Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 07:00:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975341.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_SRR975341 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975341_1.fastq.gz SRR975341_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 07:00:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975341.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,616,820
Mapped reads	4,450,809 / 96.4%
Unmapped reads	166,011 / 3.6%
Mapped paired reads	4,450,809 / 96.4%
Mapped reads, first in pair	2,223,883 / 48.17%
Mapped reads, second in pair	2,226,926 / 48.24%
Mapped reads, both in pair	4,427,142 / 95.89%
Mapped reads, singletons	23,667 / 0.51%
Secondary alignments	0
Supplementary alignments	21,621 / 0.47%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	269,713 / 5.84%
Duplication rate	3.2%
Clipped reads	2,707,849 / 58.65%

2.2. ACGT Content

Number/percentage of A's	117,876,883 / 29.07%
Number/percentage of C's	78,450,854 / 19.35%
Number/percentage of T's	120,491,960 / 29.72%
Number/percentage of G's	88,622,431 / 21.86%
Number/percentage of N's	8,317 / 0%

GC Percentage	41.21%

2.3. Coverage

Mean	0.1311
Standard Deviation	1.484

2.4. Mapping Quality

Mean Mapping Quality	52.71

2.5. Insert size

Mean	111,471.78
Standard Deviation	3,266,641.11
P25/Median/P75	134 / 167 / 213

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	3,196,697
Insertions	65,818
Mapped reads with at least one insertion	1.44%
Deletions	139,190
Mapped reads with at least one deletion	3.06%
Homopolymer indels	45.9%

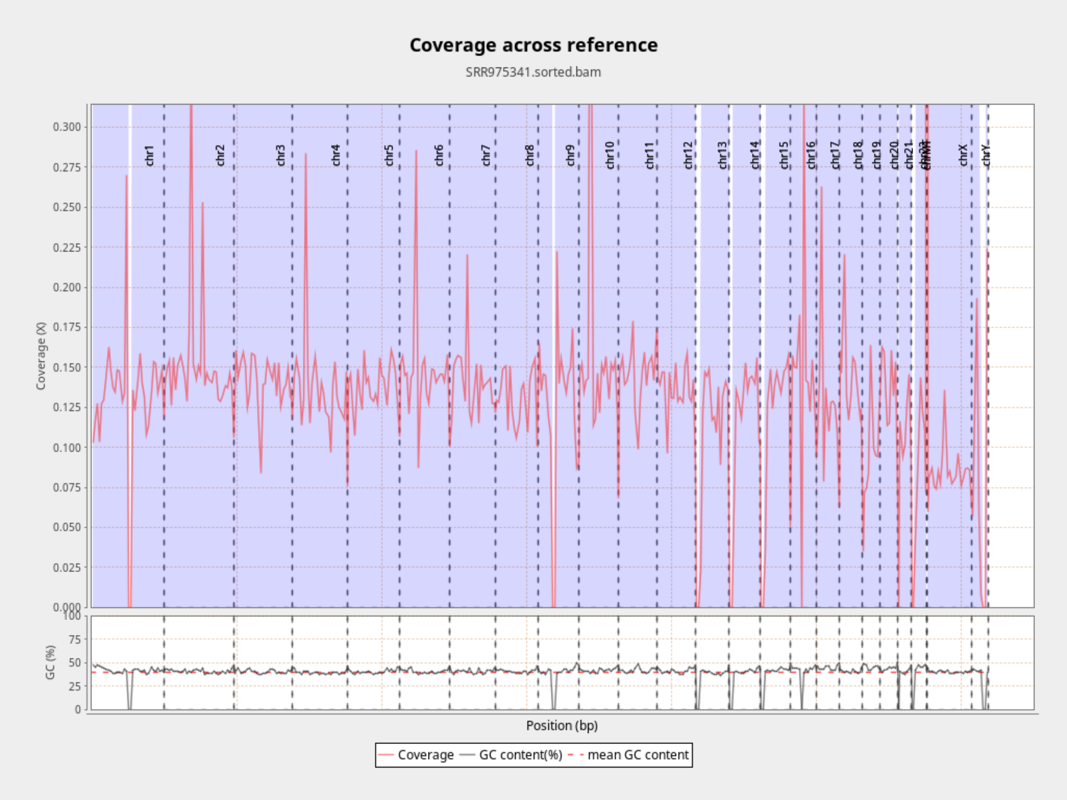
2.7. Chromosome stats

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

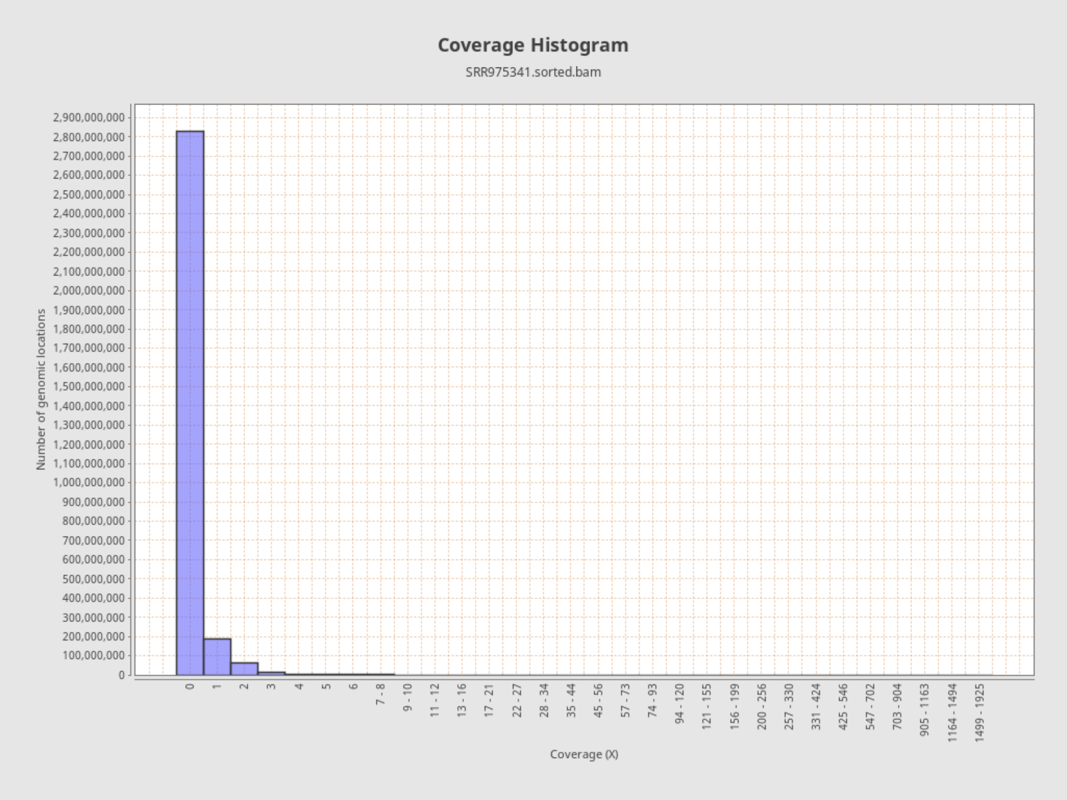
		bases	coverage	deviation
chr1	249250621	32508159	0.1304	2.0562
chr2	243199373	37238266	0.1531	1.7578
chr3	198022430	27895472	0.1409	0.5089
chr4	191154276	26483059	0.1385	1.0871
chr5	180915260	25045287	0.1384	0.5118
chr6	171115067	25270083	0.1477	1.666
chr7	159138663	22305638	0.1402	1.7321
chr8	146364022	19056244	0.1302	0.6586
chr9	141213431	17879244	0.1266	2.306
chr10	135534747	21916205	0.1617	2.8974
chr11	135006516	19485042	0.1443	1.1716
chr12	133851895	18236167	0.1362	0.4937
chr13	115169878	12273614	0.1066	0.426
chr14	107349540	12167108	0.1133	0.5113
chr15	102531392	11641107	0.1135	0.4482
chr16	90354753	12990384	0.1438	1.6207
chr17	81195210	10533542	0.1297	2.2325
chr18	78077248	11278471	0.1445	2.4279
chr19	59128983	5629471	0.0952	1.0326
chr20	63025520	8694141	0.1379	0.5619
chr21	48129895	4982656	0.1035	0.6329
chr22	51304566	4167528	0.0812	0.4306
chrMT	16571	148789	8.9789	5.6364
chrX	155270560	13122610	0.0845	0.6344

chrY	59373566	4748950	0.08	1.9088

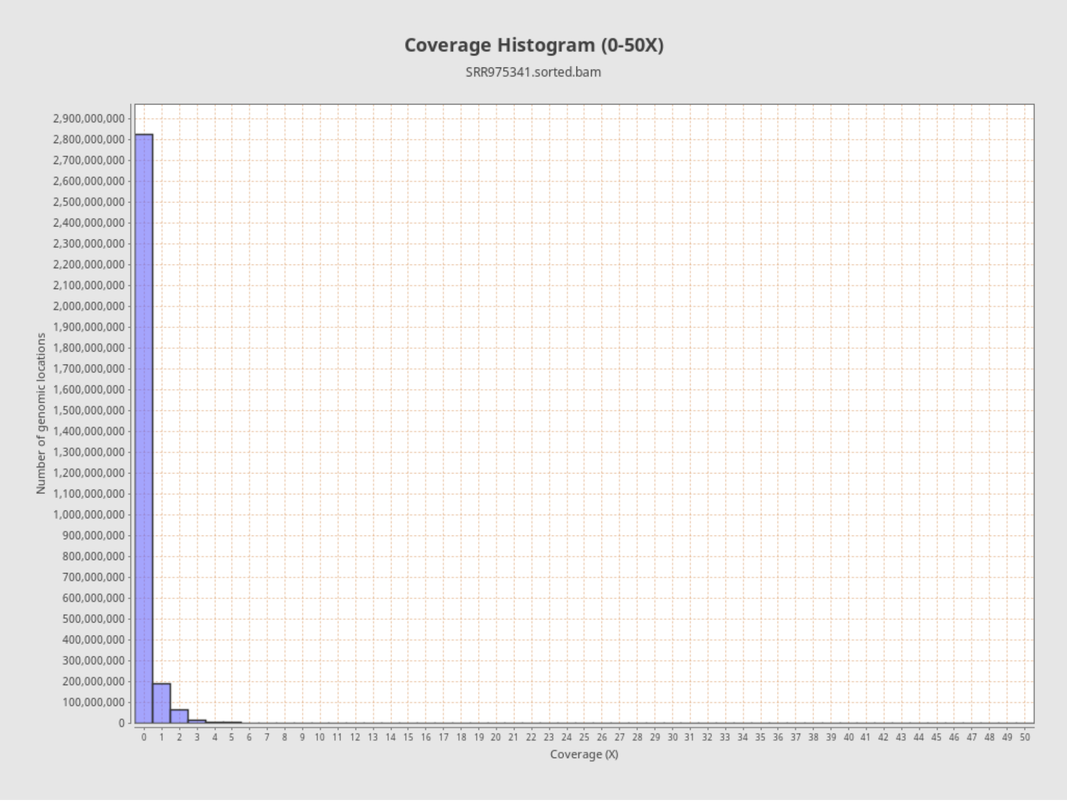
3. Results : Coverage across reference



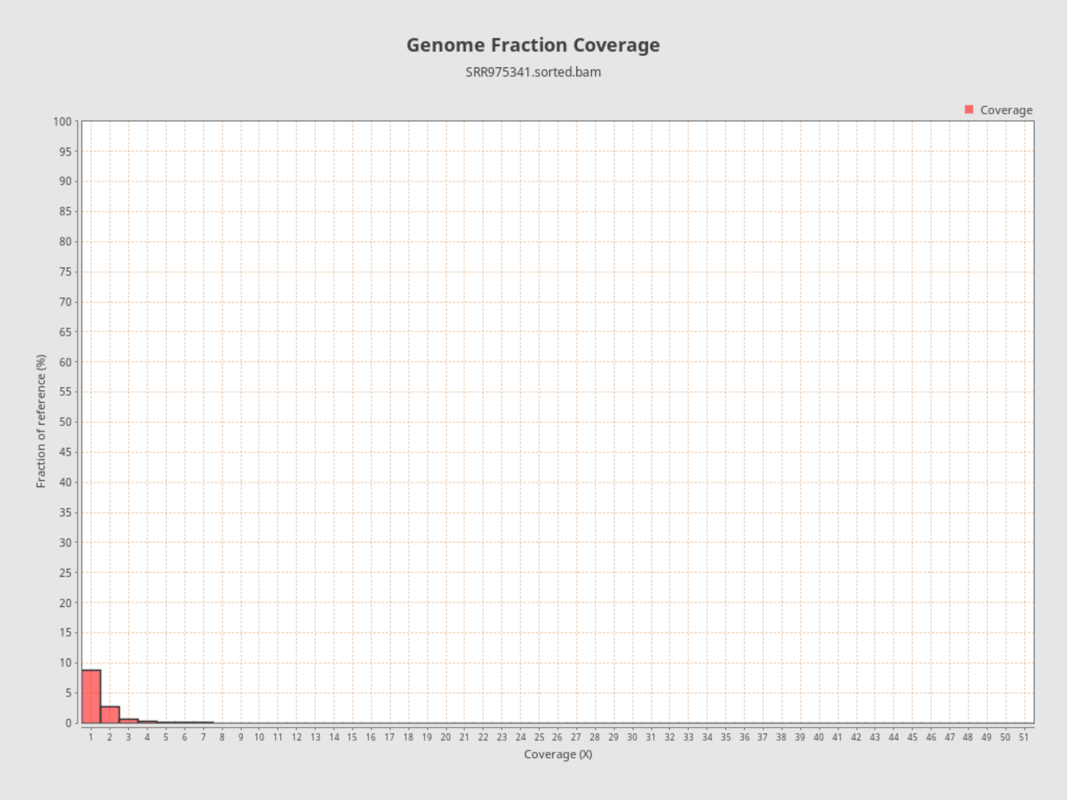
4. Results : Coverage Histogram



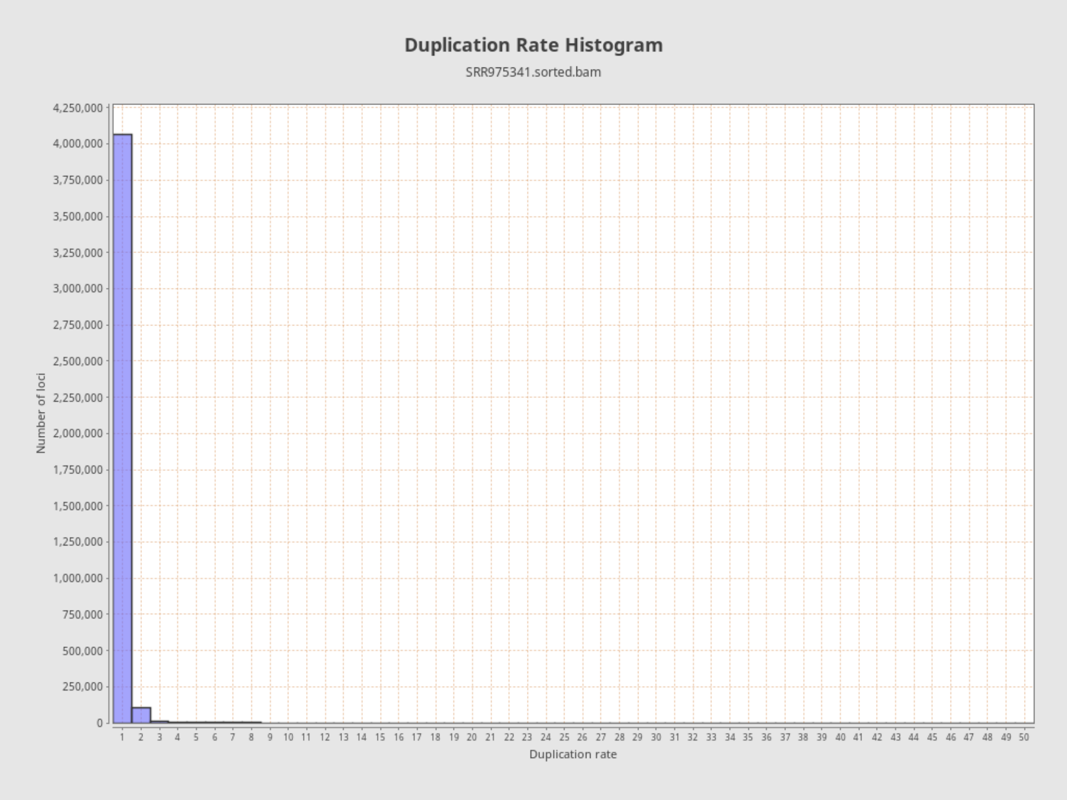
5. Results : Coverage Histogram (0-50X)



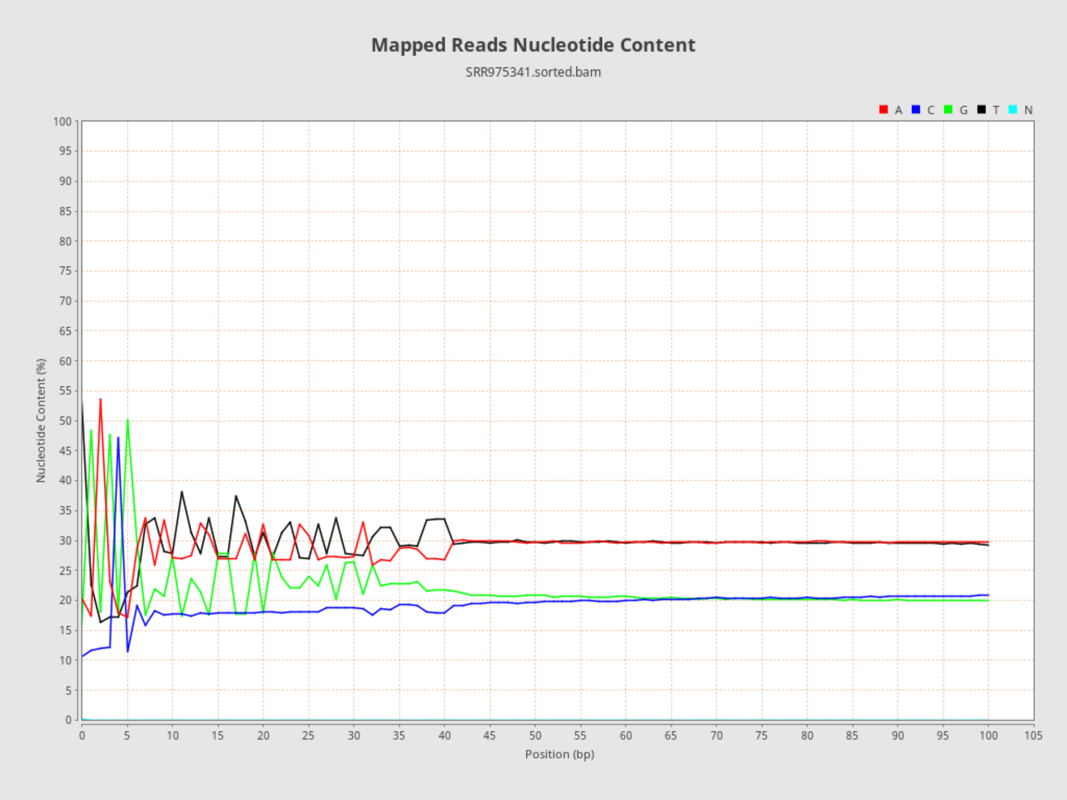
6. Results : Genome Fraction Coverage



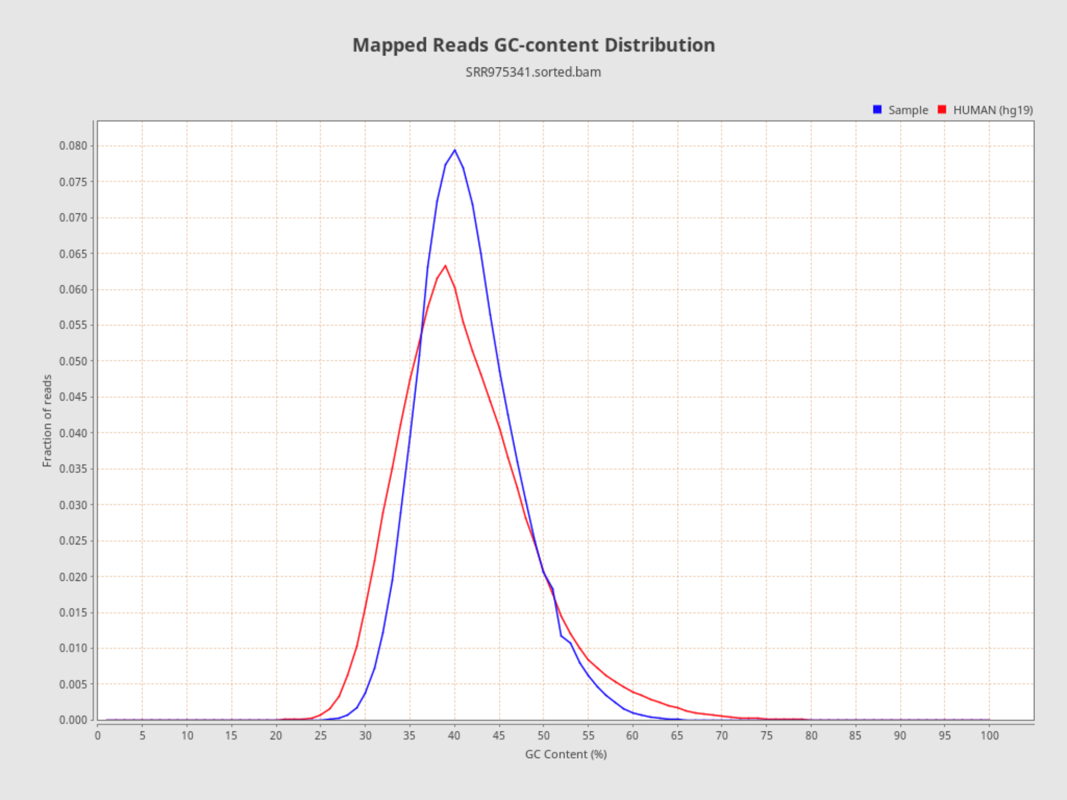
7. Results : Duplication Rate Histogram



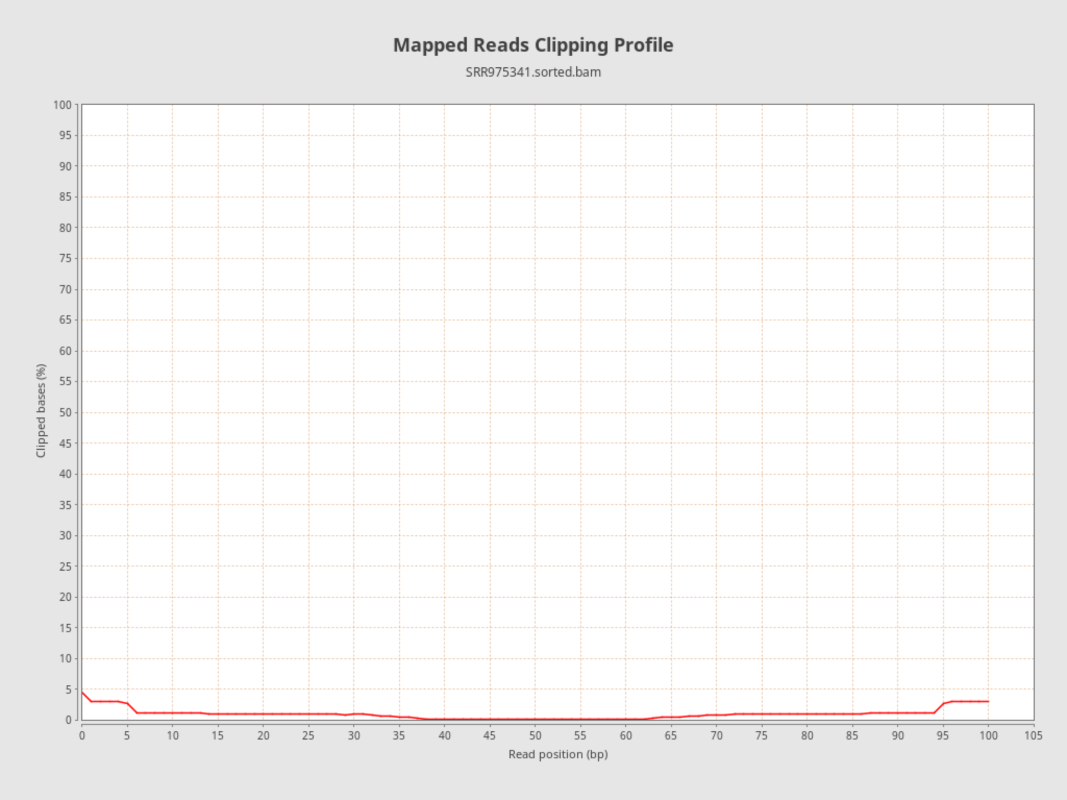
8. Results : Mapped Reads Nucleotide Content



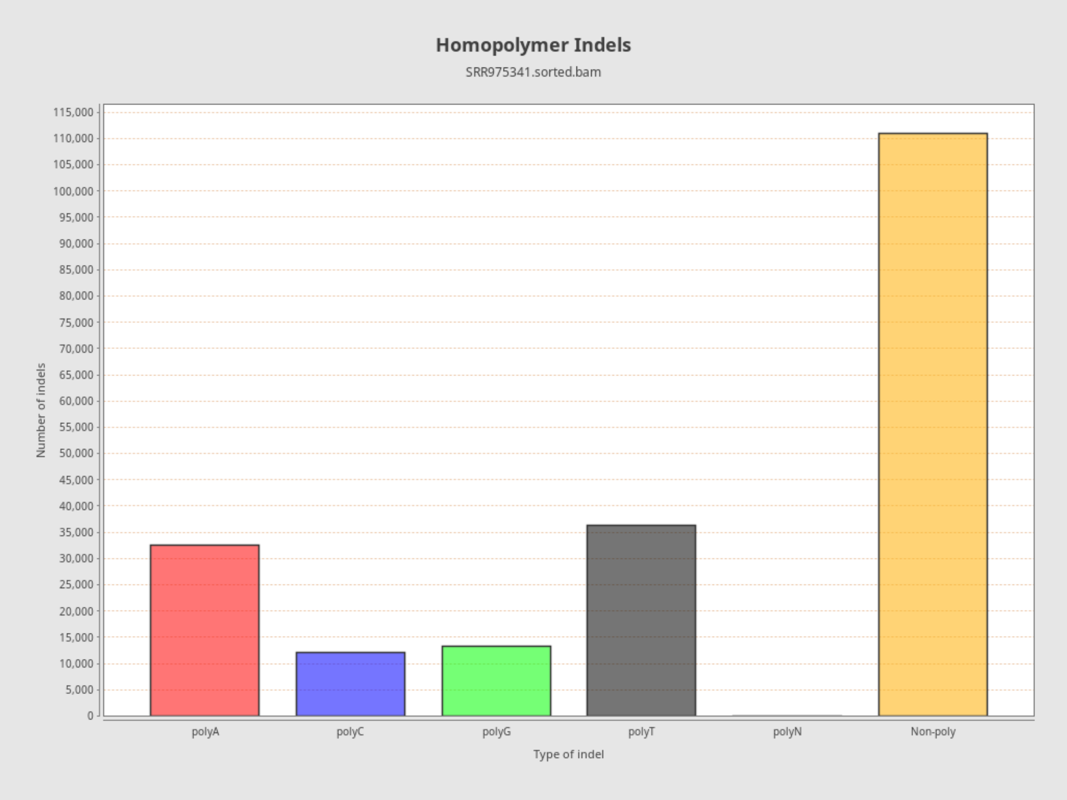
9. Results : Mapped Reads GC-content Distribution



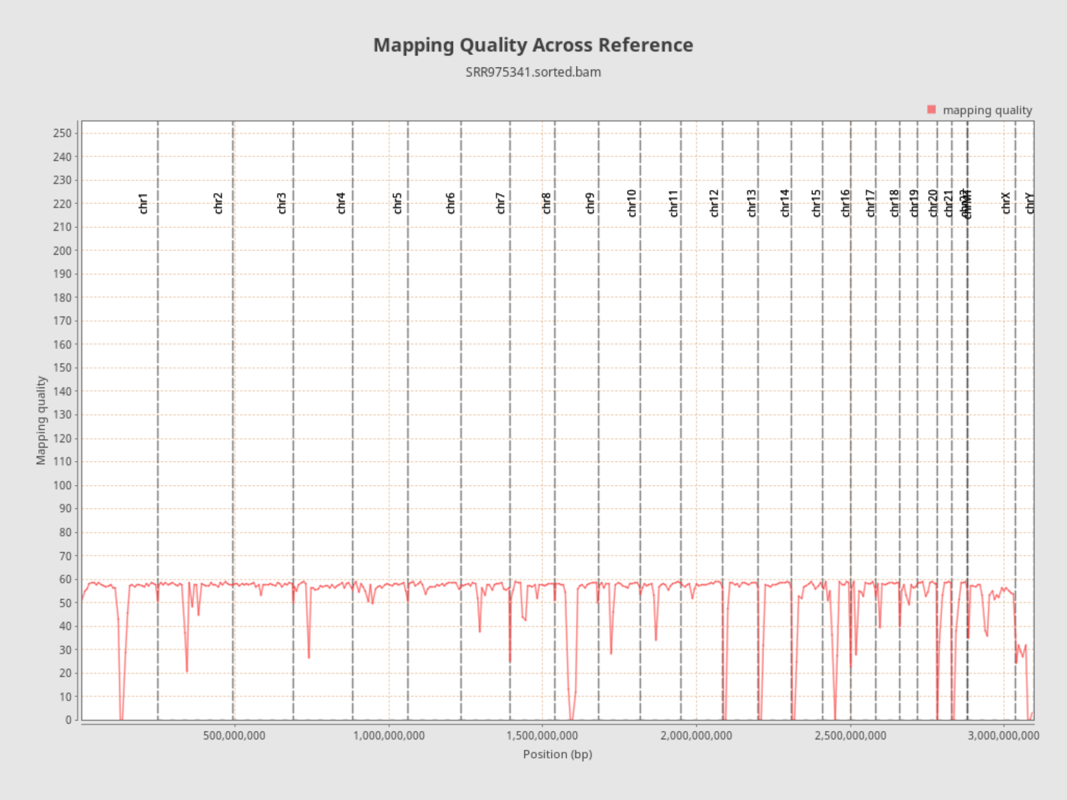
10. Results : Mapped Reads Clipping Profile



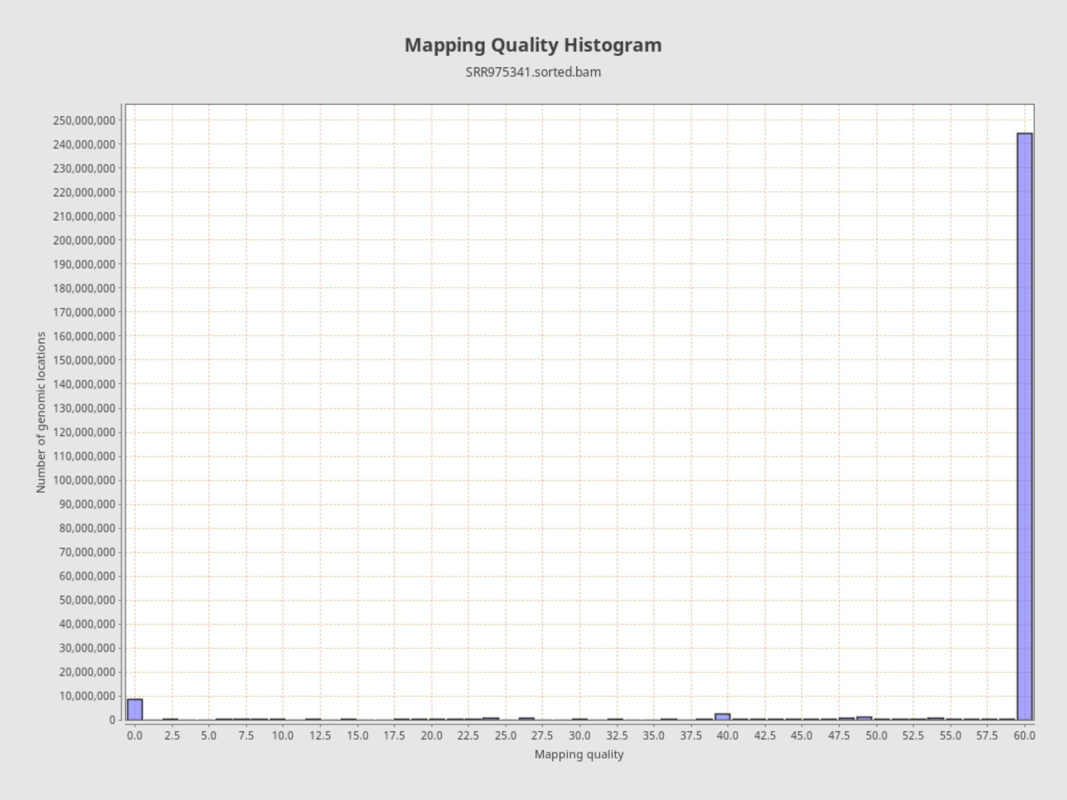
11. Results : Homopolymer Indels



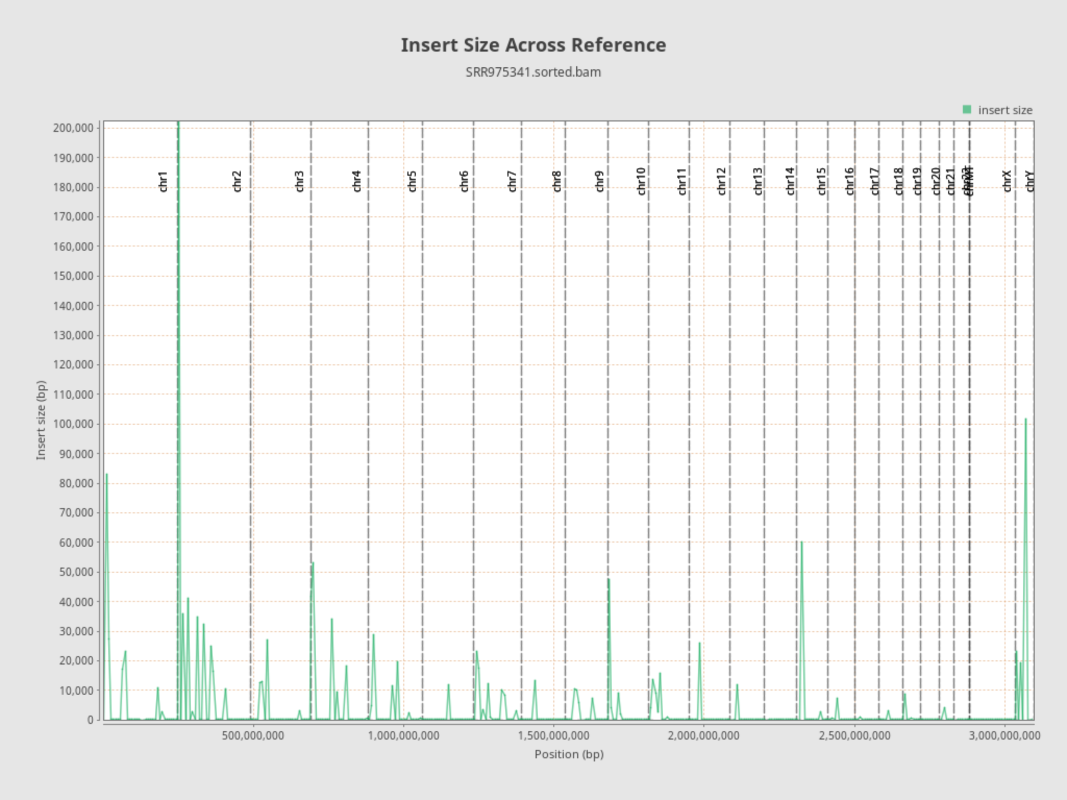
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram