Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 00:51:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975304.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_SRR975304 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975304_1.fastq.gz SRR975304_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 00:51:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975304.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,671,970
Mapped reads	3,633,824 / 98.96%
Unmapped reads	38,146 / 1.04%
Mapped paired reads	3,633,824 / 98.96%
Mapped reads, first in pair	1,816,148 / 49.46%
Mapped reads, second in pair	1,817,676 / 49.5%
Mapped reads, both in pair	3,622,794 / 98.66%
Mapped reads, singletons	11,030 / 0.3%
Secondary alignments	0
Supplementary alignments	13,973 / 0.38%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	151,250 / 4.12%
Duplication rate	2.61%
Clipped reads	2,259,938 / 61.55%

2.2. ACGT Content

Number/percentage of A's	96,122,664 / 29.07%
Number/percentage of C's	66,388,573 / 20.08%
Number/percentage of T's	97,276,444 / 29.42%
Number/percentage of G's	70,818,802 / 21.42%
Number/percentage of N's	6,899 / 0%

GC Percentage	41.5%

2.3. Coverage

Mean	0.1069
Standard Deviation	0.8905

2.4. Mapping Quality

Mean Mapping Quality	52.8

2.5. Insert size

Mean	41,973.99
Standard Deviation	1,965,302.74
P25/Median/P75	135 / 167 / 212

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	2,469,693
Insertions	48,367
Mapped reads with at least one insertion	1.3%
Deletions	105,487
Mapped reads with at least one deletion	2.84%
Homopolymer indels	46.26%

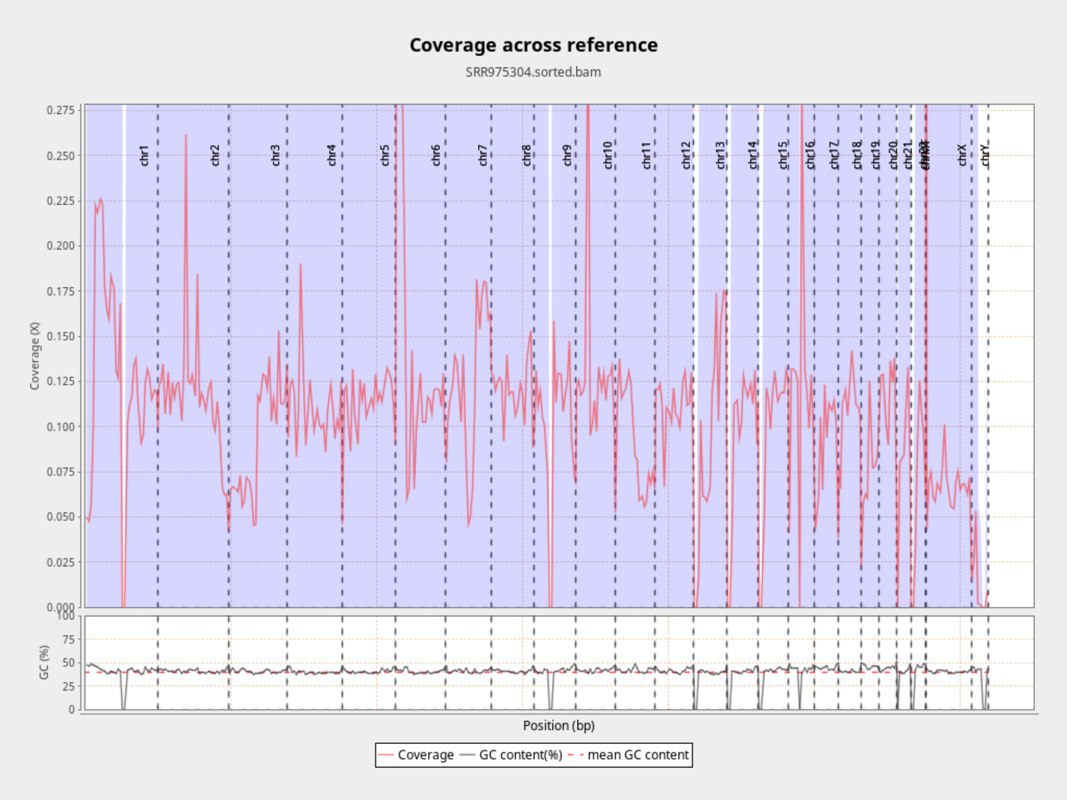
2.7. Chromosome stats

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

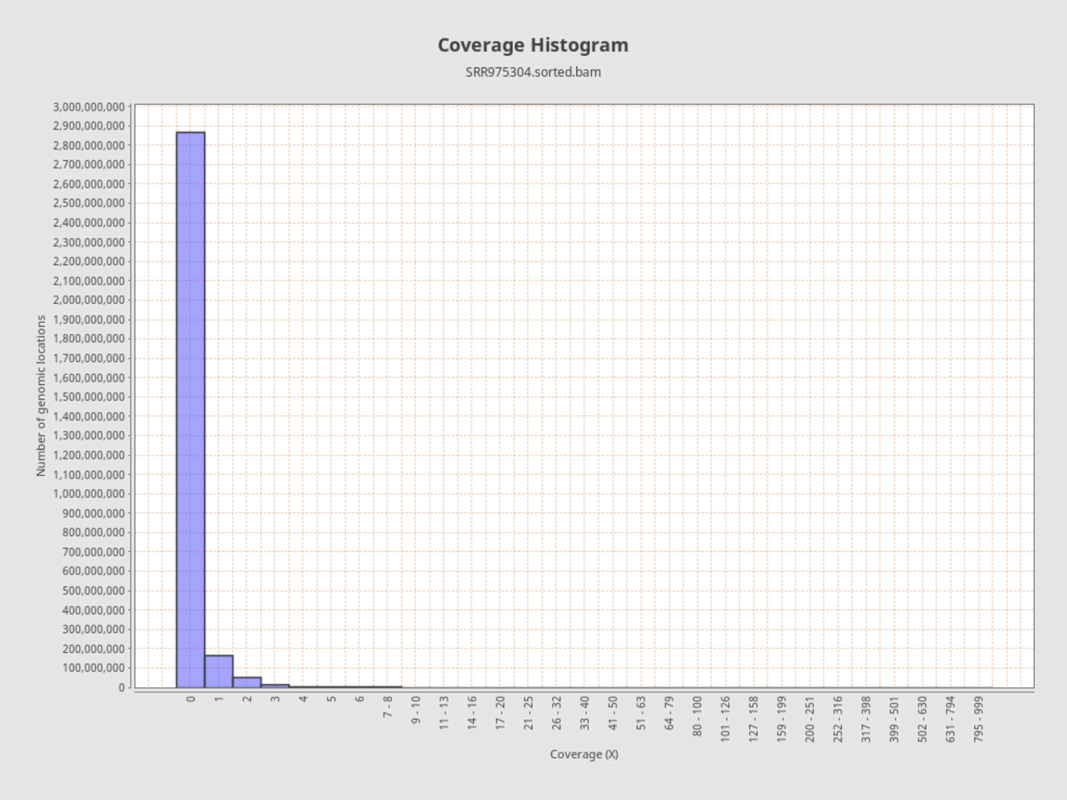
		bases	coverage	deviation
chr1	249250621	31656492	0.127	0.9089
chr2	243199373	28624785	0.1177	1.1482
chr3	198022430	18230856	0.0921	0.3938
chr4	191154276	21131007	0.1105	0.7032
chr5	180915260	20860070	0.1153	0.4409
chr6	171115067	24542823	0.1434	0.8402
chr7	159138663	19784174	0.1243	1.0127
chr8	146364022	17712768	0.121	0.5341
chr9	141213431	14395263	0.1019	1.3666
chr10	135534747	17731740	0.1308	1.877
chr11	135006516	12444092	0.0922	0.8291
chr12	133851895	14914307	0.1114	0.5959
chr13	115169878	10993461	0.0955	0.4008
chr14	107349540	10058689	0.0937	0.4317
chr15	102531392	9922968	0.0968	0.4028
chr16	90354753	10922507	0.1209	1.3255
chr17	81195210	7323756	0.0902	0.9321
chr18	78077248	8673523	0.1111	1.3891
chr19	59128983	4454617	0.0753	0.5984
chr20	63025520	7330518	0.1163	0.4671
chr21	48129895	4160352	0.0864	0.4768
chr22	51304566	3606489	0.0703	0.3582
chrMT	16571	94856	5.7242	5.3659
chrX	155270560	10452411	0.0673	0.4709

chrY	59373566	769920	0.013	0.7803

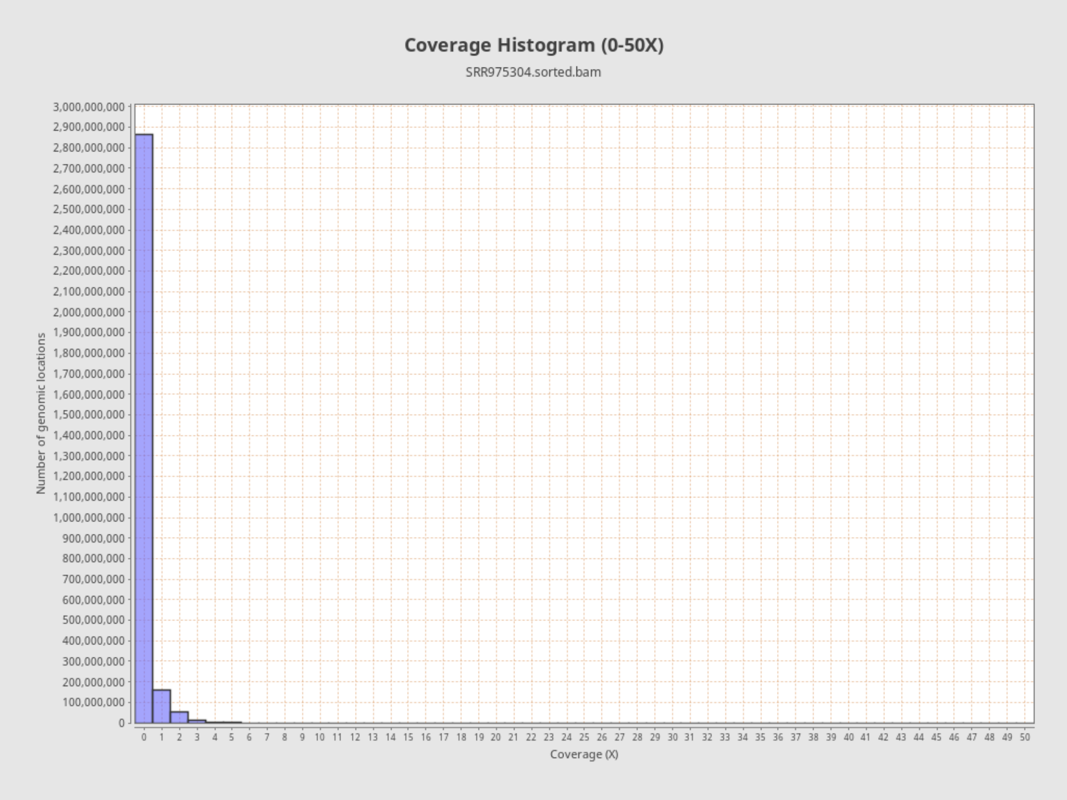
3. Results : Coverage across reference



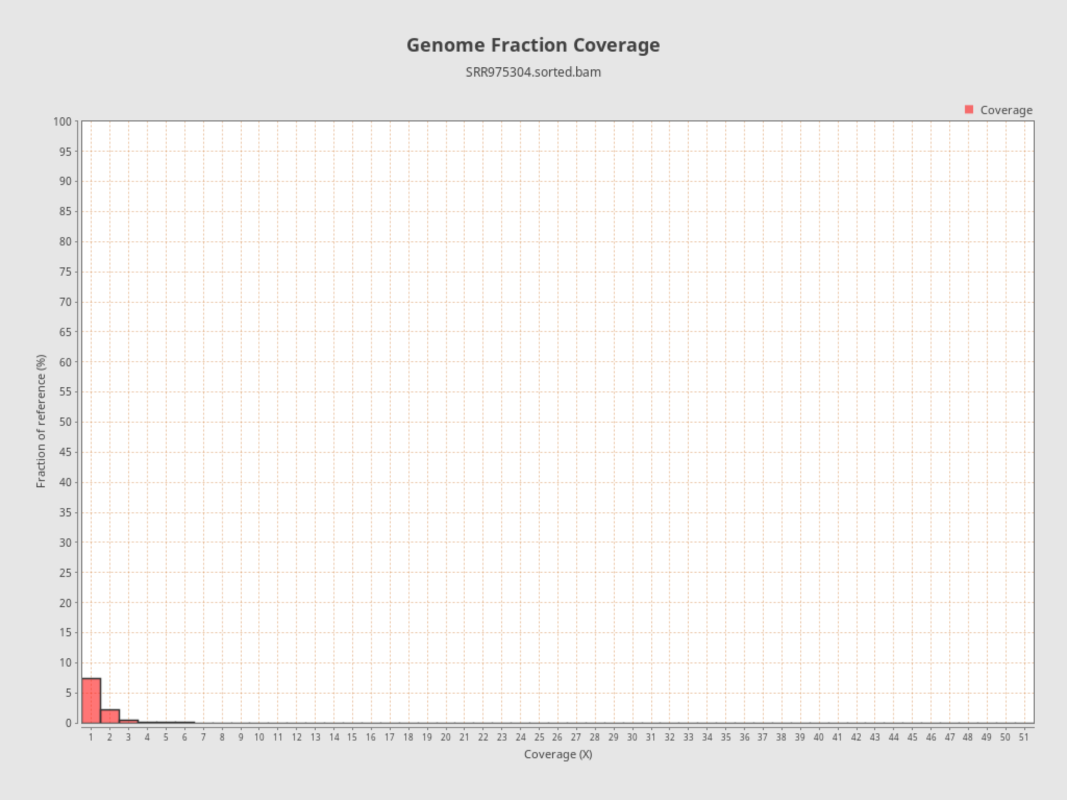
4. Results : Coverage Histogram



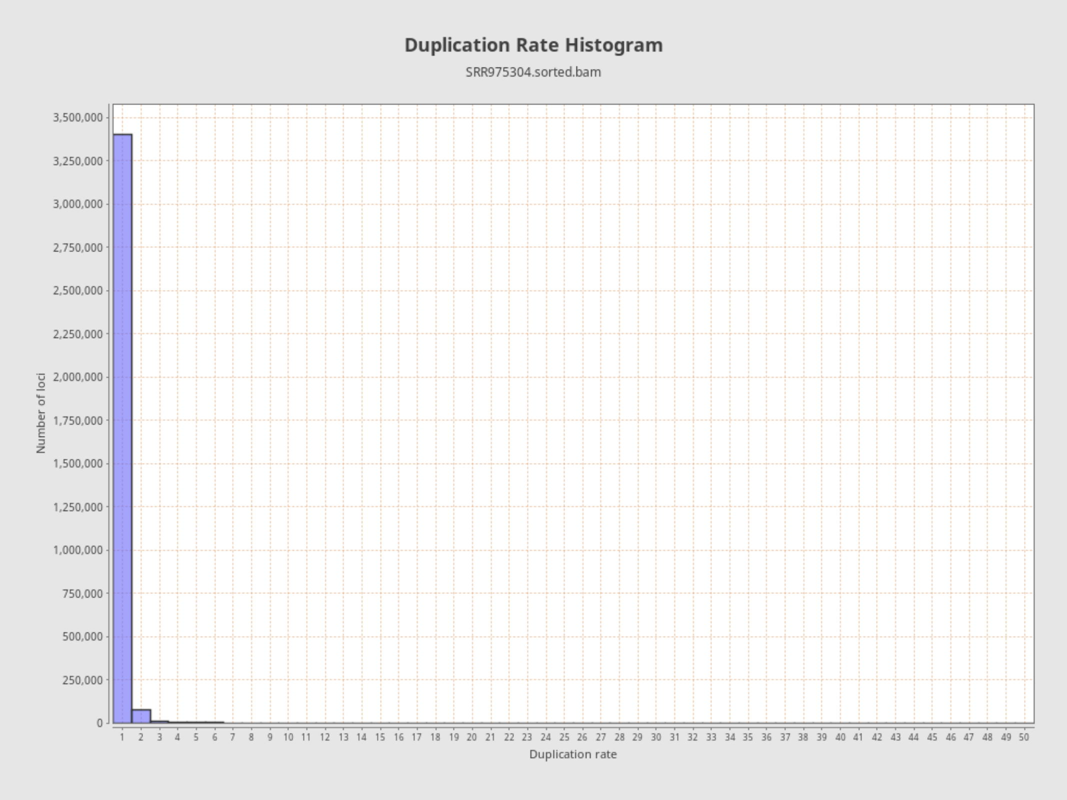
5. Results : Coverage Histogram (0-50X)



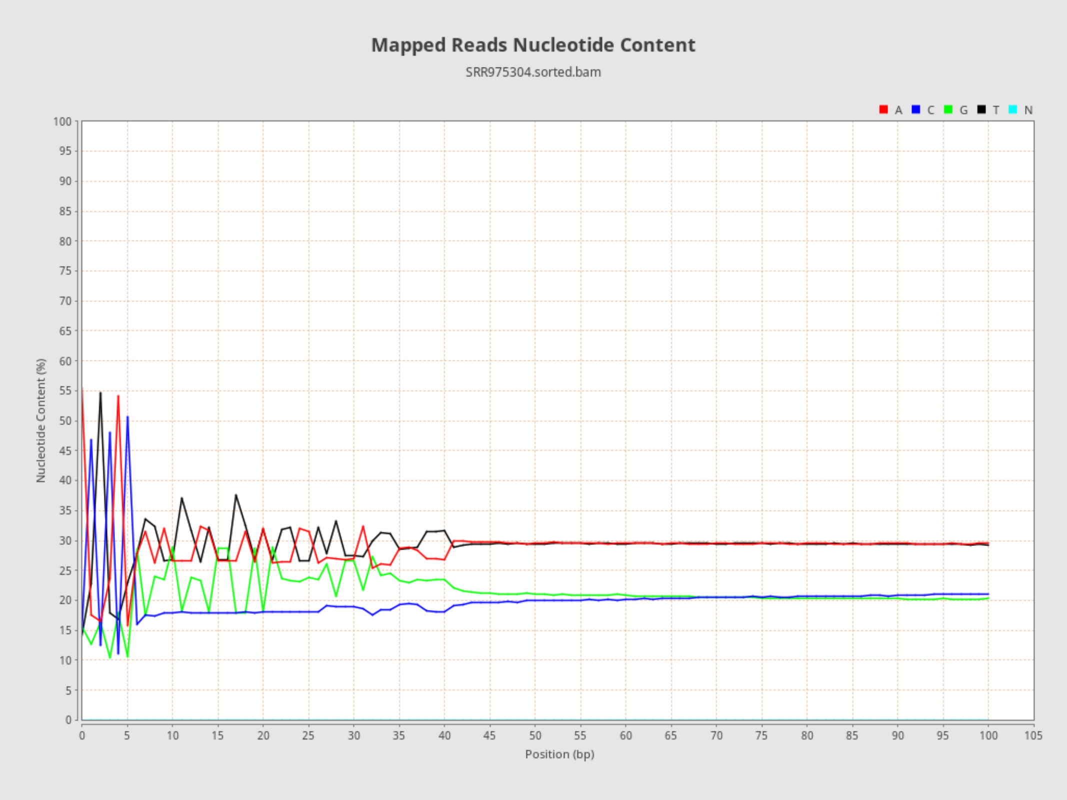
6. Results : Genome Fraction Coverage



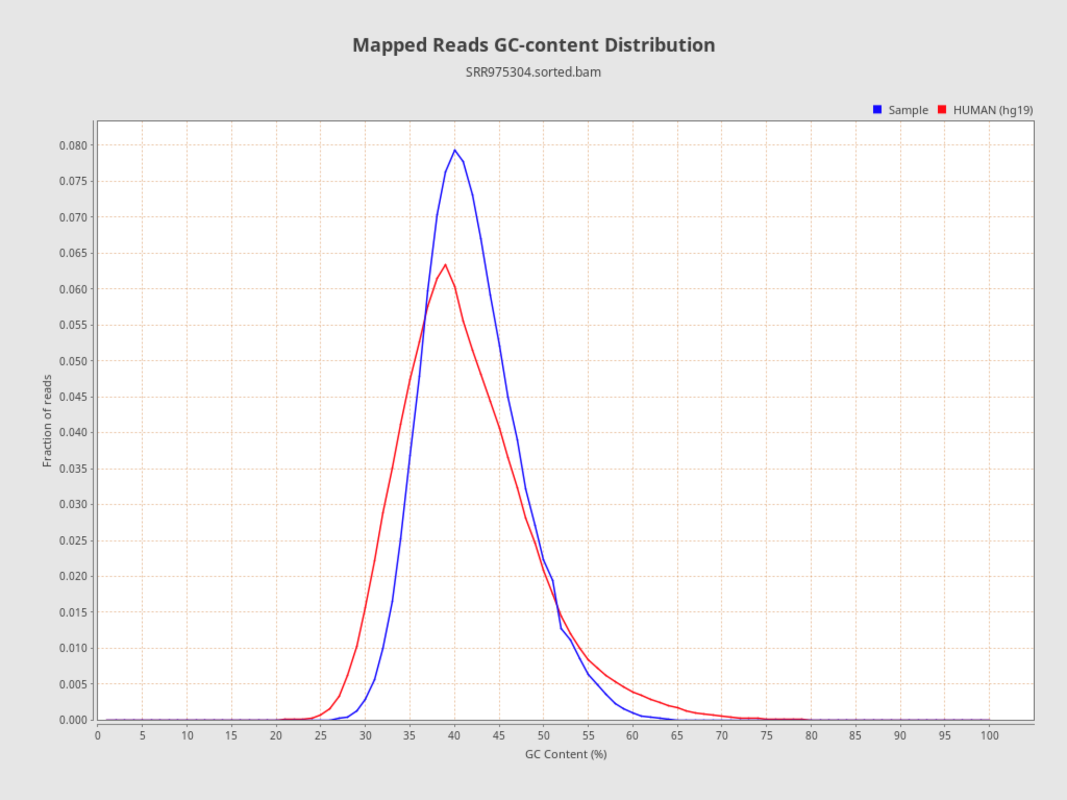
7. Results : Duplication Rate Histogram



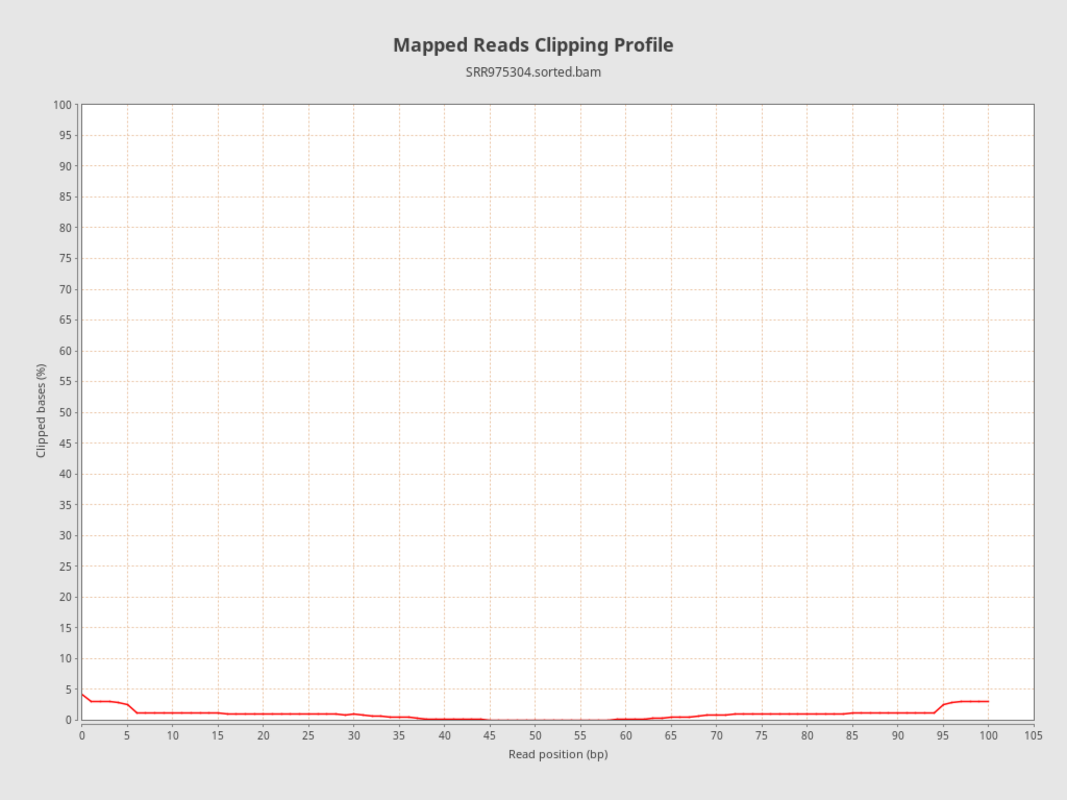
8. Results : Mapped Reads Nucleotide Content



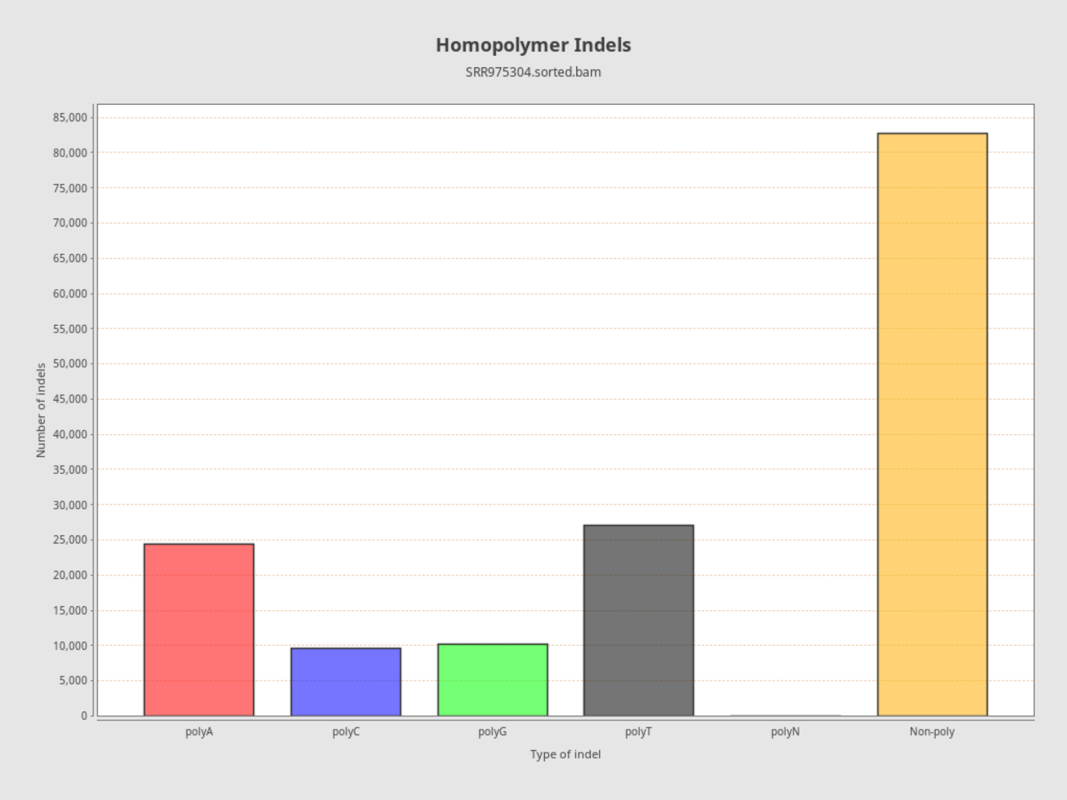
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

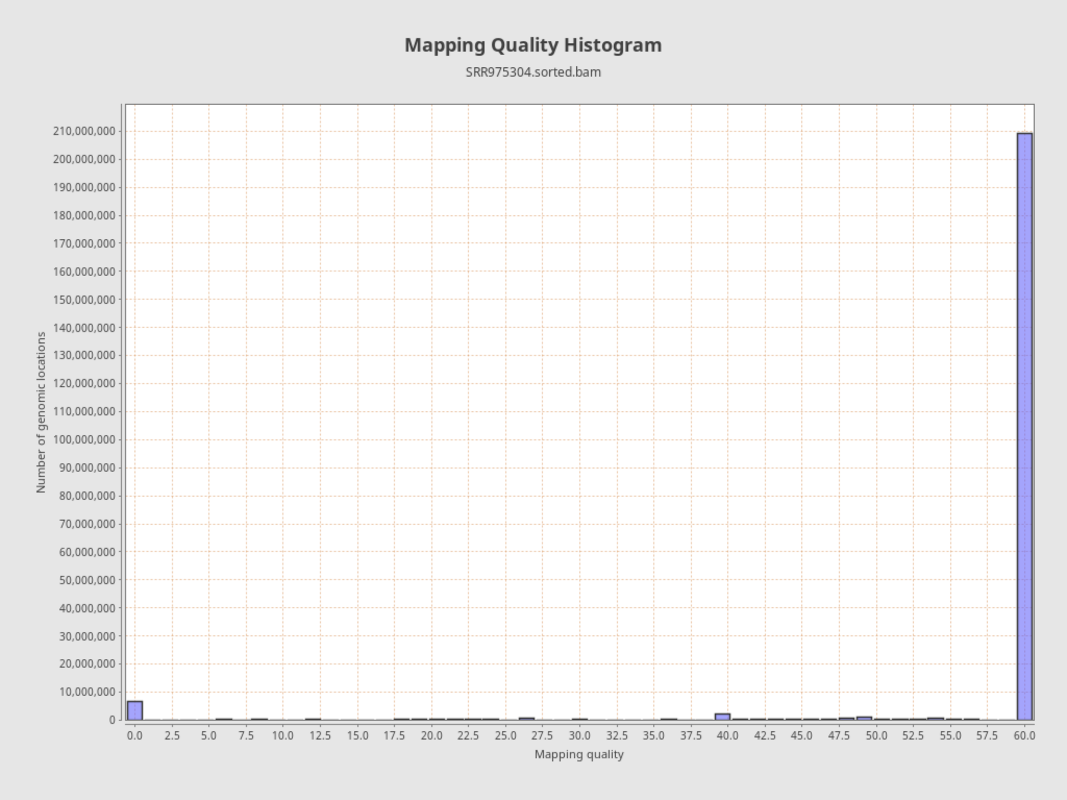


11. Results : Homopolymer Indels

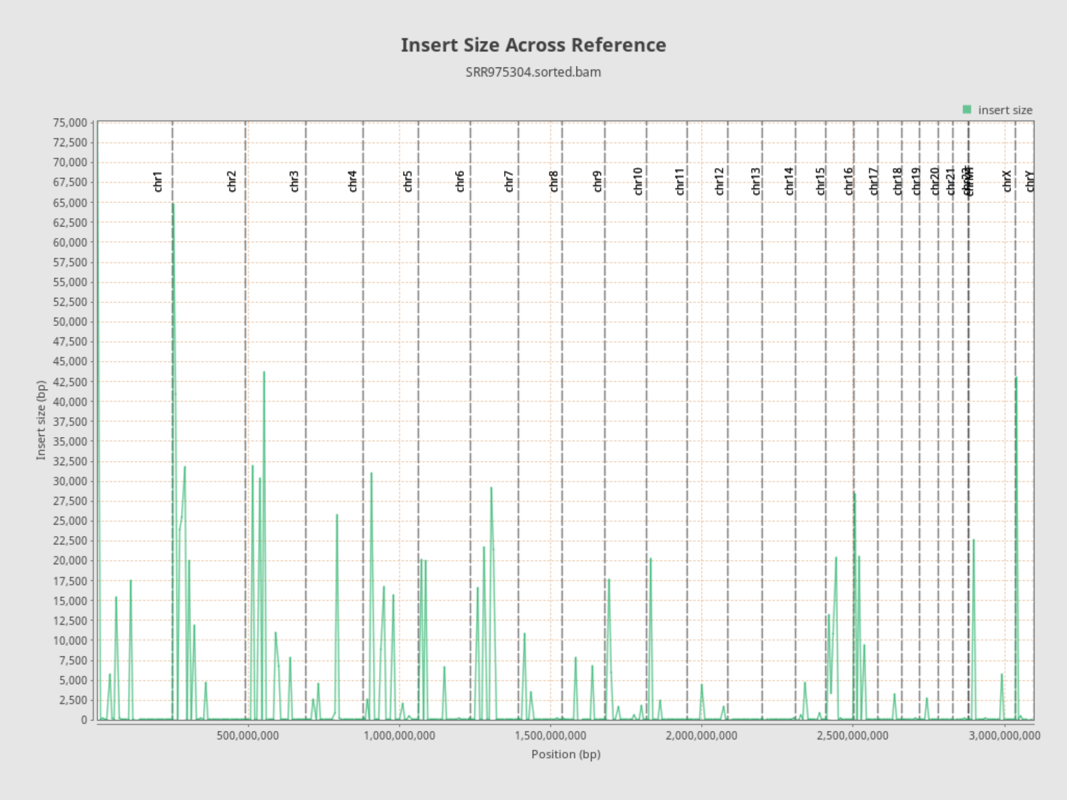


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram