Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 04:41:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975323.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_SRR975323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975323_1.fastq.gz SRR975323_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 04:41:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,476,888
Mapped reads	4,430,810 / 98.97%
Unmapped reads	46,078 / 1.03%
Mapped paired reads	4,430,810 / 98.97%
Mapped reads, first in pair	2,214,572 / 49.47%
Mapped reads, second in pair	2,216,238 / 49.5%
Mapped reads, both in pair	4,415,640 / 98.63%
Mapped reads, singletons	15,170 / 0.34%
Secondary alignments	0
Supplementary alignments	27,198 / 0.61%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	307,537 / 6.87%
Duplication rate	3.32%
Clipped reads	2,657,681 / 59.36%

2.2. ACGT Content

Number/percentage of A's	121,835,331 / 29.29%
Number/percentage of C's	84,484,881 / 20.31%
Number/percentage of T's	122,968,254 / 29.56%
Number/percentage of G's	86,683,698 / 20.84%
Number/percentage of N's	8,579 / 0%

GC Percentage	41.15%

2.3. Coverage

Mean	0.1345
Standard Deviation	2.3347

2.4. Mapping Quality

Mean Mapping Quality	52.7

2.5. Insert size

Mean	95,038.46
Standard Deviation	2,923,402.95
P25/Median/P75	141 / 174 / 222

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	3,186,630
Insertions	71,120
Mapped reads with at least one insertion	1.57%
Deletions	139,818
Mapped reads with at least one deletion	3.09%
Homopolymer indels	45.62%

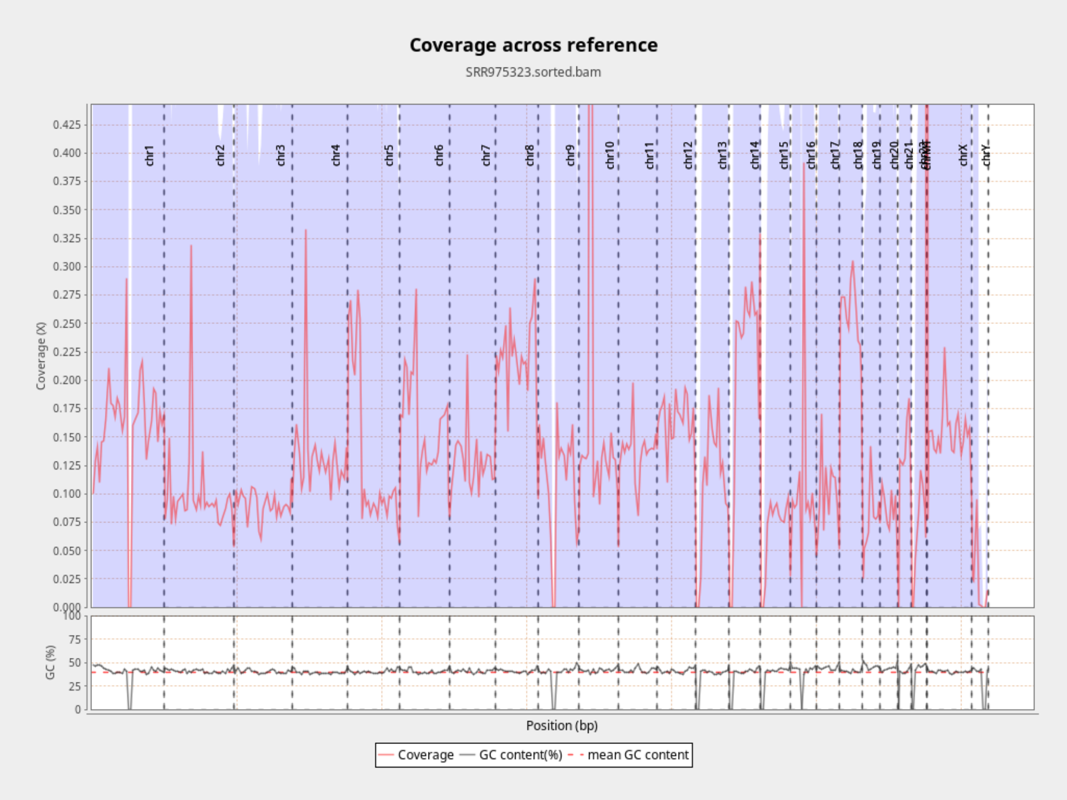
2.7. Chromosome stats

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

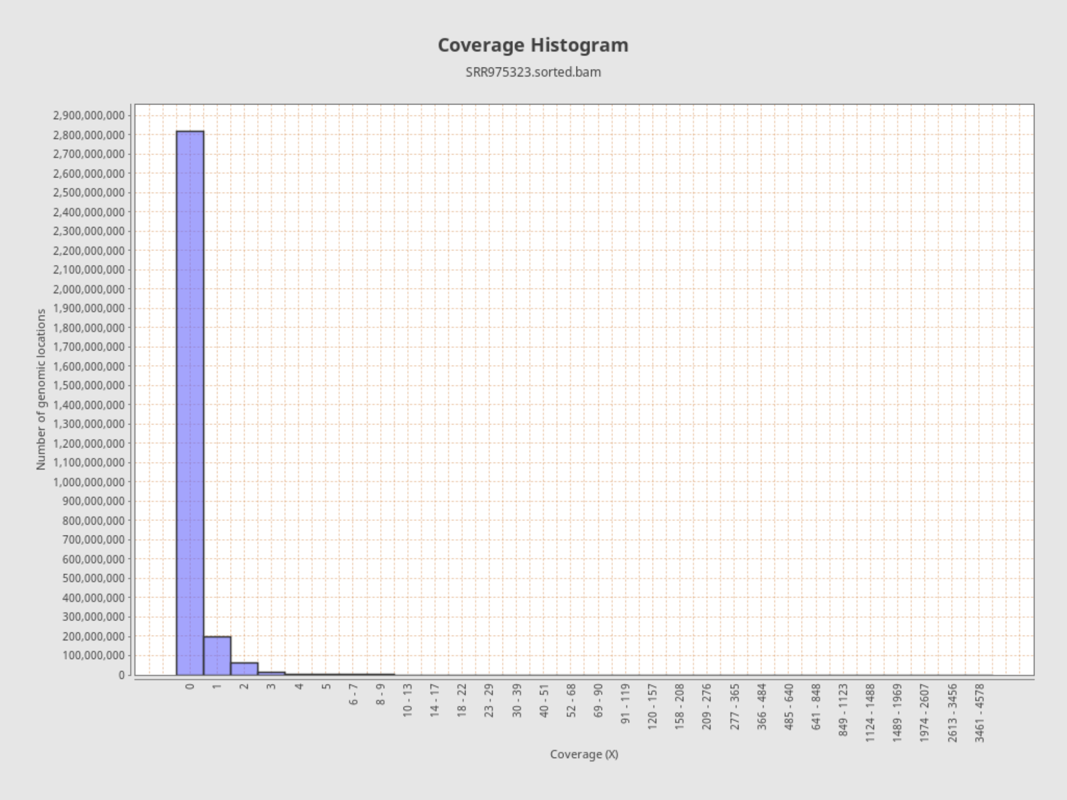
		bases	coverage	deviation
chr1	249250621	39361447	0.1579	1.7976
chr2	243199373	24310099	0.1	1.5274
chr3	198022430	17759113	0.0897	0.6319
chr4	191154276	25528489	0.1335	1.3129
chr5	180915260	23615733	0.1305	0.4764
chr6	171115067	27510209	0.1608	1.6836
chr7	159138663	20214257	0.127	1.9138
chr8	146364022	32341225	0.221	0.8434
chr9	141213431	15818255	0.112	1.7728
chr10	135534747	24744699	0.1826	9.28
chr11	135006516	18350710	0.1359	1.5783
chr12	133851895	22128503	0.1653	0.5301
chr13	115169878	12683591	0.1101	0.4238
chr14	107349540	22334596	0.2081	0.6343
chr15	102531392	6921229	0.0675	0.3244
chr16	90354753	9516298	0.1053	1.9511
chr17	81195210	8174665	0.1007	1.483
chr18	78077248	20404586	0.2613	2.5204
chr19	59128983	4575537	0.0774	0.9588
chr20	63025520	5410051	0.0858	0.4816
chr21	48129895	6159461	0.128	0.6859
chr22	51304566	3550317	0.0692	0.3416
chrMT	16571	88243	5.3251	6.4561
chrX	155270560	23529547	0.1515	0.8357

chrY	59373566	1191130	0.0201	1.1866

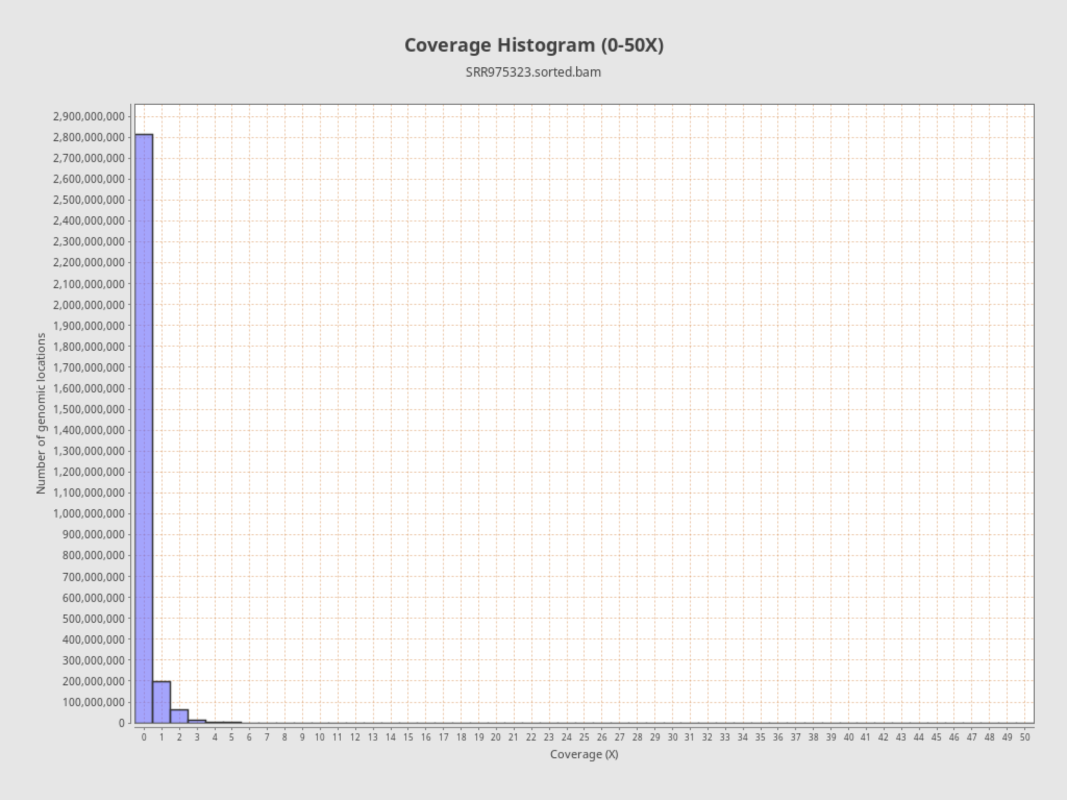
3. Results : Coverage across reference



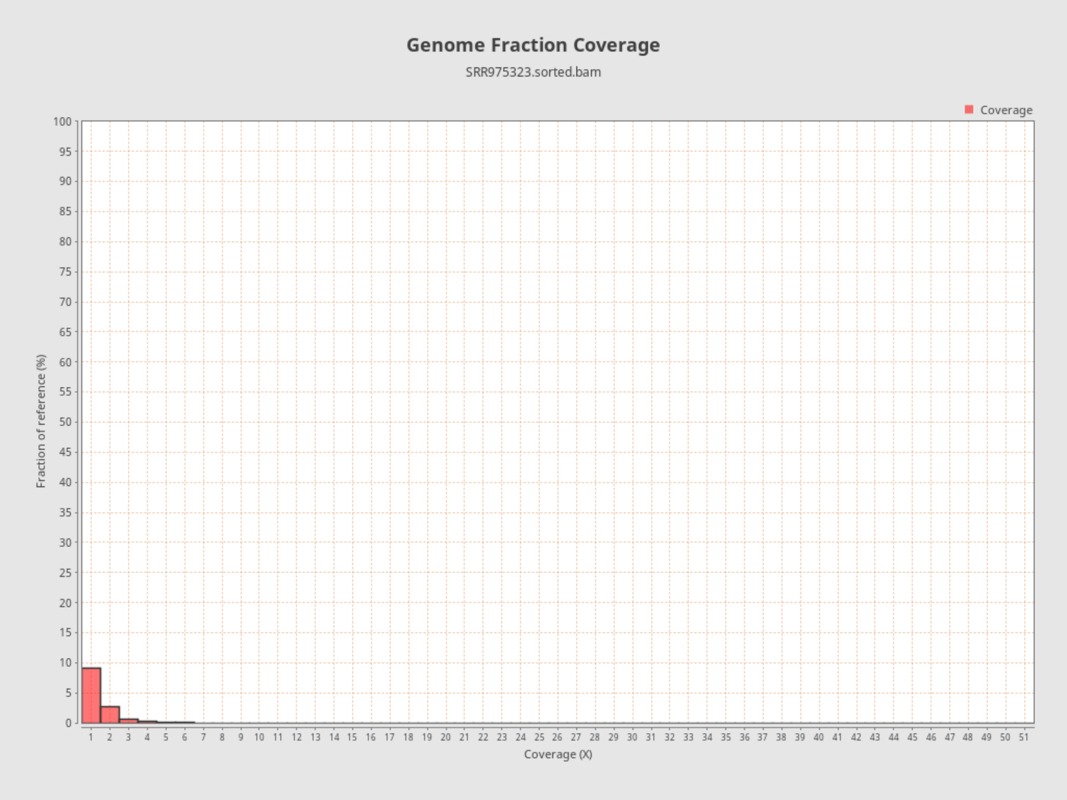
4. Results : Coverage Histogram



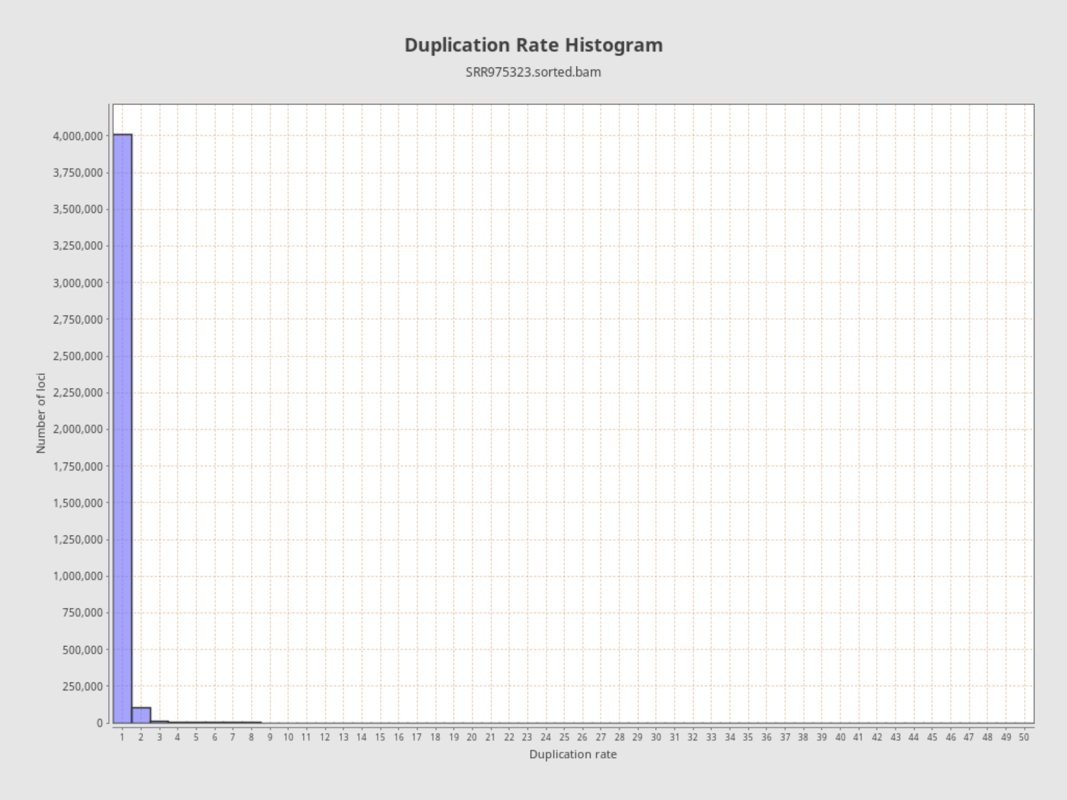
5. Results : Coverage Histogram (0-50X)



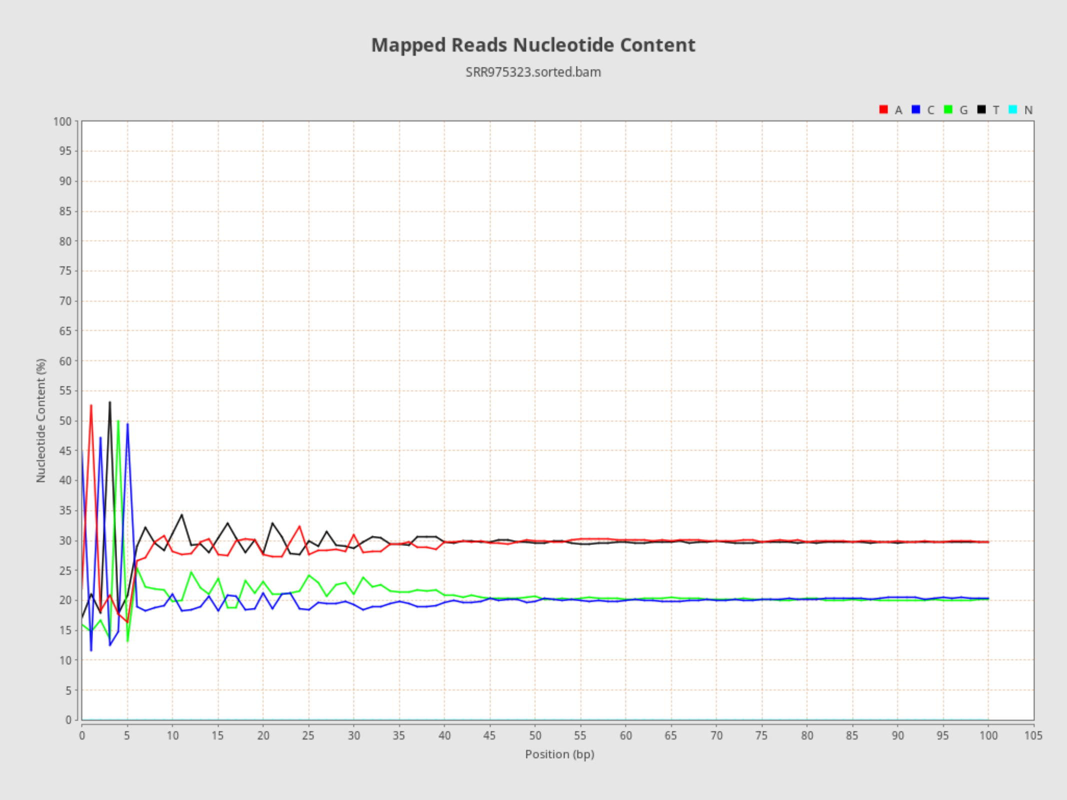
6. Results : Genome Fraction Coverage



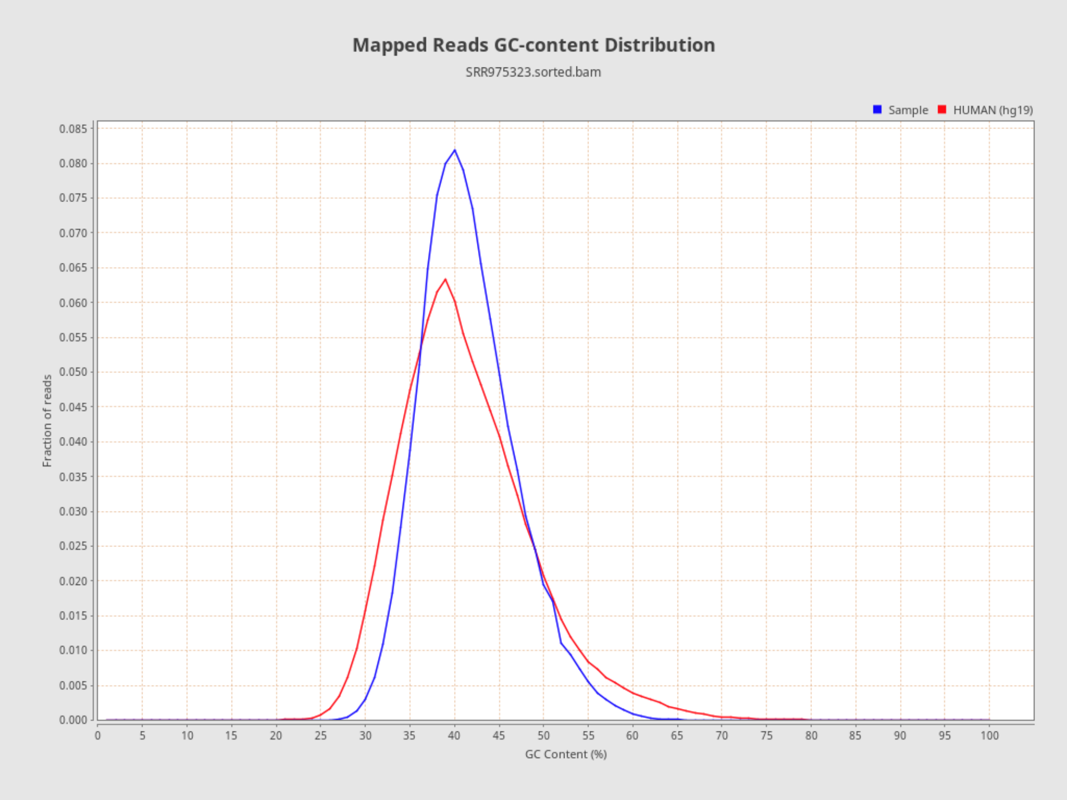
7. Results : Duplication Rate Histogram



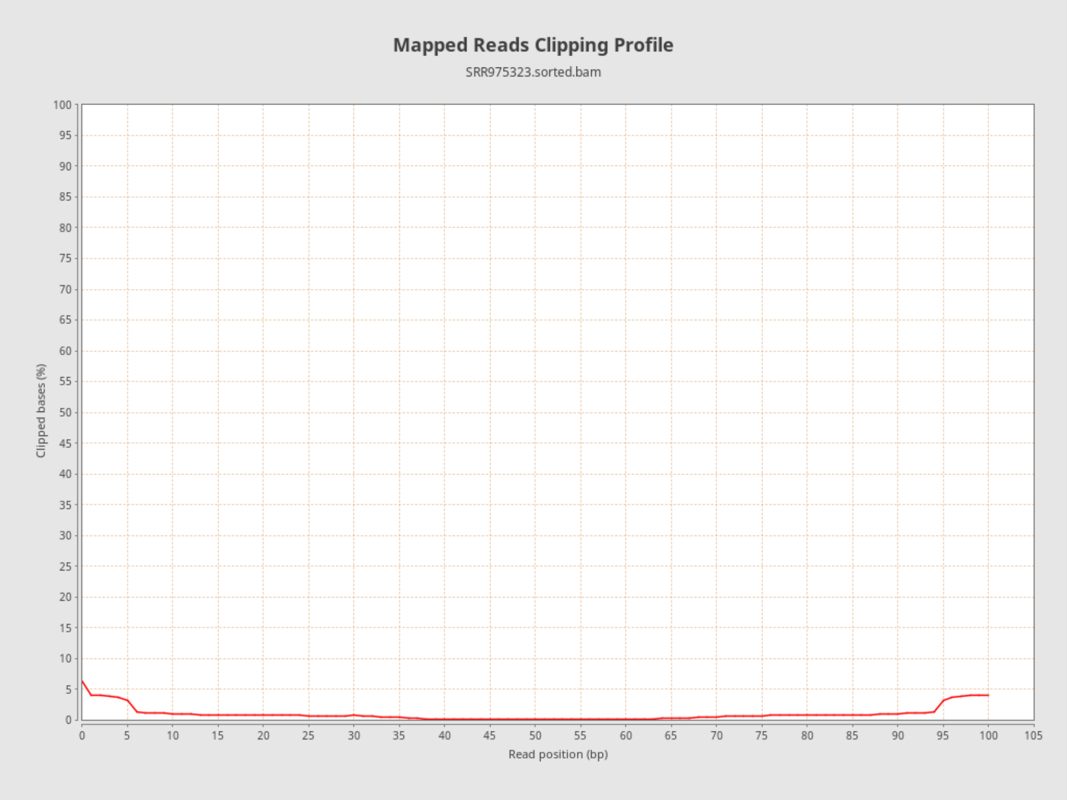
8. Results : Mapped Reads Nucleotide Content



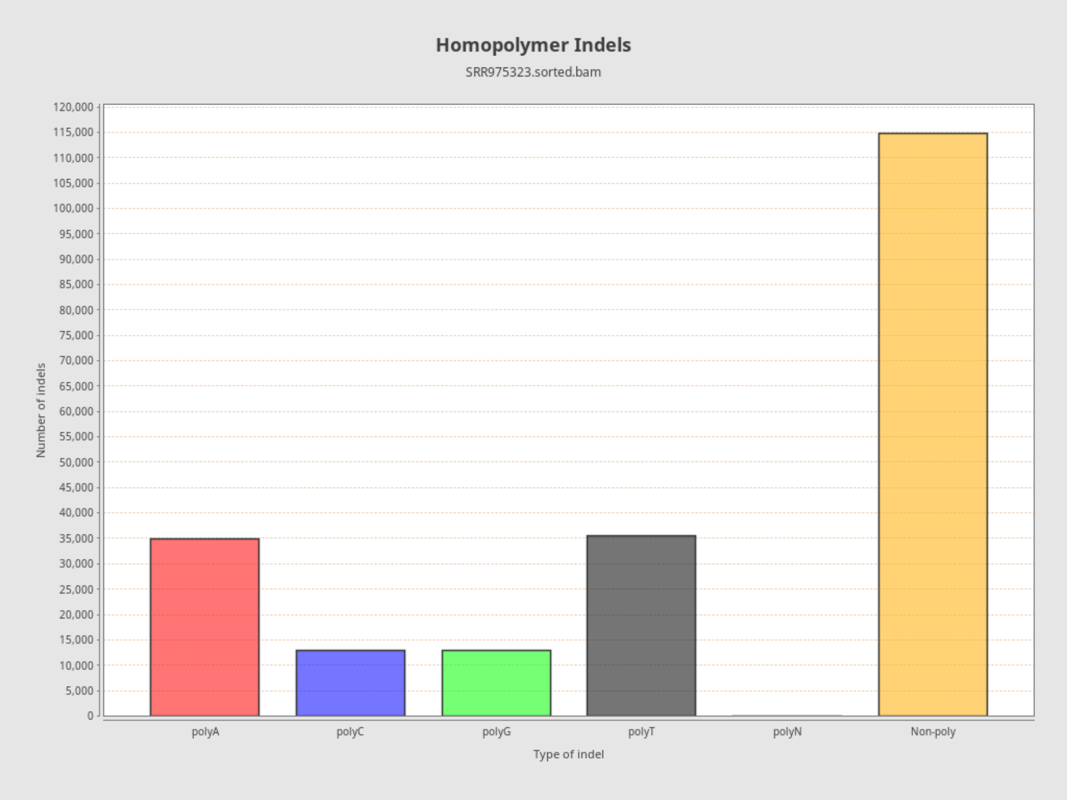
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

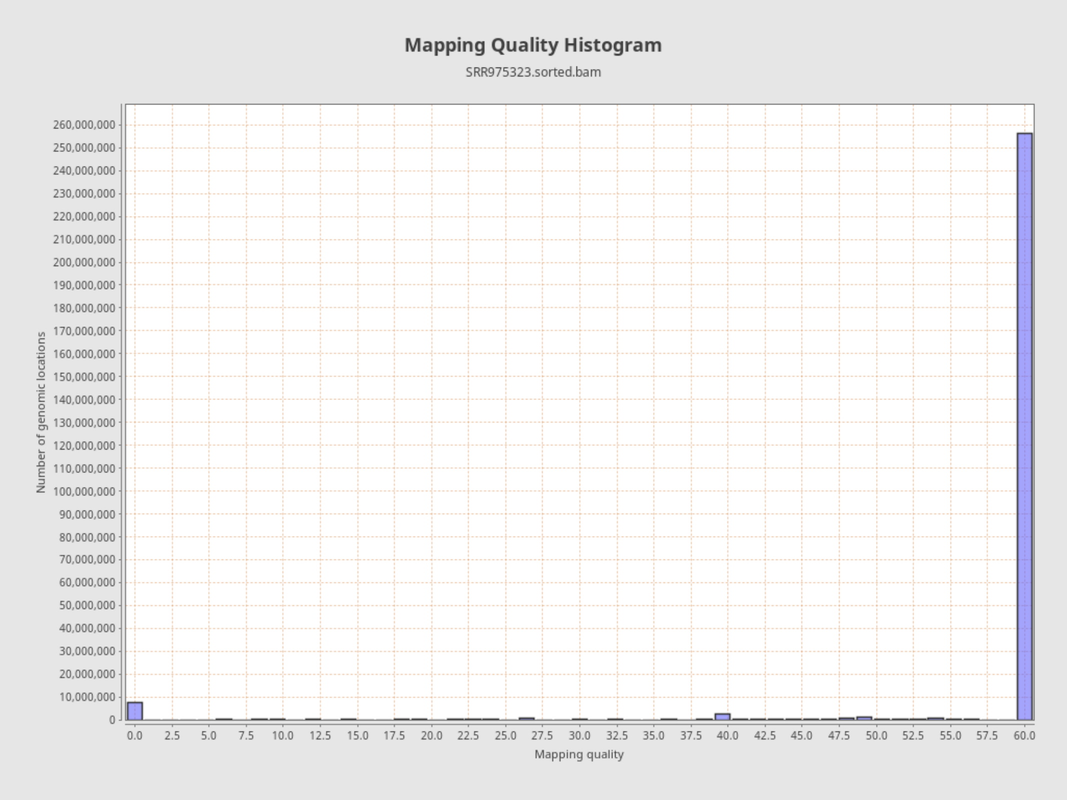


11. Results : Homopolymer Indels

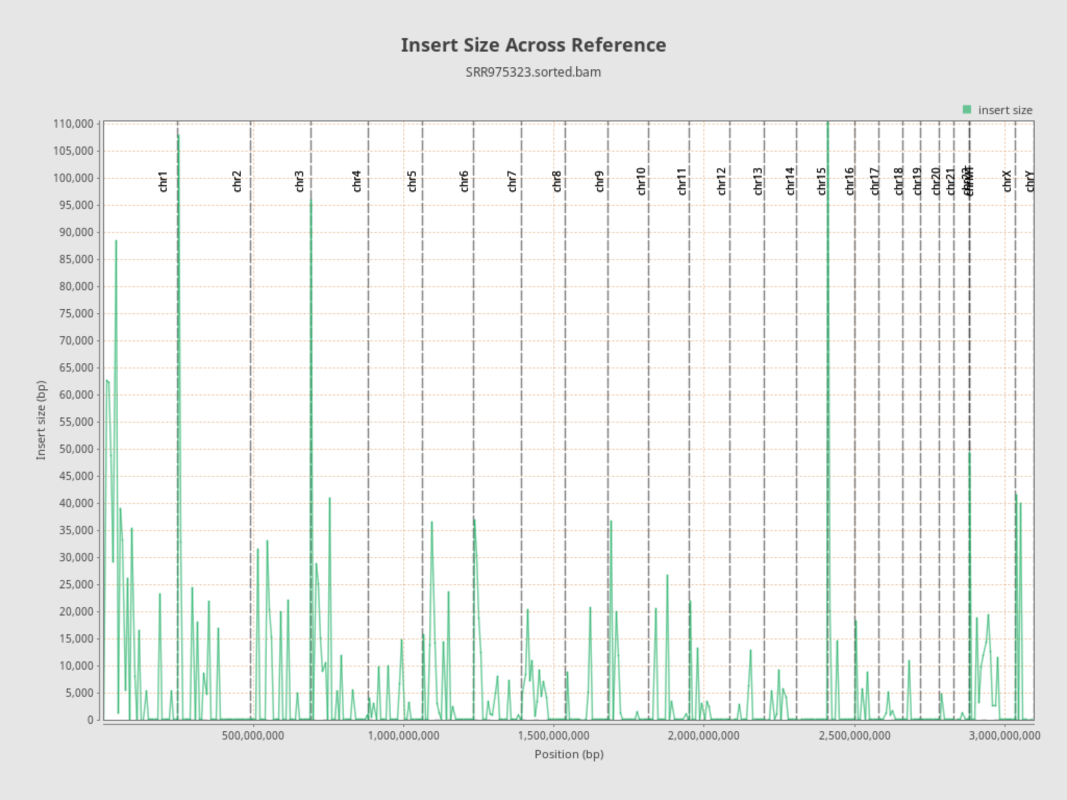


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram