Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 23:54:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975311.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_SRR975311 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975311_1.fastq.gz SRR975311_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 23:54:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975311.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	68,124,124
Mapped reads	67,927,724 / 99.71%
Unmapped reads	196,400 / 0.29%
Mapped paired reads	67,927,724 / 99.71%
Mapped reads, first in pair	33,992,048 / 49.9%
Mapped reads, second in pair	33,935,676 / 49.81%
Mapped reads, both in pair	67,839,058 / 99.58%
Mapped reads, singletons	88,666 / 0.13%
Secondary alignments	0
Supplementary alignments	110,217 / 0.16%
Read min/max/mean length	30 / 101 / 101.06
Duplicated reads (estimated)	39,465,197 / 57.93%
Duplication rate	44.91%
Clipped reads	37,913,748 / 55.65%

2.2. ACGT Content

Number/percentage of A's	1,674,643,340 / 26.42%
Number/percentage of C's	1,417,617,695 / 22.36%
Number/percentage of T's	1,719,009,410 / 27.12%
Number/percentage of G's	1,527,427,031 / 24.1%
Number/percentage of N's	260,723 / 0%

GC Percentage	46.46%

2.3. Coverage

Mean	2.0484
Standard Deviation	25.2074

2.4. Mapping Quality

Mean Mapping Quality	56.16

2.5. Insert size

Mean	60,887.33
Standard Deviation	2,442,945.9
P25/Median/P75	150 / 187 / 236

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	43,249,979
Insertions	604,725
Mapped reads with at least one insertion	0.88%
Deletions	1,531,936
Mapped reads with at least one deletion	2.22%
Homopolymer indels	47.55%

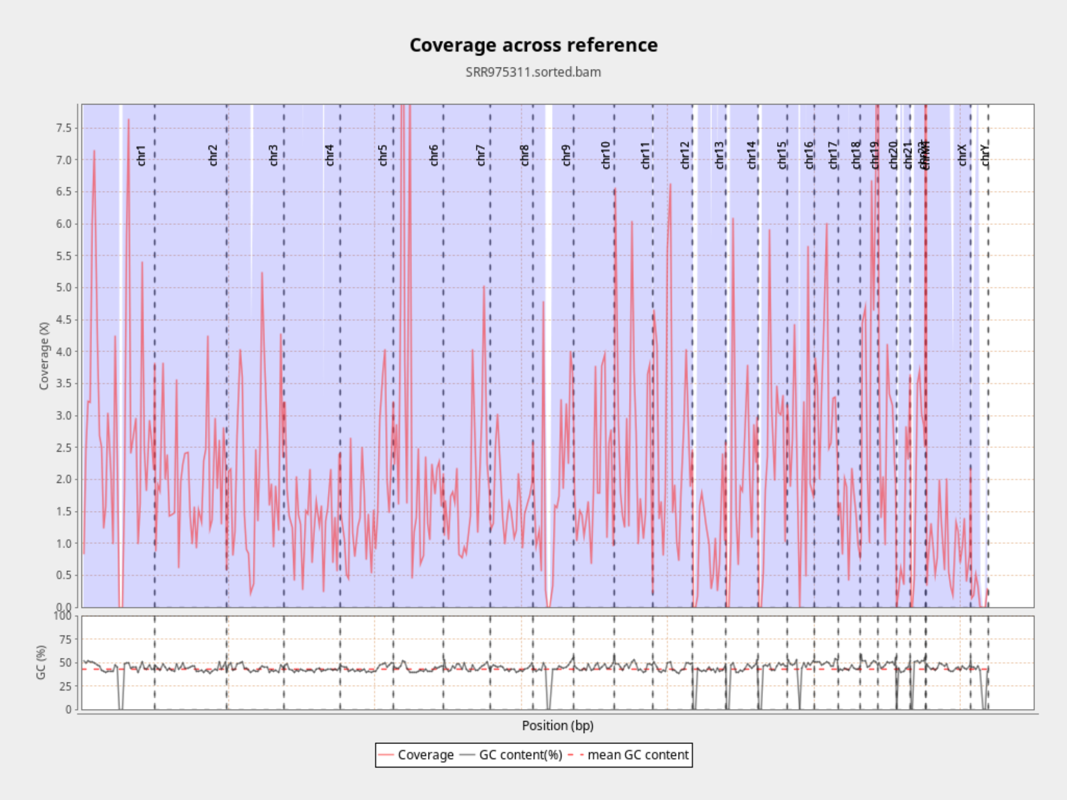
2.7. Chromosome stats

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

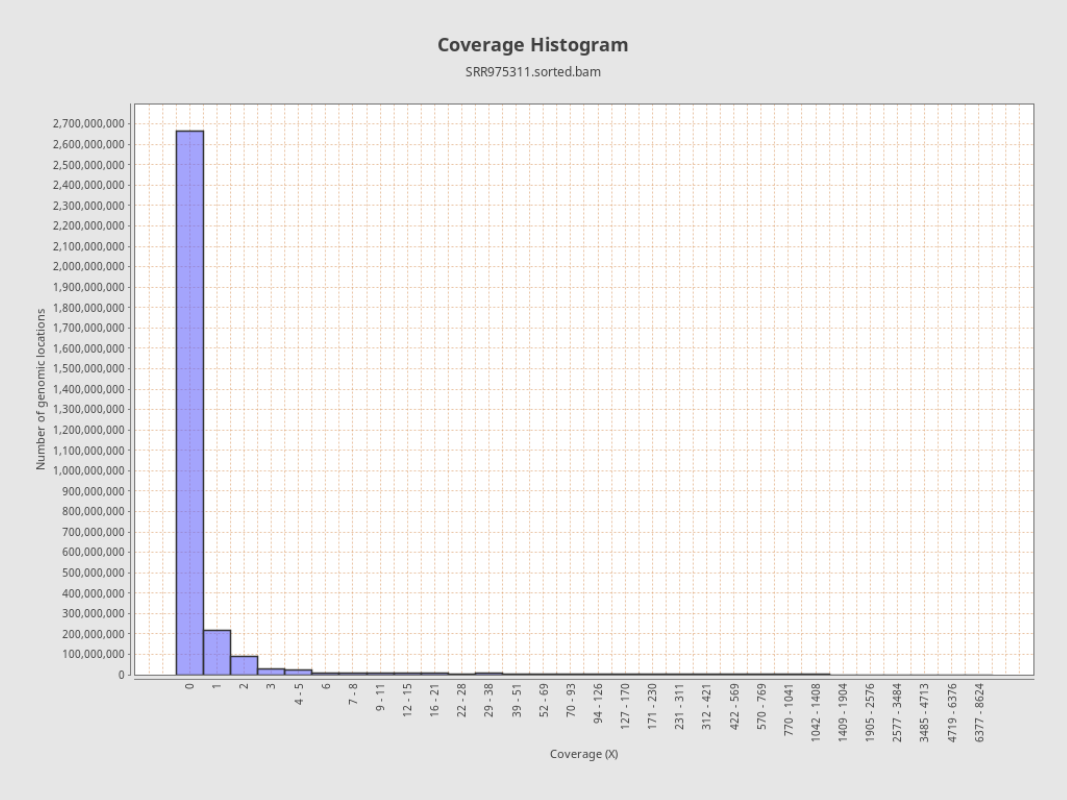
		bases	coverage	deviation
chr1	249250621	712138193	2.8571	30.3049
chr2	243199373	483894412	1.9897	23.2051
chr3	198022430	416965270	2.1056	24.9552
chr4	191154276	265441425	1.3886	19.6787
chr5	180915260	304542189	1.6833	22.0376
chr6	171115067	462924029	2.7053	39.251
chr7	159138663	297256586	1.8679	22.4138
chr8	146364022	236972060	1.6191	20.6438
chr9	141213431	261130888	1.8492	23.0945
chr10	135534747	264942338	1.9548	24.2075
chr11	135006516	349096219	2.5858	27.0407
chr12	133851895	354967274	2.6519	28.2991
chr13	115169878	110934549	0.9632	15.3334
chr14	107349540	216608115	2.0178	25.0991
chr15	102531392	238815086	2.3292	26.3747
chr16	90354753	218571217	2.419	26.3196
chr17	81195210	276690276	3.4077	30.7087
chr18	78077248	111096739	1.4229	20.2899
chr19	59128983	261893828	4.4292	37.3411
chr20	63025520	161240771	2.5583	30.2181
chr21	48129895	67154892	1.3953	19.609
chr22	51304566	109678605	2.1378	23.4145
chrMT	16571	235318	14.2006	25.1172
chrX	155270560	146711970	0.9449	13.5811

chrY	59373566	11222795	0.189	4.457

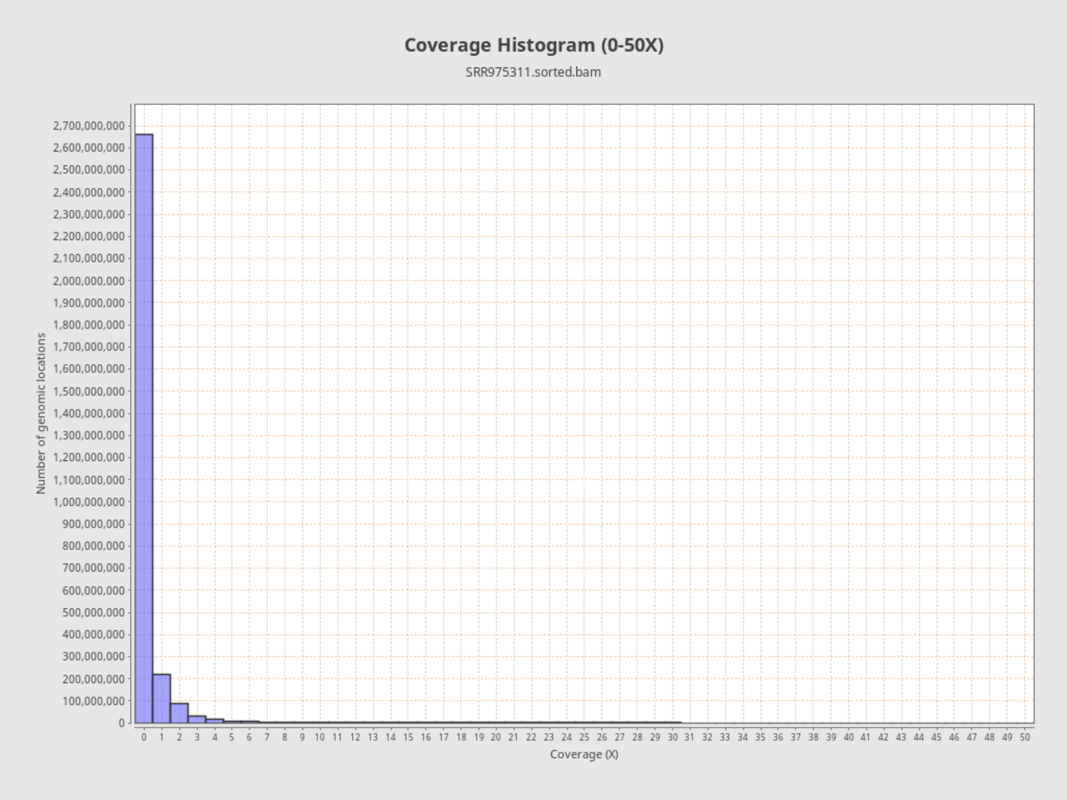
3. Results : Coverage across reference



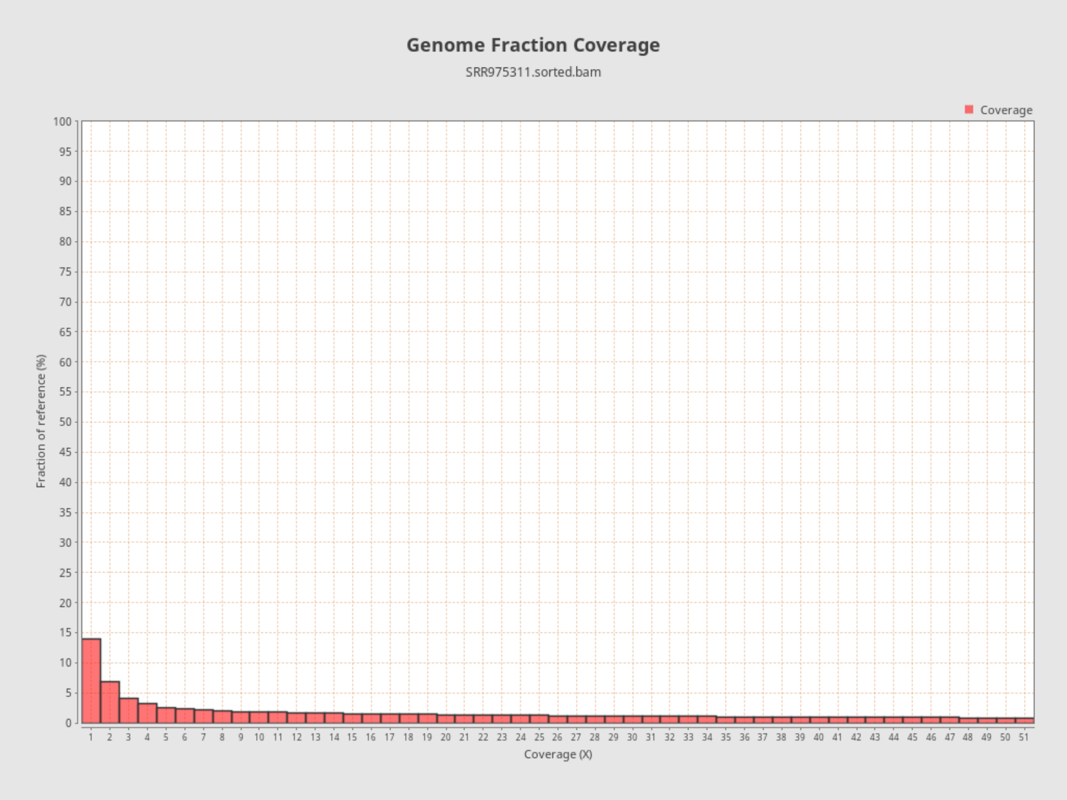
4. Results : Coverage Histogram



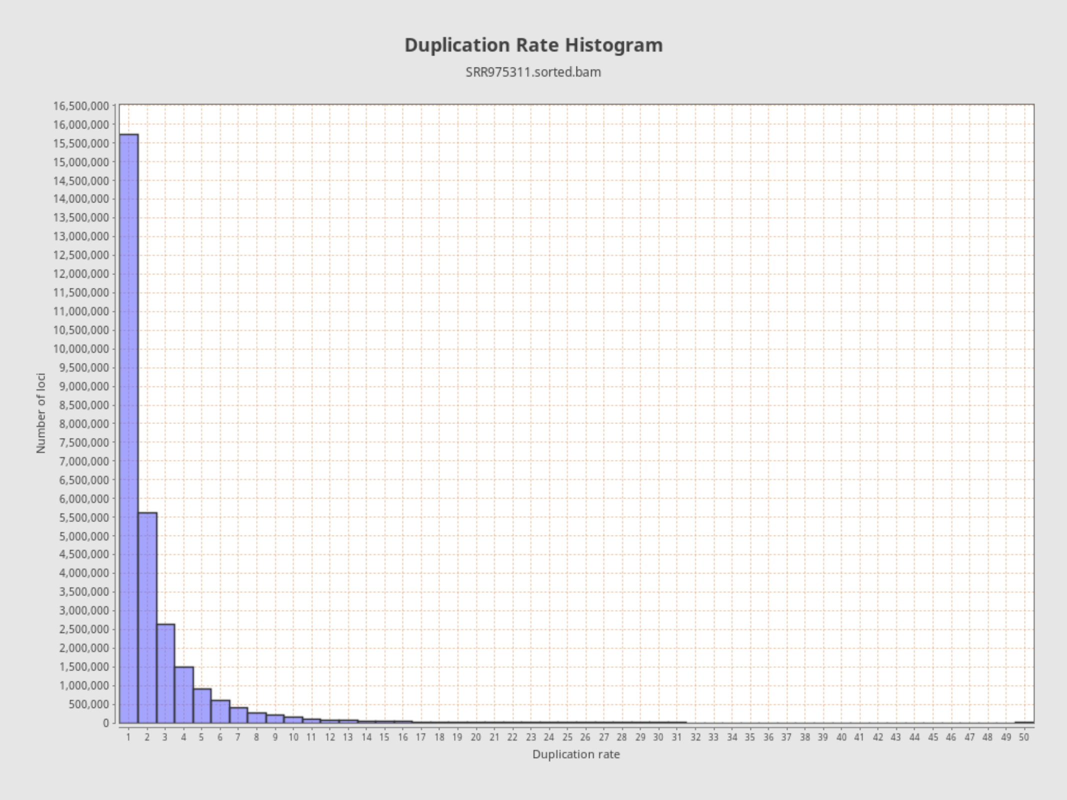
5. Results : Coverage Histogram (0-50X)



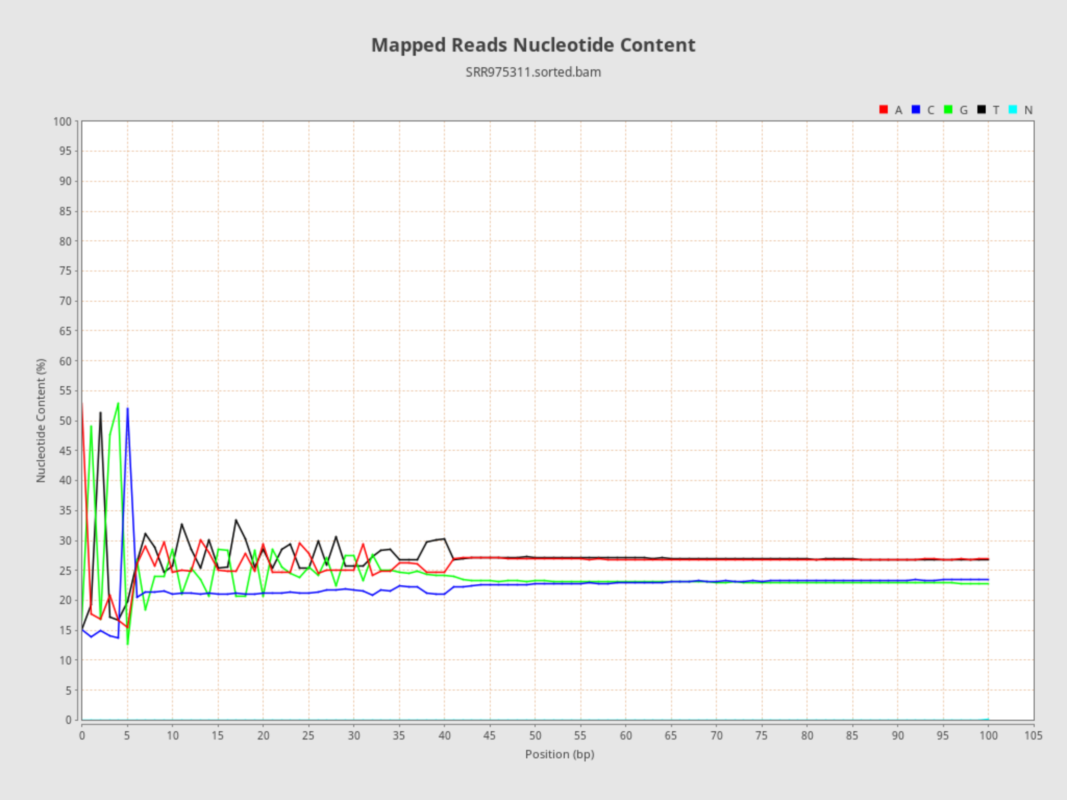
6. Results : Genome Fraction Coverage



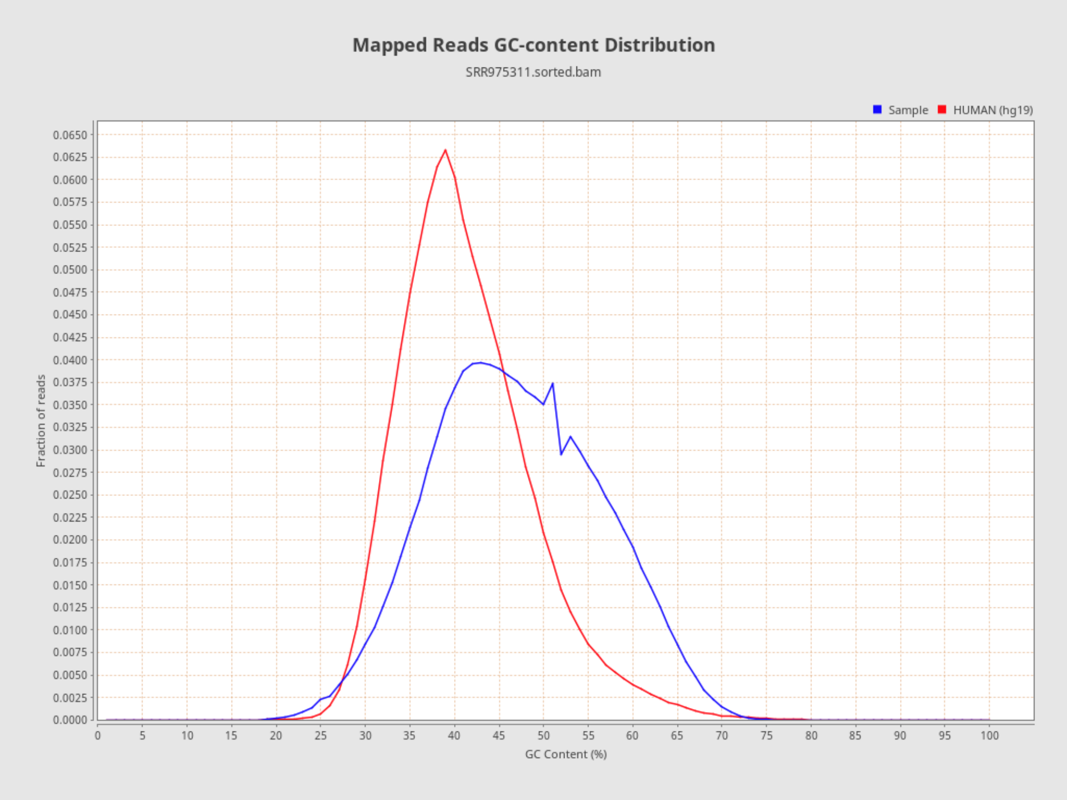
7. Results : Duplication Rate Histogram



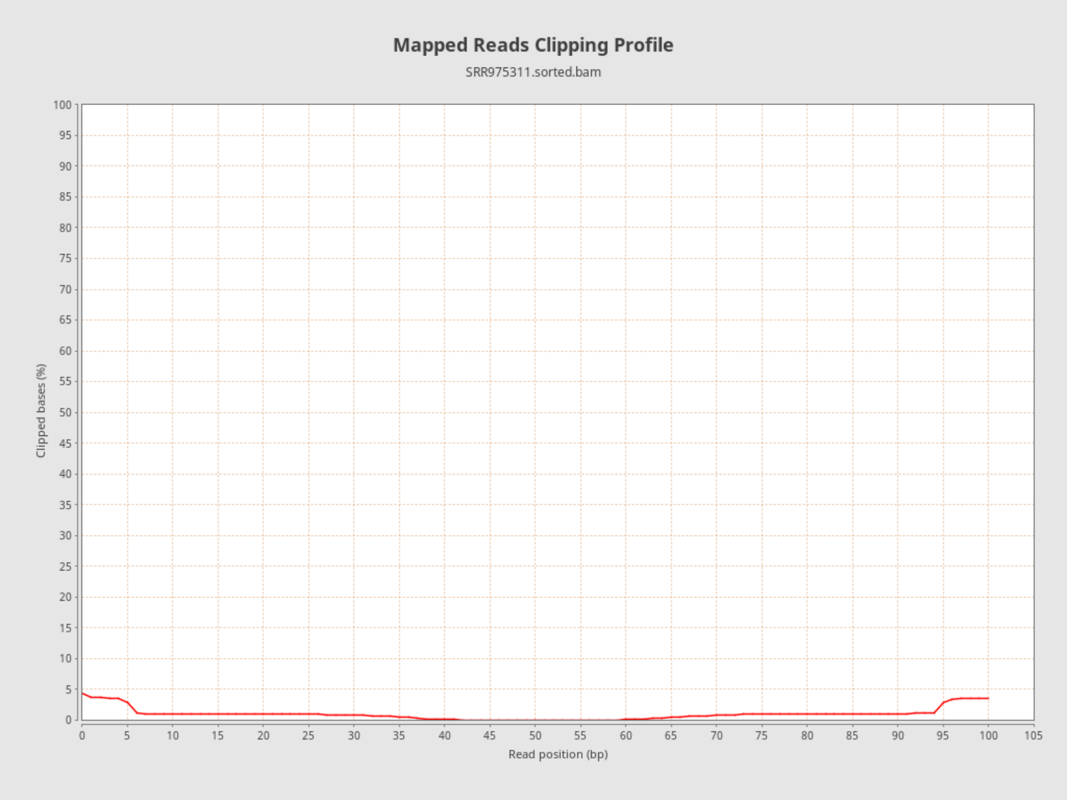
8. Results : Mapped Reads Nucleotide Content



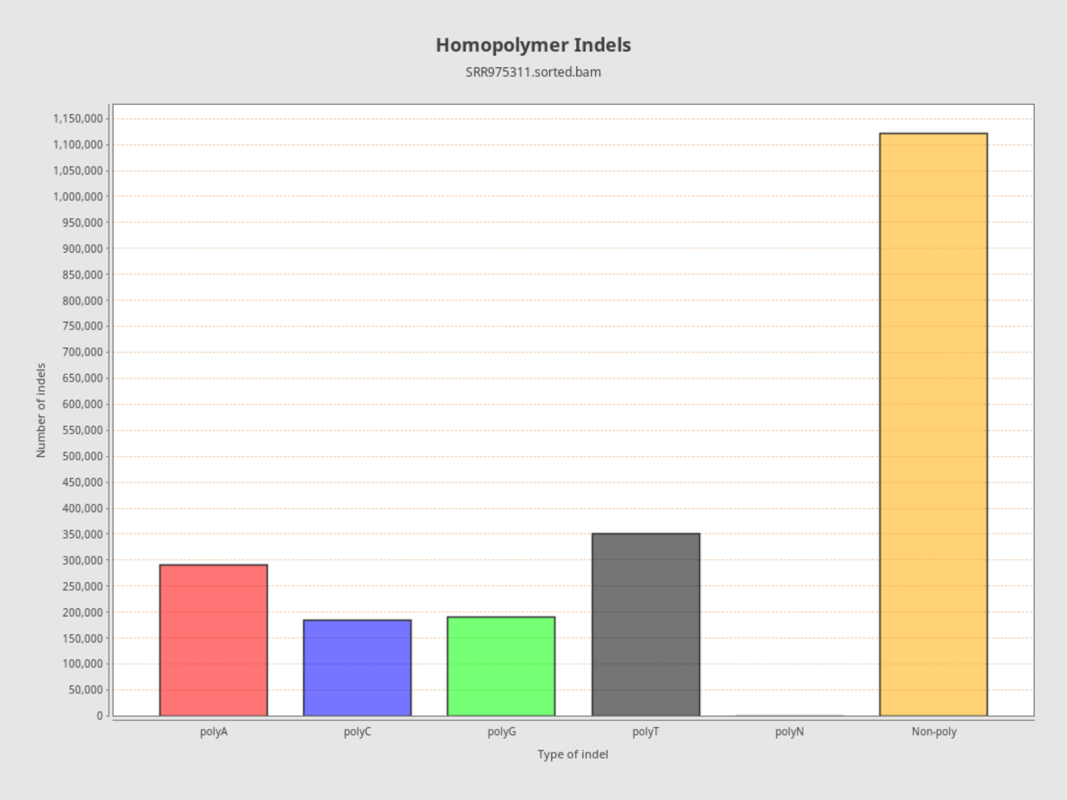
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

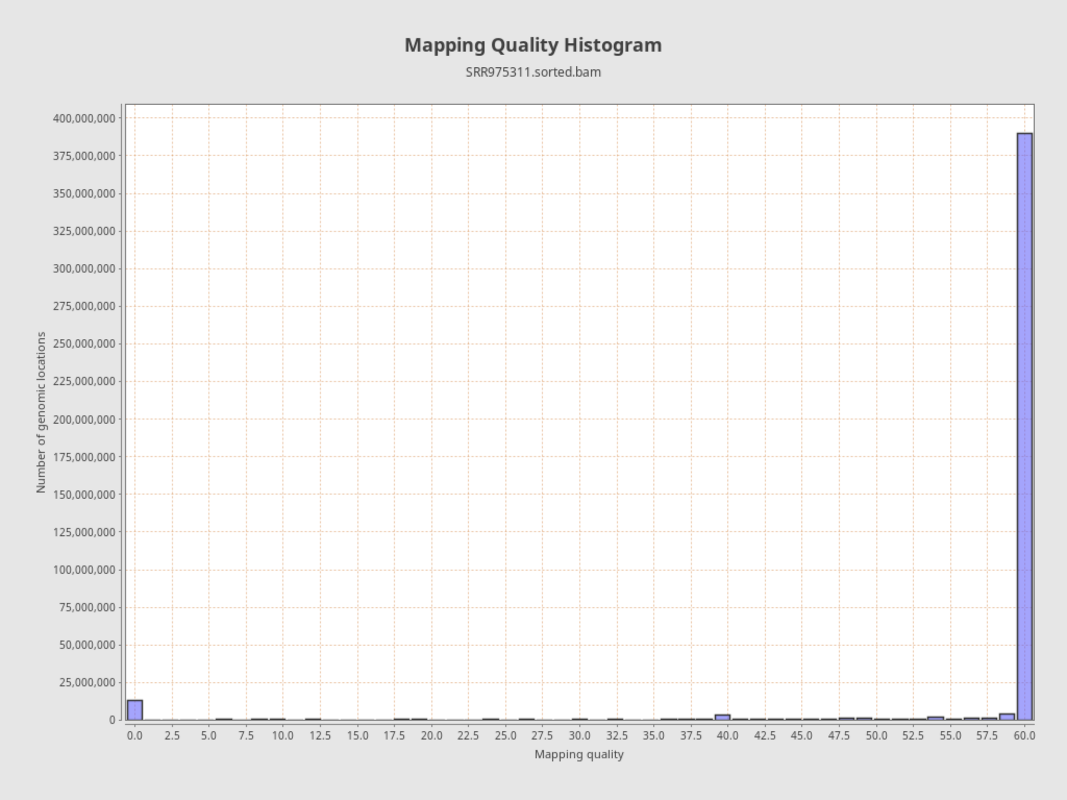


11. Results : Homopolymer Indels

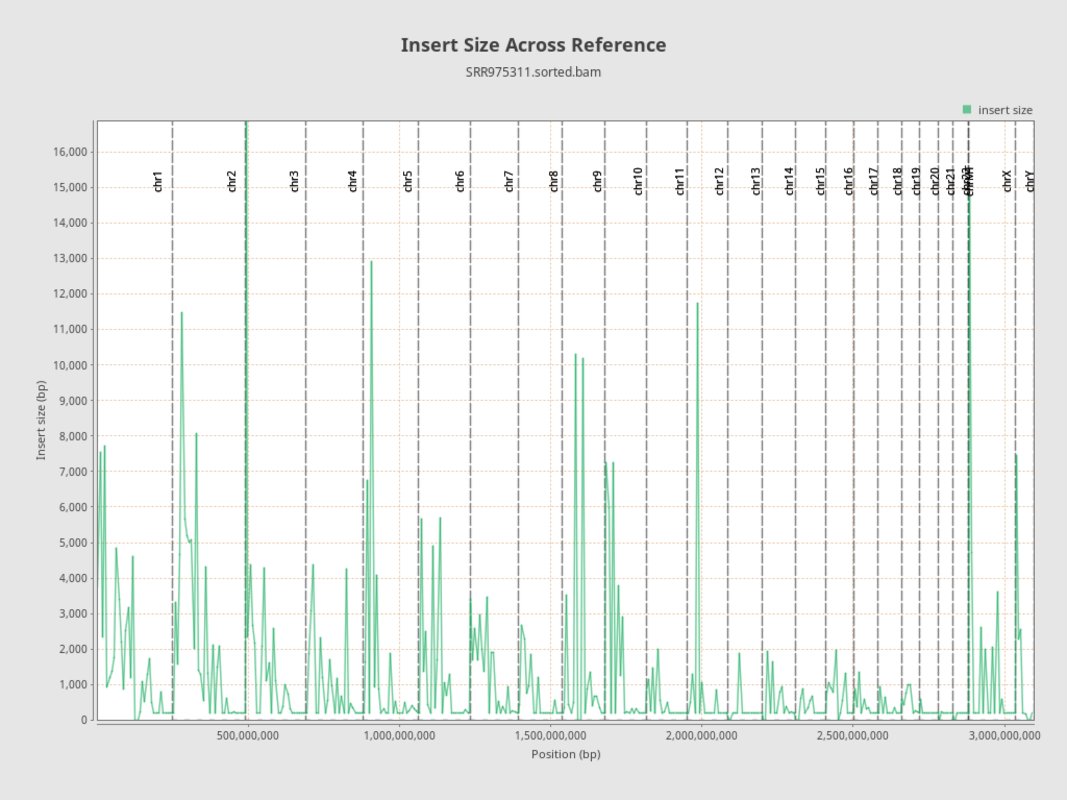


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram