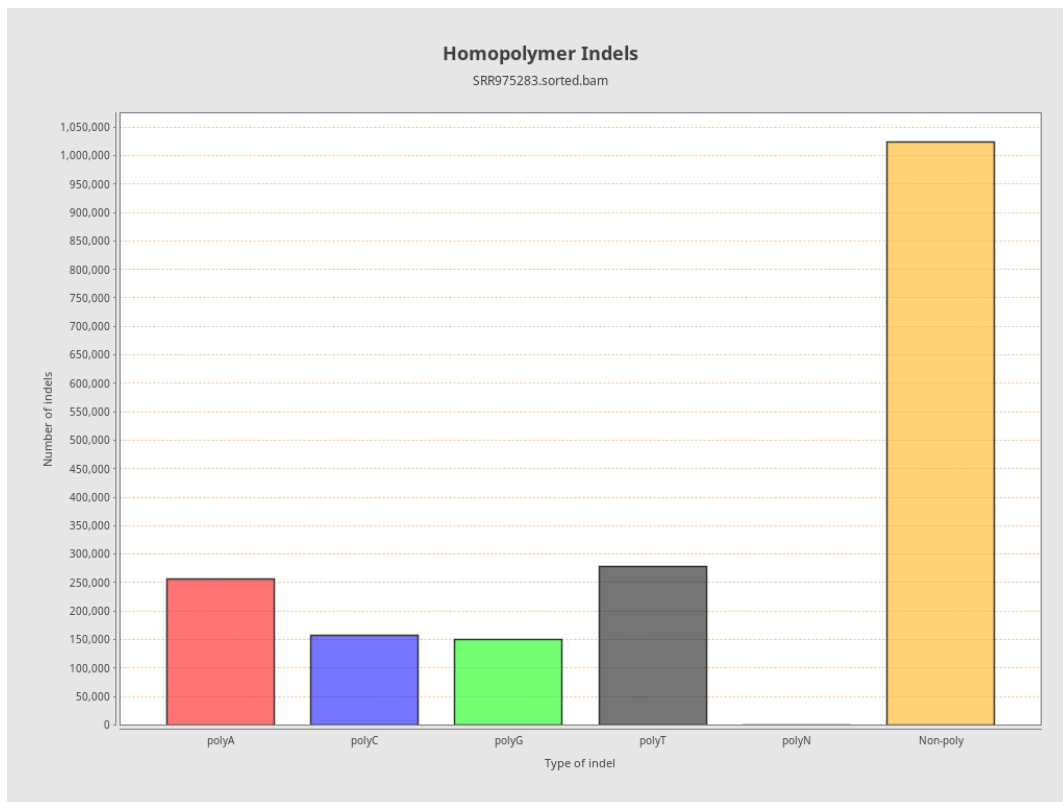
9. Results : Mapped Reads GC-content Distribution



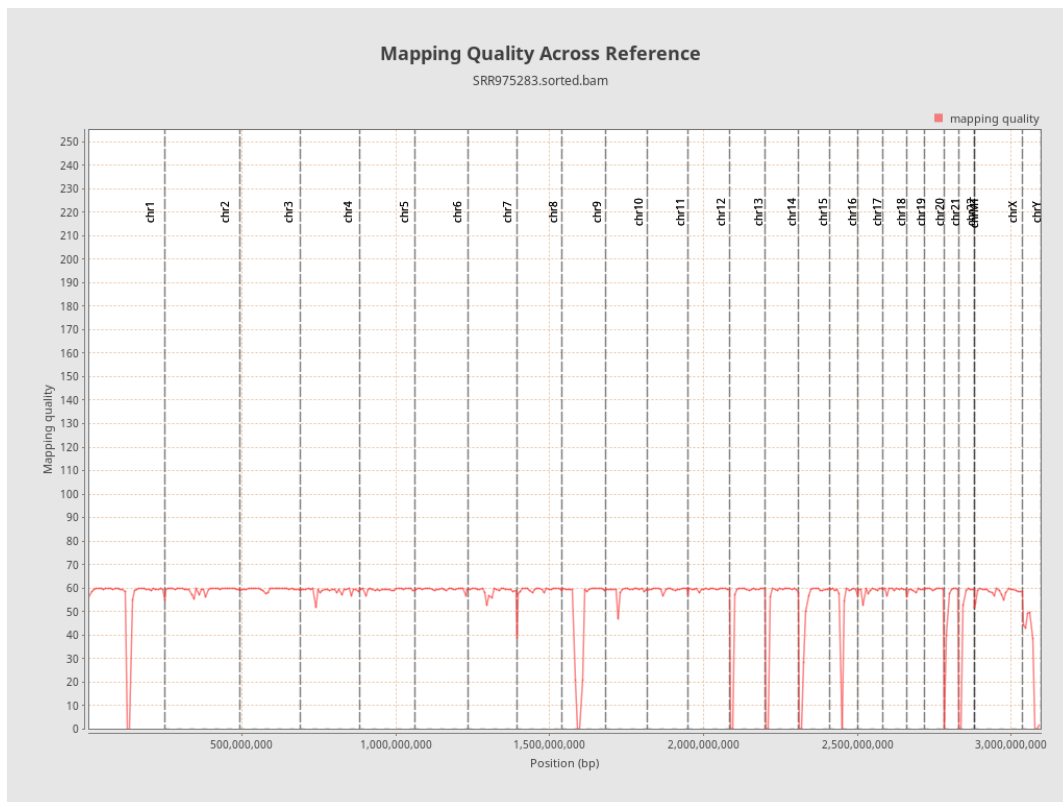
10. Results : Mapped Reads Clipping Profile



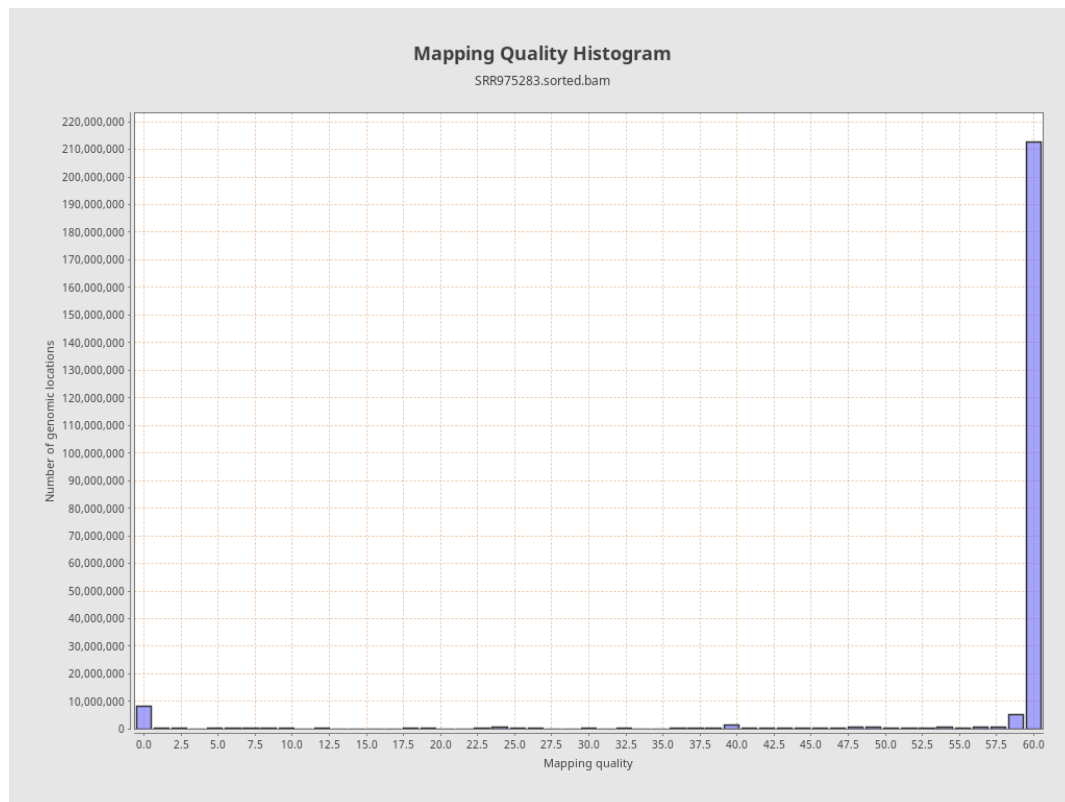
11. Results : Homopolymer Indels



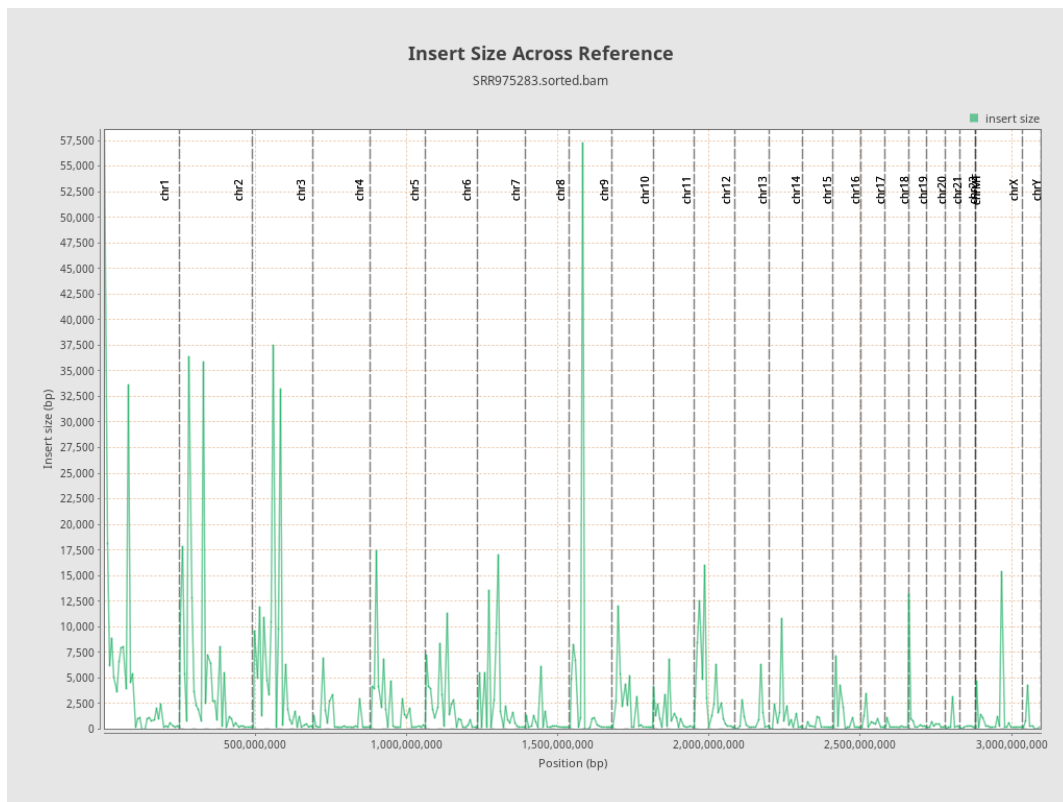
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

