Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 06:51:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975340.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_SRR975340 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975340_1.fastq.gz SRR975340_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 06:51:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975340.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,634,616
Mapped reads	4,594,331 / 99.13%
Unmapped reads	40,285 / 0.87%
Mapped paired reads	4,594,331 / 99.13%
Mapped reads, first in pair	2,297,005 / 49.56%
Mapped reads, second in pair	2,297,326 / 49.57%
Mapped reads, both in pair	4,588,620 / 99.01%
Mapped reads, singletons	5,711 / 0.12%
Secondary alignments	0
Supplementary alignments	11,363 / 0.25%
Read min/max/mean length	30 / 101 / 101.1
Duplicated reads (estimated)	97,870 / 2.11%
Duplication rate	1.44%
Clipped reads	2,388,788 / 51.54%

2.2. ACGT Content

Number/percentage of A's	136,375,167 / 30.43%
Number/percentage of C's	89,007,403 / 19.86%
Number/percentage of T's	133,637,470 / 29.82%
Number/percentage of G's	89,089,359 / 19.88%
Number/percentage of N's	8,925 / 0%

GC Percentage	39.74%

2.3. Coverage

Mean	0.1448
Standard Deviation	0.9422

2.4. Mapping Quality

Mean Mapping Quality	53.75

2.5. Insert size

Mean	41,442.11
Standard Deviation	1,982,263.19
P25/Median/P75	134 / 160 / 196

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	1,771,553
Insertions	57,065
Mapped reads with at least one insertion	1.22%
Deletions	53,618
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.81%

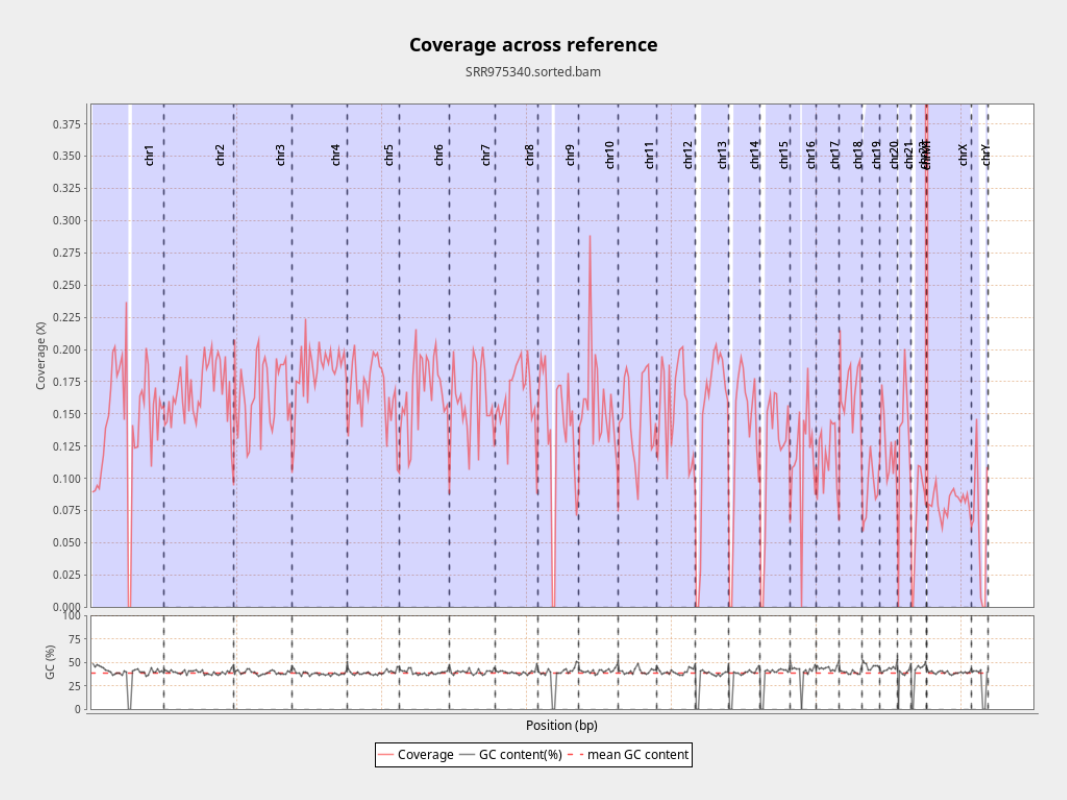
2.7. Chromosome stats

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

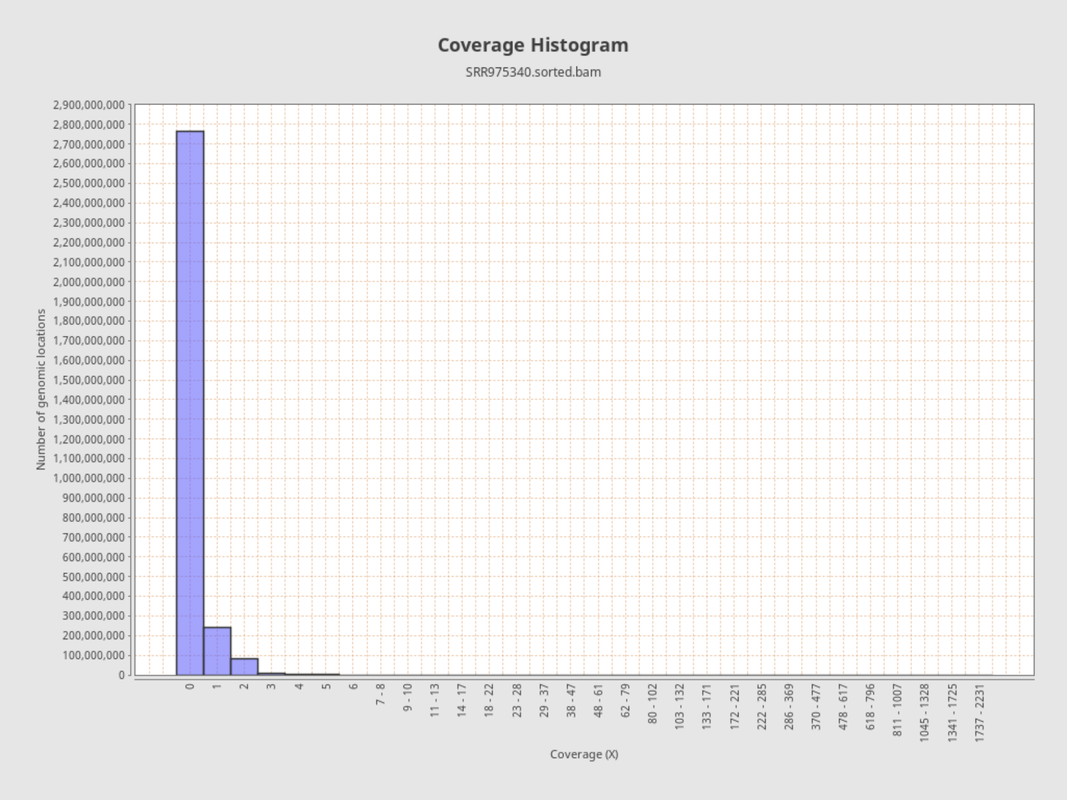
		bases	coverage	deviation
chr1	249250621	35387666	0.142	2.3477
chr2	243199373	40484719	0.1665	0.6438
chr3	198022430	32760120	0.1654	0.486
chr4	191154276	34942749	0.1828	0.7464
chr5	180915260	30255272	0.1672	0.4891
chr6	171115067	28692263	0.1677	0.6543
chr7	159138663	25216194	0.1585	0.7389
chr8	146364022	23898658	0.1633	0.633
chr9	141213431	19125668	0.1354	0.9512
chr10	135534747	21394758	0.1579	1.4191
chr11	135006516	20066426	0.1486	0.5442
chr12	133851895	20491385	0.1531	0.4692
chr13	115169878	16977525	0.1474	0.4576
chr14	107349540	14064179	0.131	0.4361
chr15	102531392	12002234	0.1171	0.408
chr16	90354753	10376247	0.1148	0.5551
chr17	81195210	9409735	0.1159	0.532
chr18	78077248	13249869	0.1697	1.1437
chr19	59128983	5272660	0.0892	0.9568
chr20	63025520	7719551	0.1225	0.4433
chr21	48129895	6480181	0.1346	0.6227
chr22	51304566	3663488	0.0714	0.6046
chrMT	16571	376837	22.7408	7.9859
chrX	155270560	12531161	0.0807	0.3723

chrY	59373566	3402168	0.0573	0.7791

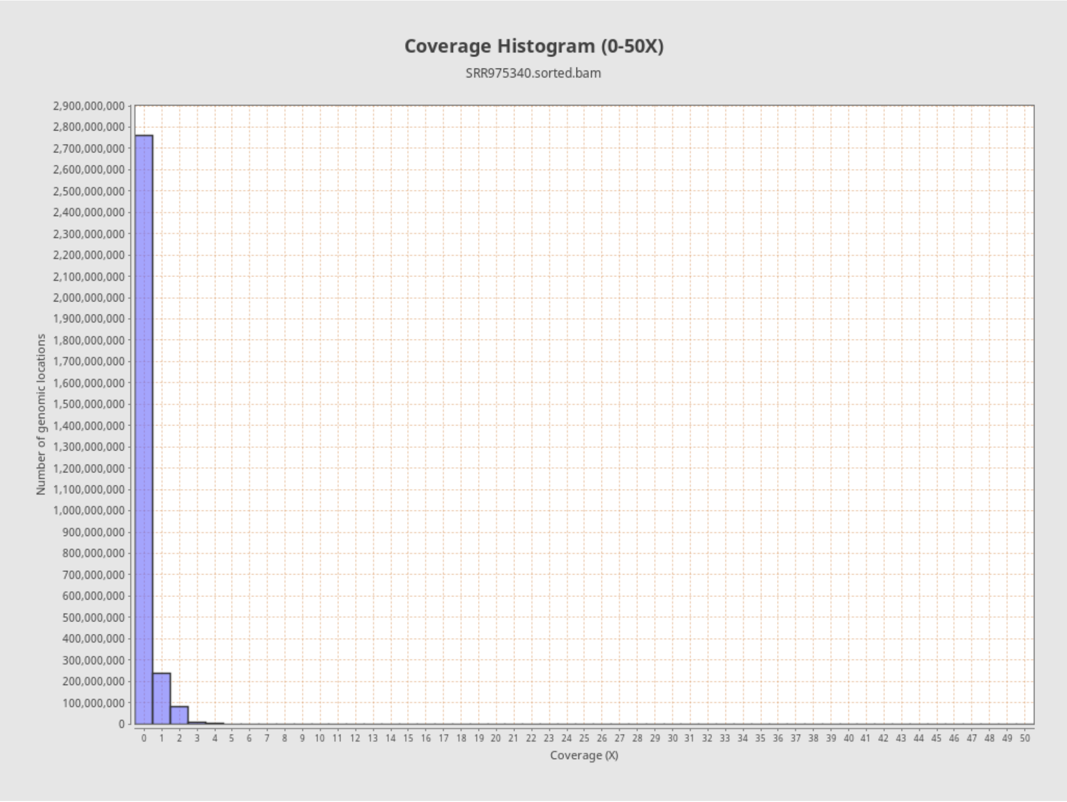
3. Results : Coverage across reference



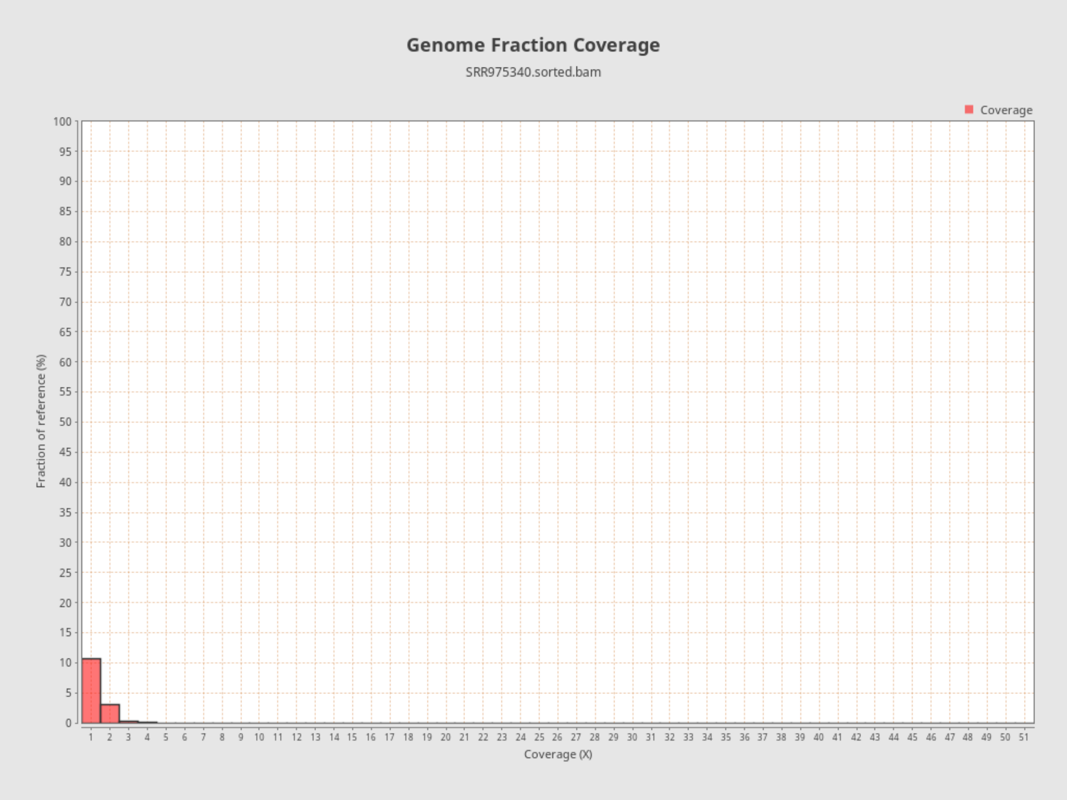
4. Results : Coverage Histogram



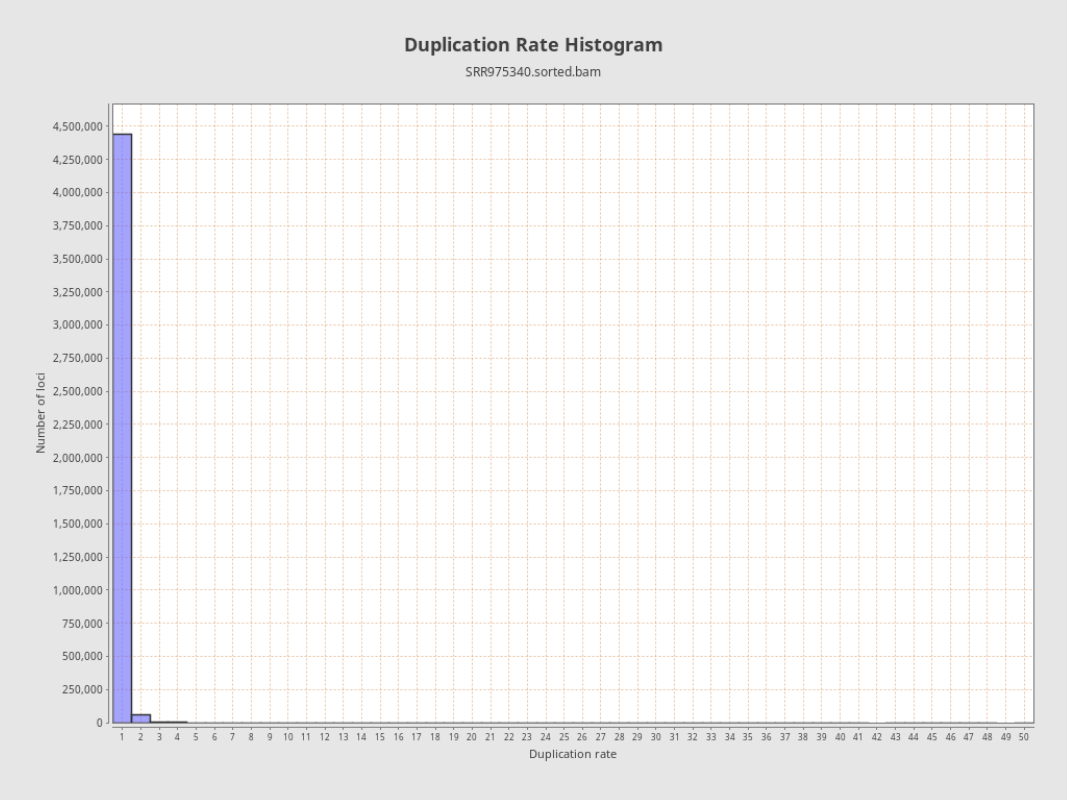
5. Results : Coverage Histogram (0-50X)



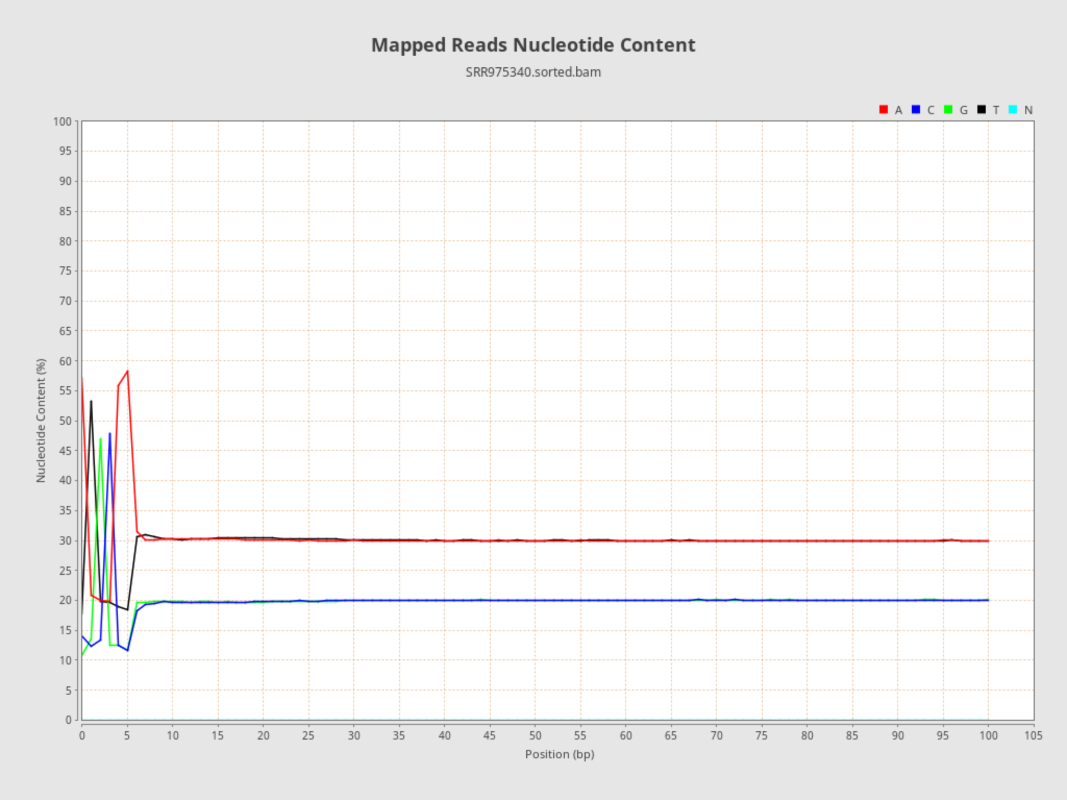
6. Results : Genome Fraction Coverage



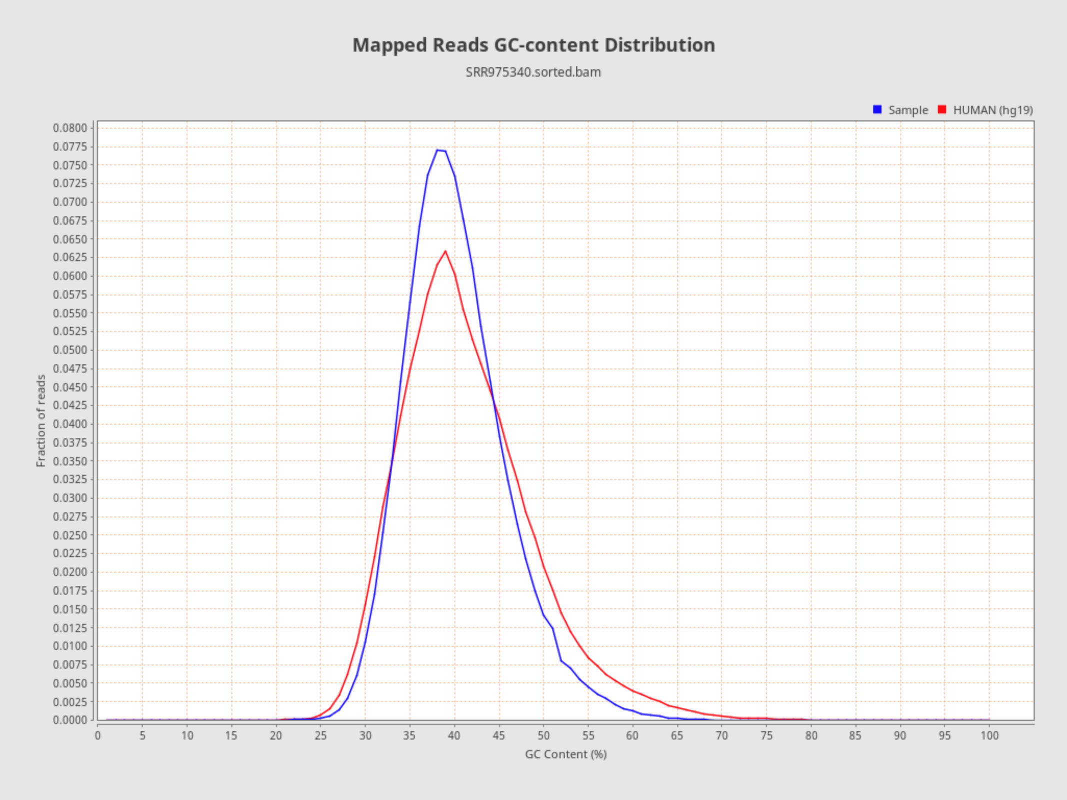
7. Results : Duplication Rate Histogram



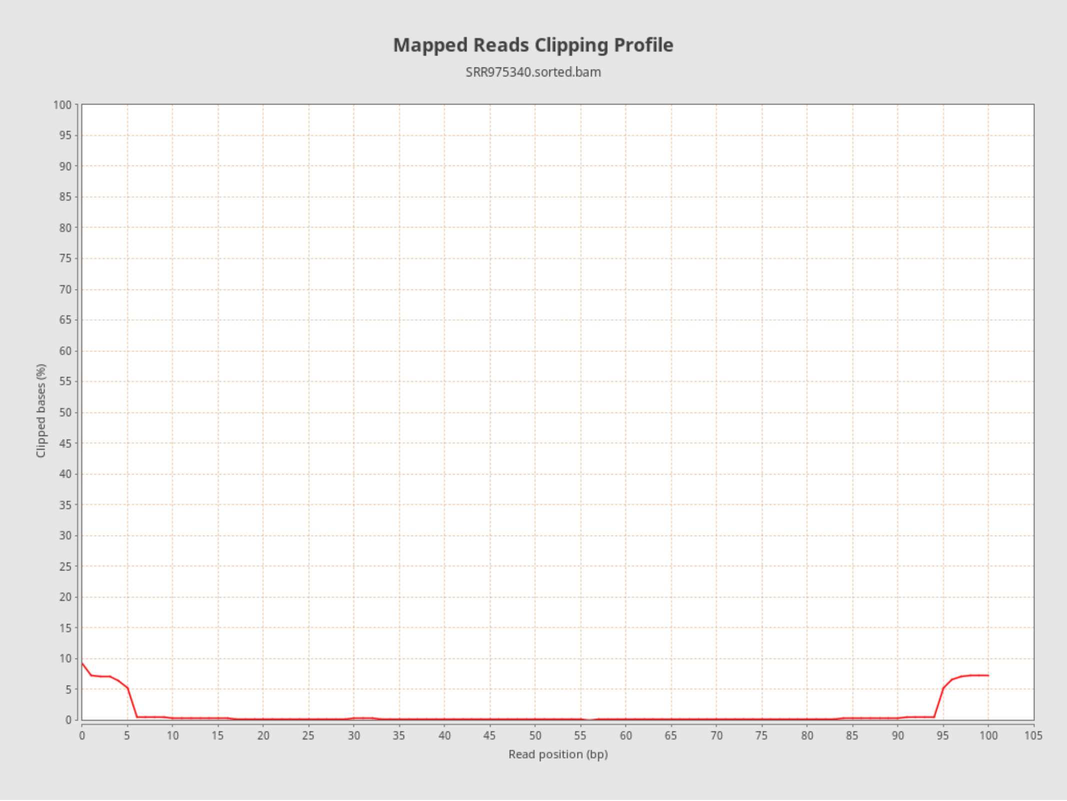
8. Results : Mapped Reads Nucleotide Content



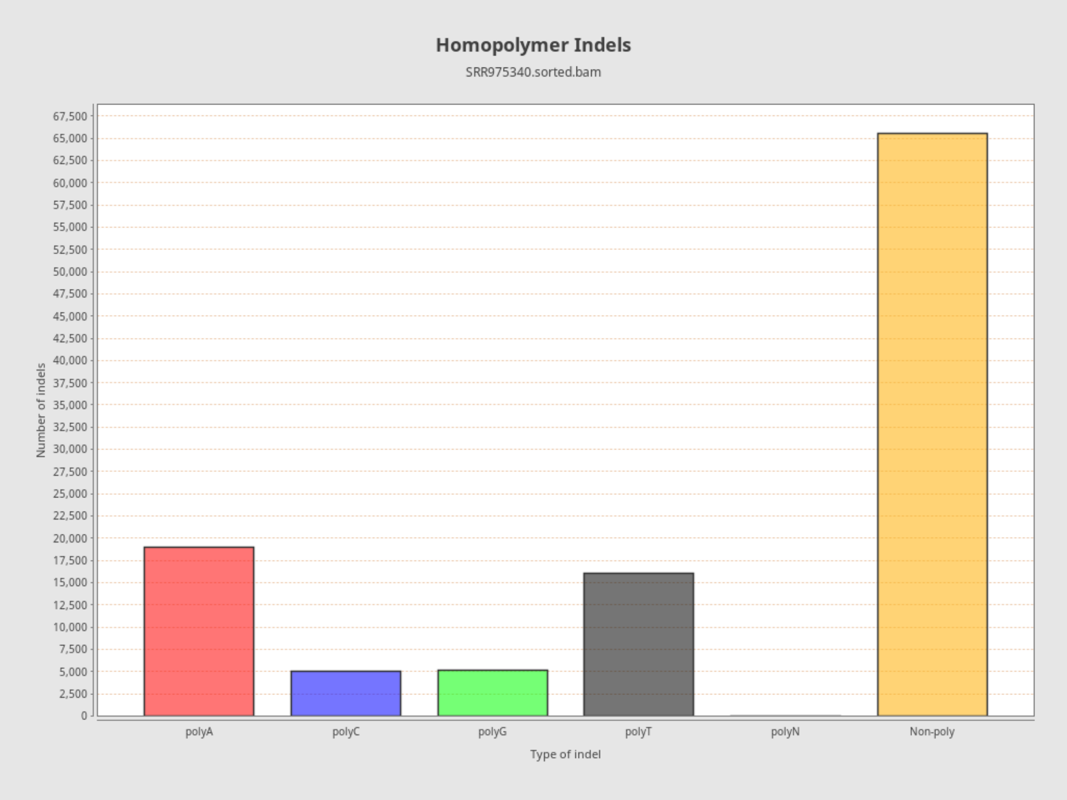
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

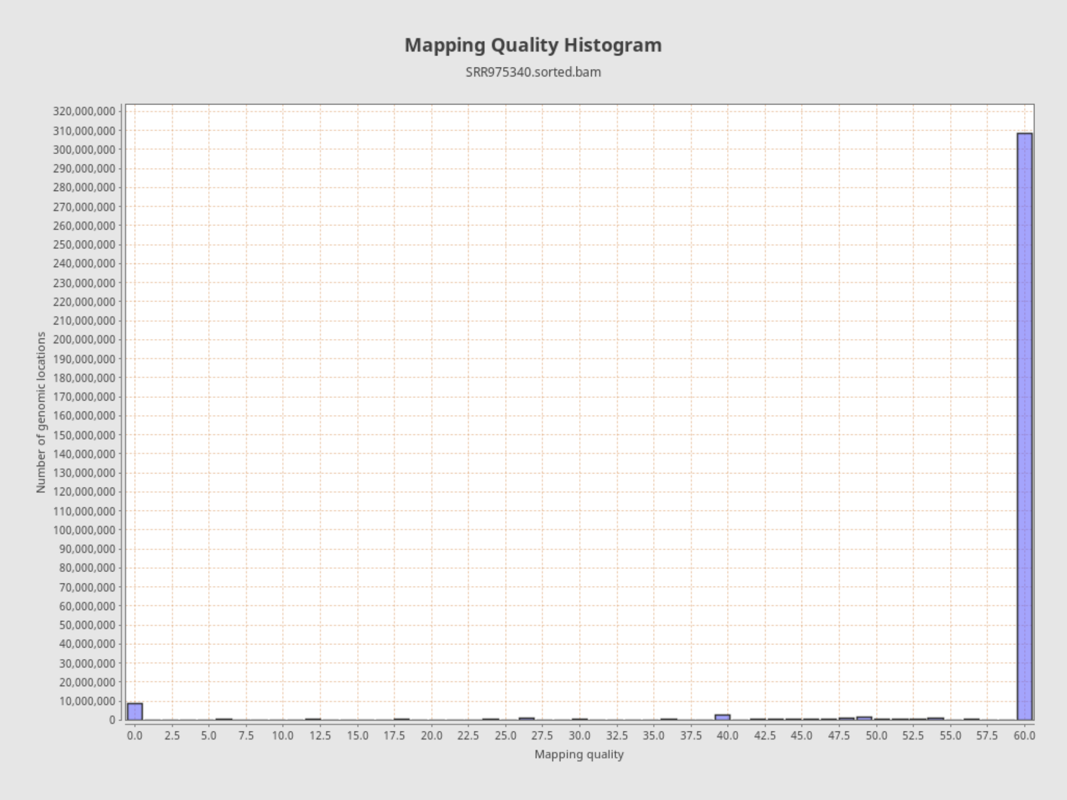


11. Results : Homopolymer Indels

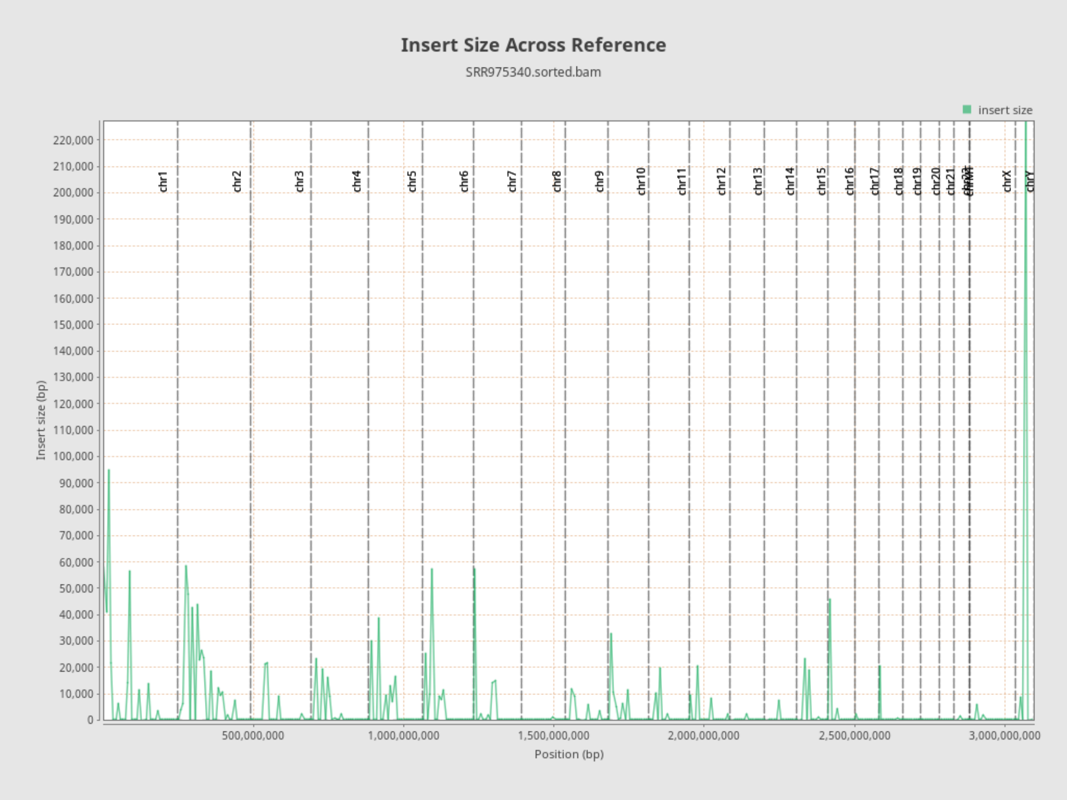


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram