Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 20:07:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975278.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_SRR975278 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975278_1.fastq.gz SRR975278_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 20:07:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975278.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,636,052
Mapped reads	2,604,408 / 98.8%
Unmapped reads	31,644 / 1.2%
Mapped paired reads	2,604,408 / 98.8%
Mapped reads, first in pair	1,304,441 / 49.48%
Mapped reads, second in pair	1,299,967 / 49.31%
Mapped reads, both in pair	2,595,106 / 98.45%
Mapped reads, singletons	9,302 / 0.35%
Secondary alignments	0
Supplementary alignments	29,790 / 1.13%
Read min/max/mean length	30 / 151 / 151.54
Duplicated reads (estimated)	437,420 / 16.59%
Duplication rate	16.12%
Clipped reads	1,925,913 / 73.06%

2.2. ACGT Content

Number/percentage of A's	104,308,455 / 29.95%
Number/percentage of C's	68,332,730 / 19.62%
Number/percentage of T's	103,503,063 / 29.72%
Number/percentage of G's	72,091,830 / 20.7%
Number/percentage of N's	23,010 / 0.01%

GC Percentage	40.32%

2.3. Coverage

Mean	0.1126
Standard Deviation	1.4281

2.4. Mapping Quality

Mean Mapping Quality	53.52

2.5. Insert size

Mean	62,128.12
Standard Deviation	2,297,296.64
P25/Median/P75	134 / 166 / 210

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	3,271,454
Insertions	68,849
Mapped reads with at least one insertion	2.5%
Deletions	111,088
Mapped reads with at least one deletion	4.1%
Homopolymer indels	45.36%

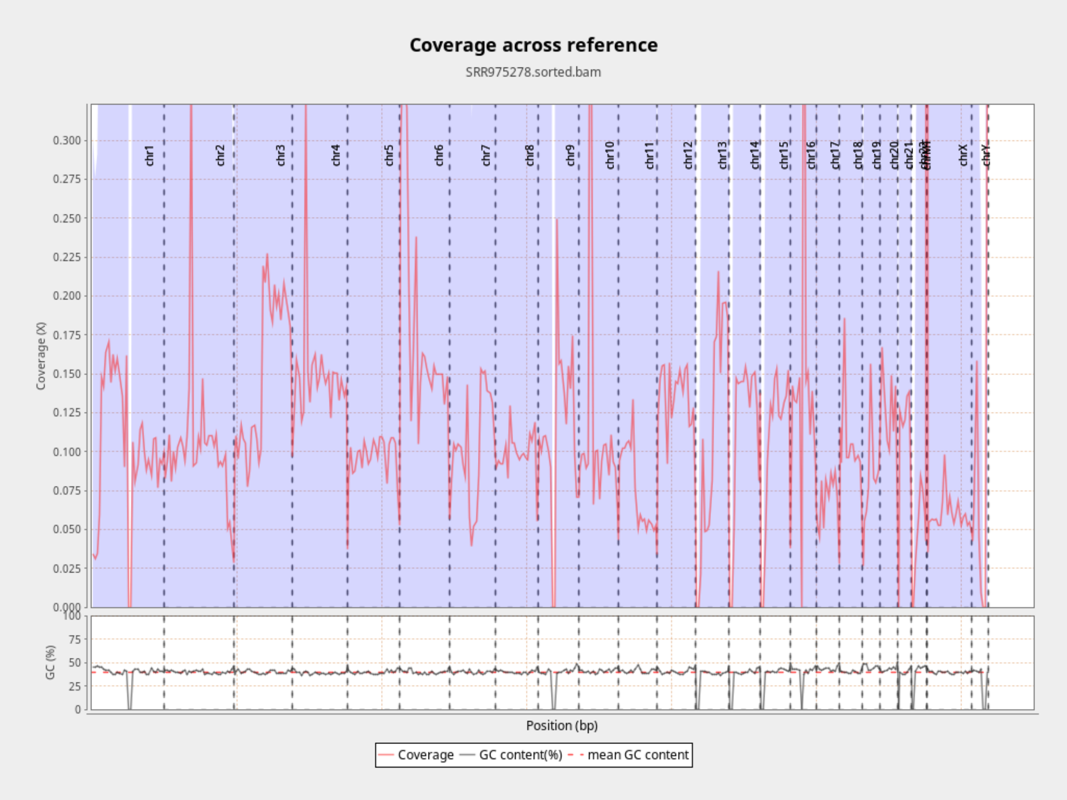
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

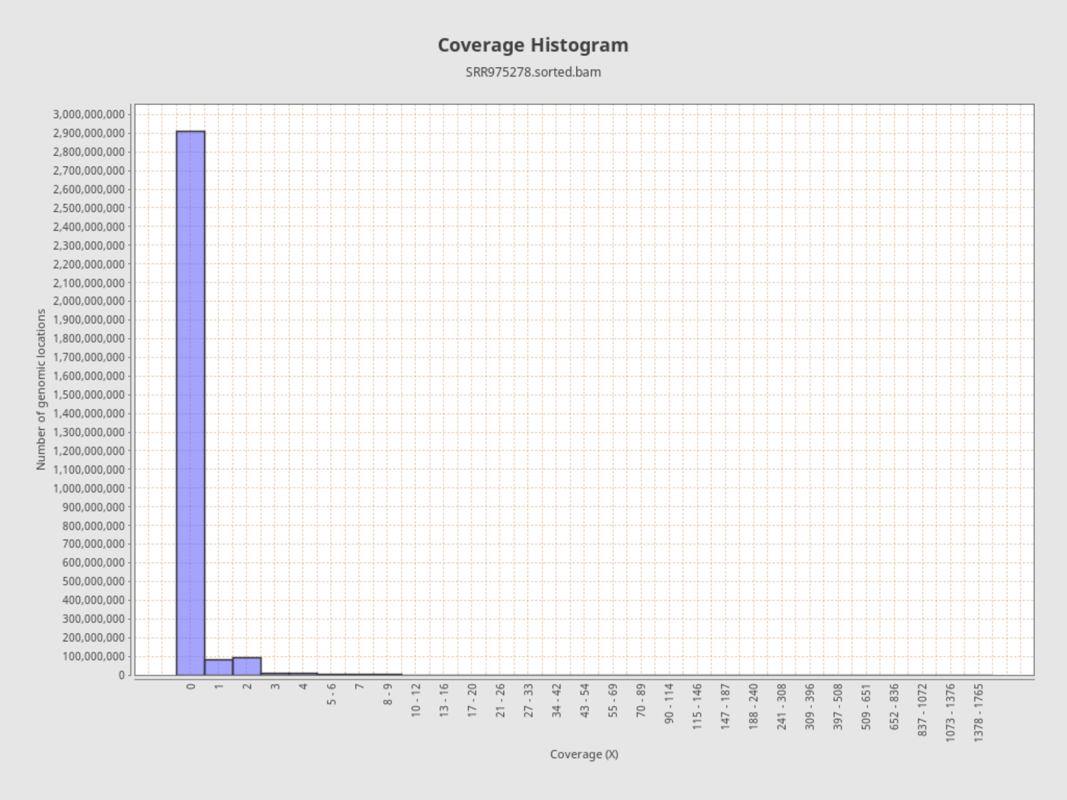
		bases	coverage	deviation
chr1	249250621	25708754	0.1031	1.3676
chr2	243199373	25374939	0.1043	1.6589
chr3	198022430	30204951	0.1525	0.5795
chr4	191154276	28640392	0.1498	1.3293
chr5	180915260	17657701	0.0976	0.445
chr6	171115067	31110804	0.1818	1.1178
chr7	159138663	16312190	0.1025	1.0425
chr8	146364022	14454415	0.0988	0.5944
chr9	141213431	16226696	0.1149	2.583
chr10	135534747	15781433	0.1164	3.3621
chr11	135006516	10265895	0.076	0.9812
chr12	133851895	18186142	0.1359	0.5281
chr13	115169878	12885923	0.1119	0.484
chr14	107349540	12298930	0.1146	0.5091
chr15	102531392	10860587	0.1059	0.4633
chr16	90354753	13793751	0.1527	2.7726
chr17	81195210	5575216	0.0687	0.7732
chr18	78077248	8253041	0.1057	2.2406
chr19	59128983	4895002	0.0828	0.9638
chr20	63025520	7906824	0.1255	0.6716
chr21	48129895	5288268	0.1099	0.8235
chr22	51304566	2462033	0.048	0.3196
chrMT	16571	79399	4.7914	3.9079
chrX	155270560	9213184	0.0593	0.4576

chrY	59373566	5062189	0.0853	2.2063

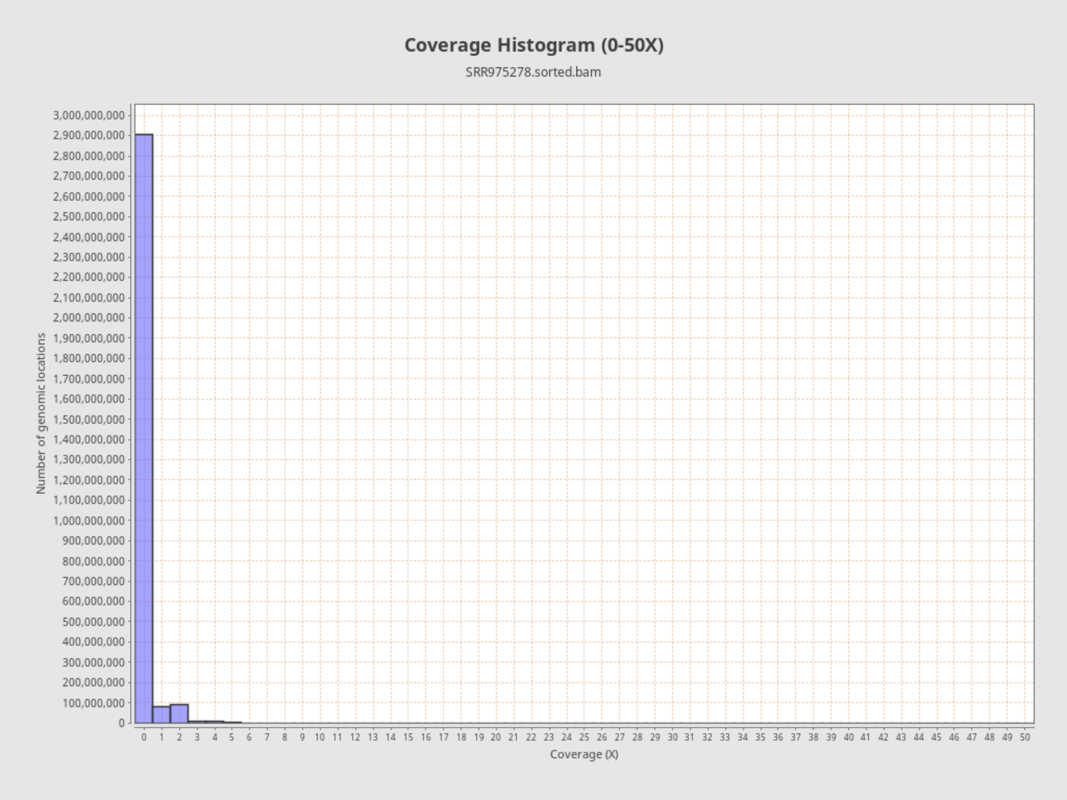
3. Results : Coverage across reference



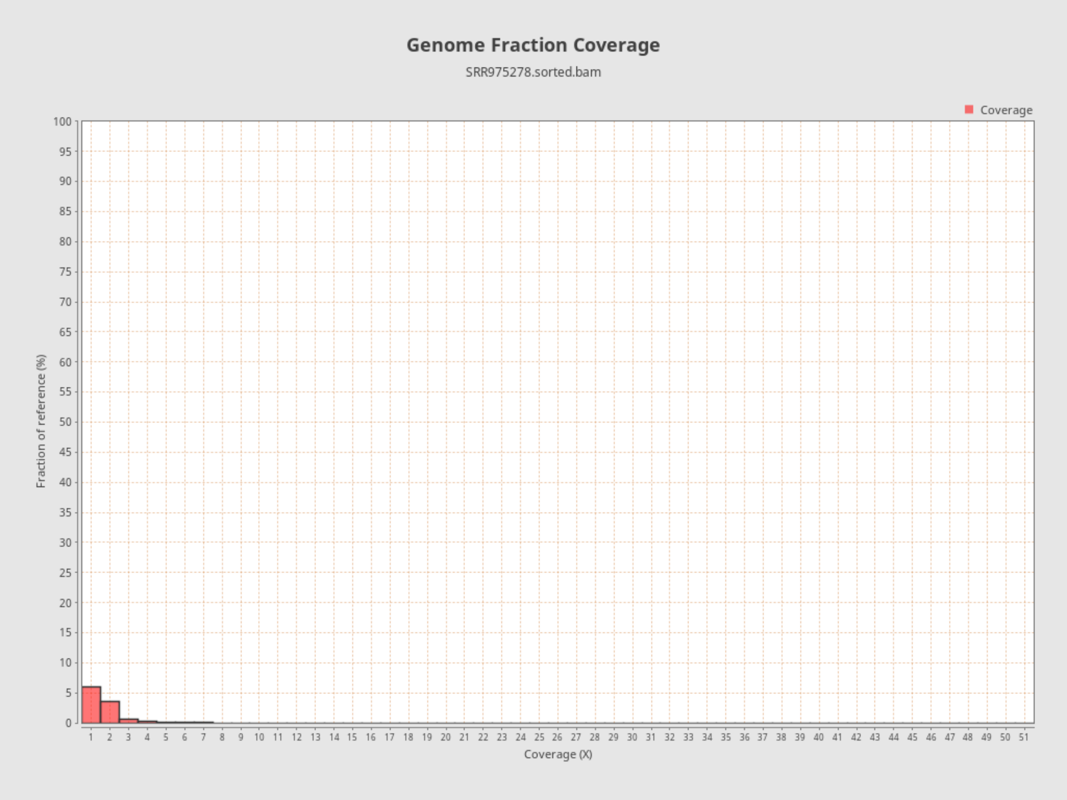
4. Results : Coverage Histogram



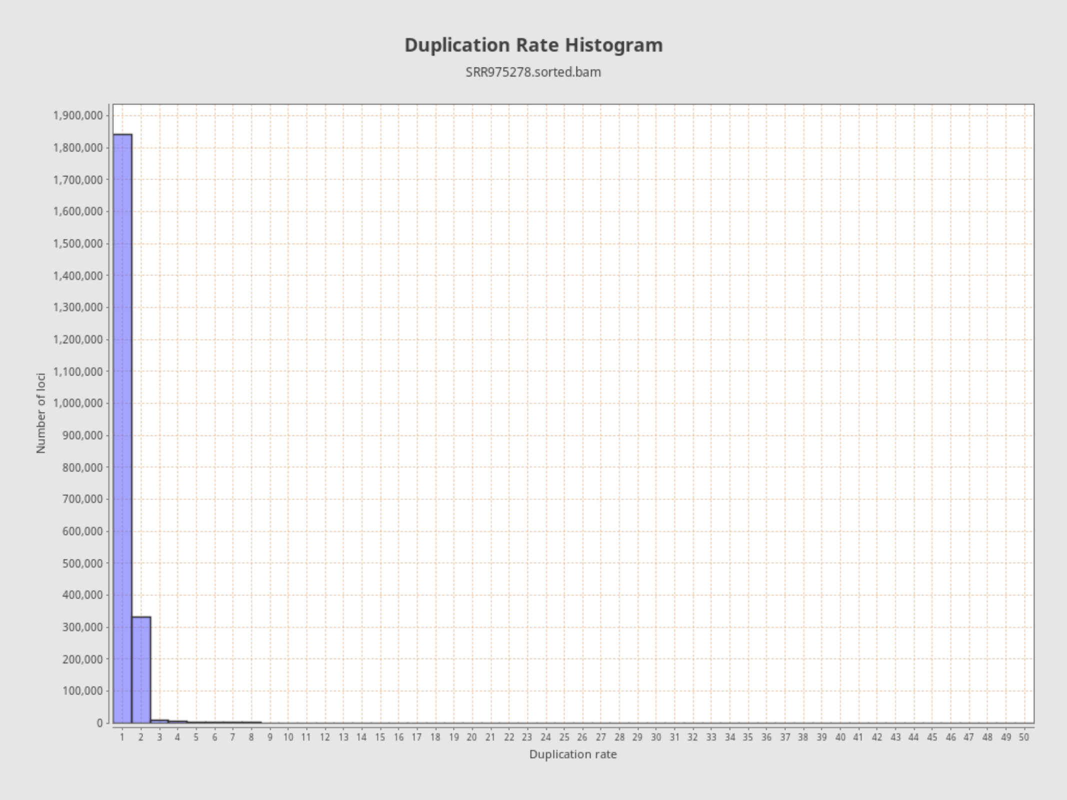
5. Results : Coverage Histogram (0-50X)



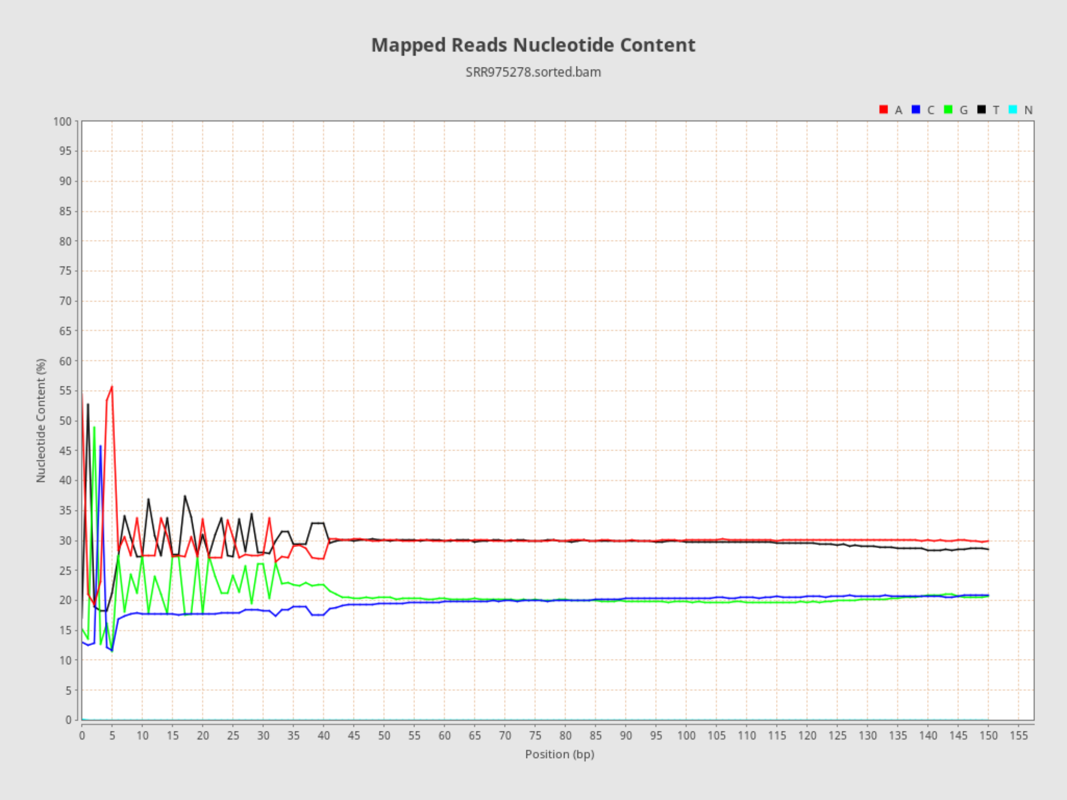
6. Results : Genome Fraction Coverage



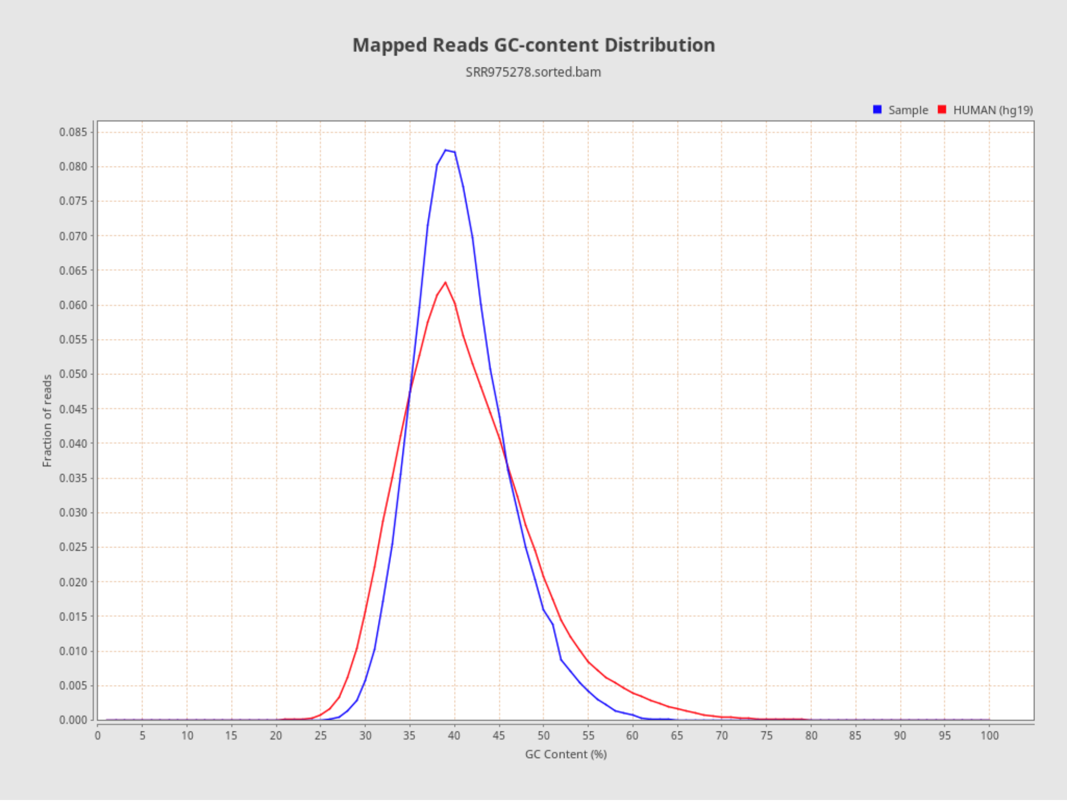
7. Results : Duplication Rate Histogram



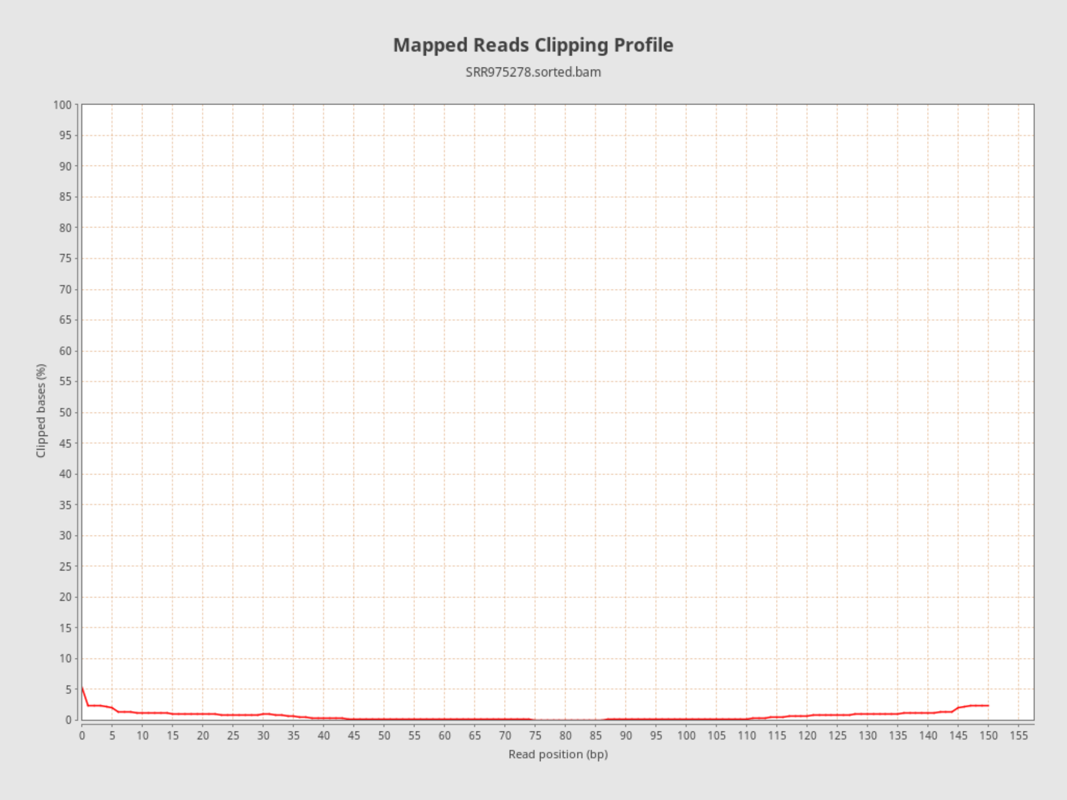
8. Results : Mapped Reads Nucleotide Content



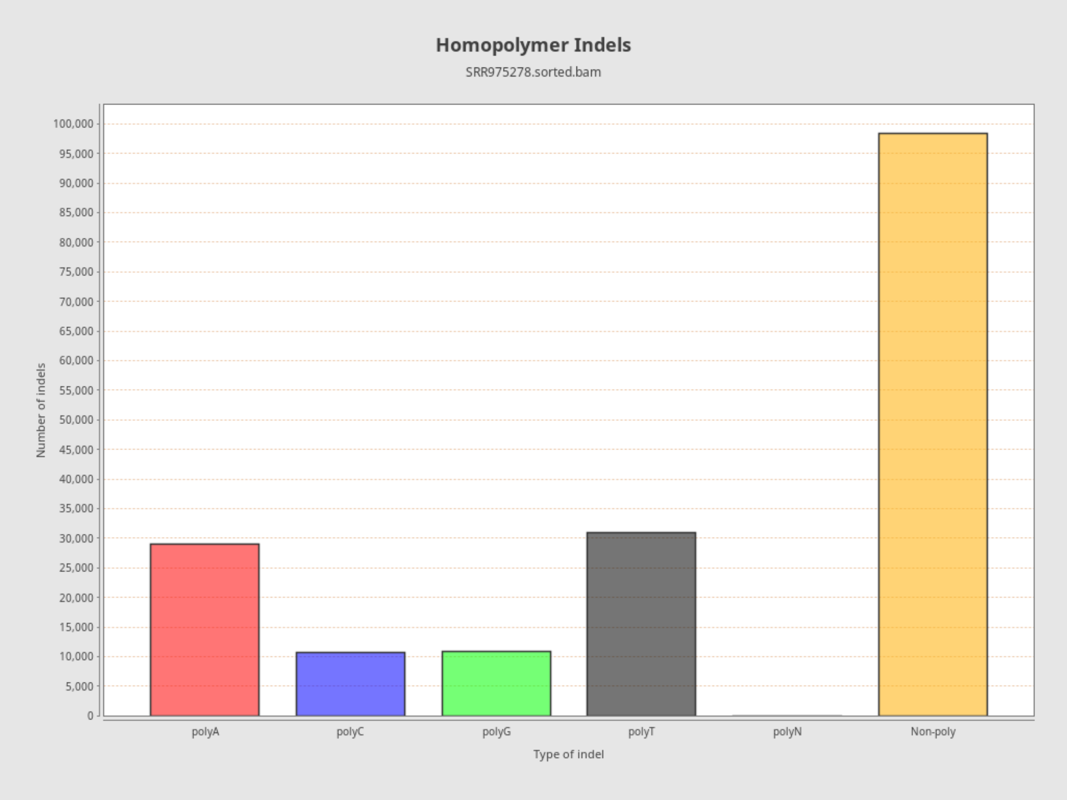
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

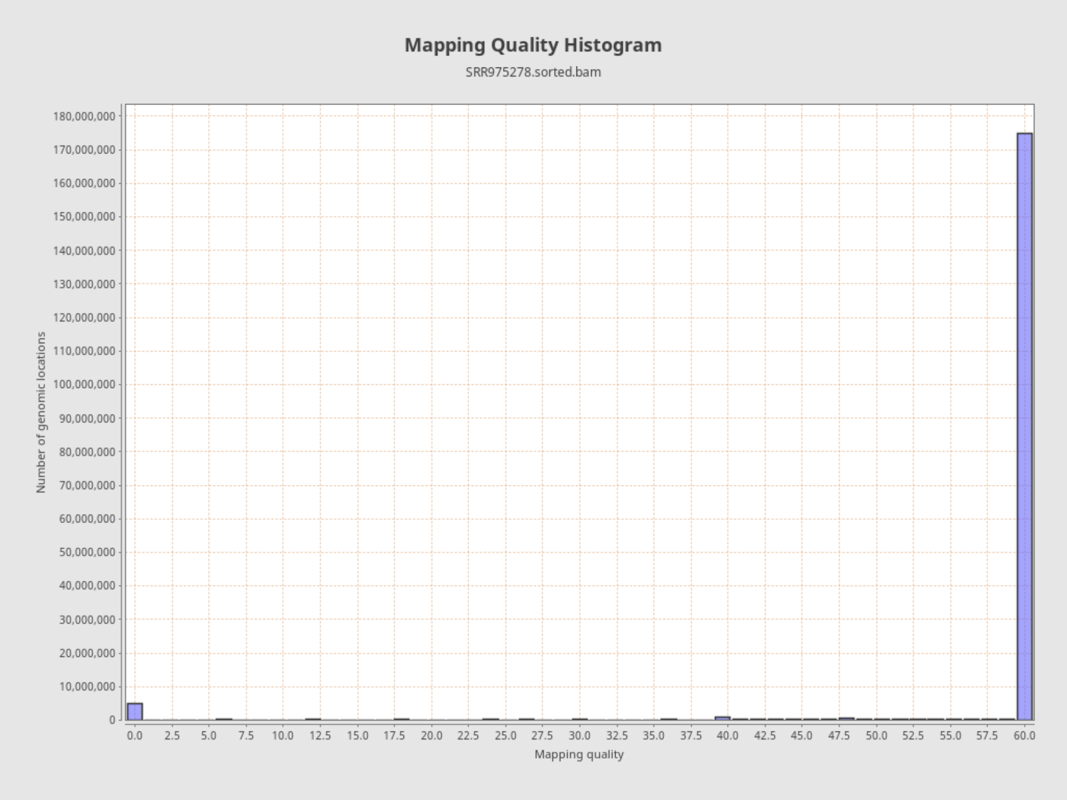


11. Results : Homopolymer Indels

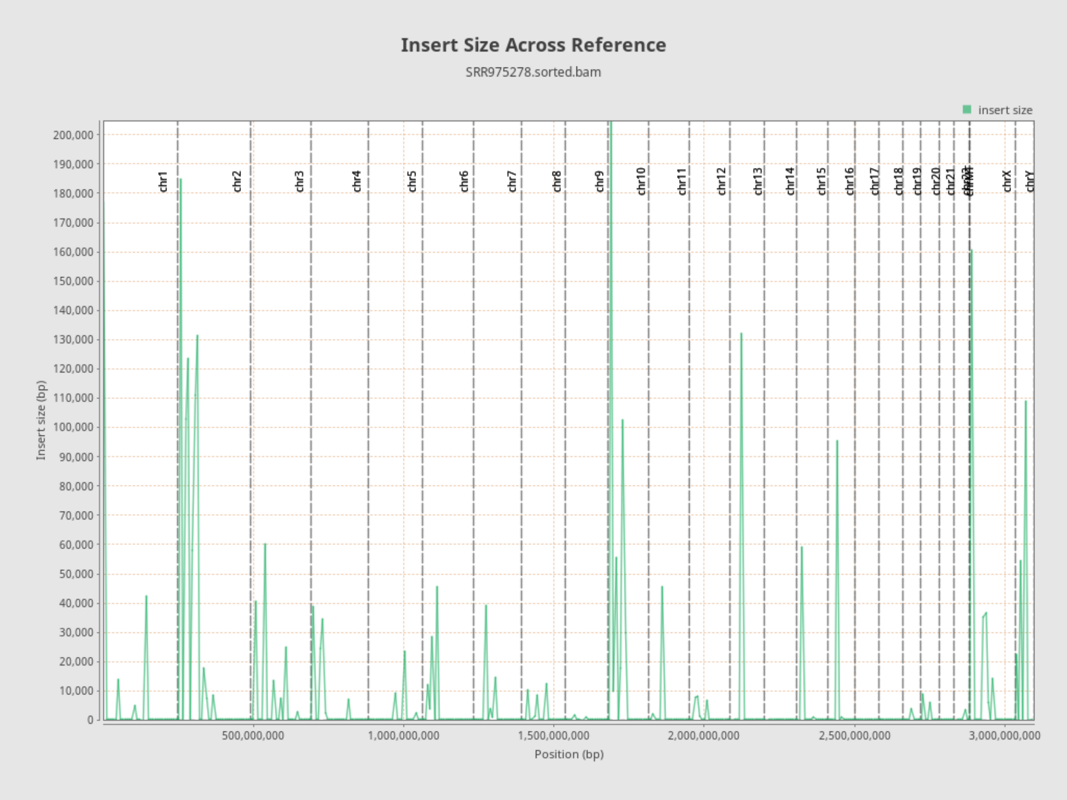


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram