Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 00:58:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975306.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_SRR975306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975306_1.fastq.gz SRR975306_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 00:58:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,972,704
Mapped reads	3,912,796 / 98.49%
Unmapped reads	59,908 / 1.51%
Mapped paired reads	3,912,796 / 98.49%
Mapped reads, first in pair	1,955,360 / 49.22%
Mapped reads, second in pair	1,957,436 / 49.27%
Mapped reads, both in pair	3,899,116 / 98.15%
Mapped reads, singletons	13,680 / 0.34%
Secondary alignments	0
Supplementary alignments	16,334 / 0.41%
Read min/max/mean length	30 / 101 / 101.16
Duplicated reads (estimated)	185,676 / 4.67%
Duplication rate	2.83%
Clipped reads	2,399,301 / 60.39%

2.2. ACGT Content

Number/percentage of A's	101,877,376 / 28.74%
Number/percentage of C's	69,066,567 / 19.48%
Number/percentage of T's	106,051,911 / 29.91%
Number/percentage of G's	77,526,994 / 21.87%
Number/percentage of N's	7,268 / 0%

GC Percentage	41.35%

2.3. Coverage

Mean	0.1146
Standard Deviation	1.0535

2.4. Mapping Quality

Mean Mapping Quality	52.67

2.5. Insert size

Mean	62,230.42
Standard Deviation	2,394,843.92
P25/Median/P75	133 / 165 / 209

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	2,629,743
Insertions	56,463
Mapped reads with at least one insertion	1.41%
Deletions	109,371
Mapped reads with at least one deletion	2.74%
Homopolymer indels	45.39%

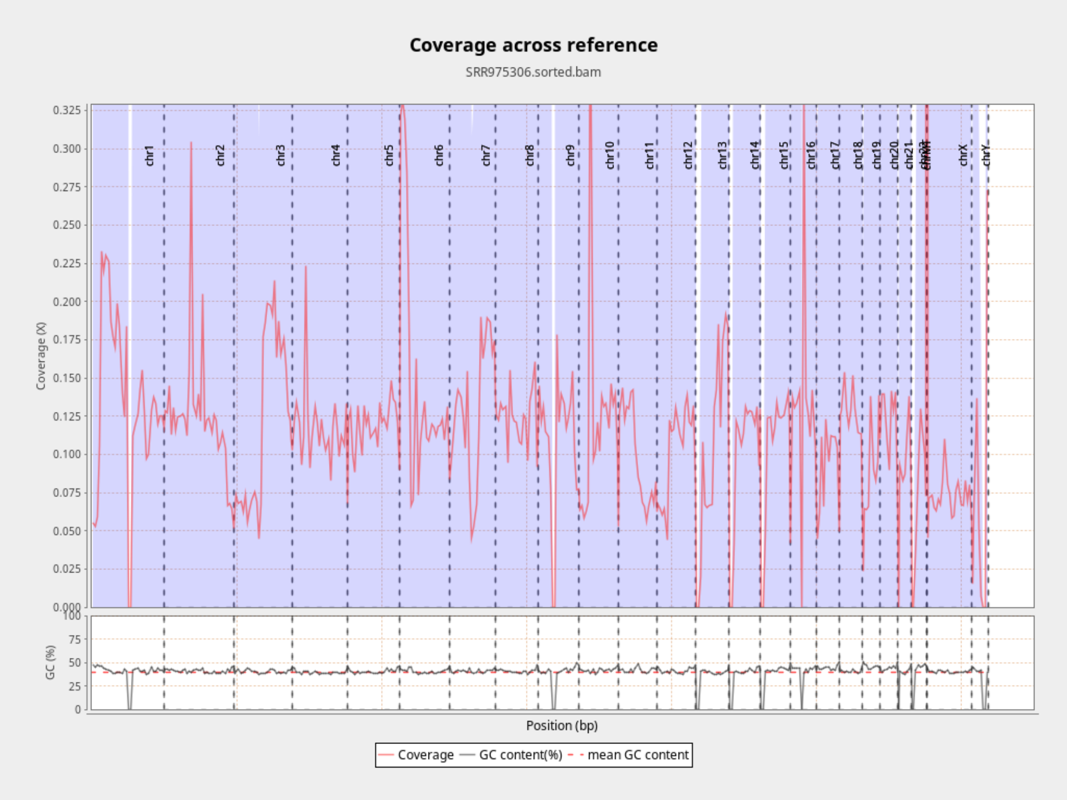
2.7. Chromosome stats

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

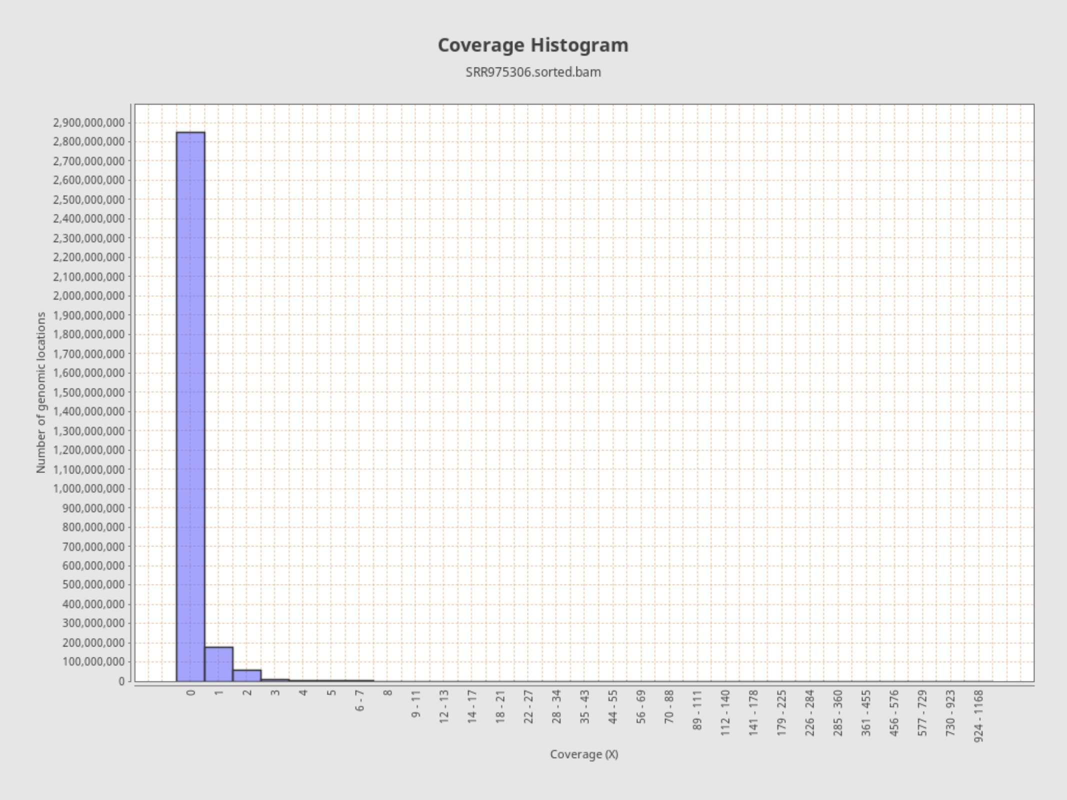
		bases	coverage	deviation
chr1	249250621	33475519	0.1343	1.0456
chr2	243199373	30303419	0.1246	1.3861
chr3	198022430	24046318	0.1214	0.4616
chr4	191154276	22543701	0.1179	0.8474
chr5	180915260	21753213	0.1202	0.4495
chr6	171115067	25614778	0.1497	0.883
chr7	159138663	20580281	0.1293	1.1128
chr8	146364022	18150382	0.124	0.5682
chr9	141213431	15528966	0.11	1.5588
chr10	135534747	16663006	0.1229	2.389
chr11	135006516	13288765	0.0984	0.9799
chr12	133851895	13884648	0.1037	0.4162
chr13	115169878	11970854	0.1039	0.417
chr14	107349540	10645860	0.0992	0.4468
chr15	102531392	10467997	0.1021	0.4104
chr16	90354753	11877623	0.1315	1.6466
chr17	81195210	7487203	0.0922	1.015
chr18	78077248	10043730	0.1286	1.5935
chr19	59128983	5015746	0.0848	0.6554
chr20	63025520	7697720	0.1221	0.4885
chr21	48129895	4382445	0.0911	0.5331
chr22	51304566	3793953	0.0739	0.3692
chrMT	16571	95071	5.7372	7.2076
chrX	155270560	11242531	0.0724	0.486

chrY	59373566	4169818	0.0702	1.573

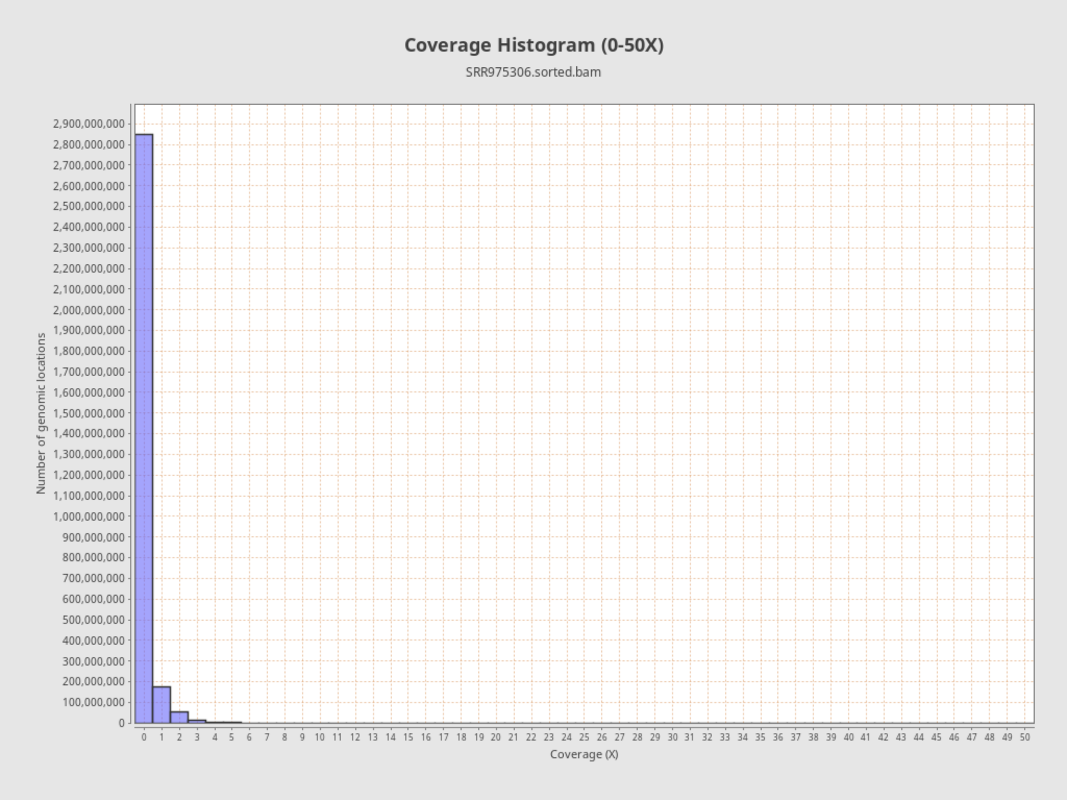
3. Results : Coverage across reference



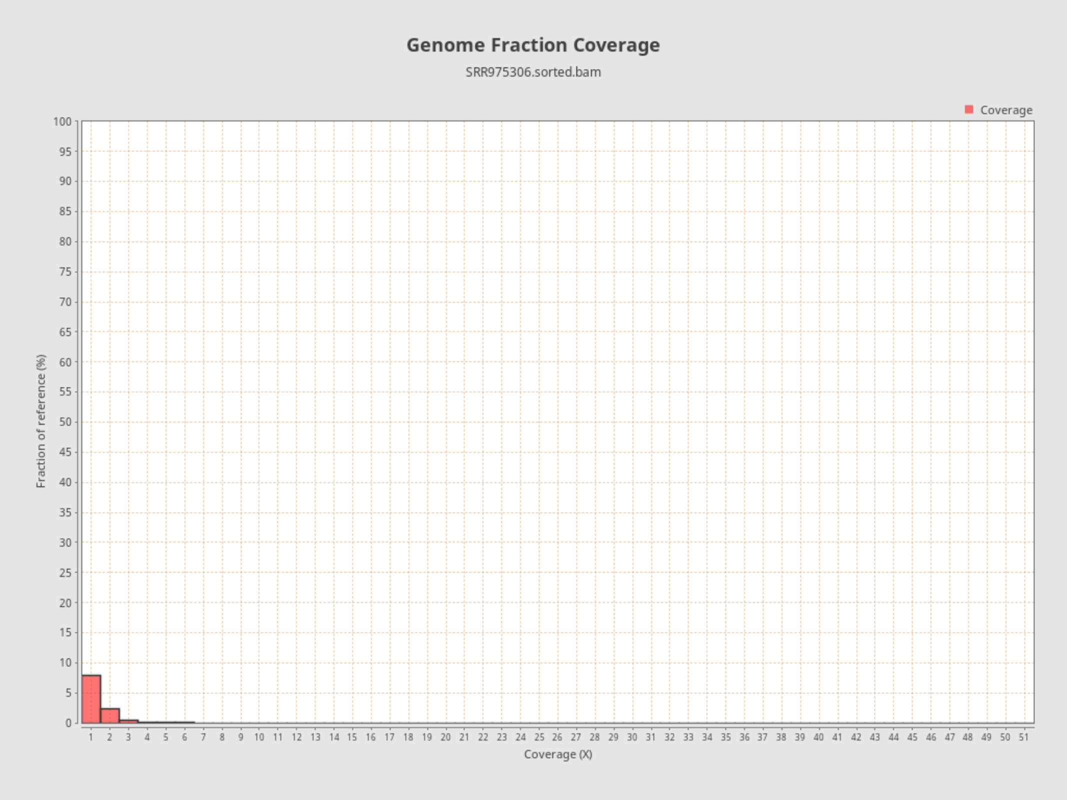
4. Results : Coverage Histogram



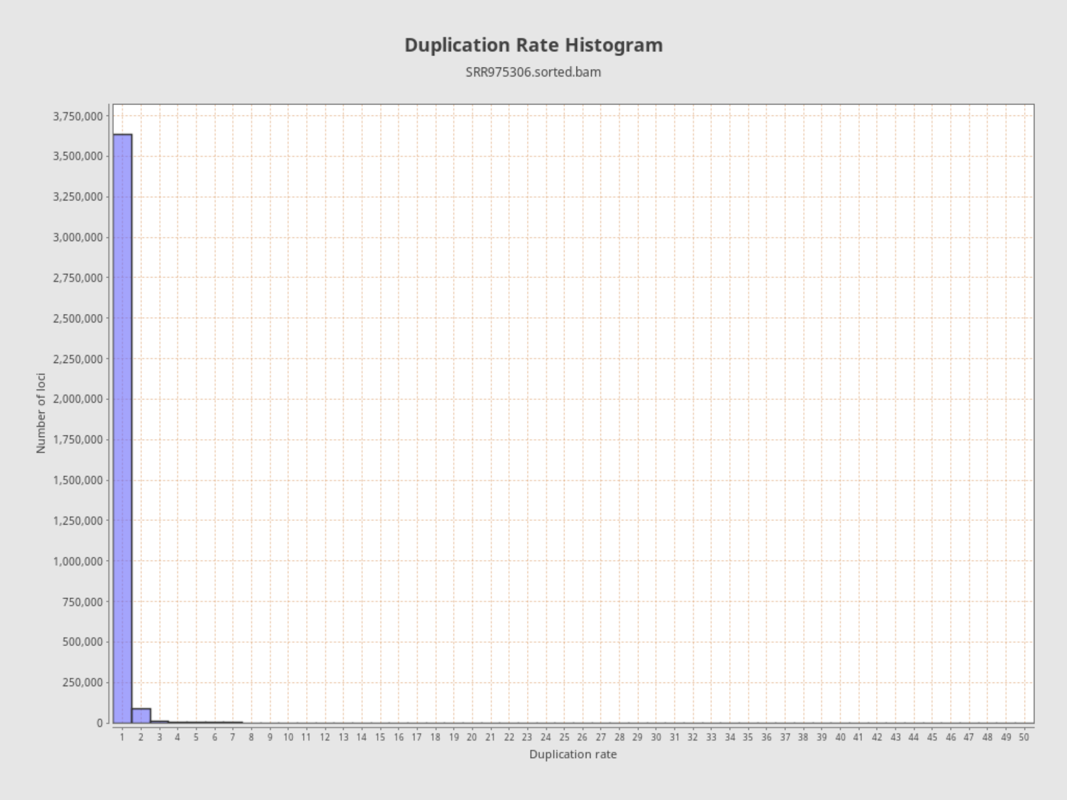
5. Results : Coverage Histogram (0-50X)



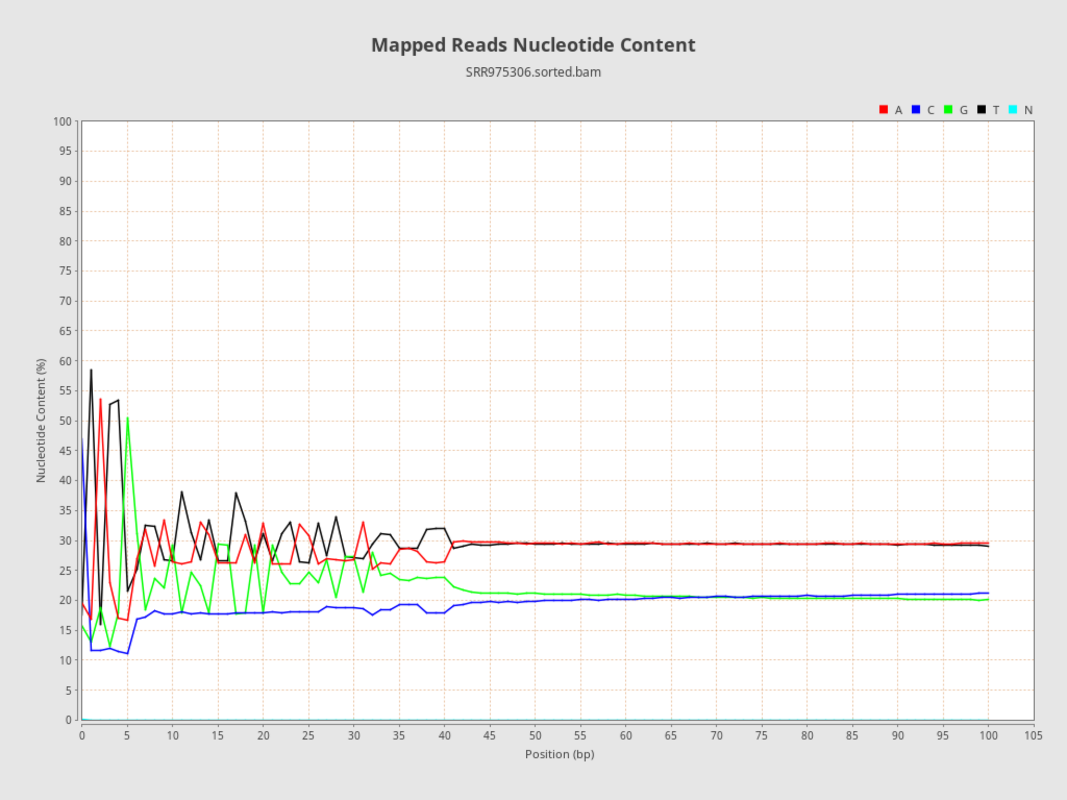
6. Results : Genome Fraction Coverage



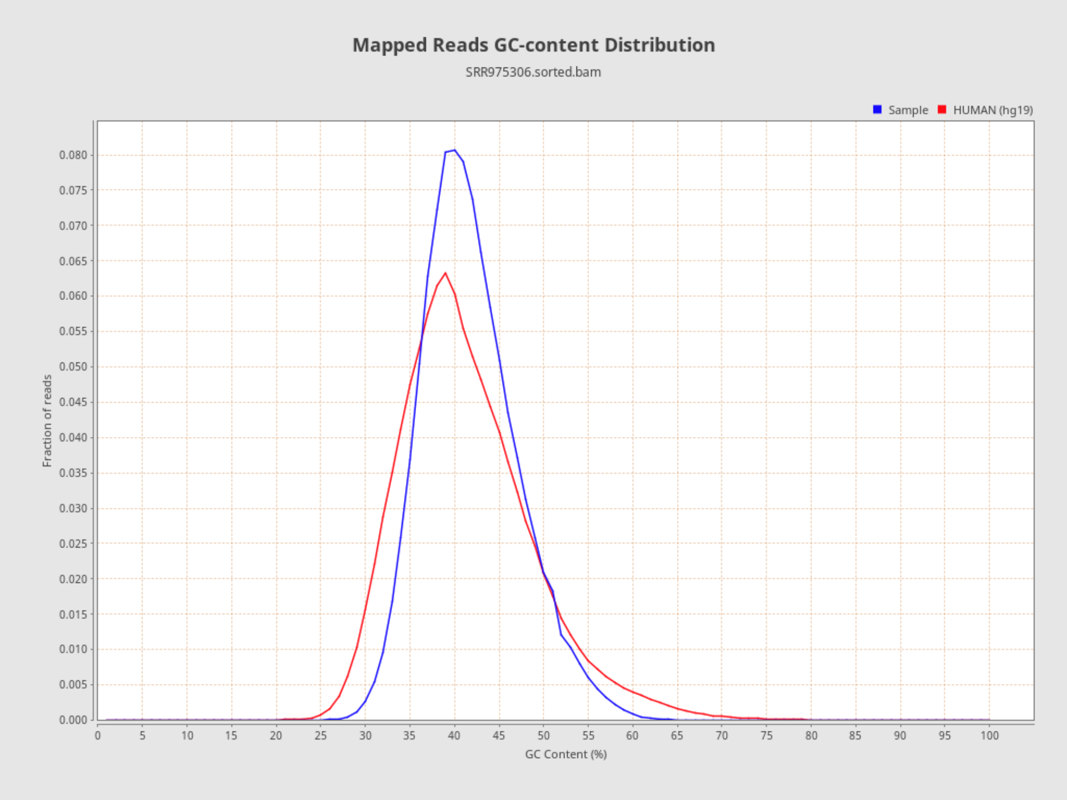
7. Results : Duplication Rate Histogram



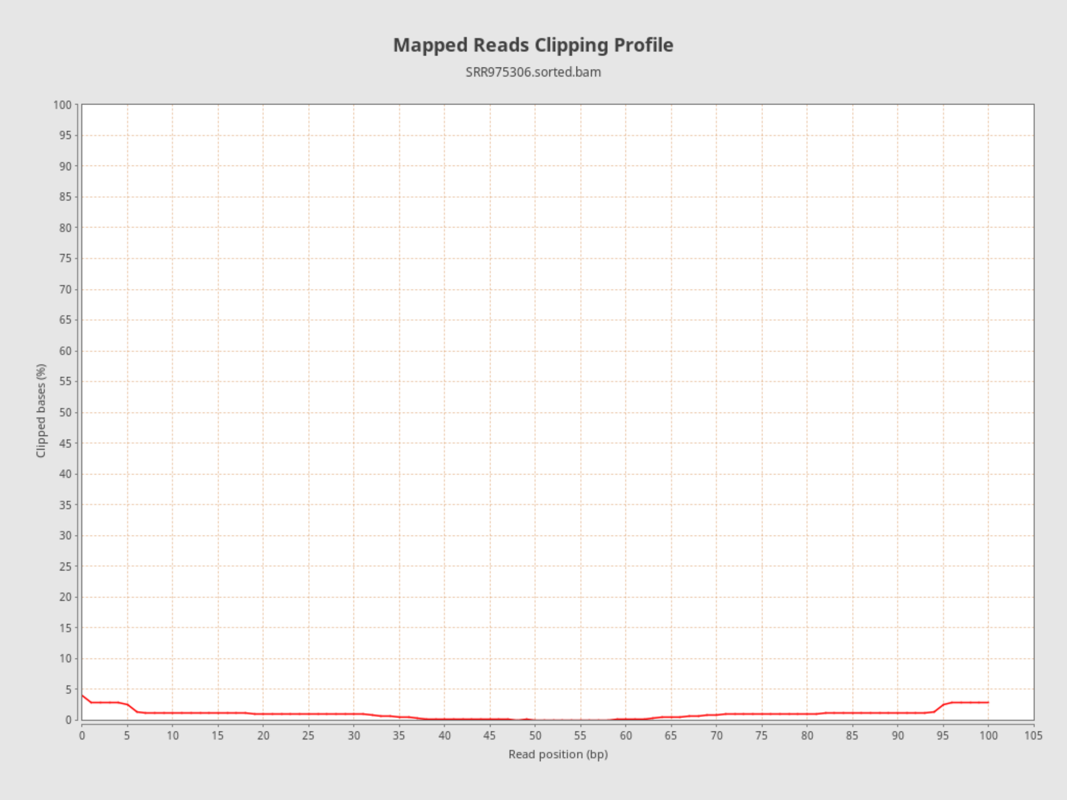
8. Results : Mapped Reads Nucleotide Content



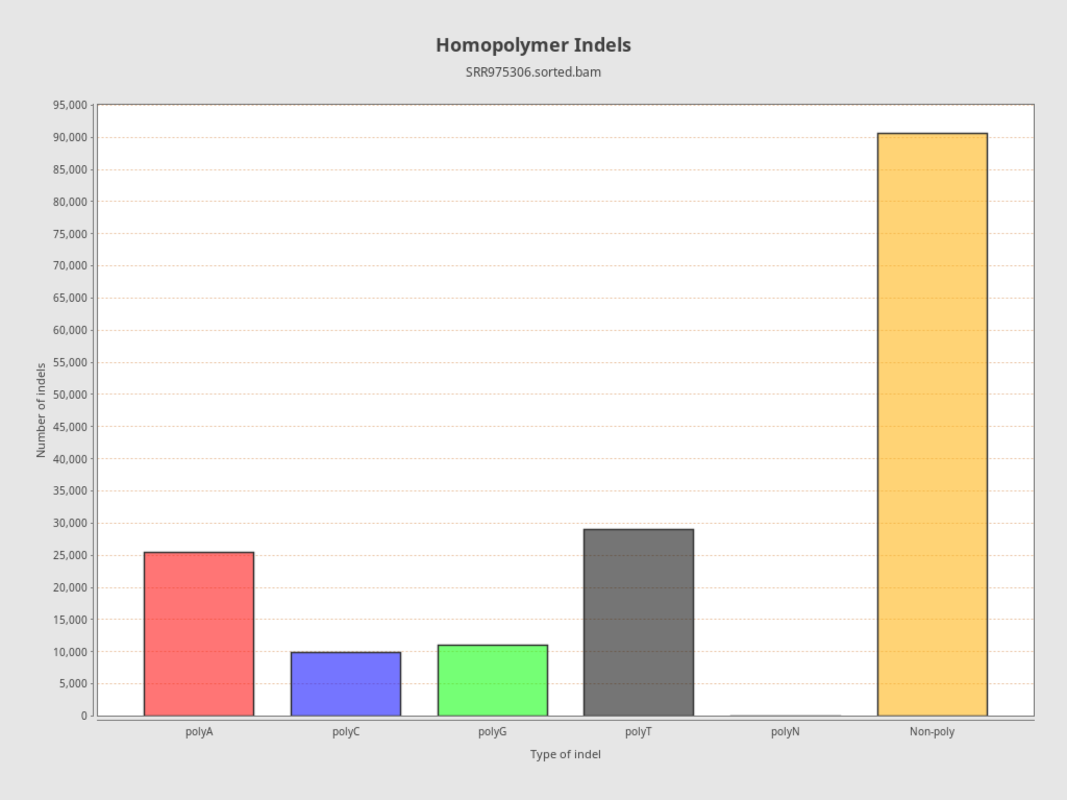
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

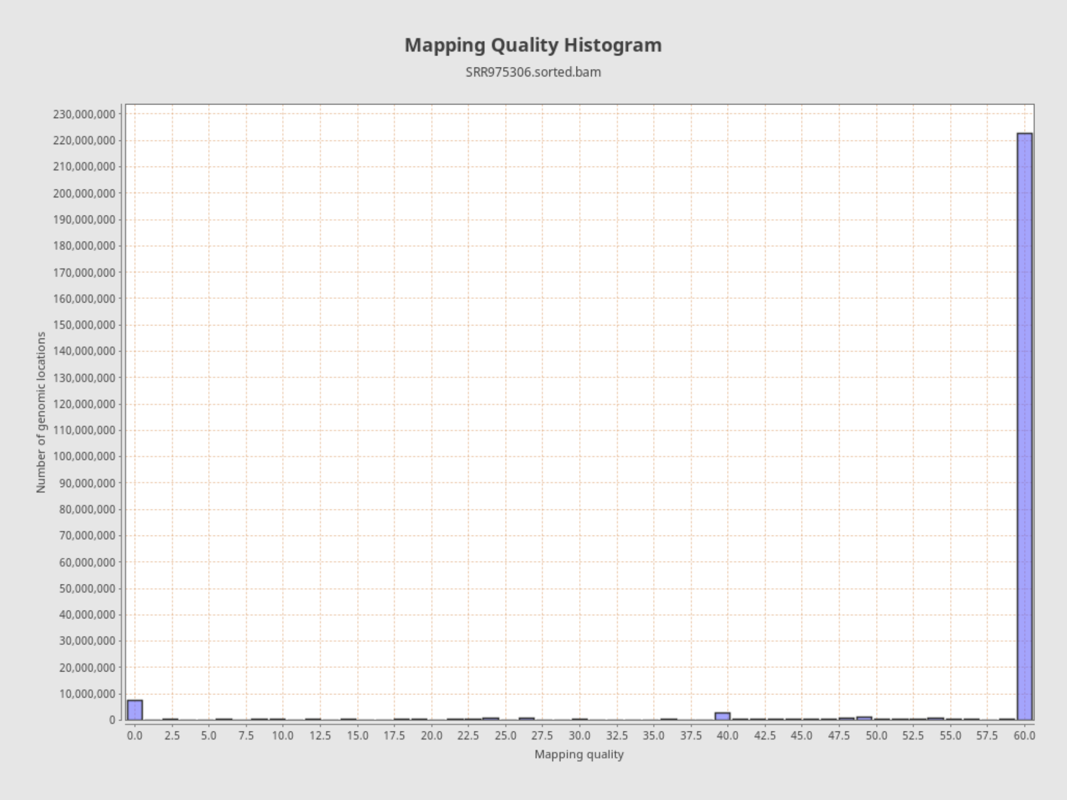


11. Results : Homopolymer Indels

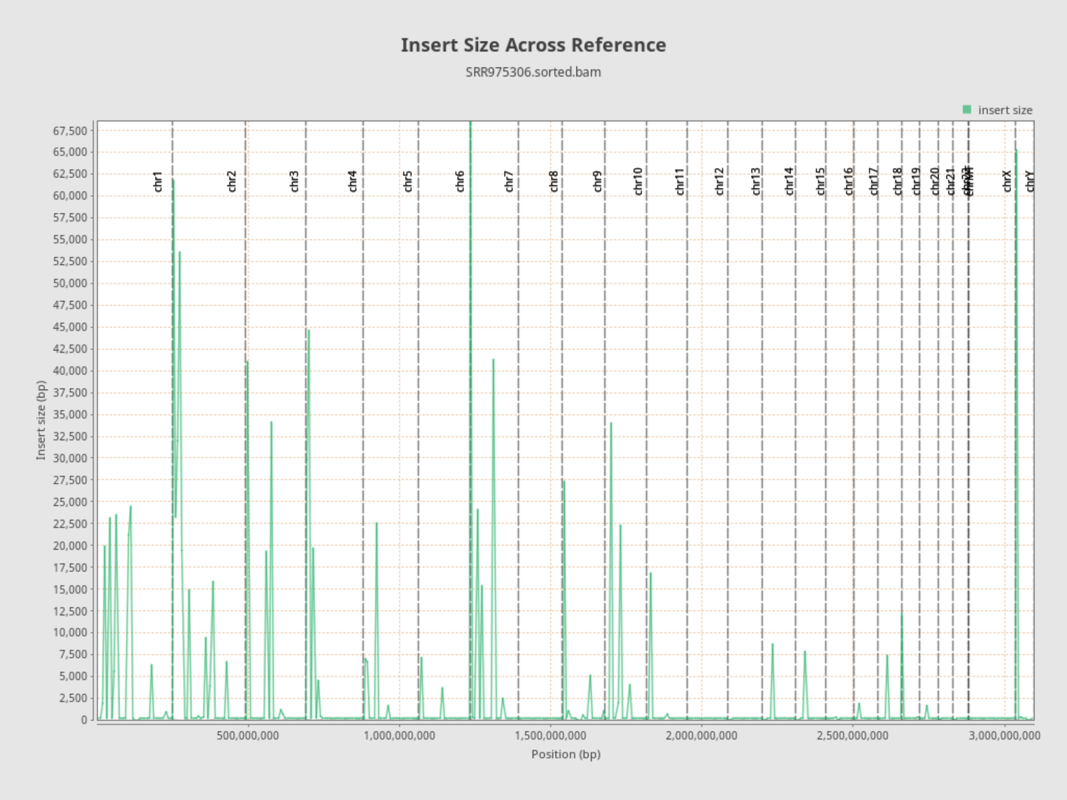


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram