Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 16:22:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975261.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_SRR975261 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975261_1.fastq.gz SRR975261_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 16:22:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975261.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,238,886
Mapped reads	5,184,991 / 98.97%
Unmapped reads	53,895 / 1.03%
Mapped paired reads	5,184,991 / 98.97%
Mapped reads, first in pair	2,591,263 / 49.46%
Mapped reads, second in pair	2,593,728 / 49.51%
Mapped reads, both in pair	5,165,806 / 98.61%
Mapped reads, singletons	19,185 / 0.37%
Secondary alignments	0
Supplementary alignments	19,088 / 0.36%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	273,469 / 5.22%
Duplication rate	3.05%
Clipped reads	3,146,550 / 60.06%

2.2. ACGT Content

Number/percentage of A's	138,171,333 / 29.3%
Number/percentage of C's	89,856,748 / 19.05%
Number/percentage of T's	141,122,036 / 29.92%
Number/percentage of G's	102,488,443 / 21.73%
Number/percentage of N's	6,673 / 0%

GC Percentage	40.78%

2.3. Coverage

Mean	0.1524
Standard Deviation	1.3804

2.4. Mapping Quality

Mean Mapping Quality	52.89

2.5. Insert size

Mean	94,655.54
Standard Deviation	2,973,035.6
P25/Median/P75	136 / 170 / 218

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	3,613,519
Insertions	78,544
Mapped reads with at least one insertion	1.48%
Deletions	154,043
Mapped reads with at least one deletion	2.91%
Homopolymer indels	45.45%

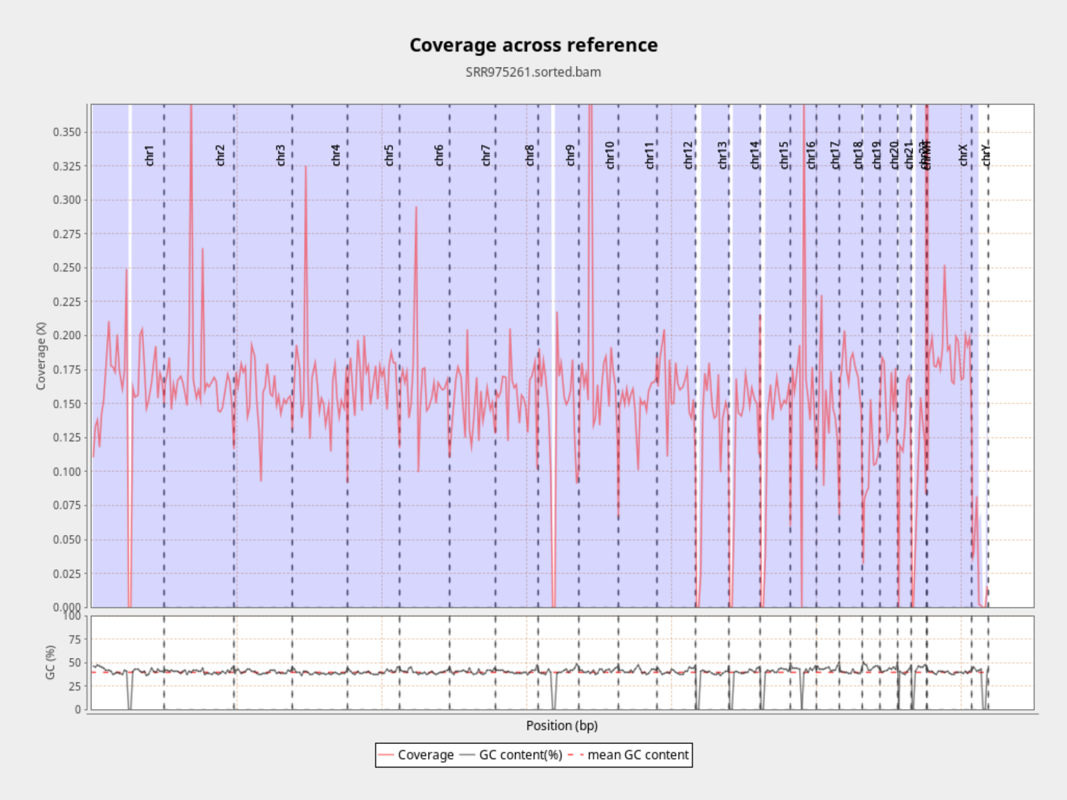
2.7. Chromosome stats

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

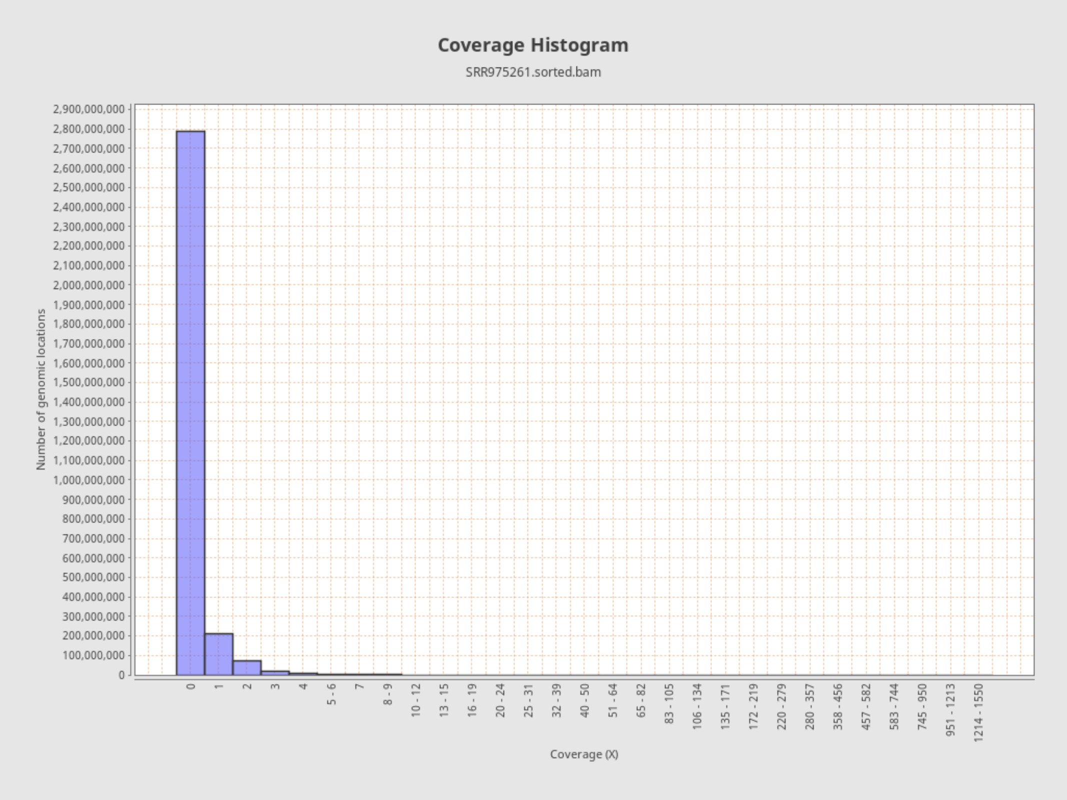
		bases	coverage	deviation
chr1	249250621	39362844	0.1579	1.3439
chr2	243199373	41743478	0.1716	1.8257
chr3	198022430	31247304	0.1578	0.5639
chr4	191154276	31055656	0.1625	1.1706
chr5	180915260	30626964	0.1693	0.5717
chr6	171115067	28040205	0.1639	1.4386
chr7	159138663	23569969	0.1481	1.3931
chr8	146364022	22962208	0.1569	0.7118
chr9	141213431	19863865	0.1407	1.8615
chr10	135534747	24926762	0.1839	3.4831
chr11	135006516	20327270	0.1506	1.0879
chr12	133851895	21743853	0.1624	0.5453
chr13	115169878	14204815	0.1233	0.4671
chr14	107349540	13548314	0.1262	0.5431
chr15	102531392	12651003	0.1234	0.4685
chr16	90354753	14579727	0.1614	1.8108
chr17	81195210	11698518	0.1441	1.5219
chr18	78077248	13604519	0.1742	2.0548
chr19	59128983	5977462	0.1011	0.803
chr20	63025520	9701812	0.1539	0.598
chr21	48129895	5975378	0.1242	0.653
chr22	51304566	4576645	0.0892	0.4293
chrMT	16571	64237	3.8765	2.92
chrX	155270560	28581750	0.1841	0.7982

chrY	59373566	1279872	0.0216	1.2848

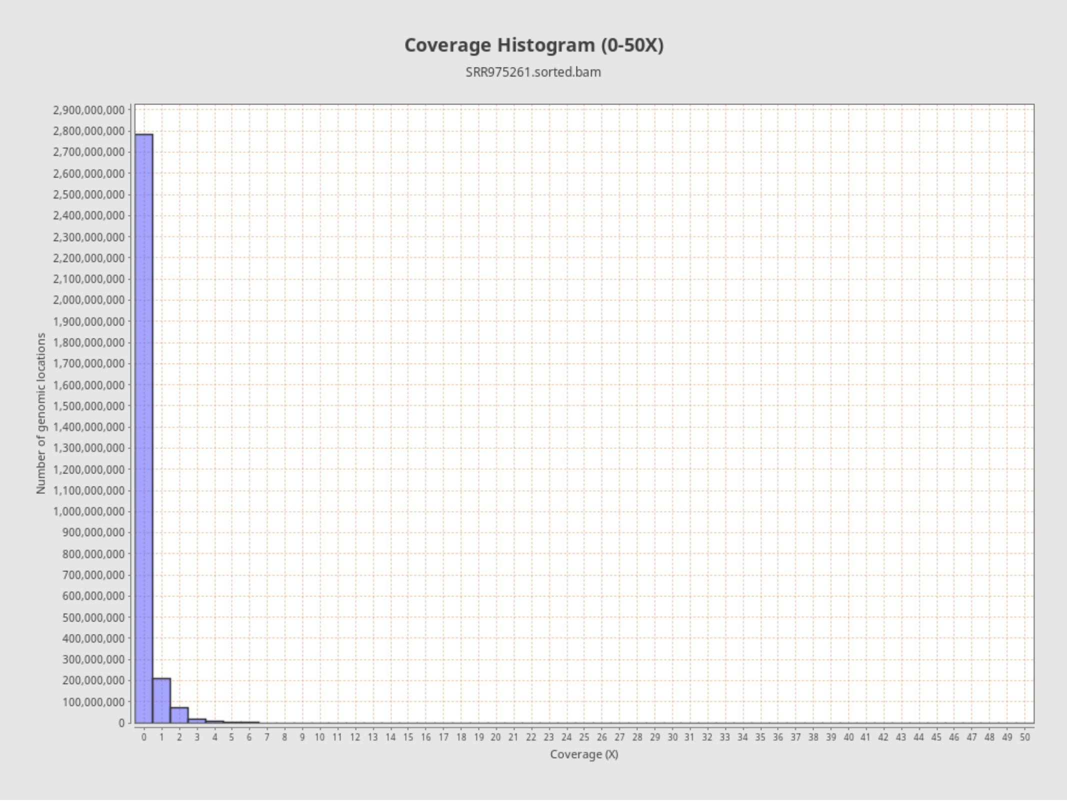
3. Results : Coverage across reference



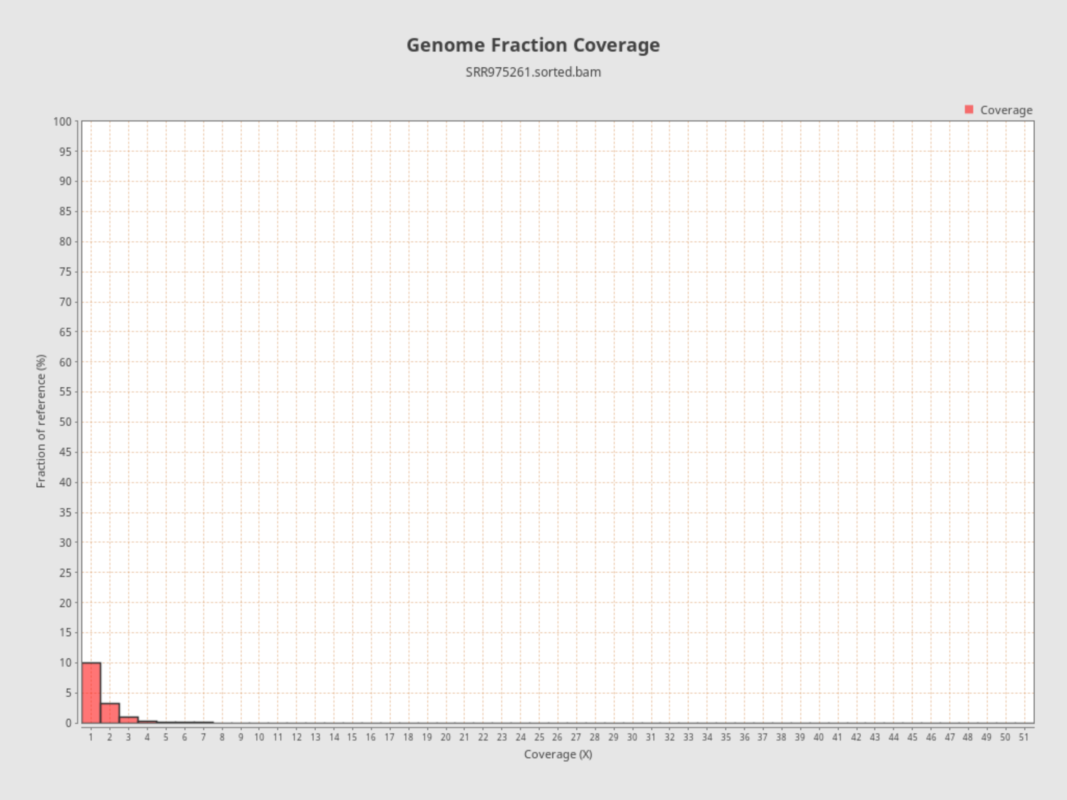
4. Results : Coverage Histogram



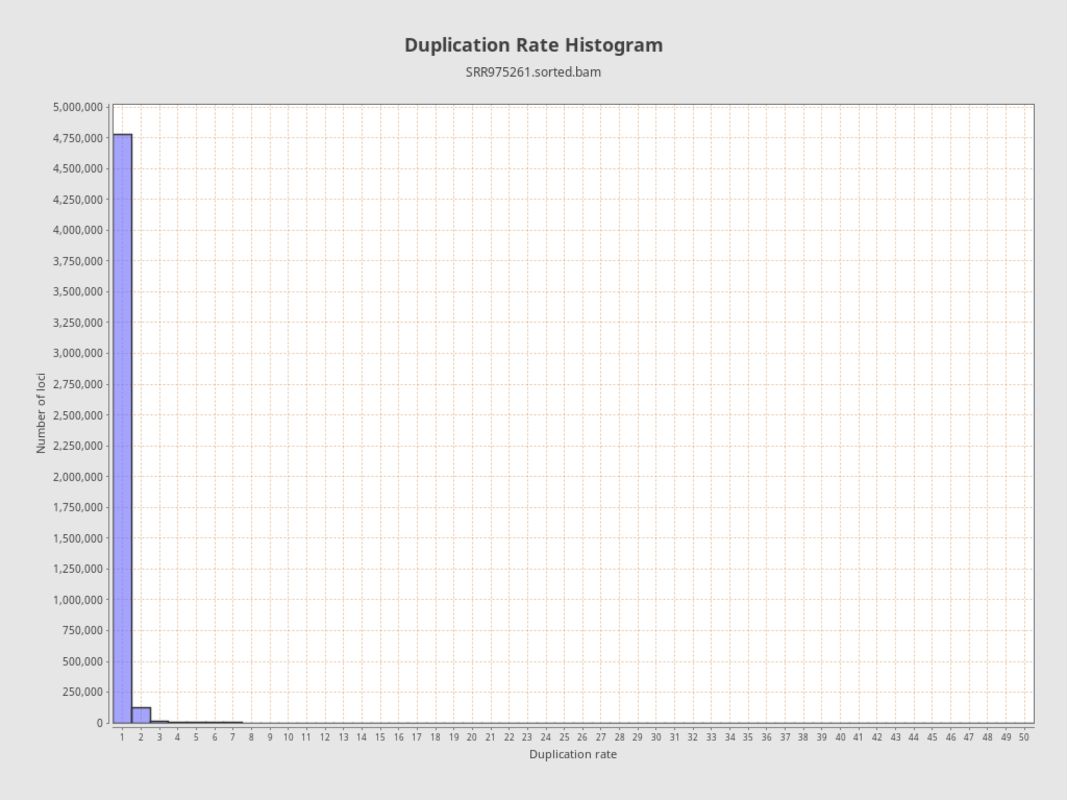
5. Results : Coverage Histogram (0-50X)



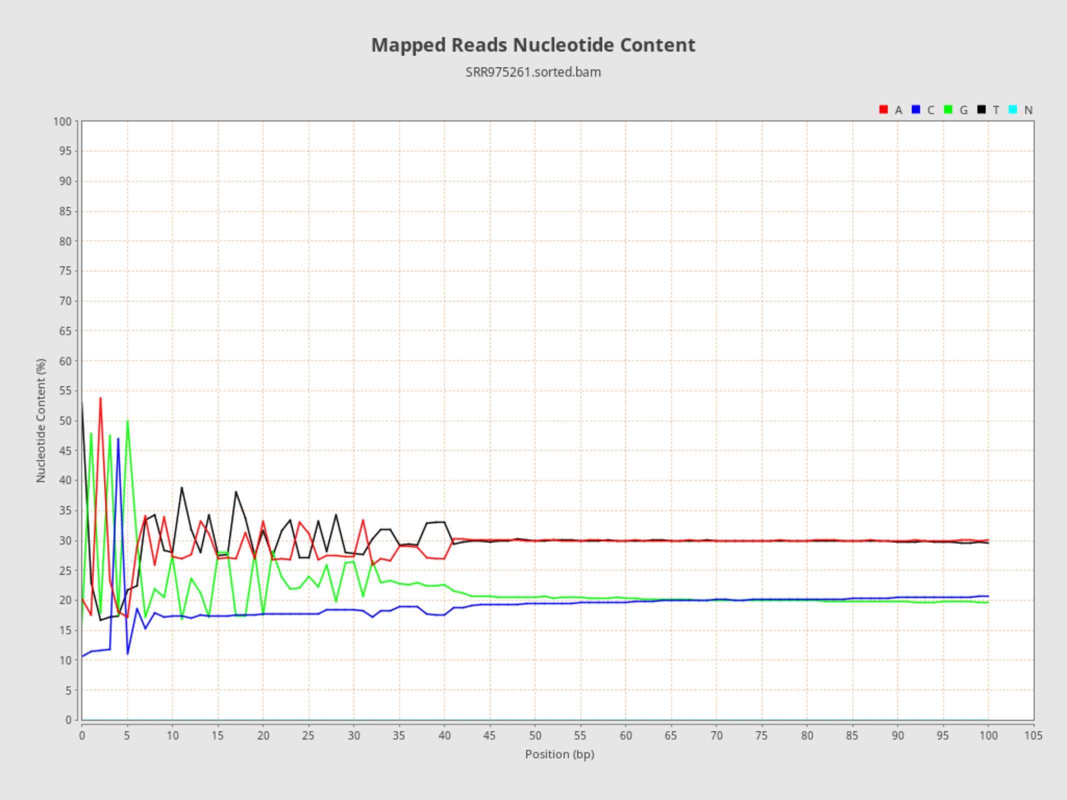
6. Results : Genome Fraction Coverage



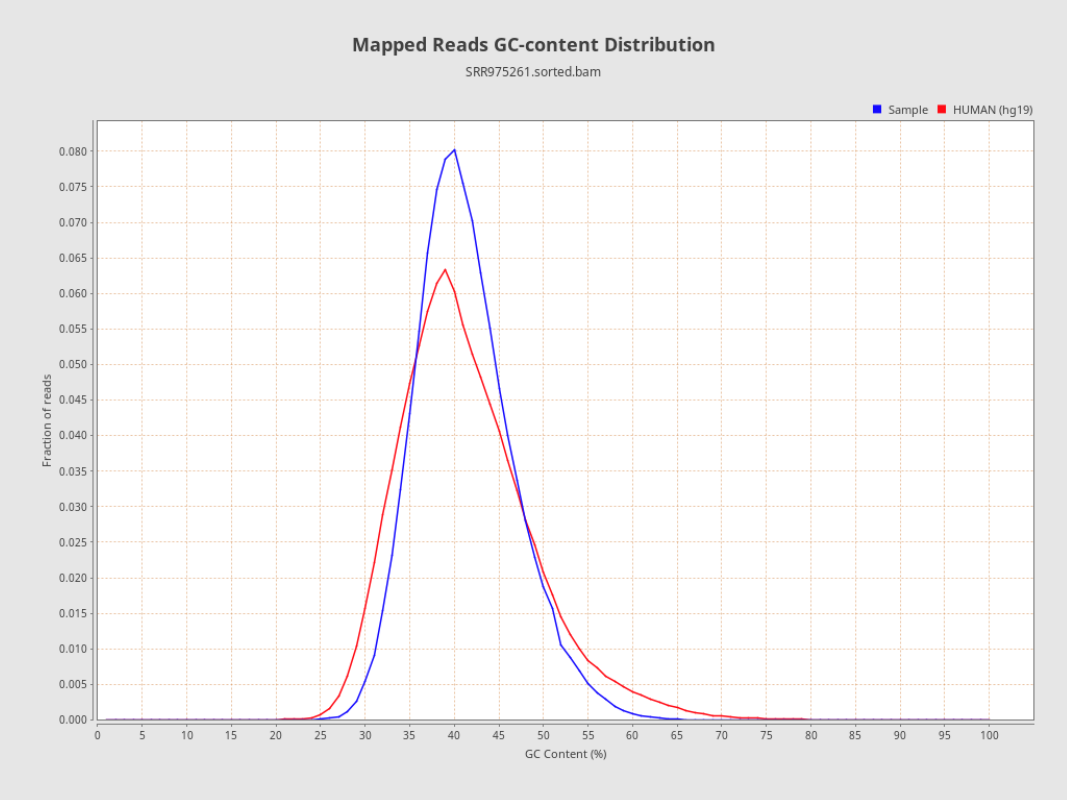
7. Results : Duplication Rate Histogram



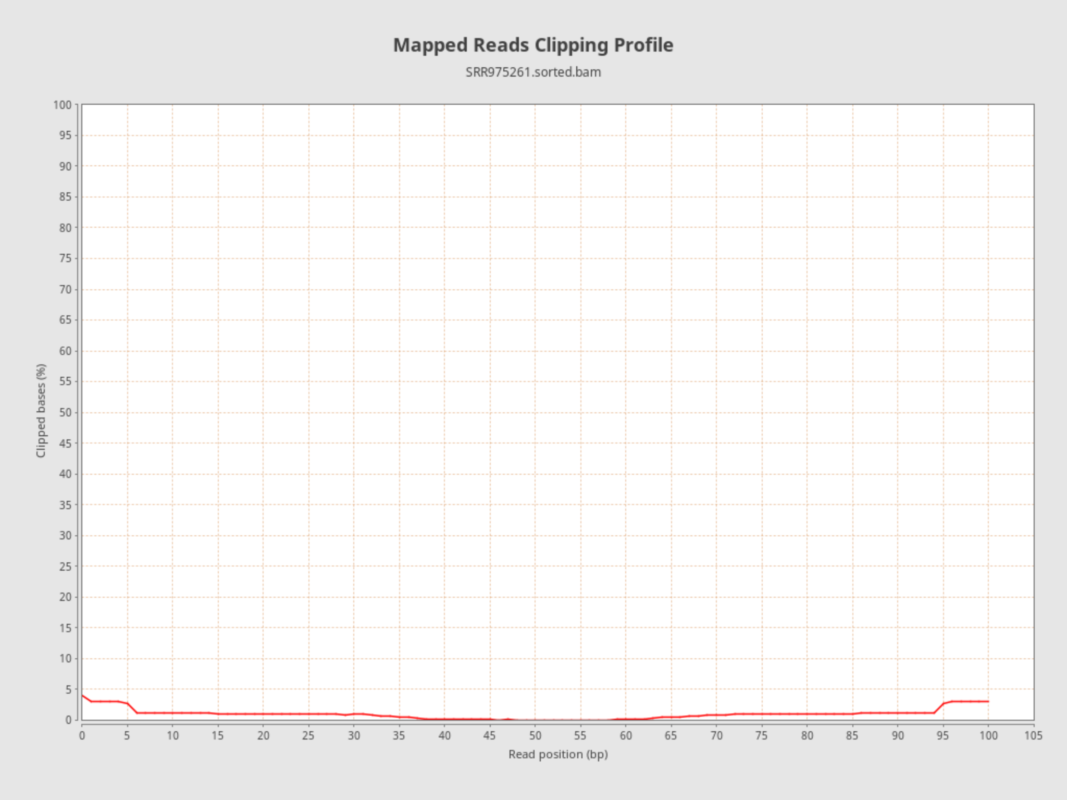
8. Results : Mapped Reads Nucleotide Content



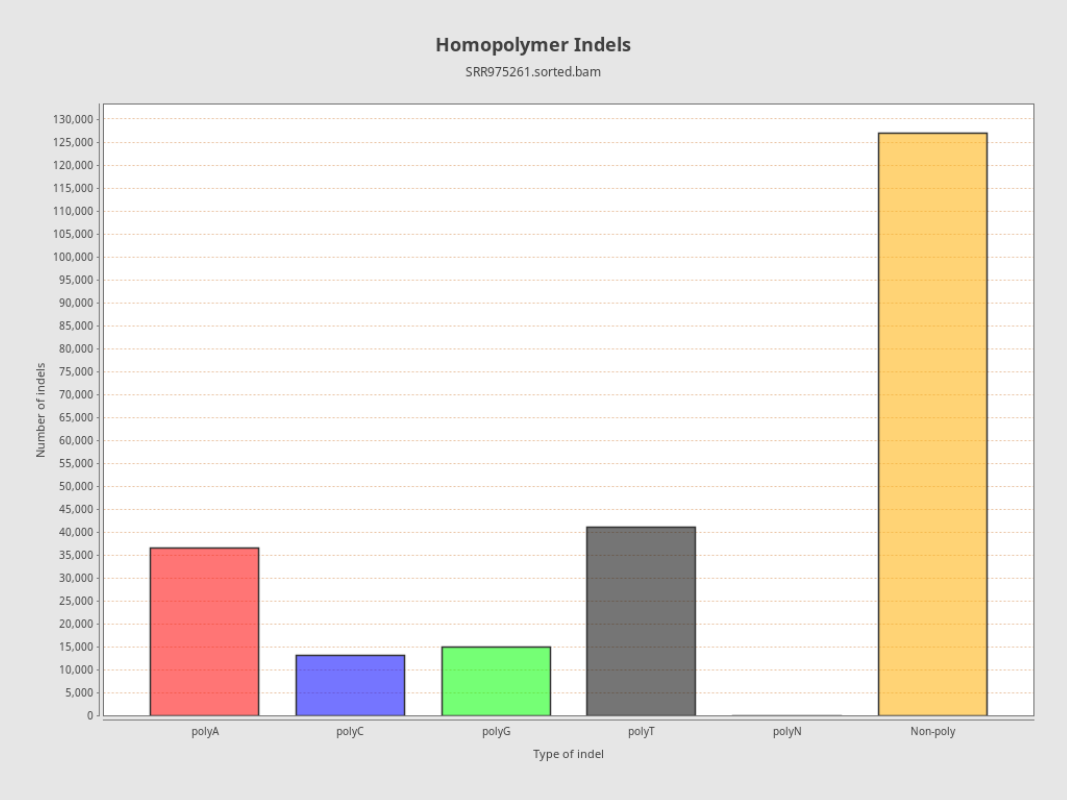
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

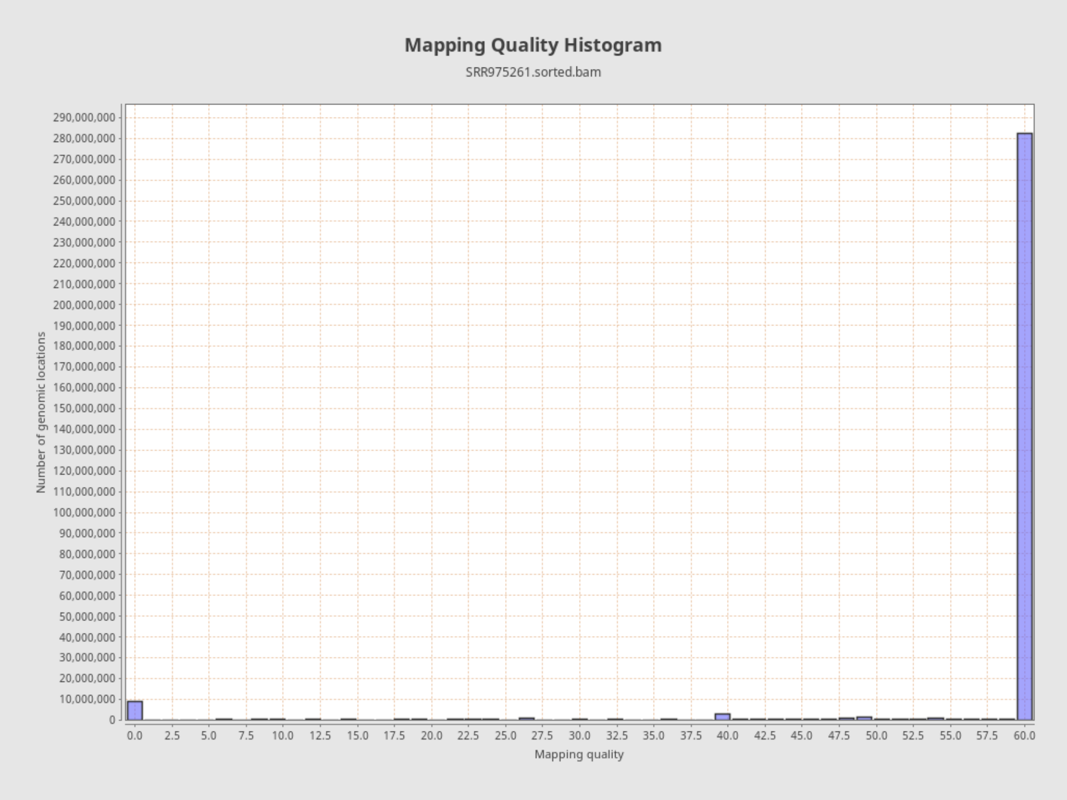


11. Results : Homopolymer Indels

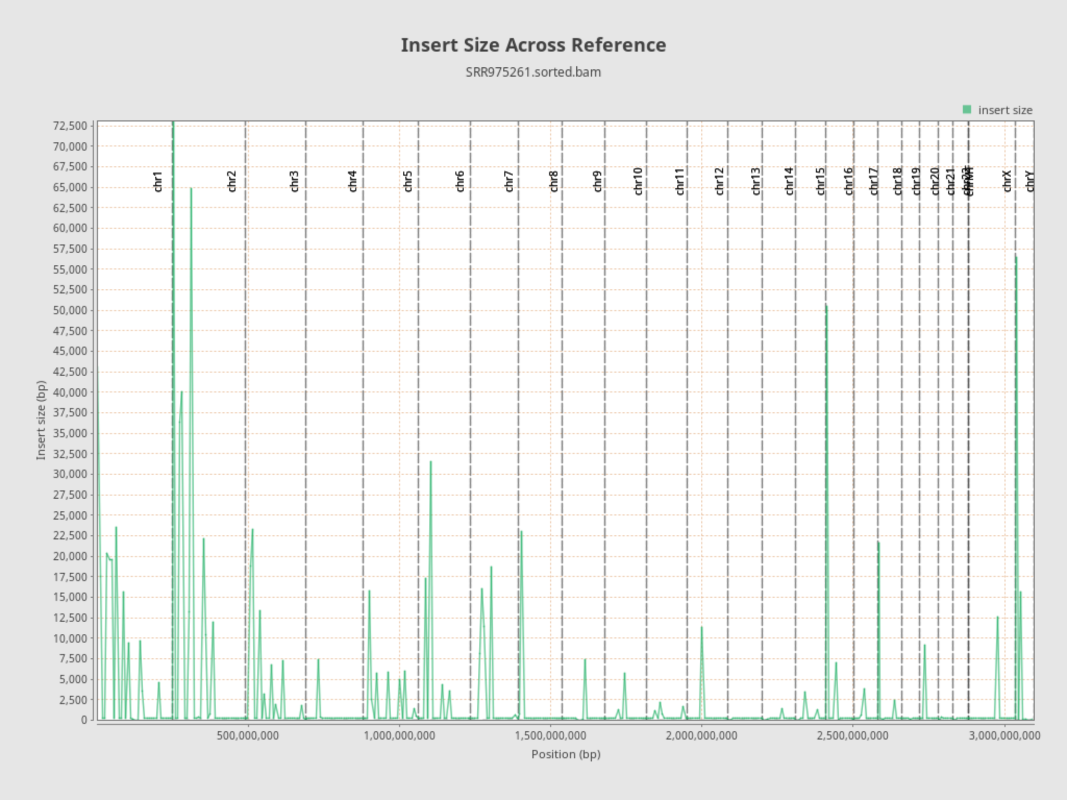


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram