Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 17:07:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975264.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_SRR975264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975264_1.fastq.gz SRR975264_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 17:07:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,649,790
Mapped reads	11,505,539 / 98.76%
Unmapped reads	144,251 / 1.24%
Mapped paired reads	11,505,539 / 98.76%
Mapped reads, first in pair	5,756,966 / 49.42%
Mapped reads, second in pair	5,748,573 / 49.34%
Mapped reads, both in pair	11,467,778 / 98.44%
Mapped reads, singletons	37,761 / 0.32%
Secondary alignments	0
Supplementary alignments	72,082 / 0.62%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	695,757 / 5.97%
Duplication rate	3.47%
Clipped reads	7,010,233 / 60.17%

2.2. ACGT Content

Number/percentage of A's	302,446,363 / 29.03%
Number/percentage of C's	209,348,788 / 20.09%
Number/percentage of T's	303,237,630 / 29.1%
Number/percentage of G's	226,932,518 / 21.78%
Number/percentage of N's	10,037 / 0%

GC Percentage	41.87%

2.3. Coverage

Mean	0.3368
Standard Deviation	2.7254

2.4. Mapping Quality

Mean Mapping Quality	52.67

2.5. Insert size

Mean	72,384.17
Standard Deviation	2,579,619.86
P25/Median/P75	133 / 164 / 208

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	7,800,570
Insertions	167,460
Mapped reads with at least one insertion	1.42%
Deletions	358,726
Mapped reads with at least one deletion	3.06%
Homopolymer indels	46.35%

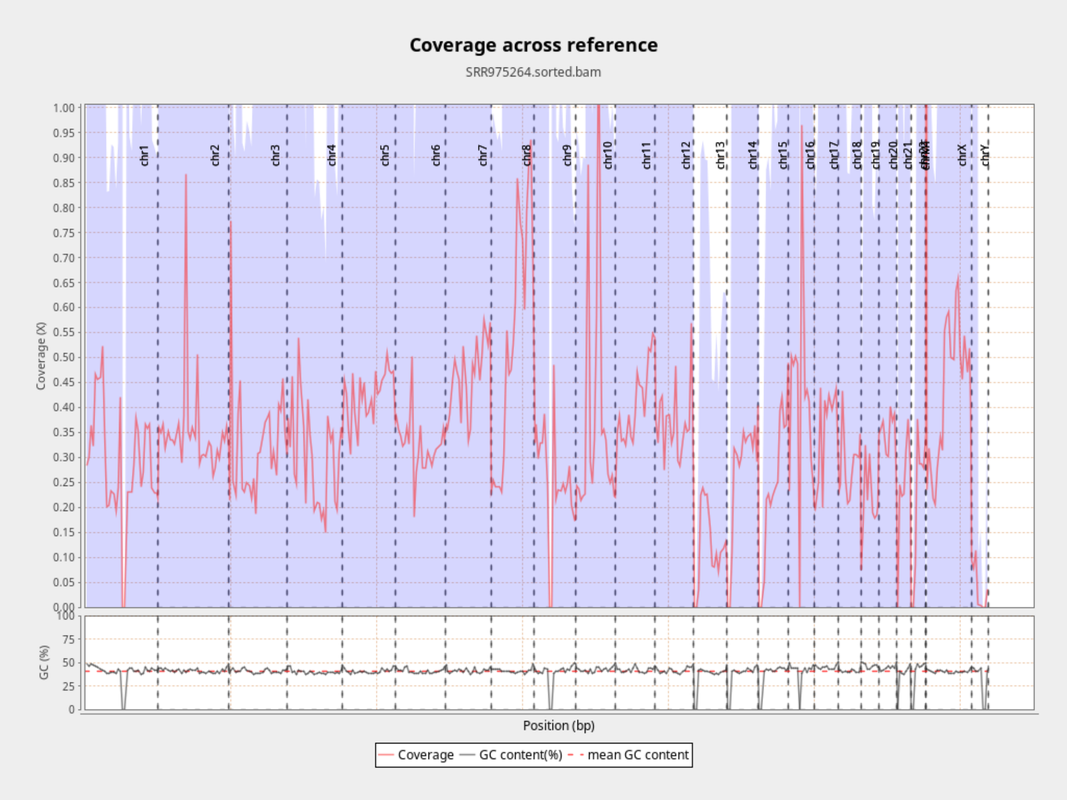
2.7. Chromosome stats

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

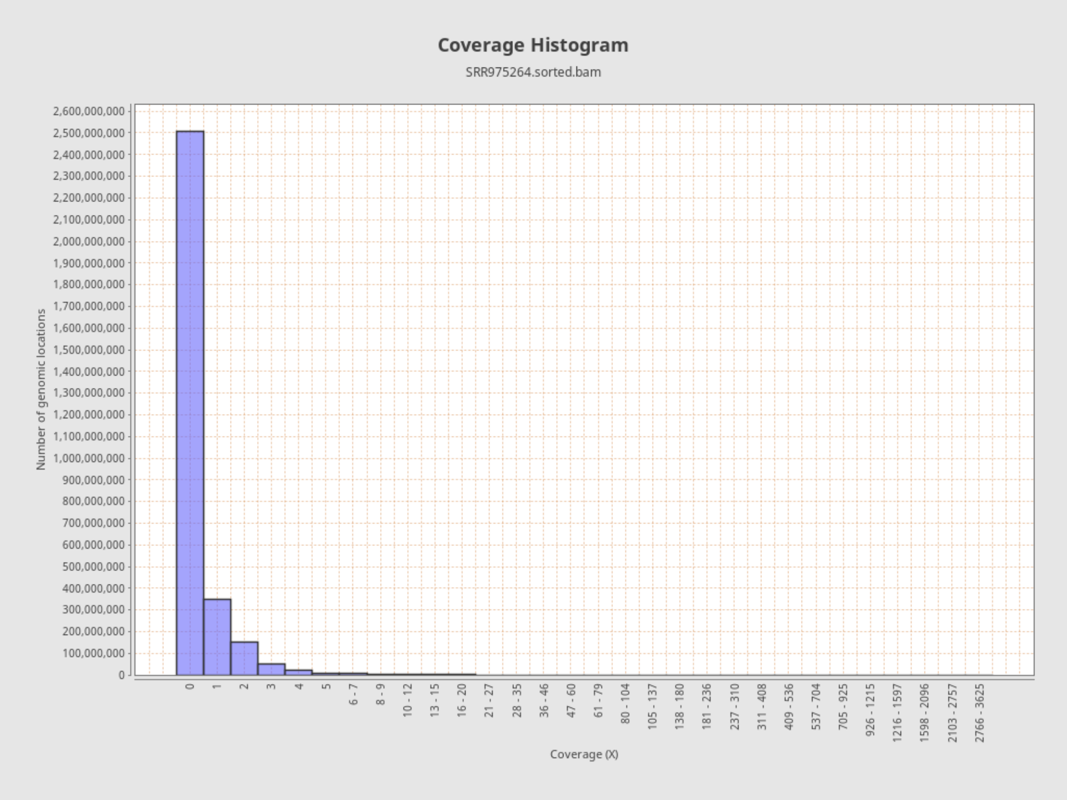
		bases	coverage	deviation
chr1	249250621	72020107	0.2889	3.2143
chr2	243199373	85782481	0.3527	3.6498
chr3	198022430	65221263	0.3294	0.8724
chr4	191154276	57805881	0.3024	1.8078
chr5	180915260	76768519	0.4243	0.9792
chr6	171115067	55338290	0.3234	1.9763
chr7	159138663	73699046	0.4631	3.4674
chr8	146364022	79889102	0.5458	1.836
chr9	141213431	35415494	0.2508	4.8708
chr10	135534747	51206705	0.3778	4.7457
chr11	135006516	54626380	0.4046	2.2657
chr12	133851895	49335794	0.3686	0.9124
chr13	115169878	14249783	0.1237	0.4759
chr14	107349540	28756969	0.2679	0.862
chr15	102531392	24271292	0.2367	0.7004
chr16	90354753	37991307	0.4205	4.4553
chr17	81195210	28712847	0.3536	3.6369
chr18	78077248	22155010	0.2838	4.8342
chr19	59128983	12832695	0.217	1.9917
chr20	63025520	22041738	0.3497	0.9618
chr21	48129895	12128513	0.252	1.0861
chr22	51304566	10890459	0.2123	0.725
chrMT	16571	1281061	77.3074	38.0381
chrX	155270560	67828750	0.4368	1.5686

chrY	59373566	2315750	0.039	1.7892

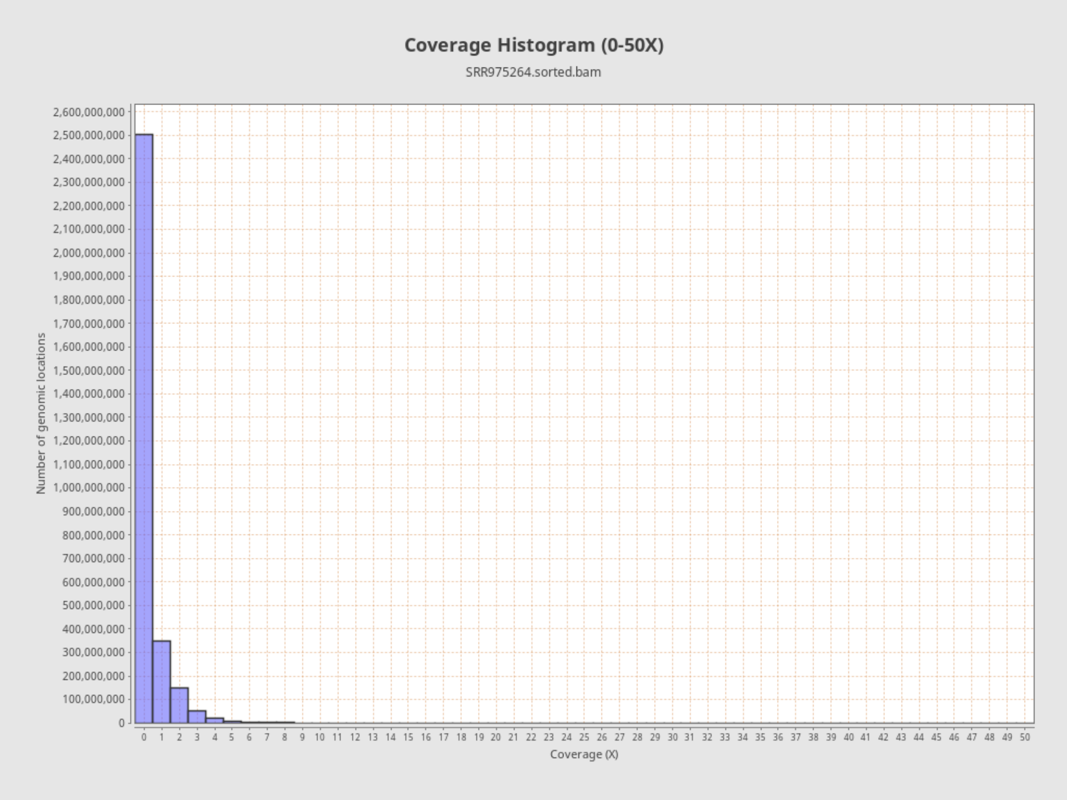
3. Results : Coverage across reference



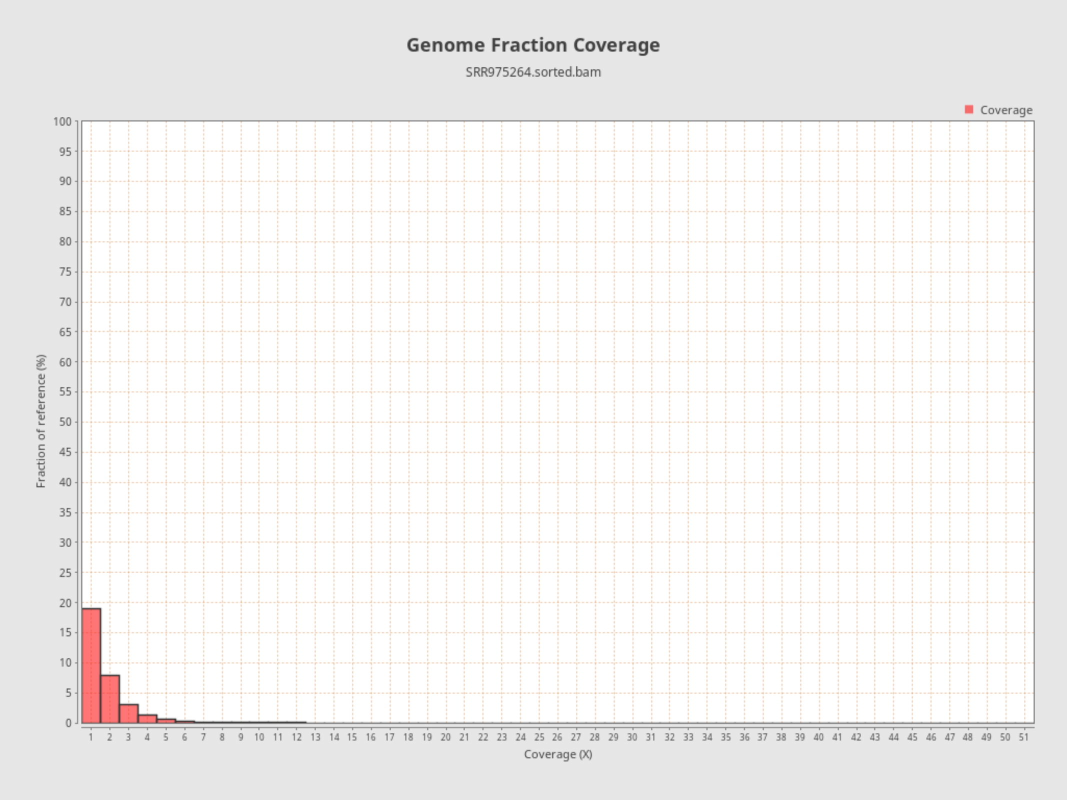
4. Results : Coverage Histogram



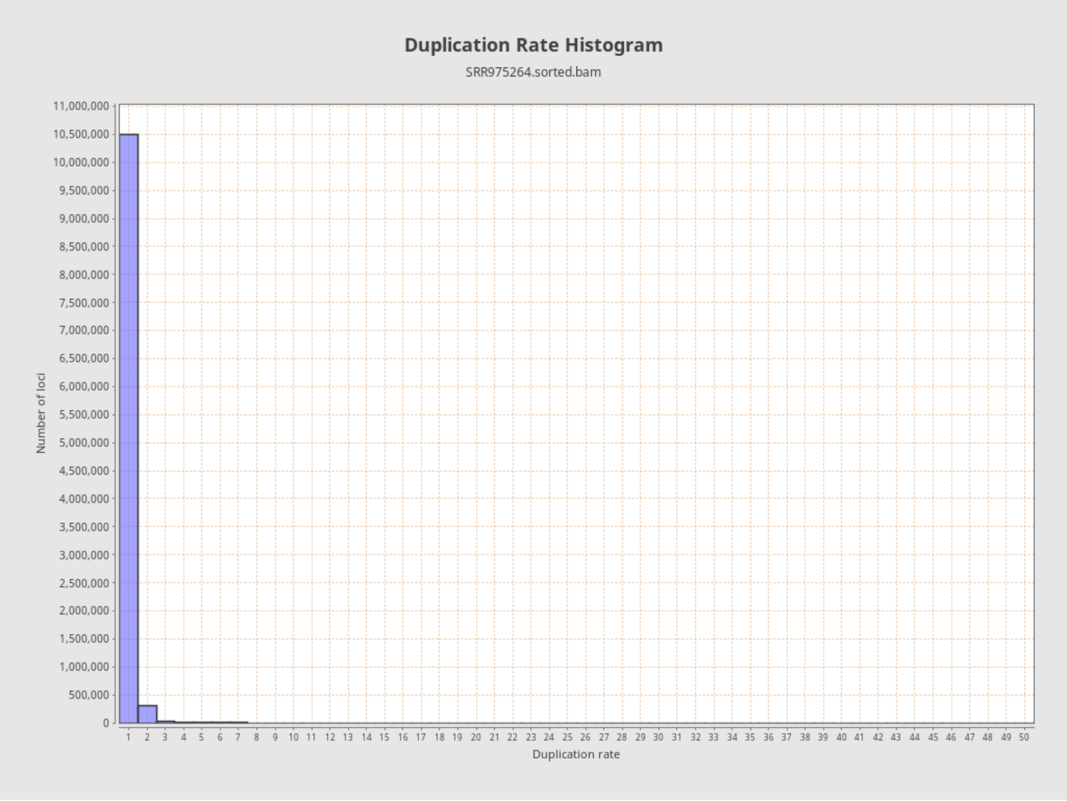
5. Results : Coverage Histogram (0-50X)



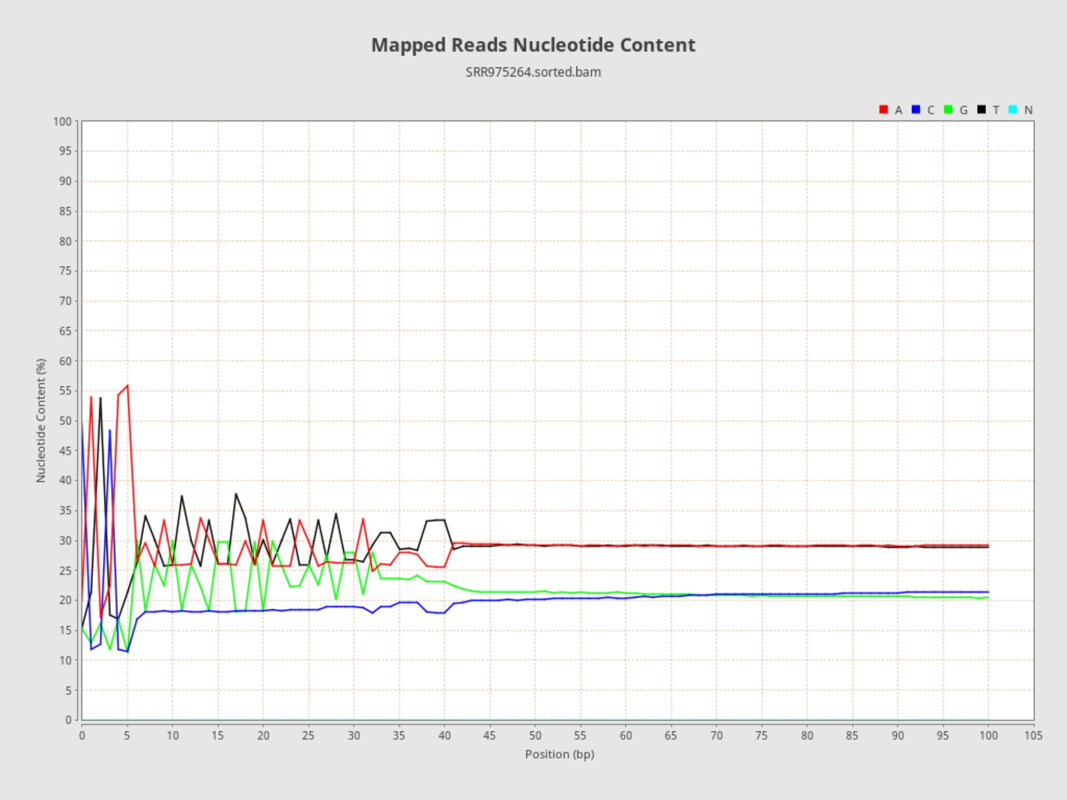
6. Results : Genome Fraction Coverage



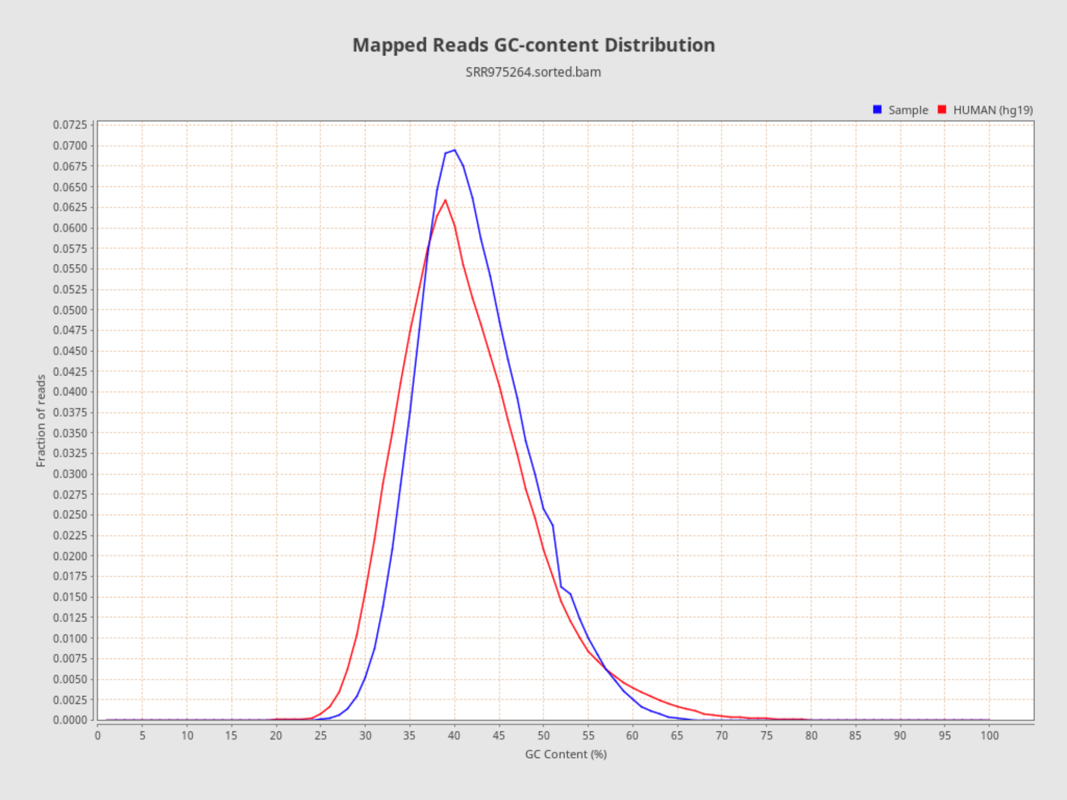
7. Results : Duplication Rate Histogram



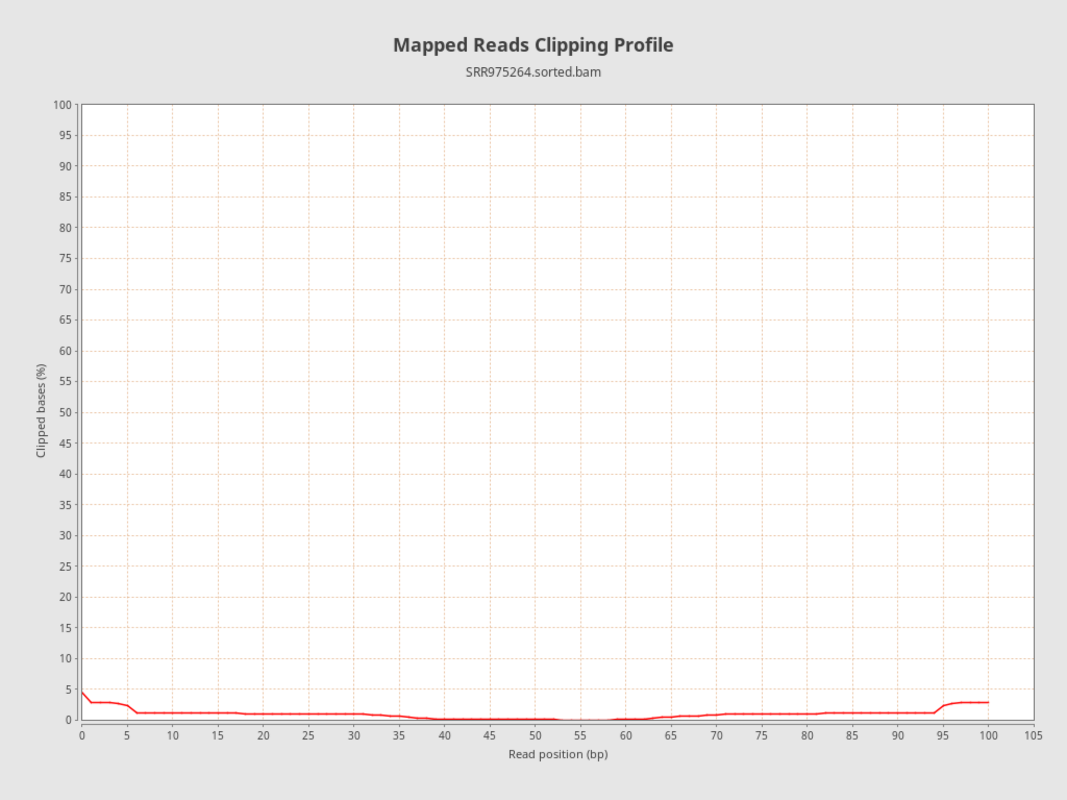
8. Results : Mapped Reads Nucleotide Content



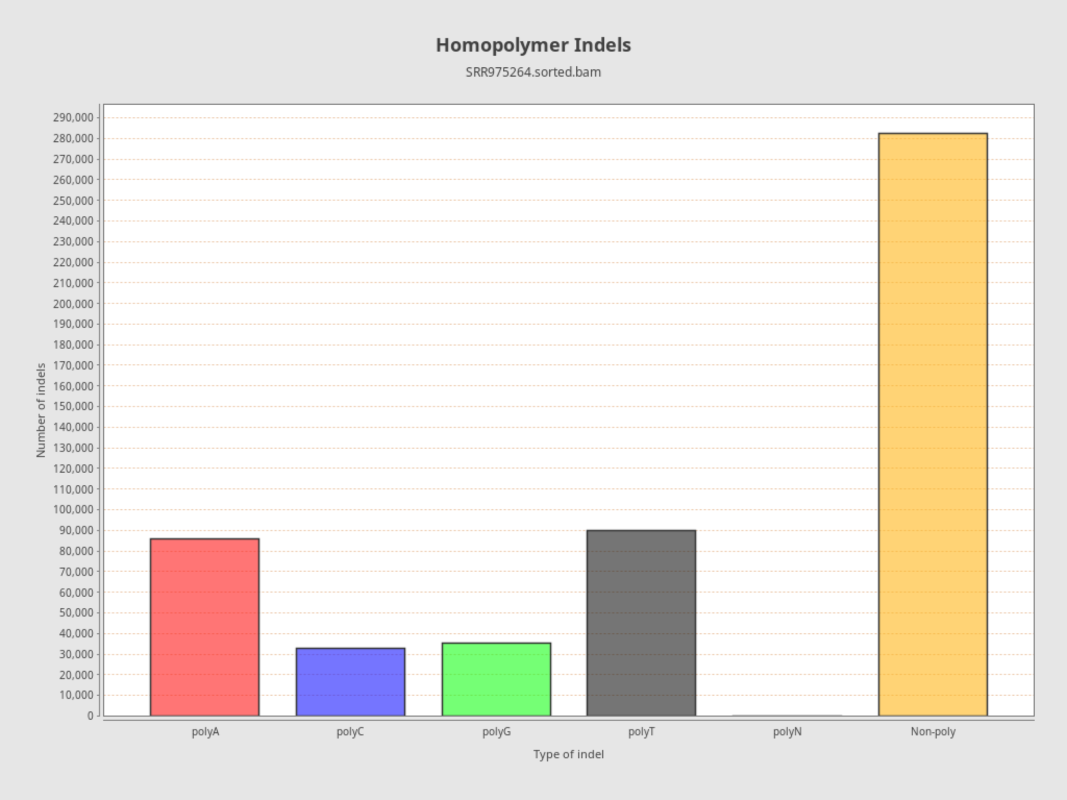
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

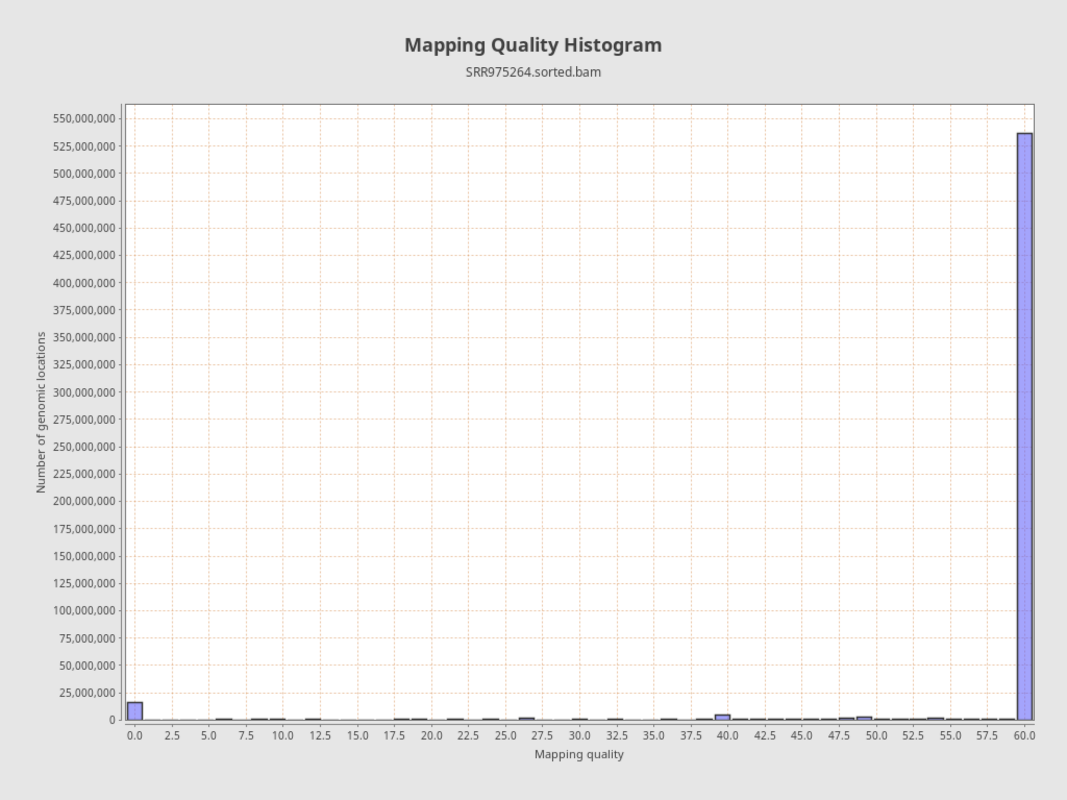


11. Results : Homopolymer Indels

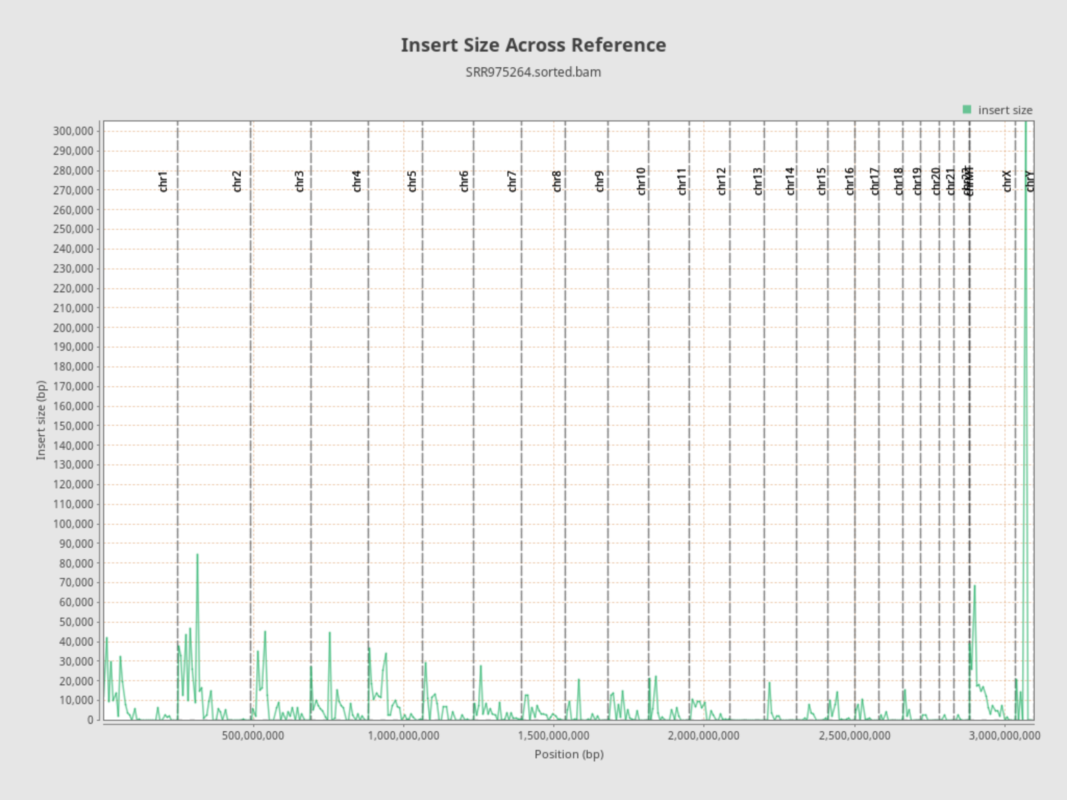


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram