Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 02:13:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975310.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_SRR975310 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975310_1.fastq.gz SRR975310_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 02:13:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975310.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,278,512
Mapped reads	4,194,880 / 98.05%
Unmapped reads	83,632 / 1.95%
Mapped paired reads	4,194,880 / 98.05%
Mapped reads, first in pair	2,096,739 / 49.01%
Mapped reads, second in pair	2,098,141 / 49.04%
Mapped reads, both in pair	4,180,656 / 97.71%
Mapped reads, singletons	14,224 / 0.33%
Secondary alignments	0
Supplementary alignments	16,973 / 0.4%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	207,134 / 4.84%
Duplication rate	2.94%
Clipped reads	2,623,686 / 61.32%

2.2. ACGT Content

Number/percentage of A's	110,184,937 / 28.89%
Number/percentage of C's	73,938,069 / 19.39%
Number/percentage of T's	113,851,046 / 29.85%
Number/percentage of G's	83,389,059 / 21.87%
Number/percentage of N's	7,592 / 0%

GC Percentage	41.25%

2.3. Coverage

Mean	0.1233
Standard Deviation	1.1359

2.4. Mapping Quality

Mean Mapping Quality	52.82

2.5. Insert size

Mean	46,046.08
Standard Deviation	2,055,482.58
P25/Median/P75	134 / 166 / 211

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	2,822,697
Insertions	64,144
Mapped reads with at least one insertion	1.49%
Deletions	121,213
Mapped reads with at least one deletion	2.83%
Homopolymer indels	44.92%

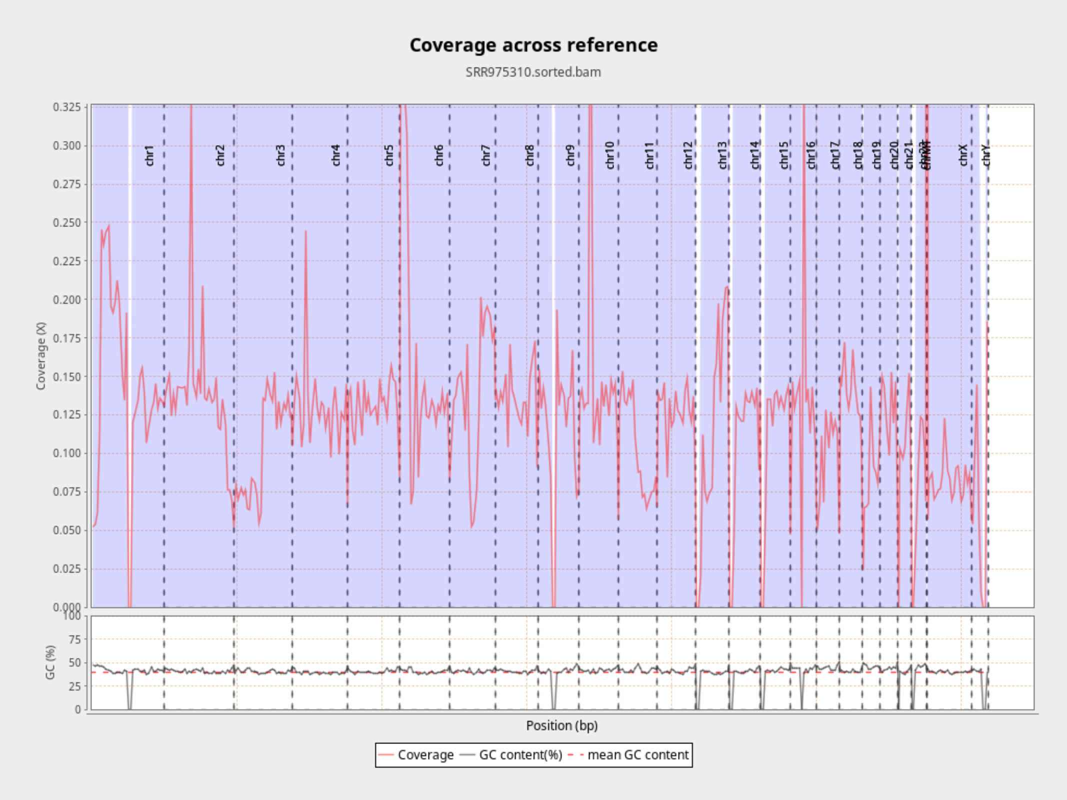
2.7. Chromosome stats

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

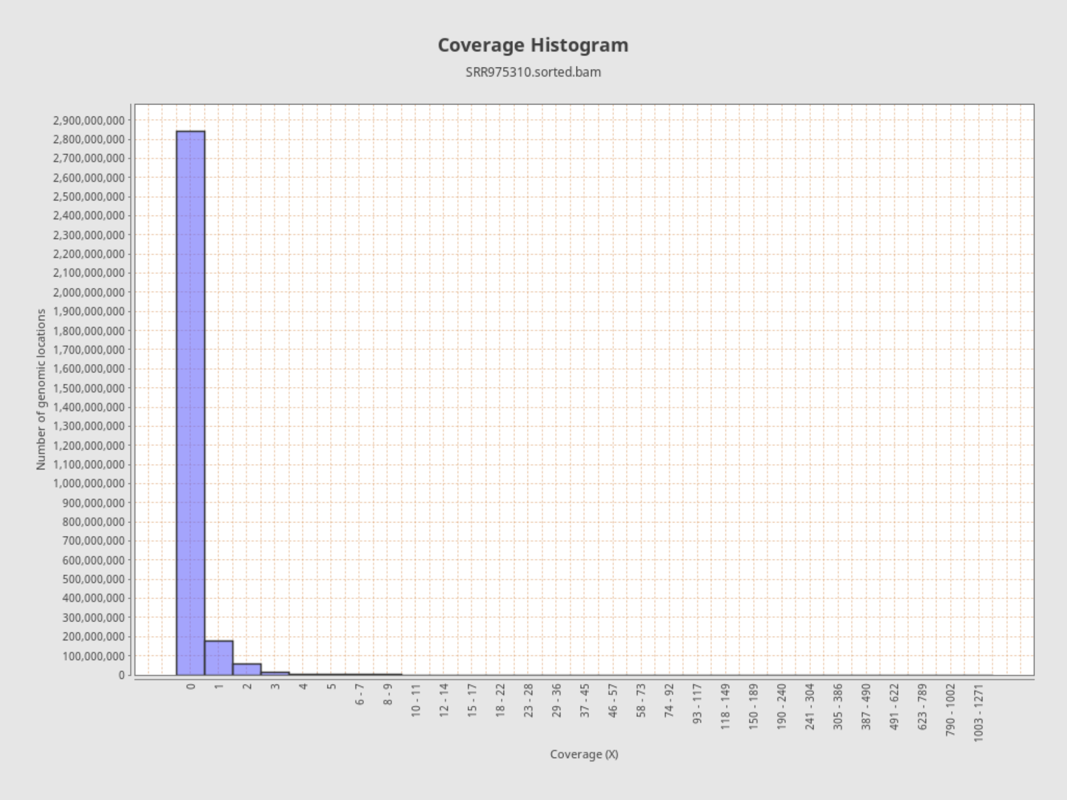
		bases	coverage	deviation
chr1	249250621	35650145	0.143	1.1351
chr2	243199373	33714008	0.1386	1.4533
chr3	198022430	20491606	0.1035	0.4362
chr4	191154276	24994630	0.1308	0.8598
chr5	180915260	23951992	0.1324	0.4842
chr6	171115067	27640613	0.1615	0.9849
chr7	159138663	22054029	0.1386	1.2998
chr8	146364022	19828277	0.1355	0.6209
chr9	141213431	16318399	0.1156	1.701
chr10	135534747	20426593	0.1507	2.7268
chr11	135006516	13946695	0.1033	0.9823
chr12	133851895	17188250	0.1284	0.4757
chr13	115169878	13131236	0.114	0.4485
chr14	107349540	11389877	0.1061	0.4782
chr15	102531392	11222395	0.1095	0.4368
chr16	90354753	12247260	0.1355	1.6724
chr17	81195210	7946336	0.0979	0.9676
chr18	78077248	11034919	0.1413	1.7981
chr19	59128983	4916145	0.0831	0.738
chr20	63025520	8000505	0.1269	0.5083
chr21	48129895	4923971	0.1023	0.5844
chr22	51304566	3819255	0.0744	0.3836
chrMT	16571	116851	7.0515	6.4851
chrX	155270560	12675027	0.0816	0.5307

chrY	59373566	3953323	0.0666	1.3103

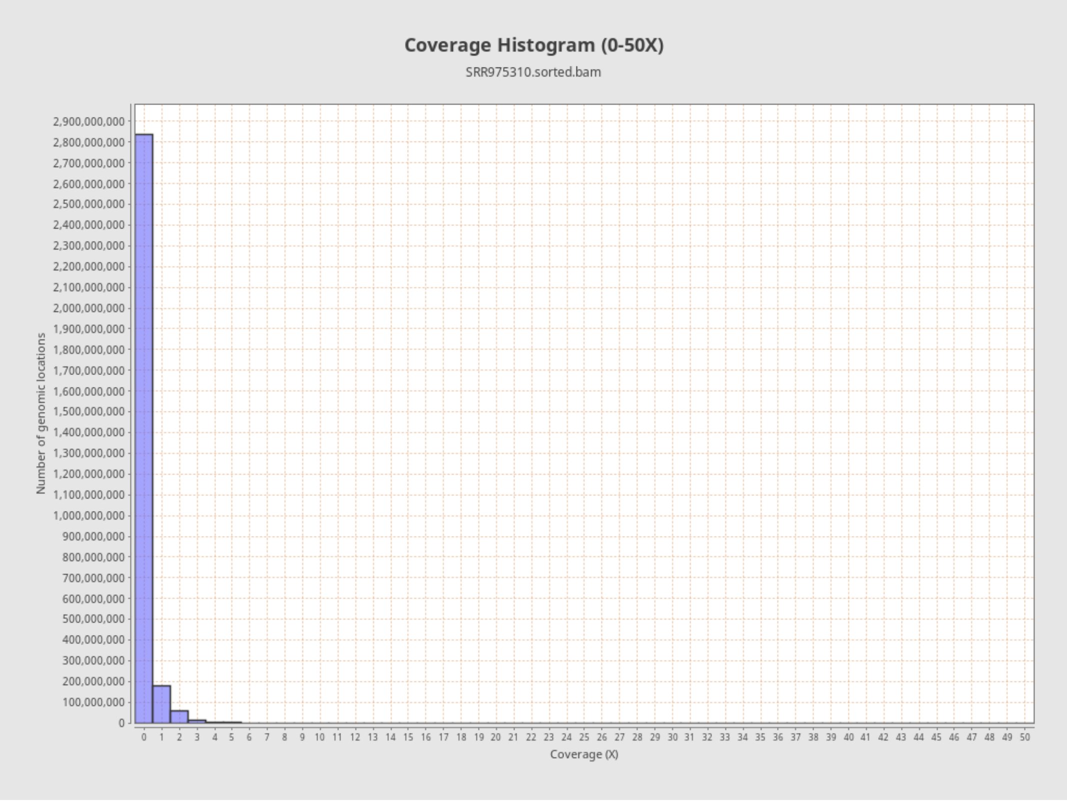
3. Results : Coverage across reference



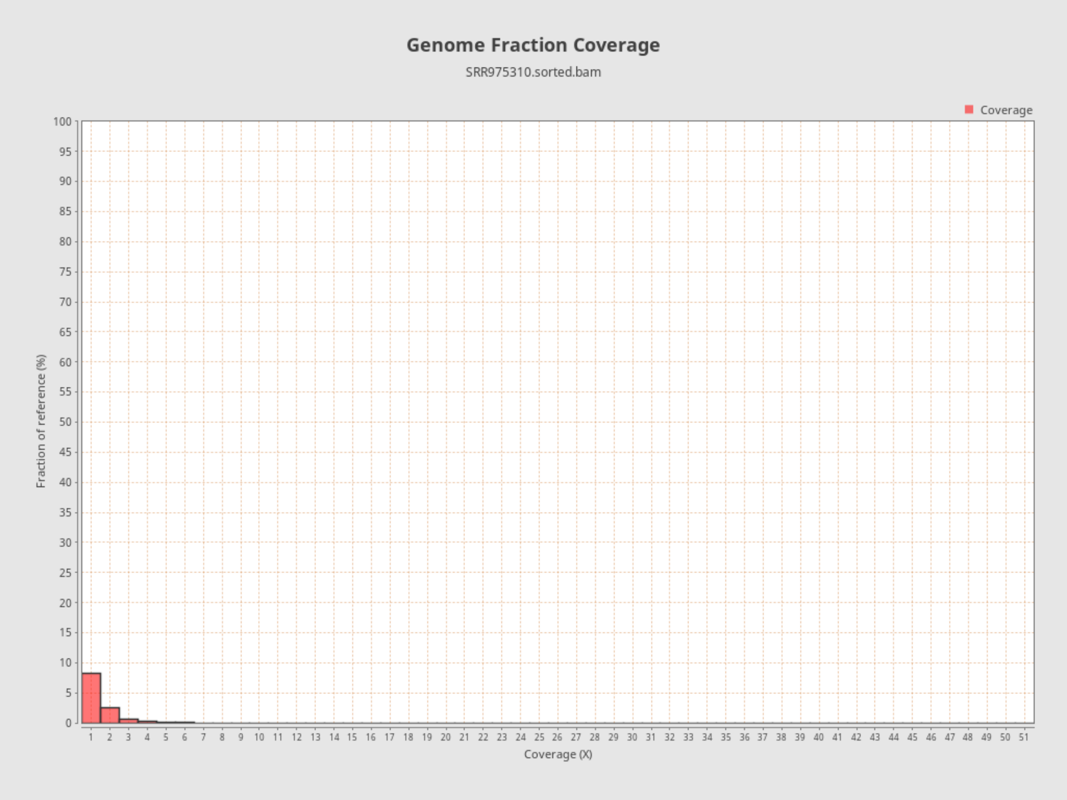
4. Results : Coverage Histogram



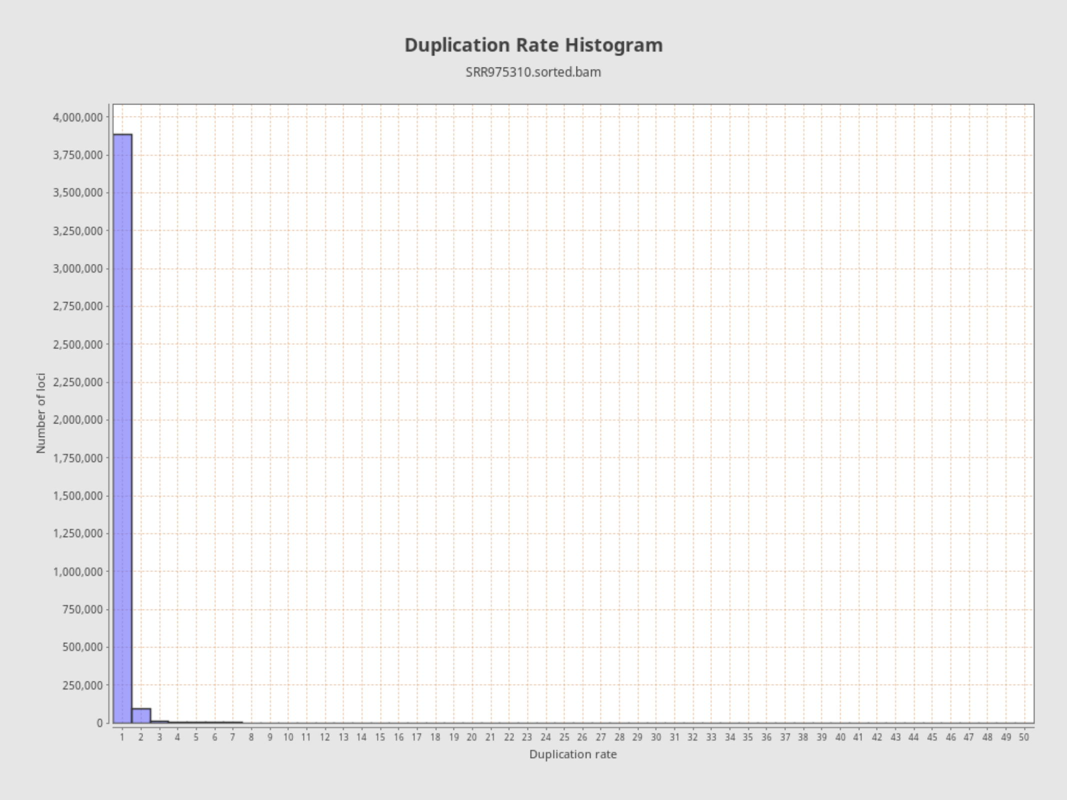
5. Results : Coverage Histogram (0-50X)



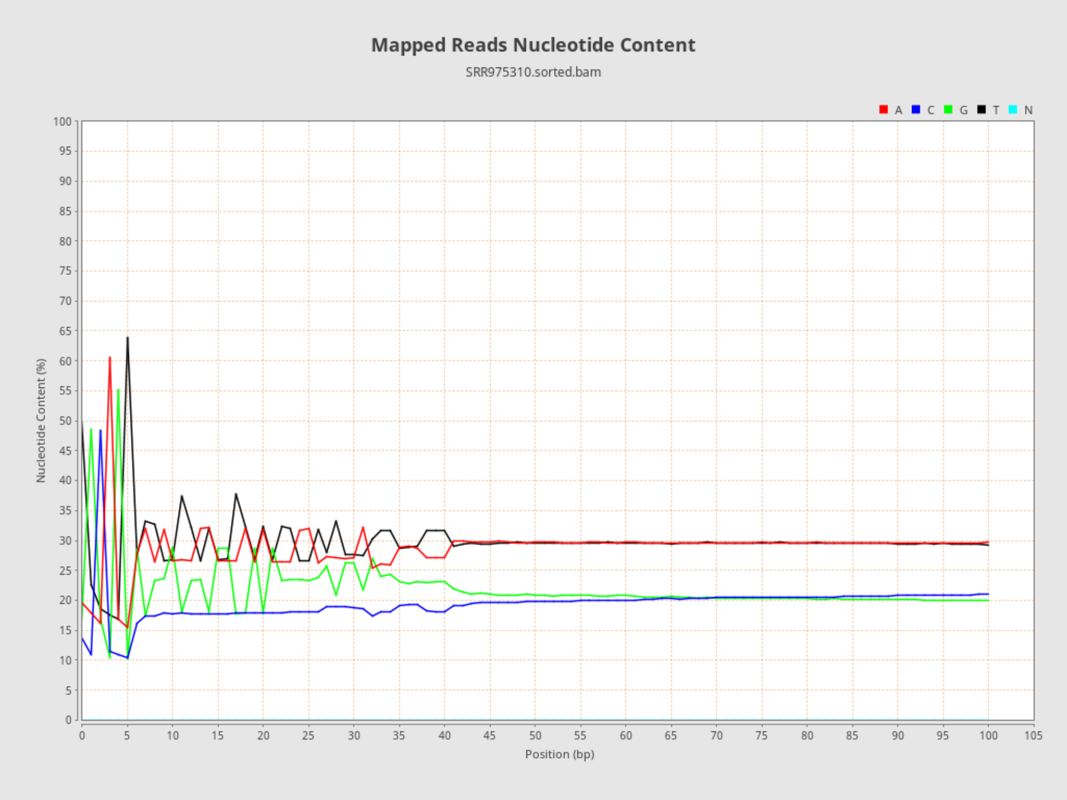
6. Results : Genome Fraction Coverage



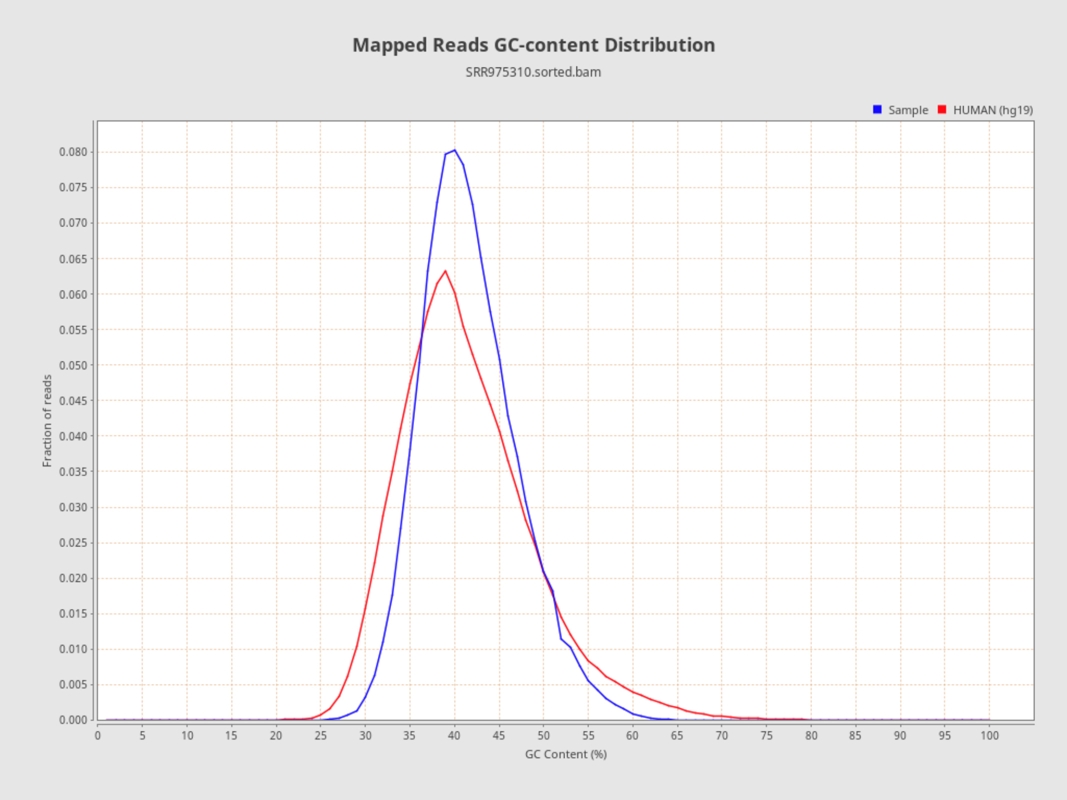
7. Results : Duplication Rate Histogram



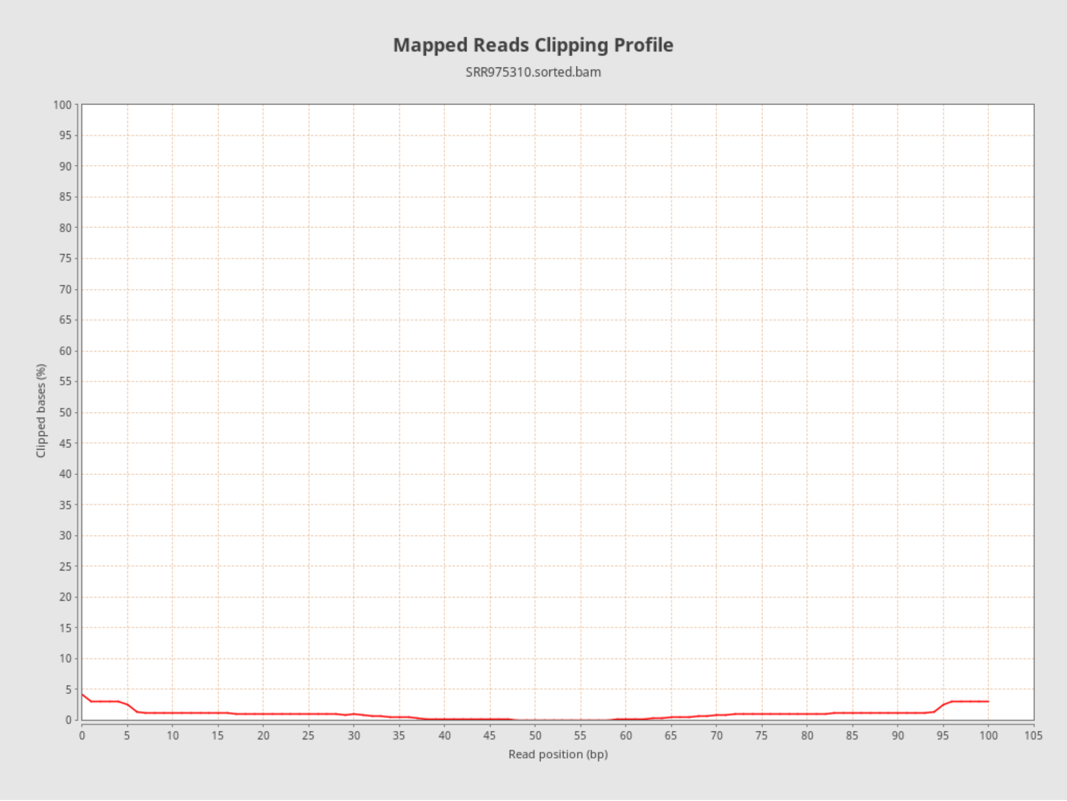
8. Results : Mapped Reads Nucleotide Content



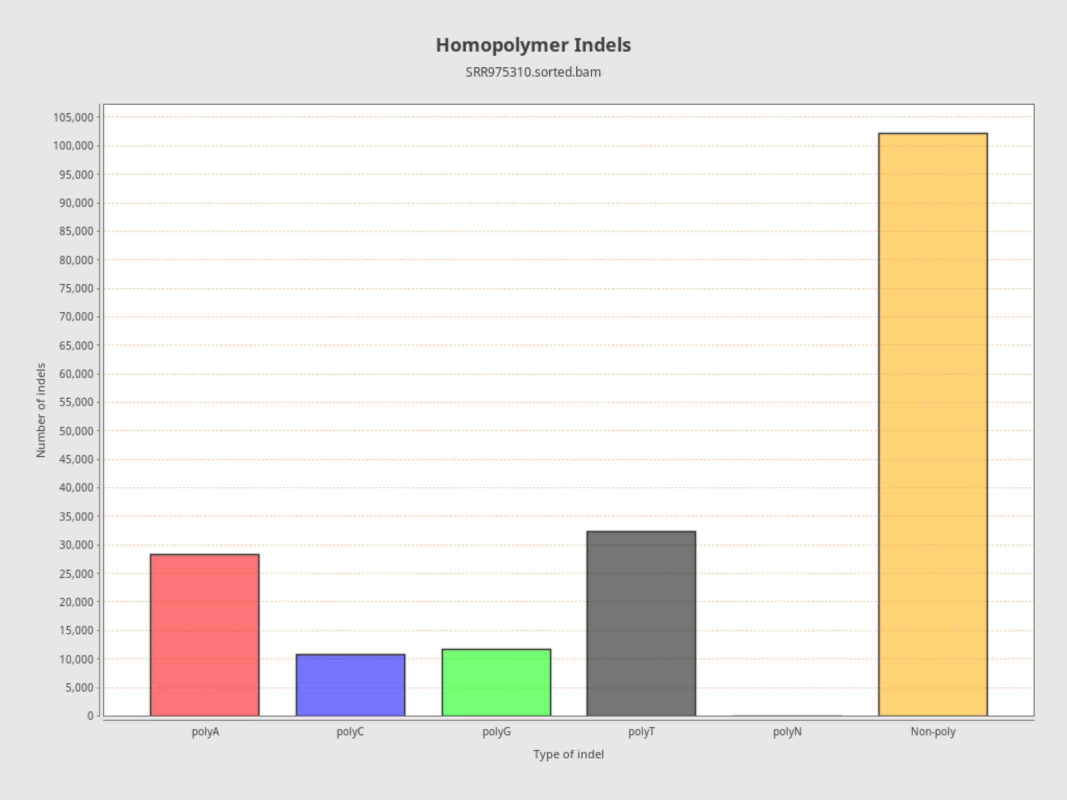
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

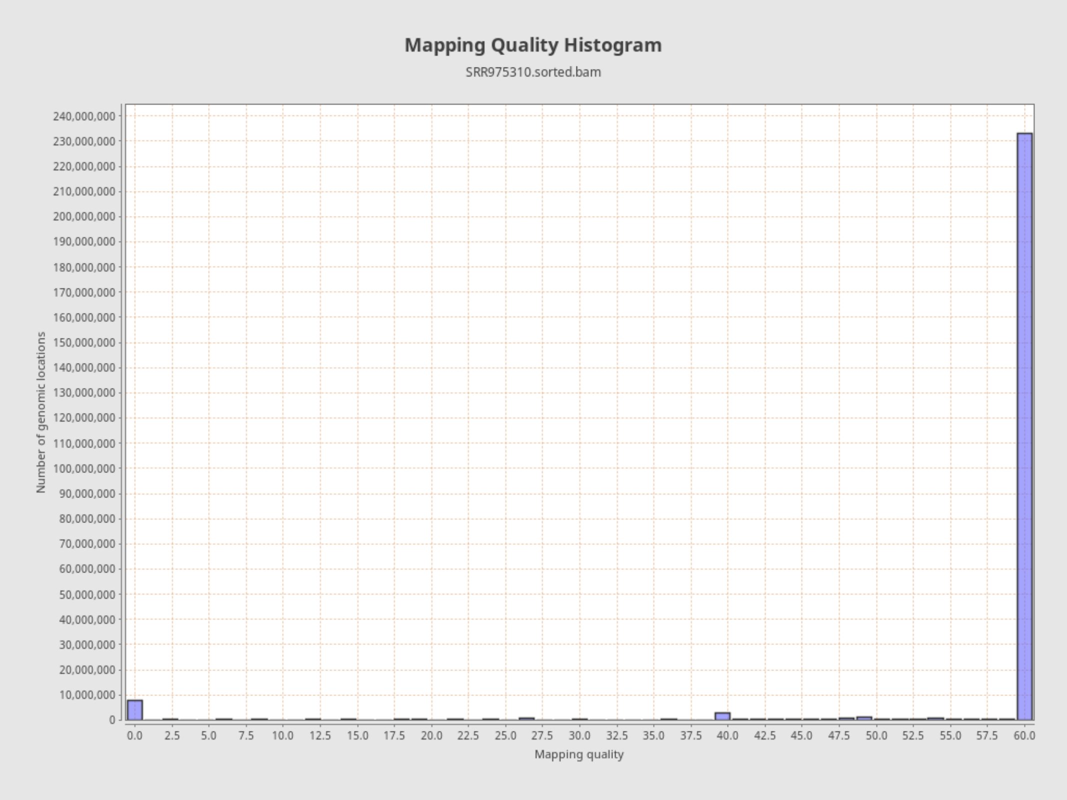


11. Results : Homopolymer Indels

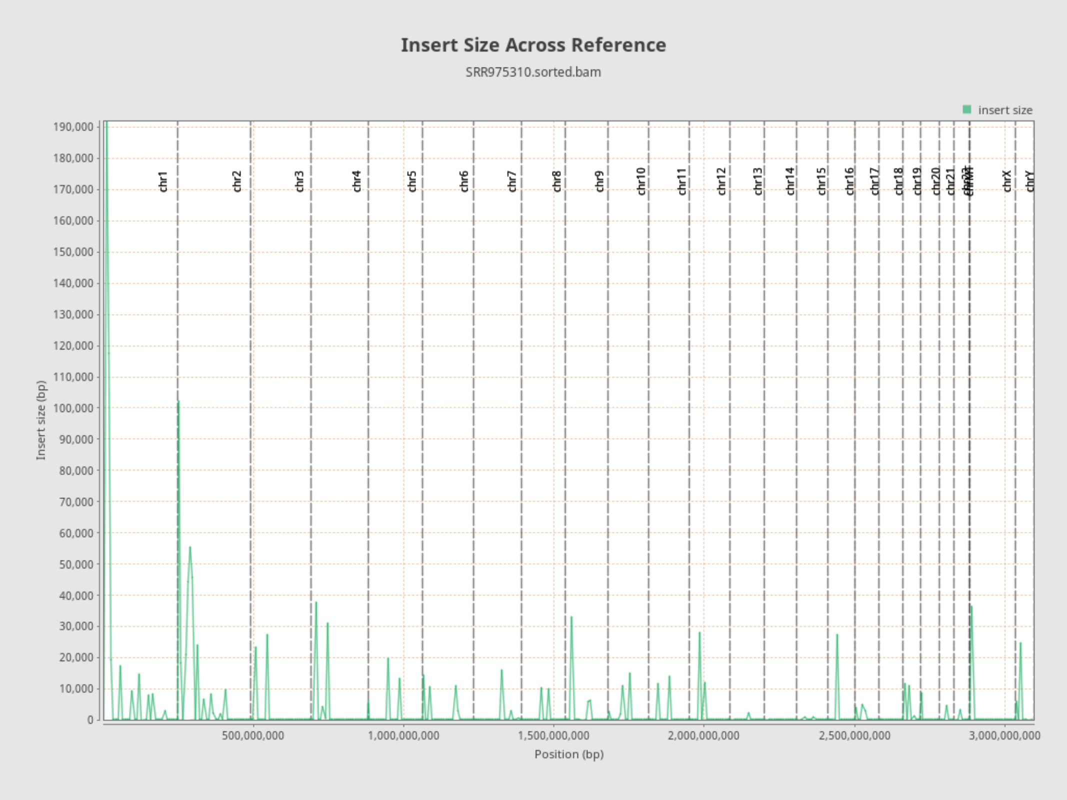


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram