Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:10:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975231.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_SRR975231 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975231_1.fastq.gz SRR975231_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:10:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975231.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,464,408
Mapped reads	3,200,547 / 92.38%
Unmapped reads	263,861 / 7.62%
Mapped paired reads	3,200,547 / 92.38%
Mapped reads, first in pair	1,599,758 / 46.18%
Mapped reads, second in pair	1,600,789 / 46.21%
Mapped reads, both in pair	3,191,496 / 92.12%
Mapped reads, singletons	9,051 / 0.26%
Secondary alignments	0
Supplementary alignments	157,820 / 4.56%
Read min/max/mean length	30 / 101 / 102.89
Duplicated reads (estimated)	379,719 / 10.96%
Duplication rate	8.57%
Clipped reads	2,156,339 / 62.24%

2.2. ACGT Content

Number/percentage of A's	83,877,947 / 27.68%
Number/percentage of C's	66,863,212 / 22.06%
Number/percentage of T's	85,236,375 / 28.12%
Number/percentage of G's	67,087,102 / 22.14%
Number/percentage of N's	4,074 / 0%

GC Percentage	44.2%

2.3. Coverage

Mean	0.0979
Standard Deviation	1.9468

2.4. Mapping Quality

Mean Mapping Quality	51.09

2.5. Insert size

Mean	314,071.83
Standard Deviation	5,467,586.88
P25/Median/P75	106 / 126 / 150

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	2,194,070
Insertions	62,966
Mapped reads with at least one insertion	1.91%
Deletions	57,652
Mapped reads with at least one deletion	1.74%
Homopolymer indels	36.78%

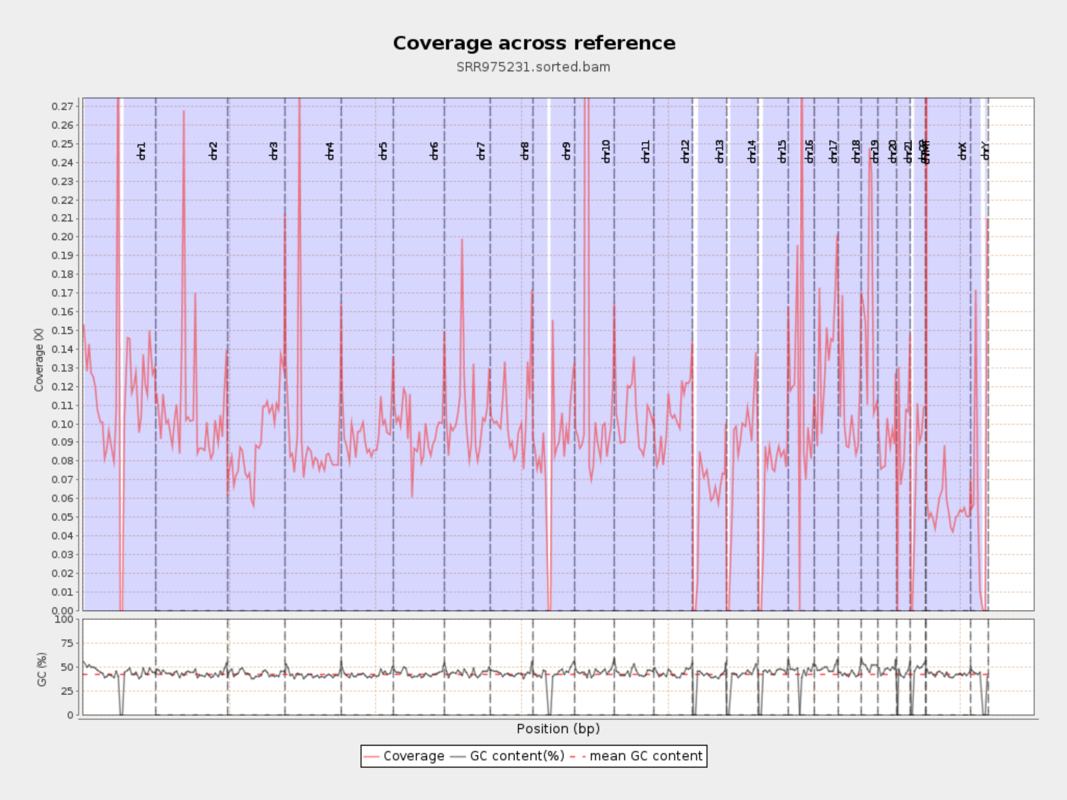
2.7. Chromosome stats

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

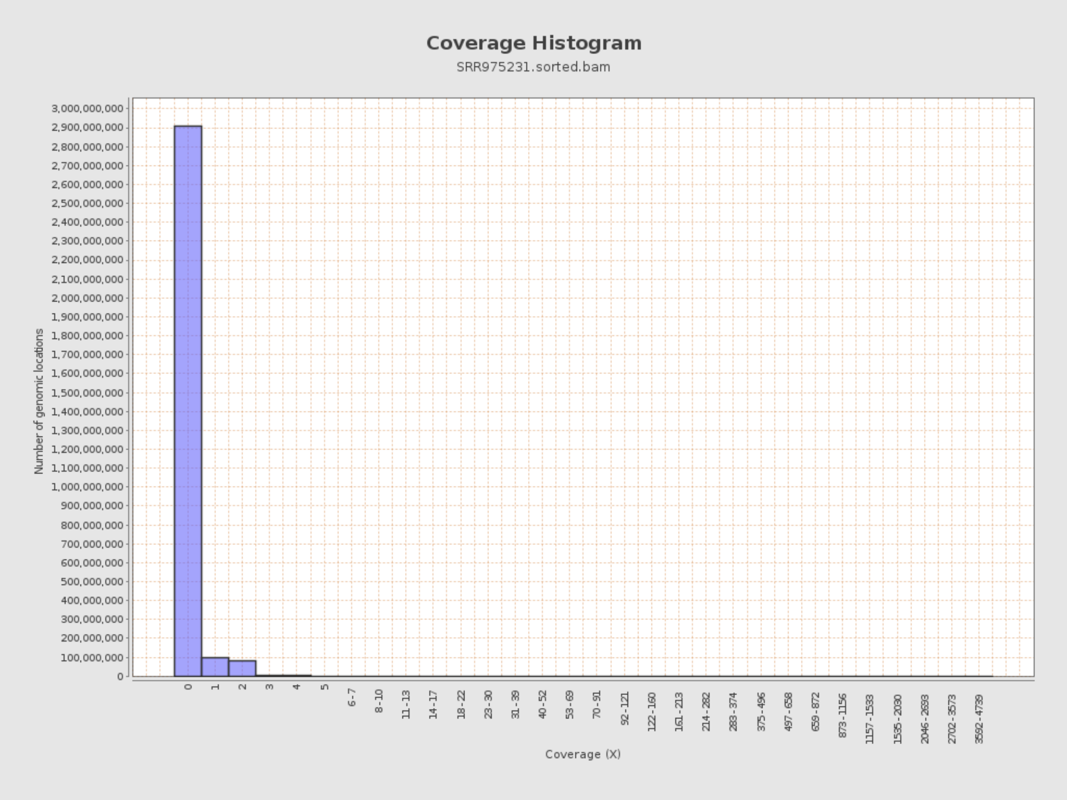
		bases	coverage	deviation
chr1	249250621	28893048	0.1159	4.5375
chr2	243199373	26081790	0.1072	1.1865
chr3	198022430	18124018	0.0915	0.7605
chr4	191154276	17879473	0.0935	1.3081
chr5	180915260	17299593	0.0956	0.4185
chr6	171115067	16345891	0.0955	0.5424
chr7	159138663	17094646	0.1074	1.3521
chr8	146364022	15139173	0.1034	0.8175
chr9	141213431	11972816	0.0848	1.3448
chr10	135534747	17191658	0.1268	5.2198
chr11	135006516	14014239	0.1038	0.85
chr12	133851895	13900679	0.1039	0.4459
chr13	115169878	6766324	0.0588	0.3167
chr14	107349540	9139576	0.0851	0.4081
chr15	102531392	6841333	0.0667	0.3364
chr16	90354753	11058710	0.1224	1.6691
chr17	81195210	11097903	0.1367	1.0928
chr18	78077248	8316815	0.1065	1.8692
chr19	59128983	9452873	0.1599	2.377
chr20	63025520	5636329	0.0894	0.5654
chr21	48129895	4531967	0.0942	0.8734
chr22	51304566	3635945	0.0709	0.6188
chrMT	16571	162185	9.7873	4.9037
chrX	155270560	8443177	0.0544	0.5293

chrY	59373566	4188128	0.0705	1.612

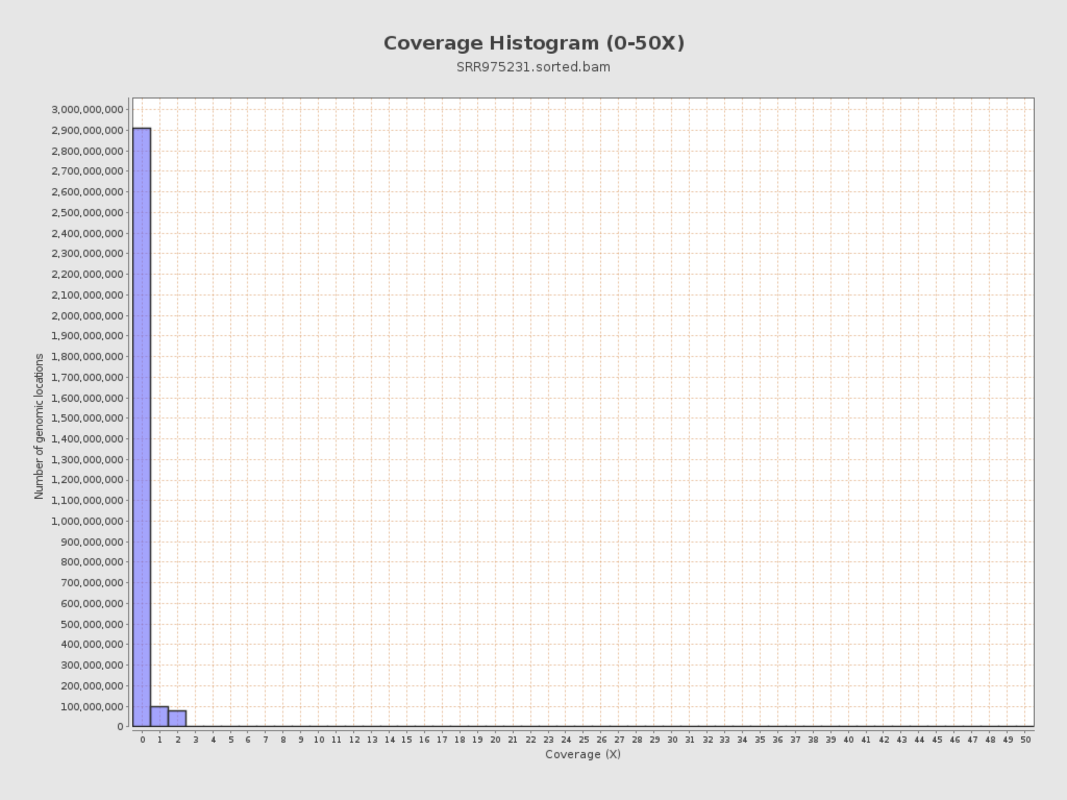
3. Results : Coverage across reference



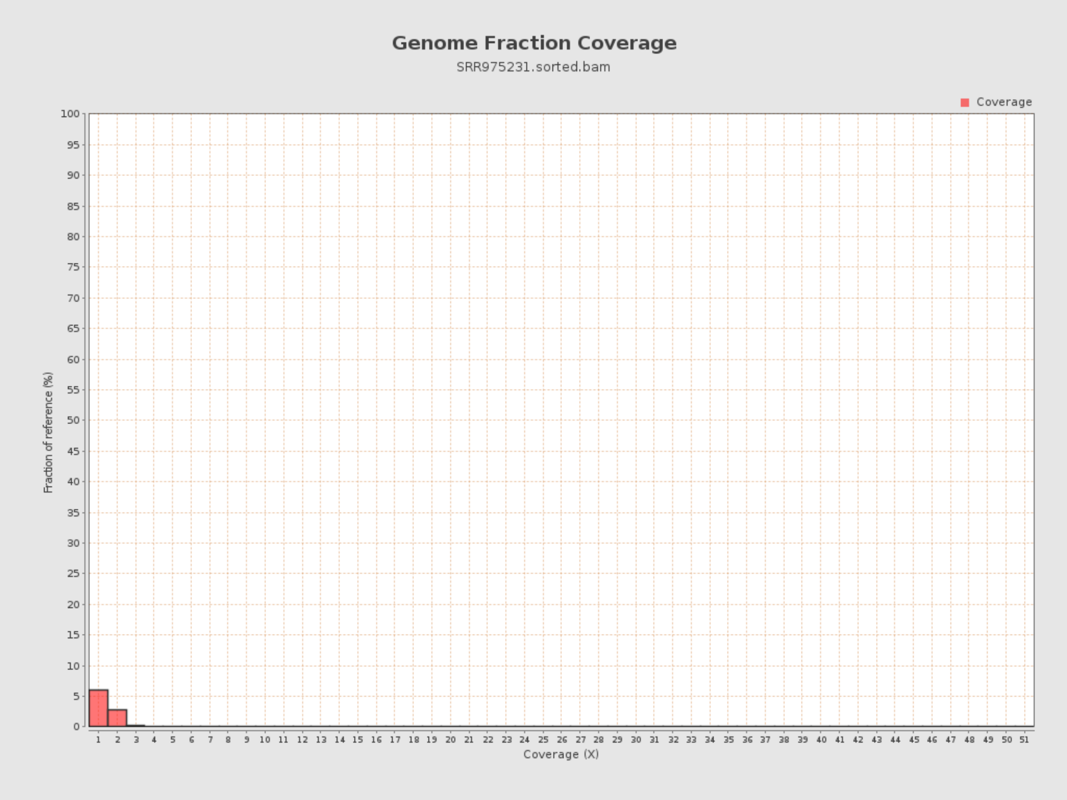
4. Results : Coverage Histogram



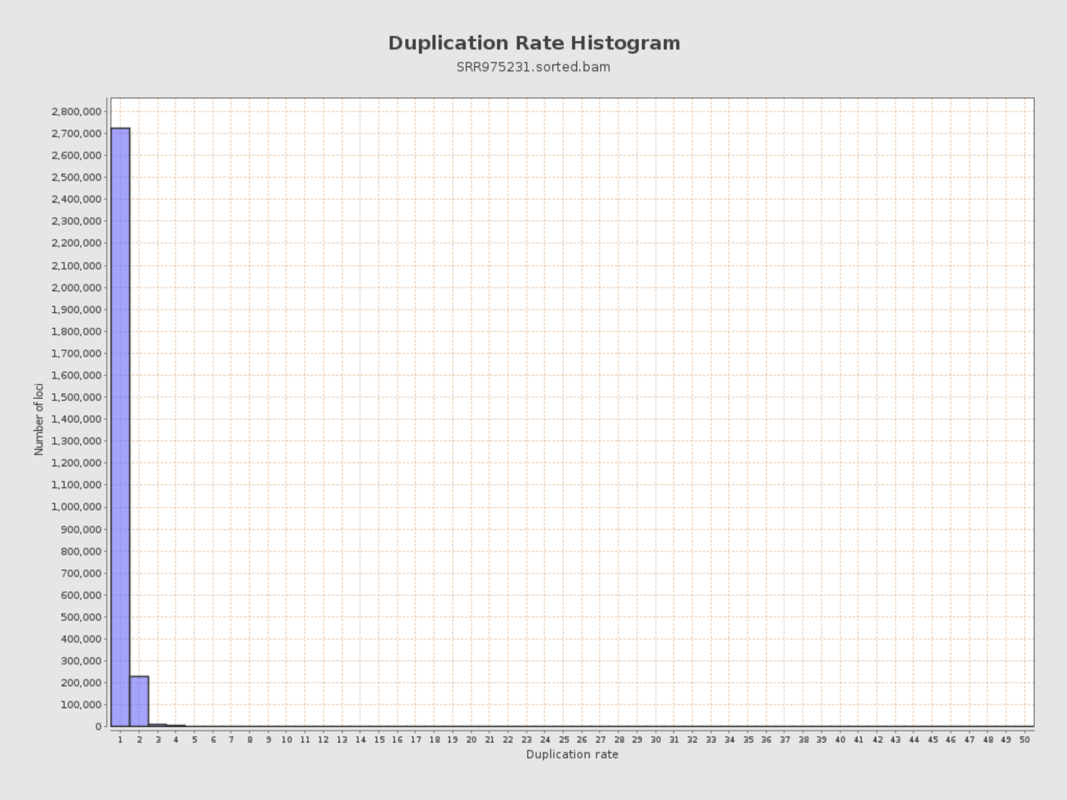
5. Results : Coverage Histogram (0-50X)



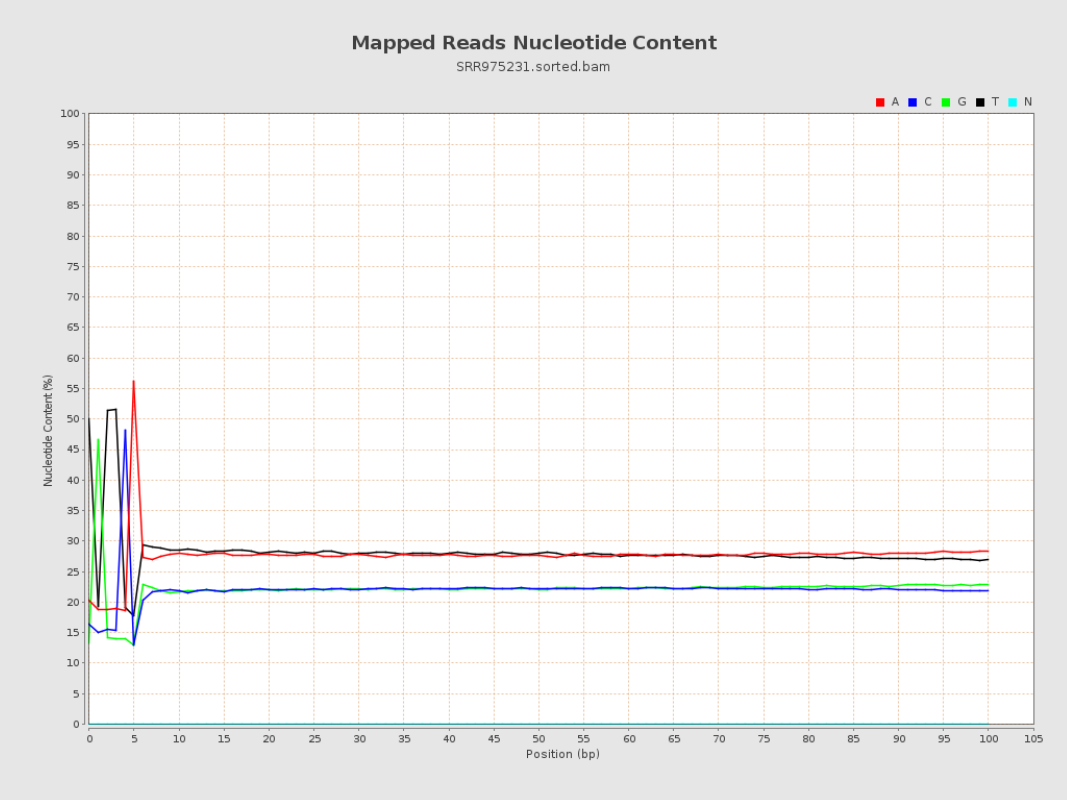
6. Results : Genome Fraction Coverage



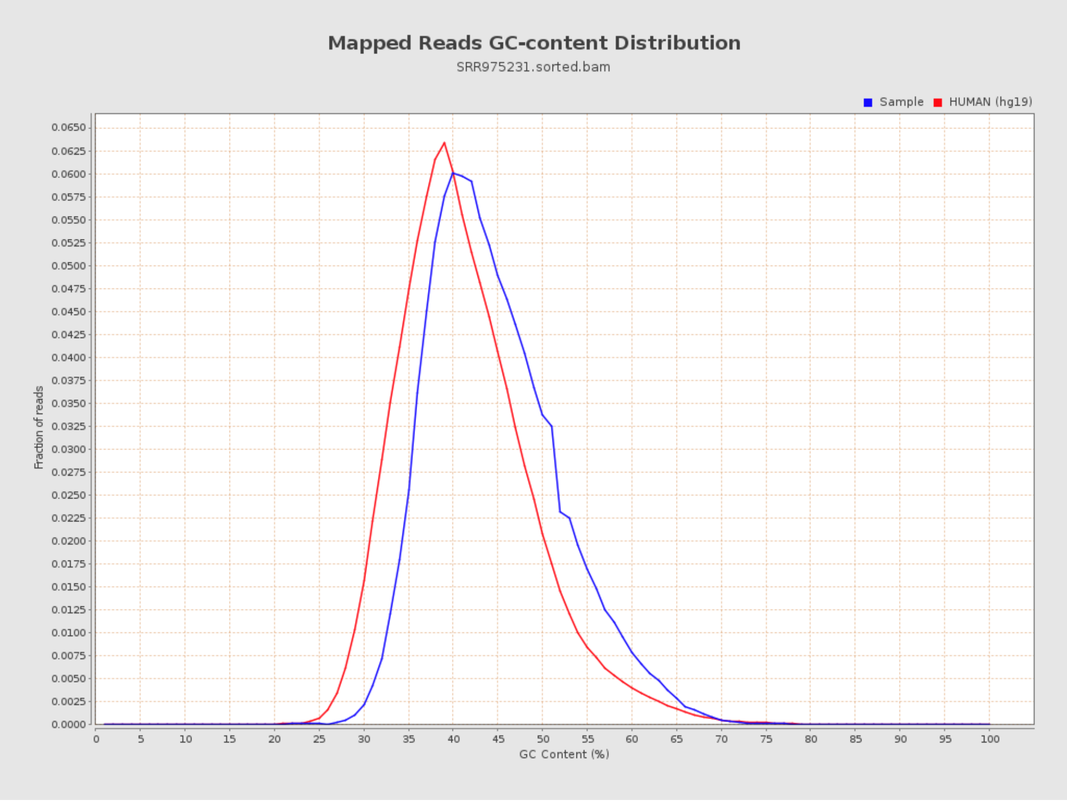
7. Results : Duplication Rate Histogram



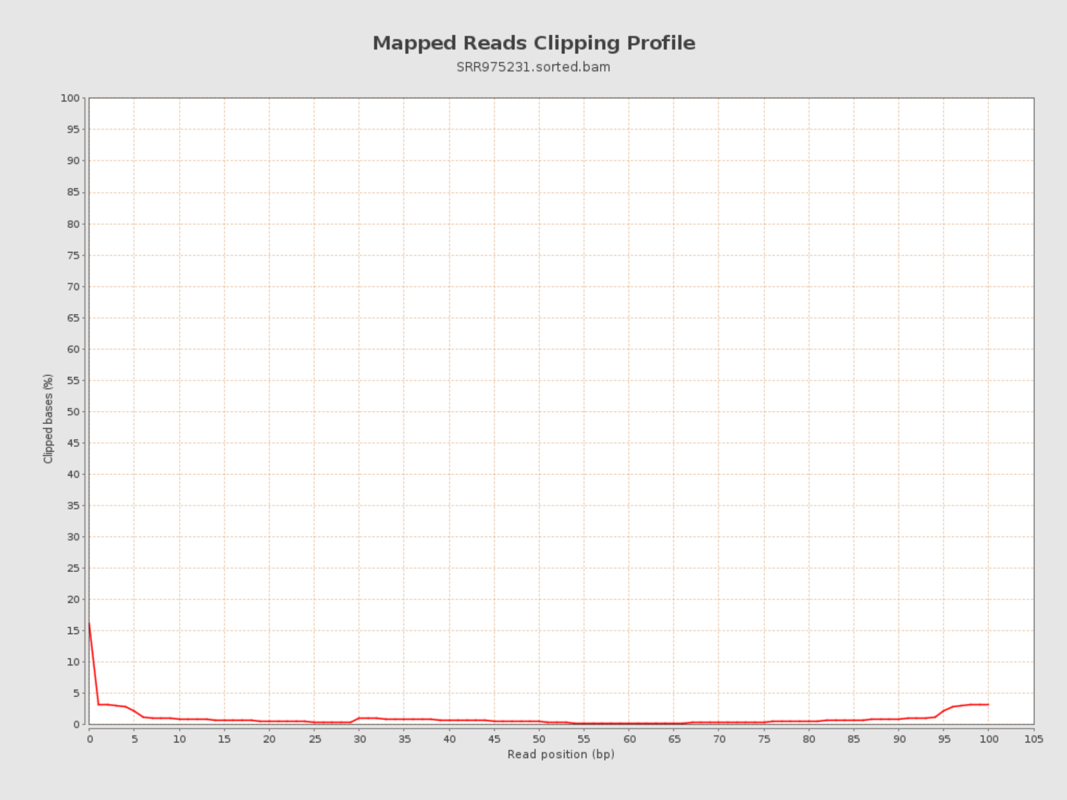
8. Results : Mapped Reads Nucleotide Content



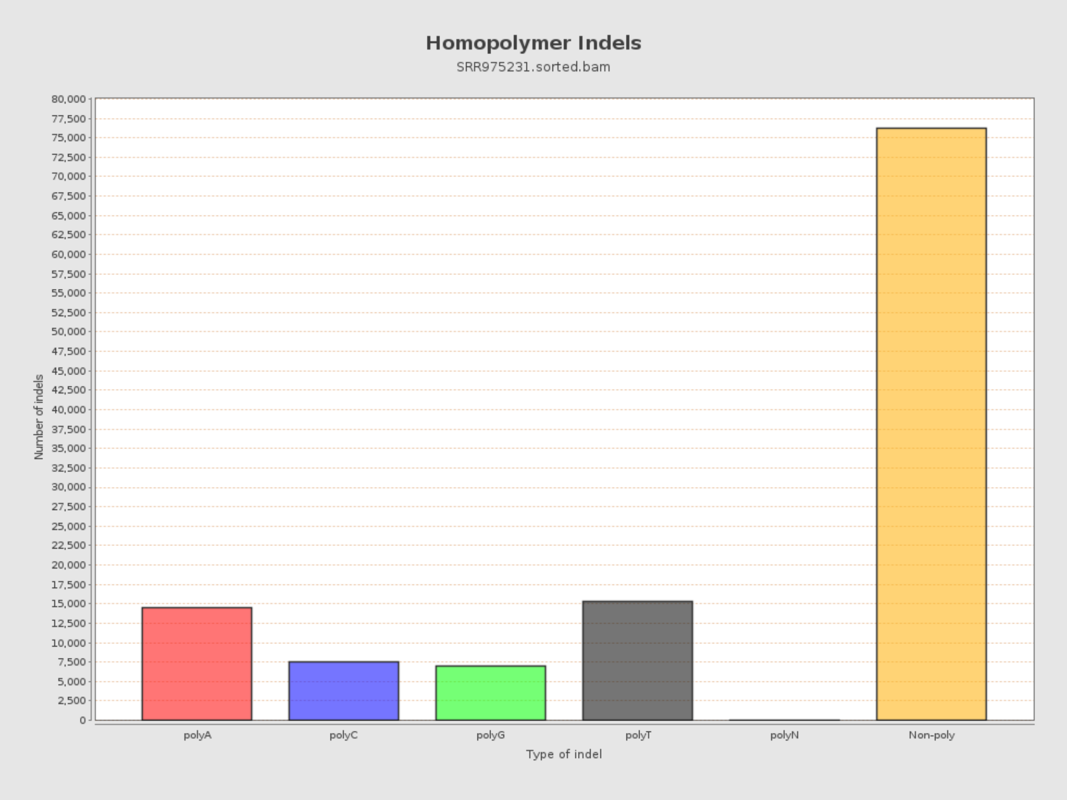
9. Results : Mapped Reads GC-content Distribution



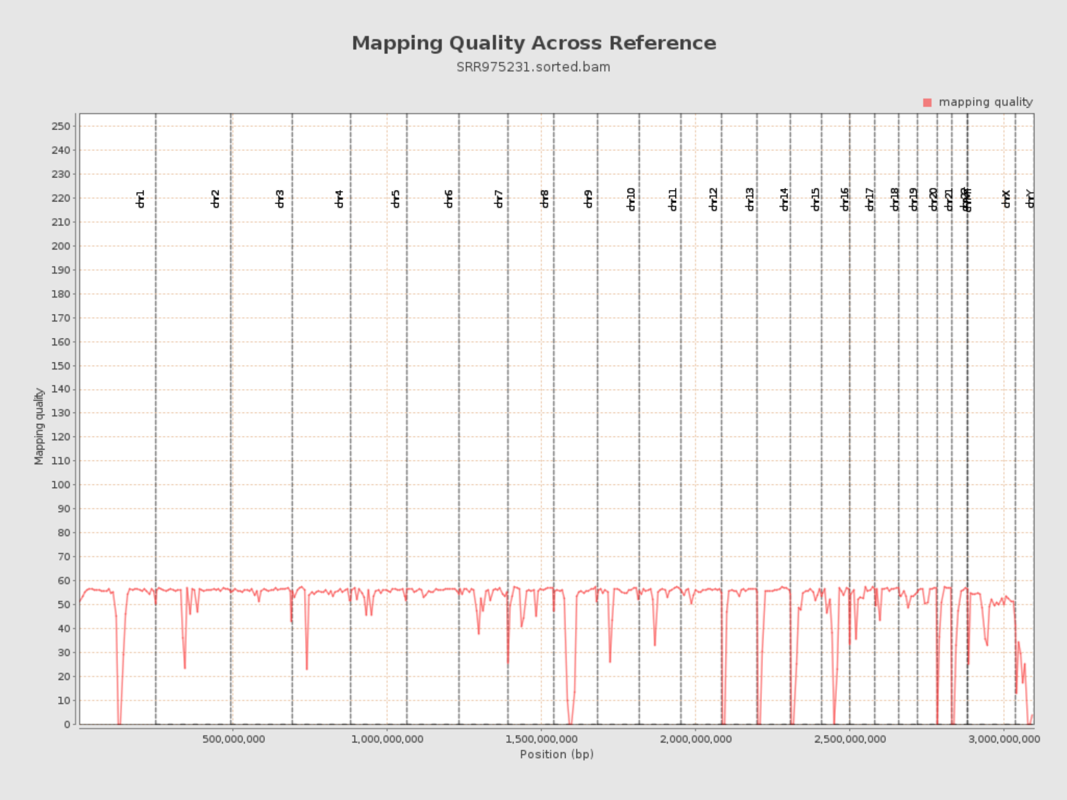
10. Results : Mapped Reads Clipping Profile



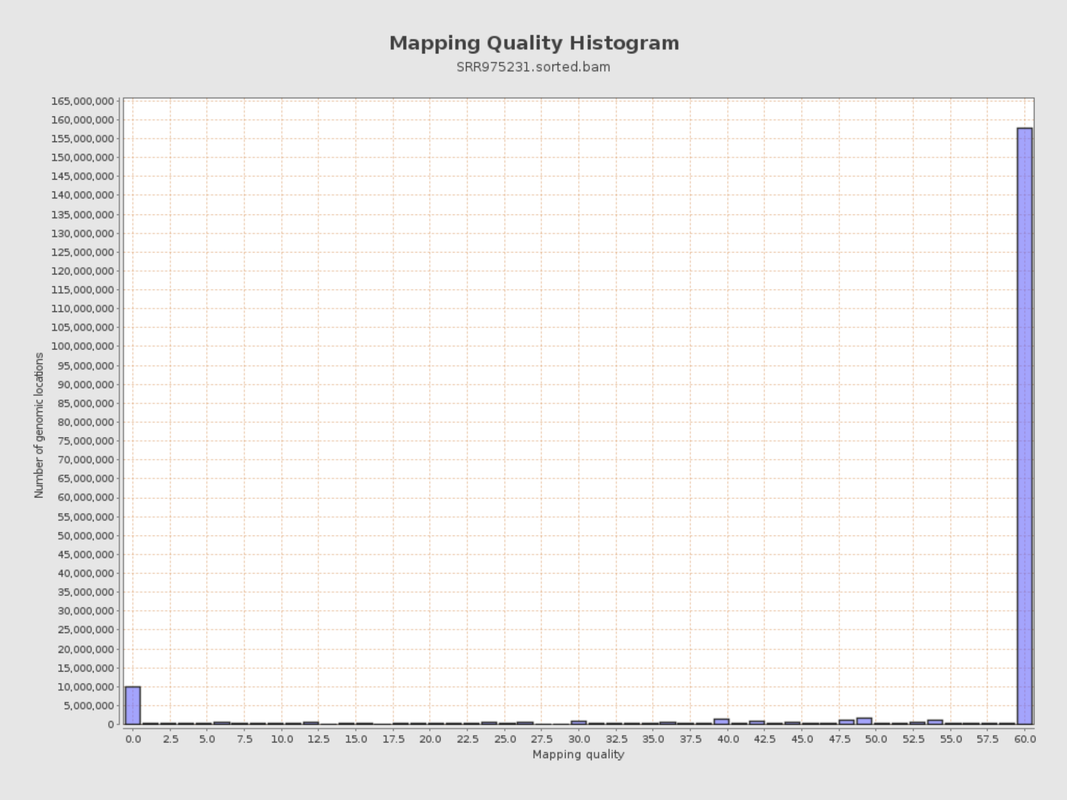
11. Results : Homopolymer Indels



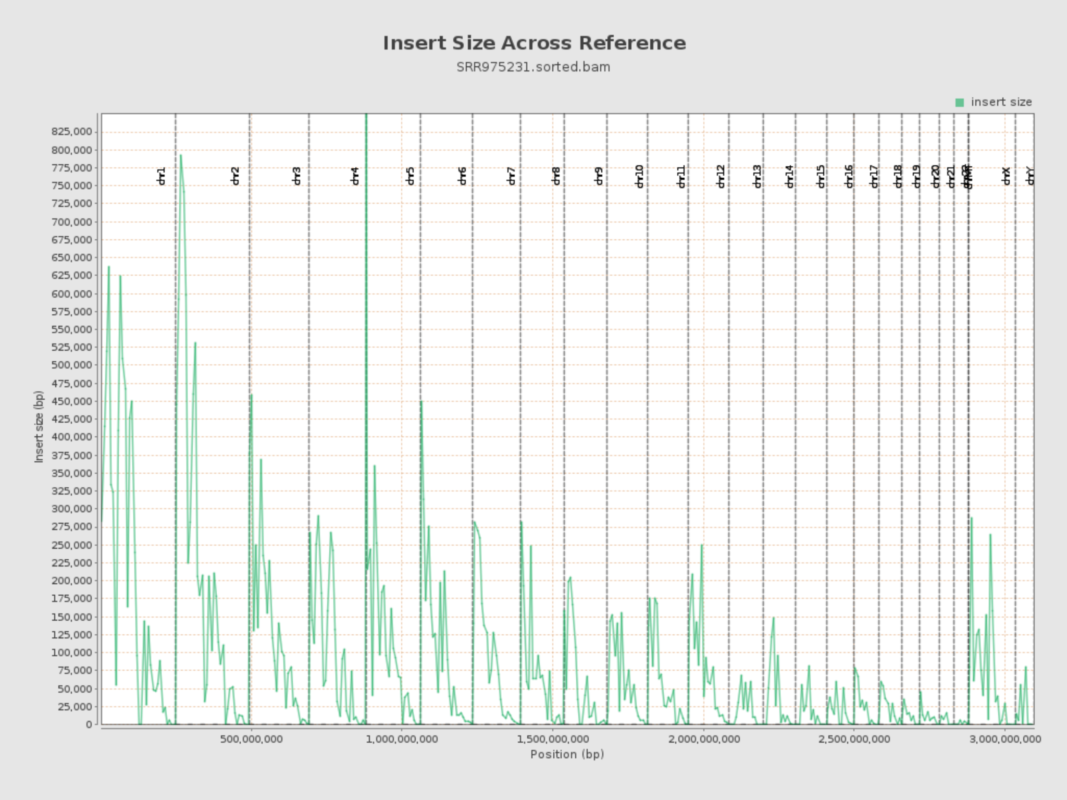
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram