Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 16:05:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975257.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_SRR975257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975257_1.fastq.gz SRR975257_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 16:05:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,973,390
Mapped reads	5,935,498 / 99.37%
Unmapped reads	37,892 / 0.63%
Mapped paired reads	5,935,498 / 99.37%
Mapped reads, first in pair	2,967,502 / 49.68%
Mapped reads, second in pair	2,967,996 / 49.69%
Mapped reads, both in pair	5,924,766 / 99.19%
Mapped reads, singletons	10,732 / 0.18%
Secondary alignments	0
Supplementary alignments	15,290 / 0.26%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	181,009 / 3.03%
Duplication rate	2.12%
Clipped reads	3,565,360 / 59.69%

2.2. ACGT Content

Number/percentage of A's	157,466,313 / 28.67%
Number/percentage of C's	109,350,679 / 19.91%
Number/percentage of T's	163,323,281 / 29.73%
Number/percentage of G's	119,172,346 / 21.69%
Number/percentage of N's	7,616 / 0%

GC Percentage	41.6%

2.3. Coverage

Mean	0.1775
Standard Deviation	1.0355

2.4. Mapping Quality

Mean Mapping Quality	52.89

2.5. Insert size

Mean	60,549.36
Standard Deviation	2,381,289.67
P25/Median/P75	138 / 171 / 218

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	3,367,697
Insertions	75,240
Mapped reads with at least one insertion	1.25%
Deletions	140,078
Mapped reads with at least one deletion	2.32%
Homopolymer indels	46.02%

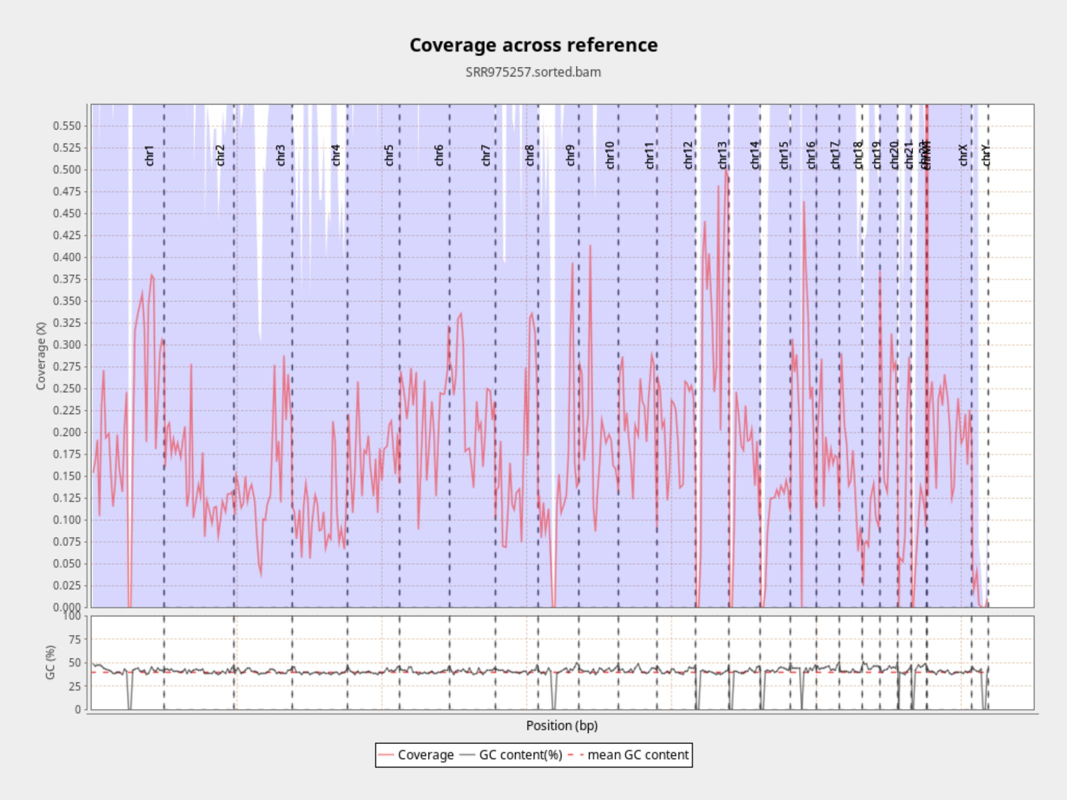
2.7. Chromosome stats

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

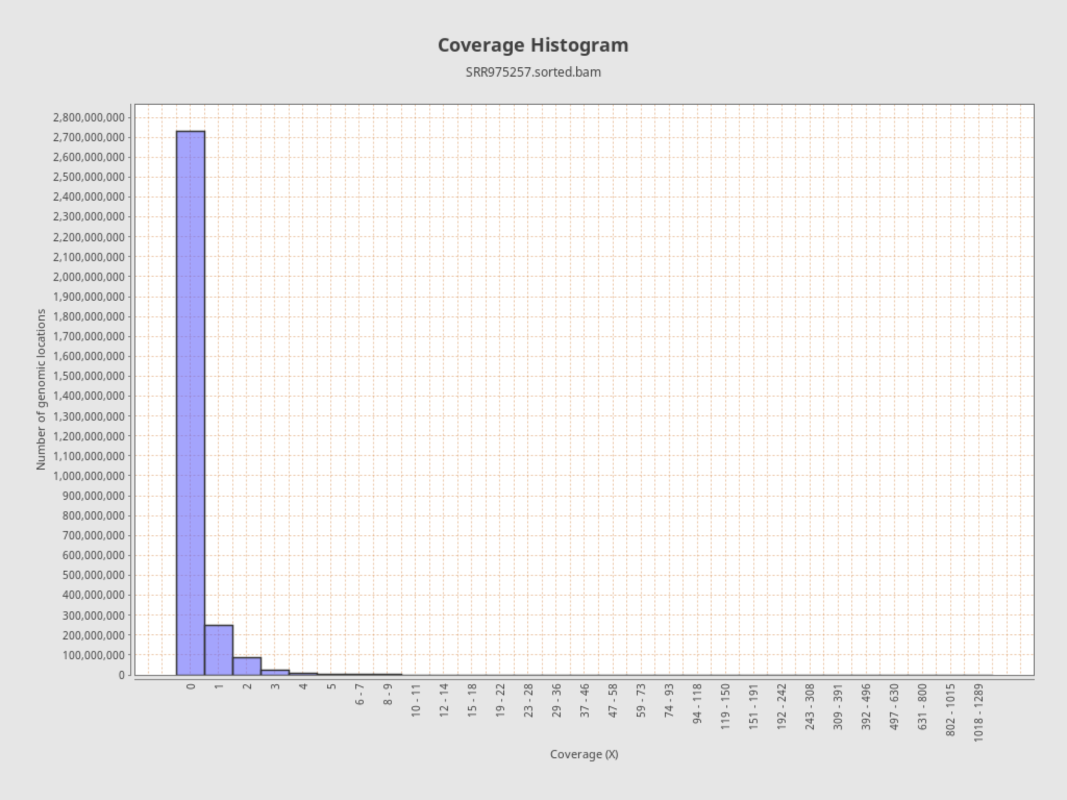
		bases	coverage	deviation
chr1	249250621	54851950	0.2201	1.065
chr2	243199373	35269509	0.145	1.1318
chr3	198022430	29677737	0.1499	0.5133
chr4	191154276	20085757	0.1051	0.5469
chr5	180915260	31151767	0.1722	0.5334
chr6	171115067	37382835	0.2185	1.105
chr7	159138663	36341727	0.2284	1.2548
chr8	146364022	25289577	0.1728	0.624
chr9	141213431	18766347	0.1329	1.0246
chr10	135534747	26356846	0.1945	2.5443
chr11	135006516	29260884	0.2167	0.8622
chr12	133851895	28310937	0.2115	0.603
chr13	115169878	35875191	0.3115	0.8052
chr14	107349540	16942442	0.1578	0.5332
chr15	102531392	10301070	0.1005	0.4002
chr16	90354753	22746911	0.2518	1.5921
chr17	81195210	14932814	0.1839	1.4207
chr18	78077248	12369206	0.1584	1.5139
chr19	59128983	5542424	0.0937	0.6219
chr20	63025520	14975607	0.2376	0.6566
chr21	48129895	6361828	0.1322	0.5024
chr22	51304566	4221974	0.0823	0.3672
chrMT	16571	48466	2.9247	2.7701
chrX	155270560	31690058	0.2041	0.7282

chrY	59373566	803167	0.0135	0.5564

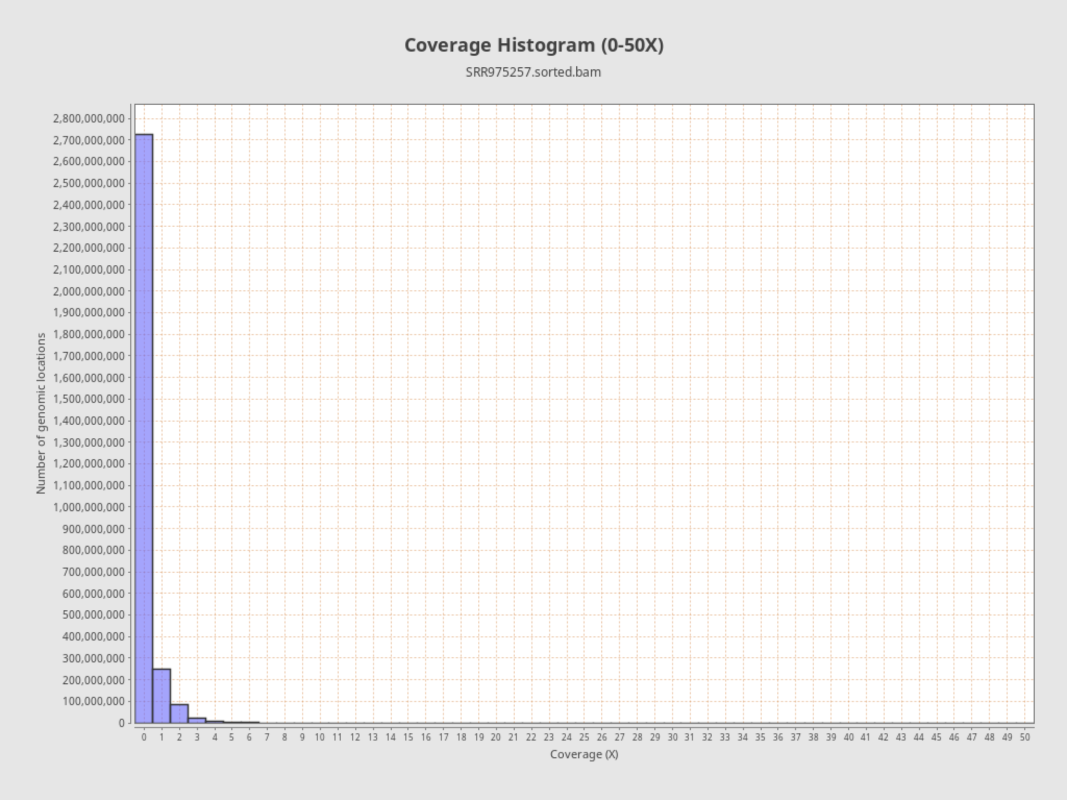
3. Results : Coverage across reference



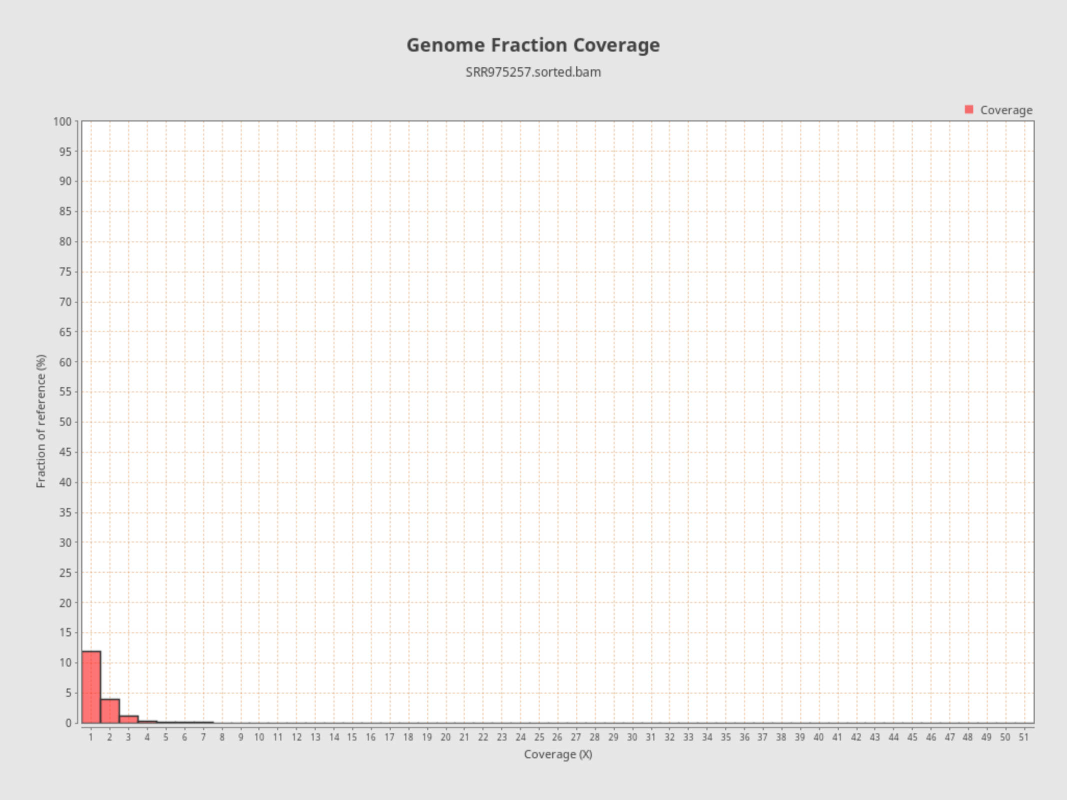
4. Results : Coverage Histogram



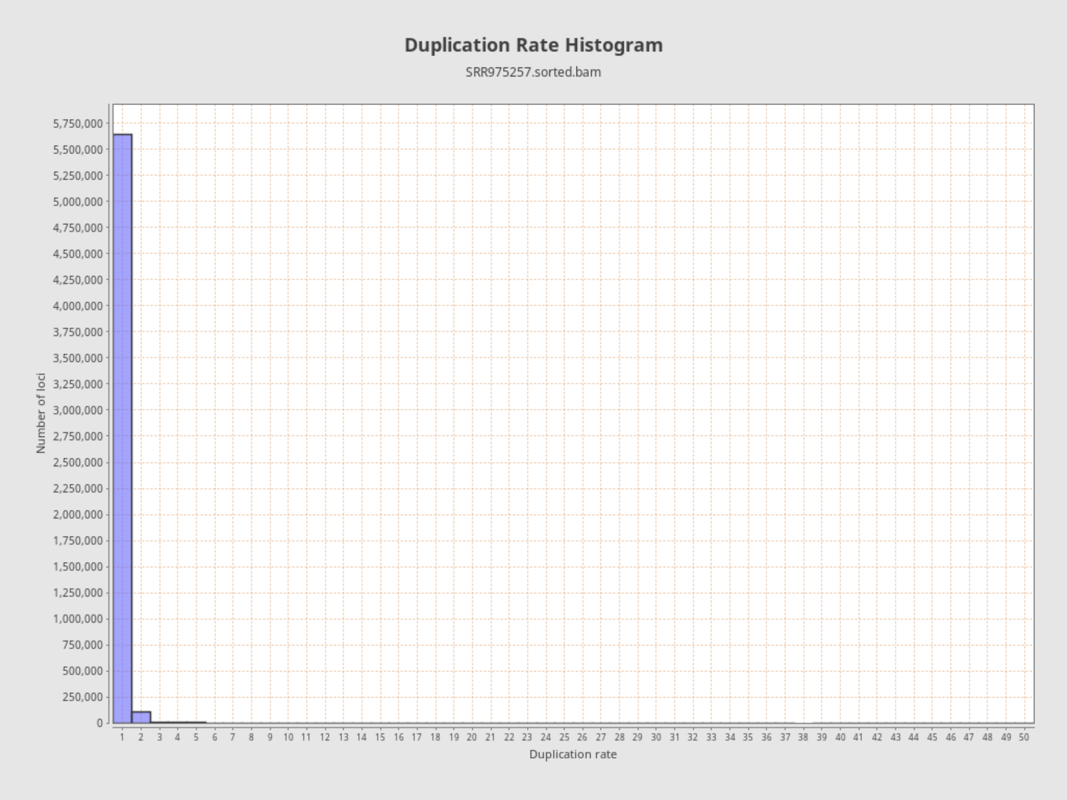
5. Results : Coverage Histogram (0-50X)



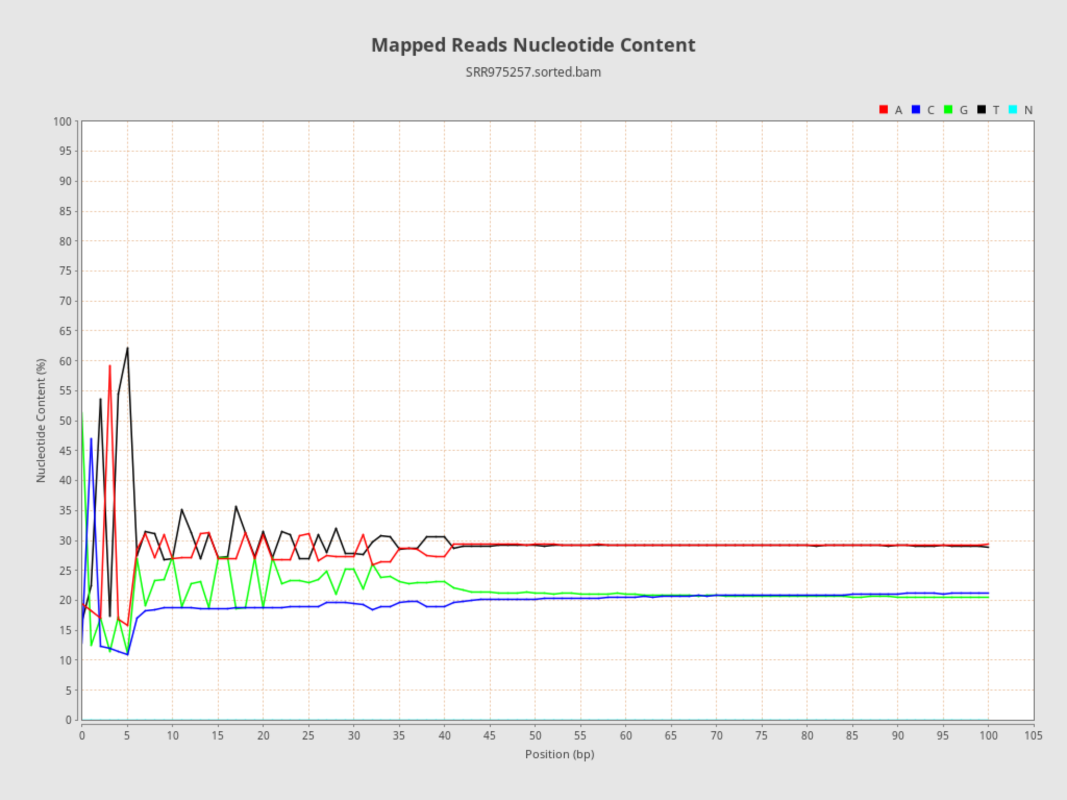
6. Results : Genome Fraction Coverage



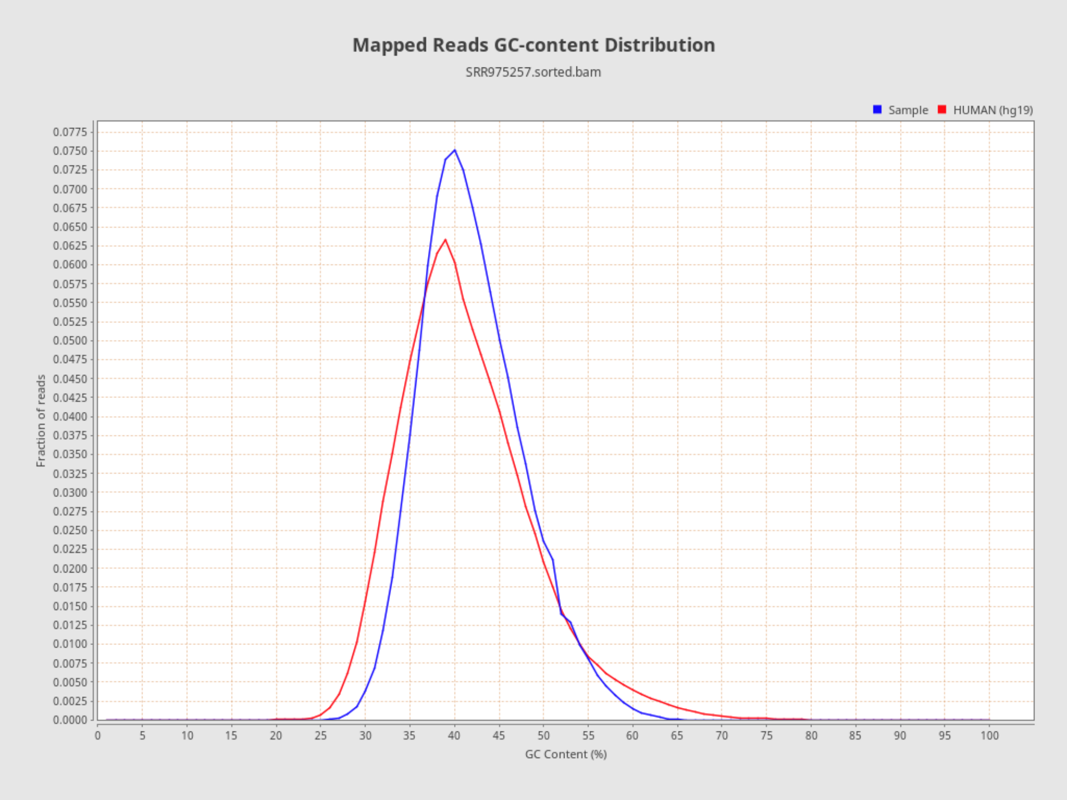
7. Results : Duplication Rate Histogram



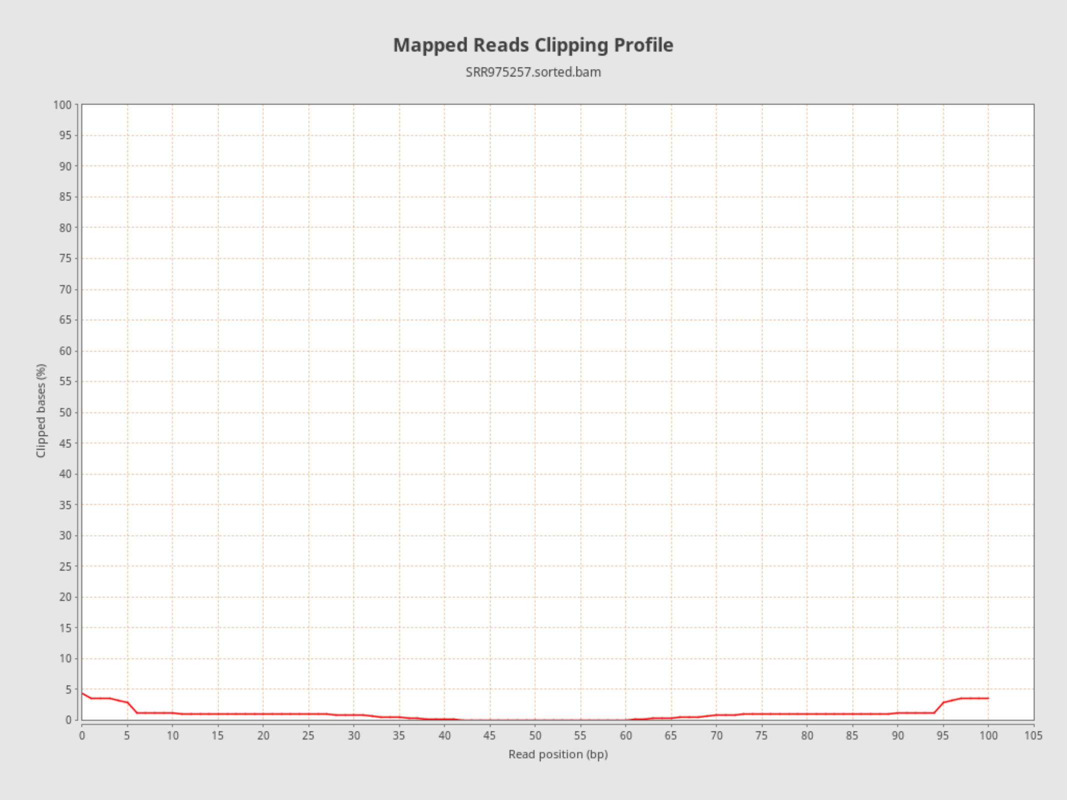
8. Results : Mapped Reads Nucleotide Content



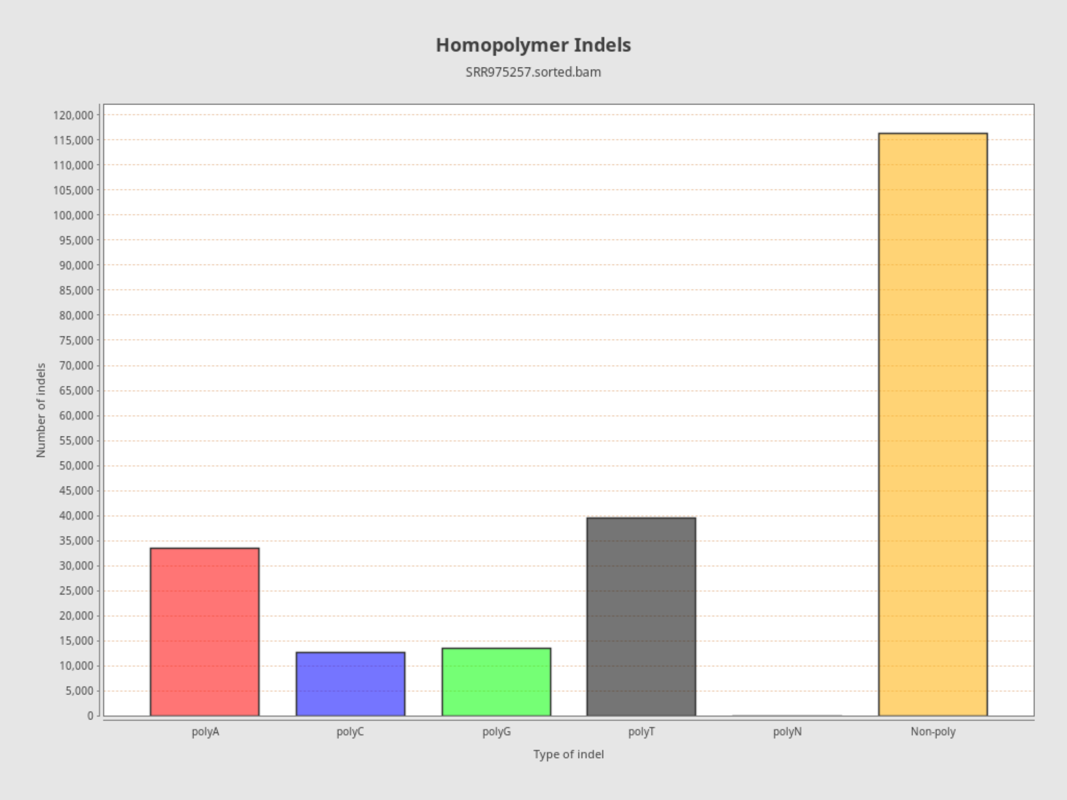
9. Results : Mapped Reads GC-content Distribution



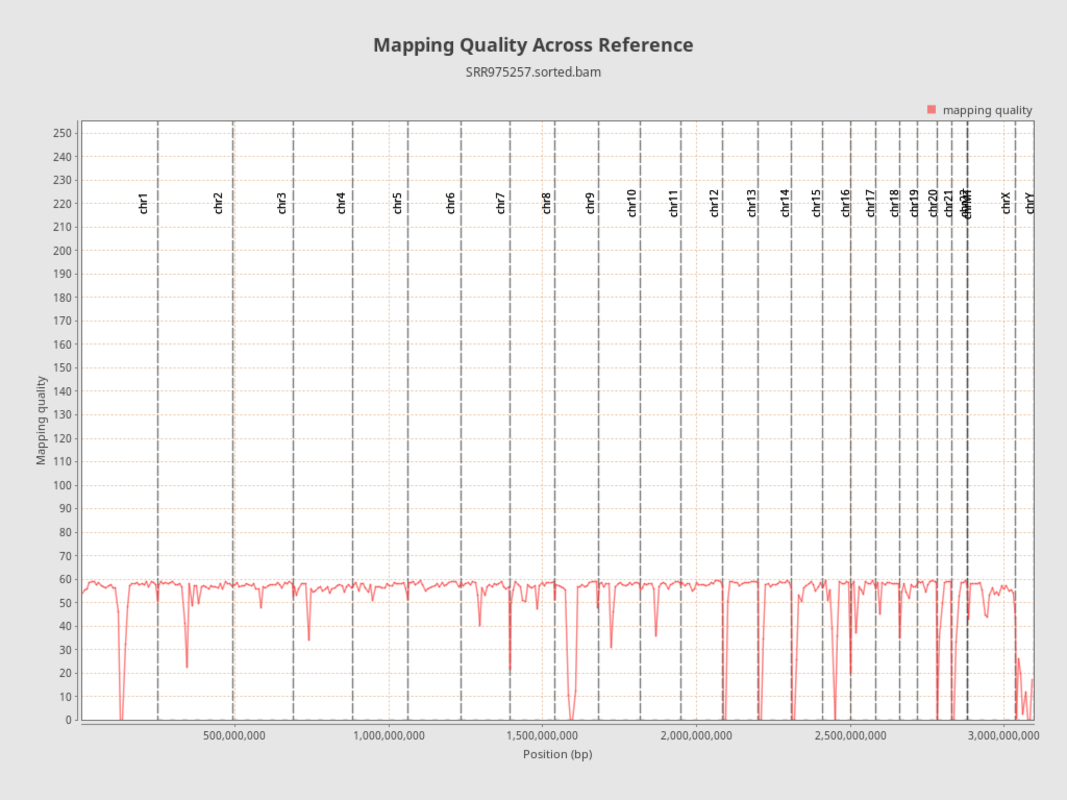
10. Results : Mapped Reads Clipping Profile



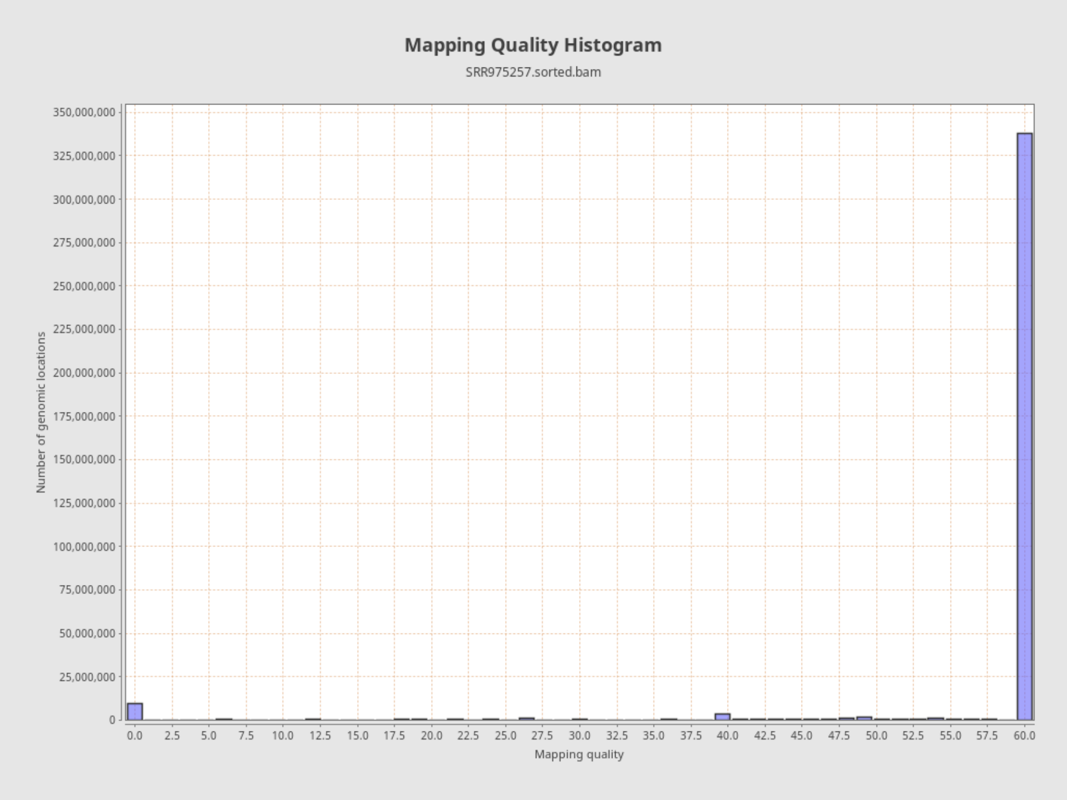
11. Results : Homopolymer Indels



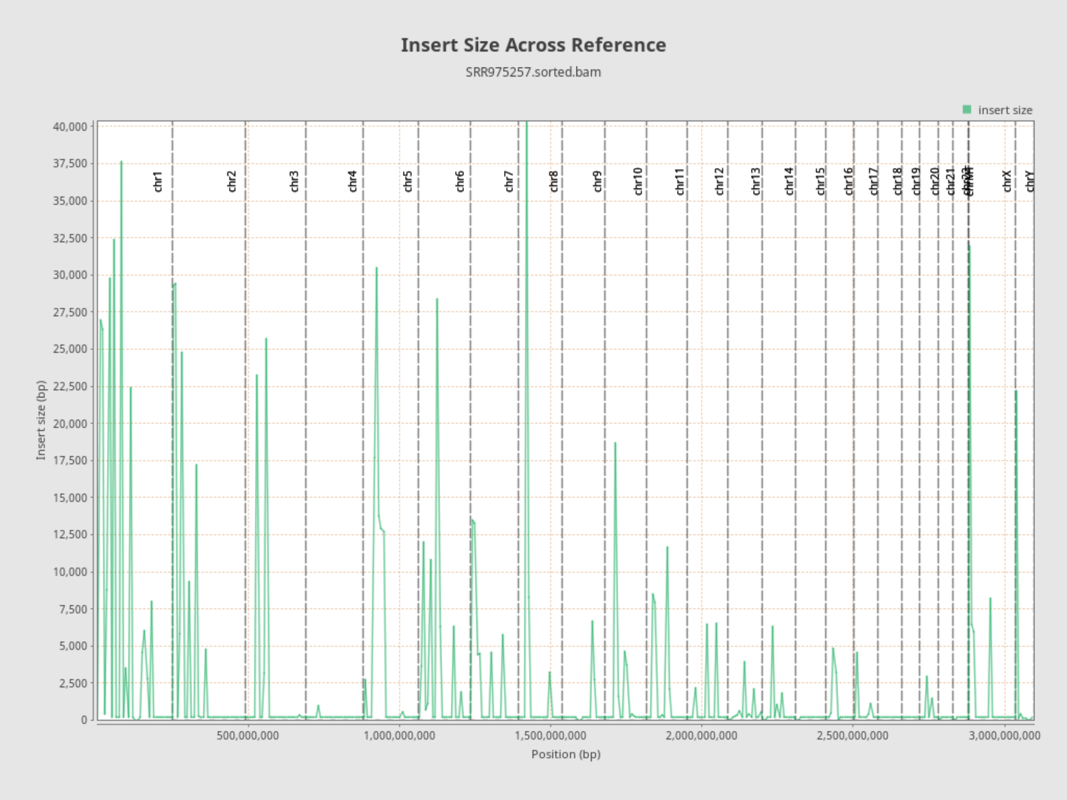
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram