Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/09 04:04:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR980244.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_SRR980244 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR980244_1.fastq.gz SRR980244_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 09 04:04:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR980244.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	90,113,462
Mapped reads	89,994,768 / 99.87%
Unmapped reads	118,694 / 0.13%
Mapped paired reads	89,994,768 / 99.87%
Mapped reads, first in pair	44,997,525 / 49.93%
Mapped reads, second in pair	44,997,243 / 49.93%
Mapped reads, both in pair	89,948,772 / 99.82%
Mapped reads, singletons	45,996 / 0.05%
Secondary alignments	0
Supplementary alignments	466,542 / 0.52%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	57,044,525 / 63.3%
Duplication rate	61.54%
Clipped reads	46,160,976 / 51.23%

2.2. ACGT Content

Number/percentage of A's	2,233,464,510 / 25.37%
Number/percentage of C's	2,215,439,135 / 25.17%
Number/percentage of T's	2,249,026,779 / 25.55%
Number/percentage of G's	2,104,585,173 / 23.91%
Number/percentage of N's	301,446 / 0%

GC Percentage	49.08%

2.3. Coverage

Mean	2.8439
Standard Deviation	25.5489

2.4. Mapping Quality

Mean Mapping Quality	56.45

2.5. Insert size

Mean	81,904.29
Standard Deviation	2,838,716.99
P25/Median/P75	164 / 197 / 235

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	35,441,451
Insertions	476,957
Mapped reads with at least one insertion	0.52%
Deletions	478,910
Mapped reads with at least one deletion	0.52%
Homopolymer indels	37.46%

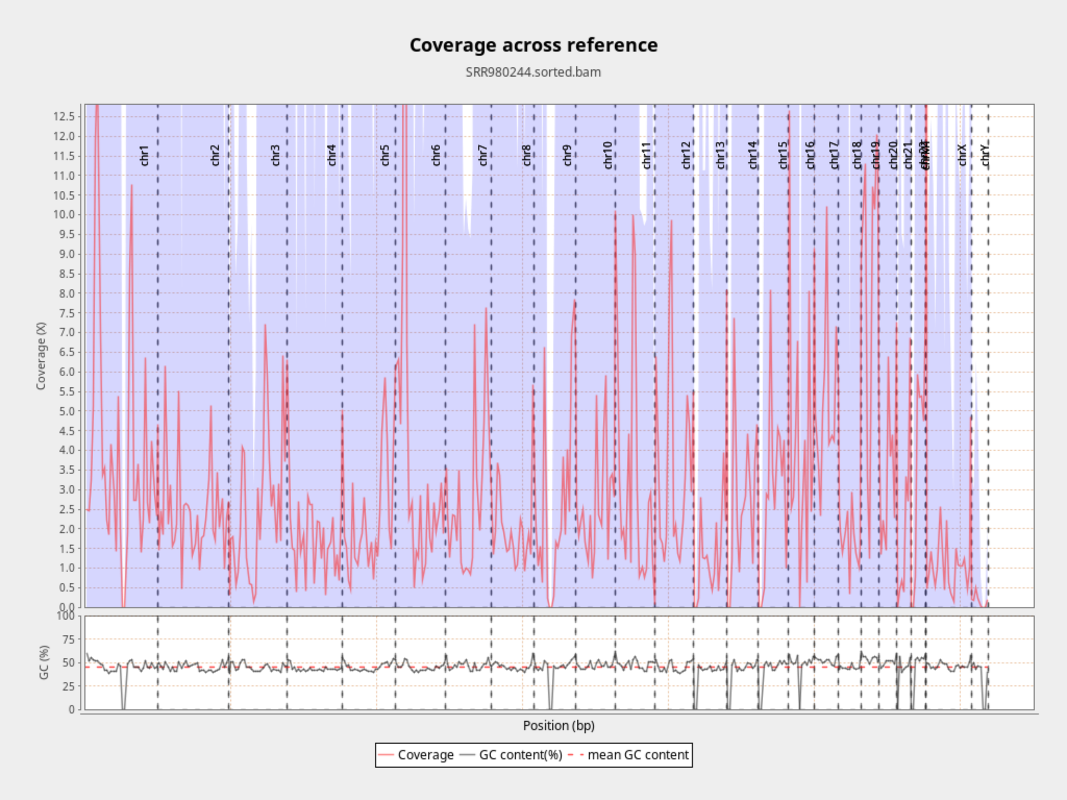
2.7. Chromosome stats

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

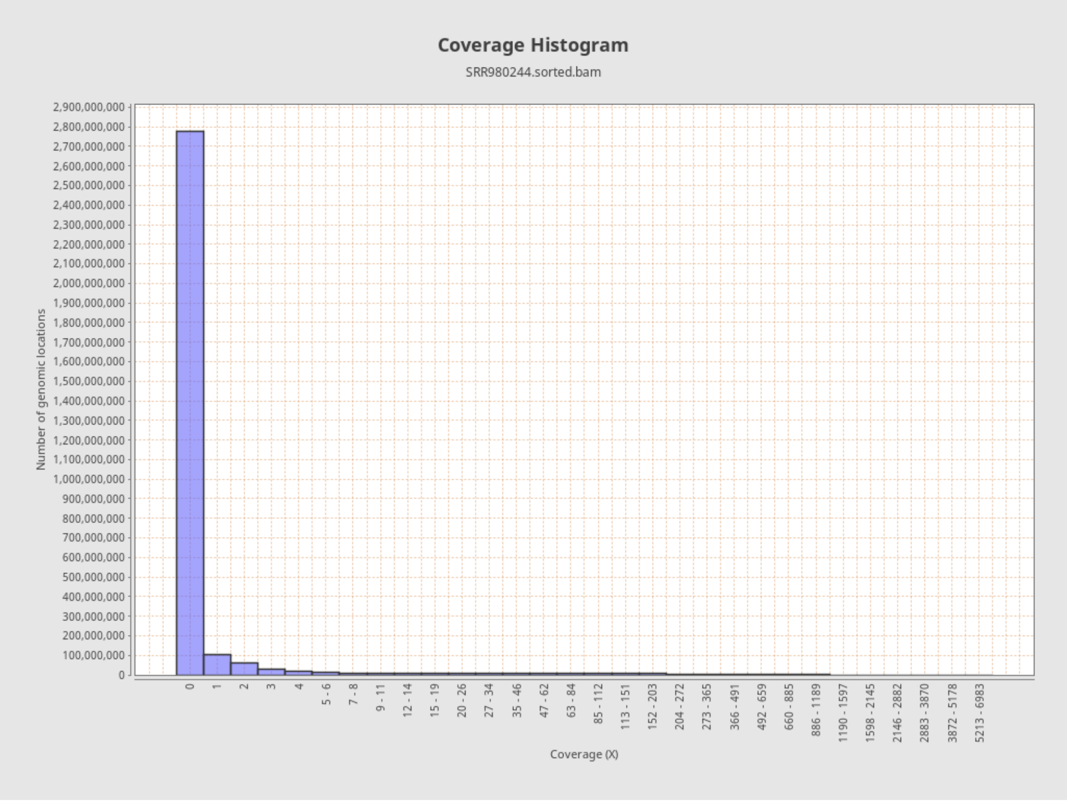
		bases	coverage	deviation
chr1	249250621	993912733	3.9876	33.1148
chr2	243199373	586936752	2.4134	20.5456
chr3	198022430	517678404	2.6142	23.7521
chr4	191154276	335190602	1.7535	17.3158
chr5	180915260	397704956	2.1983	19.9582
chr6	171115067	743720441	4.3463	44.8577
chr7	159138663	452348206	2.8425	26.3671
chr8	146364022	292755981	2.0002	18.8357
chr9	141213431	352904738	2.4991	21.957
chr10	135534747	356446036	2.6299	22.9481
chr11	135006516	440904334	3.2658	25.1015
chr12	133851895	476081879	3.5568	27.4144
chr13	115169878	162759325	1.4132	16.9688
chr14	107349540	281715581	2.6243	22.7268
chr15	102531392	301681321	2.9423	23.9504
chr16	90354753	358819578	3.9712	29.4507
chr17	81195210	425973125	5.2463	32.1561
chr18	78077248	134786970	1.7263	17.797
chr19	59128983	505622419	8.5512	43.2224
chr20	63025520	221541566	3.5151	26.5804
chr21	48129895	92379210	1.9194	19.3954
chr22	51304566	188464412	3.6734	26.7154
chrMT	16571	4553068	274.7612	362.1053
chrX	155270560	169423939	1.0912	10.8744

chrY	59373566	9567209	0.1611	2.979

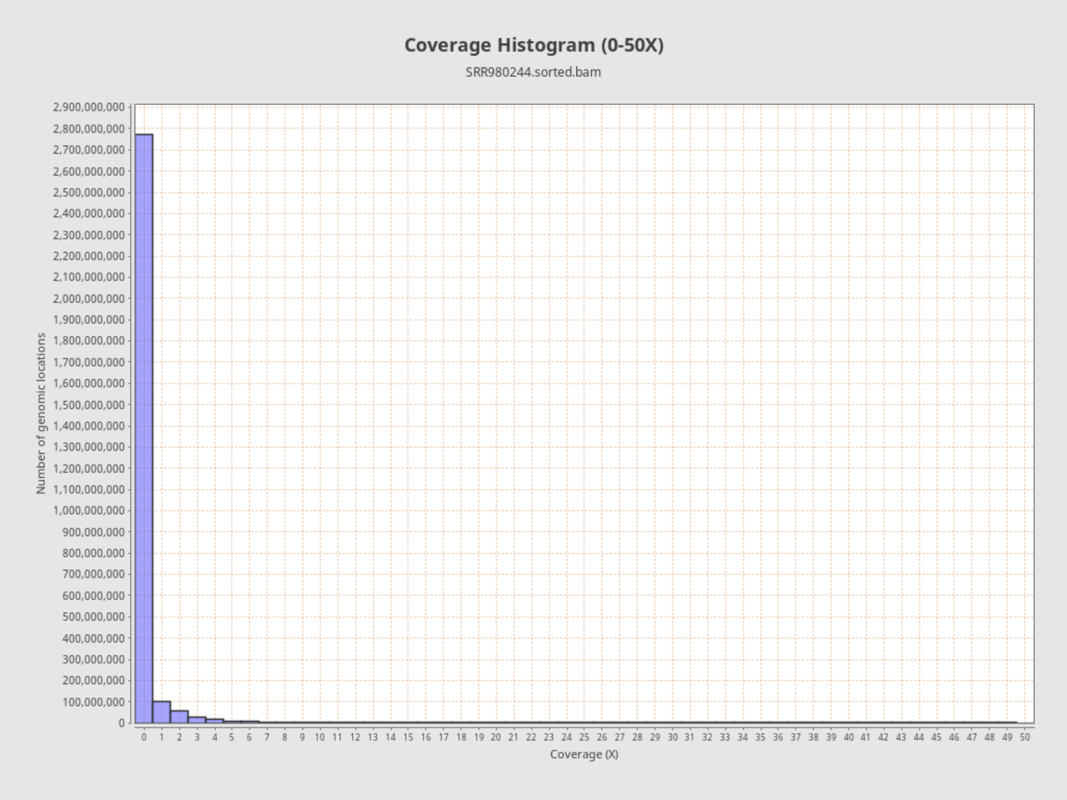
3. Results : Coverage across reference



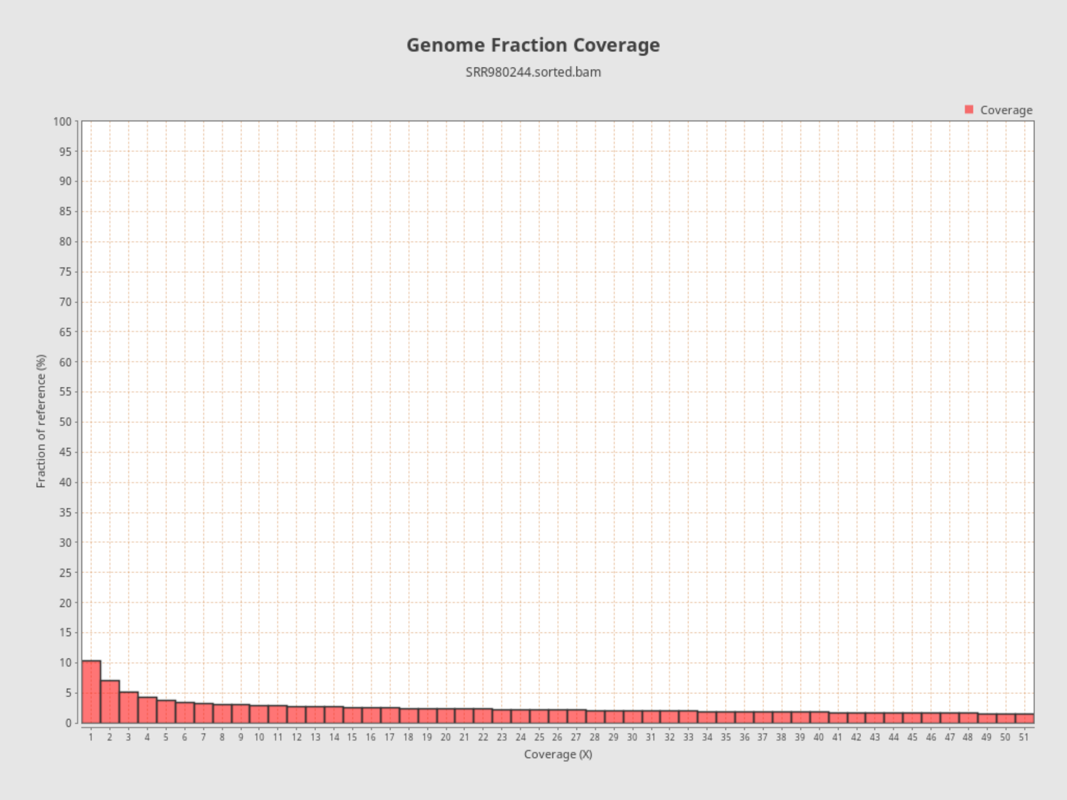
4. Results : Coverage Histogram



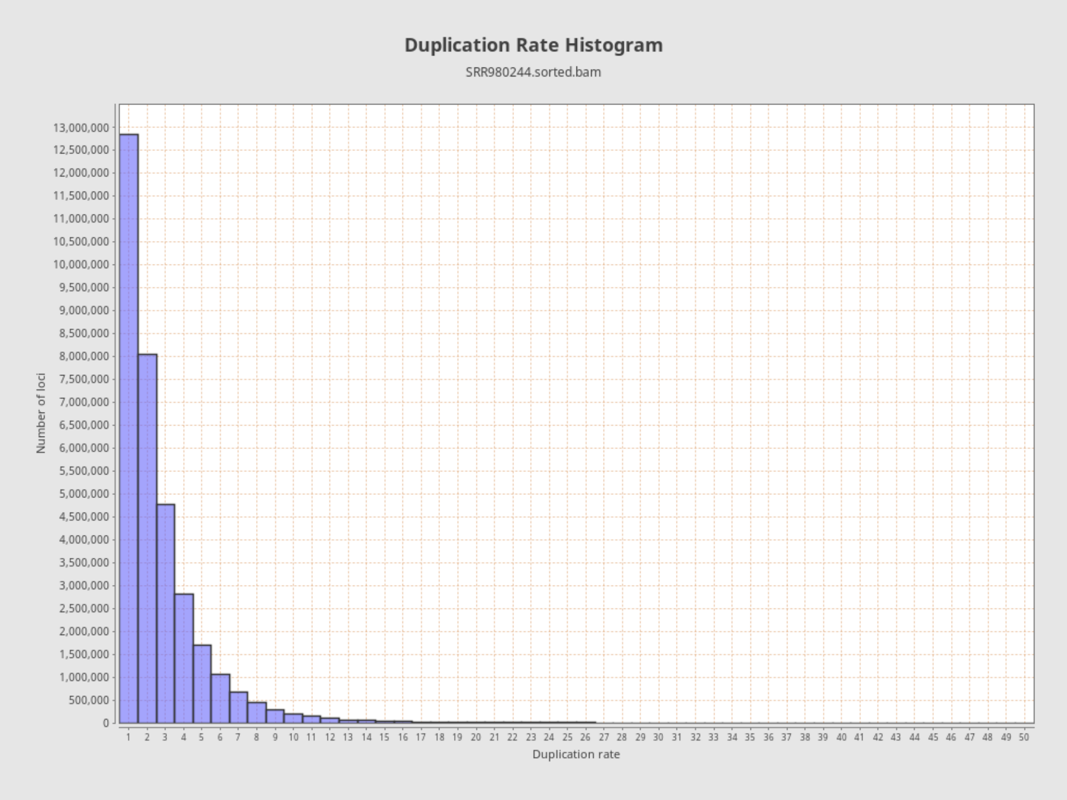
5. Results : Coverage Histogram (0-50X)



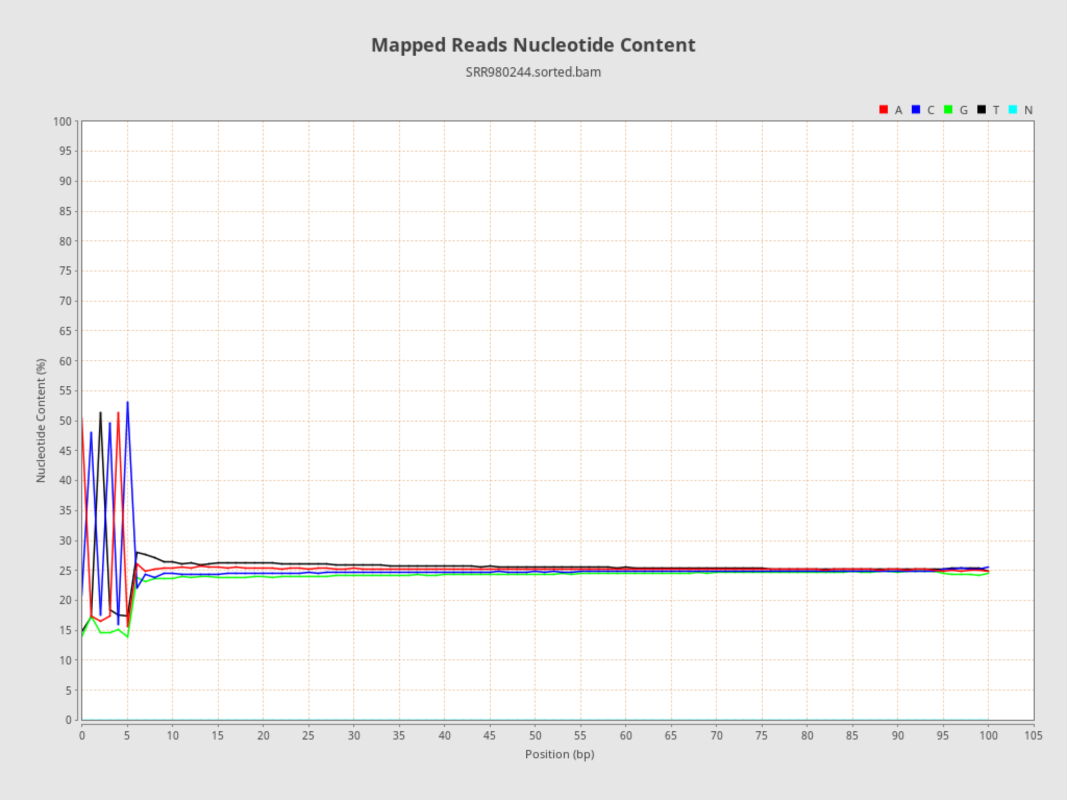
6. Results : Genome Fraction Coverage



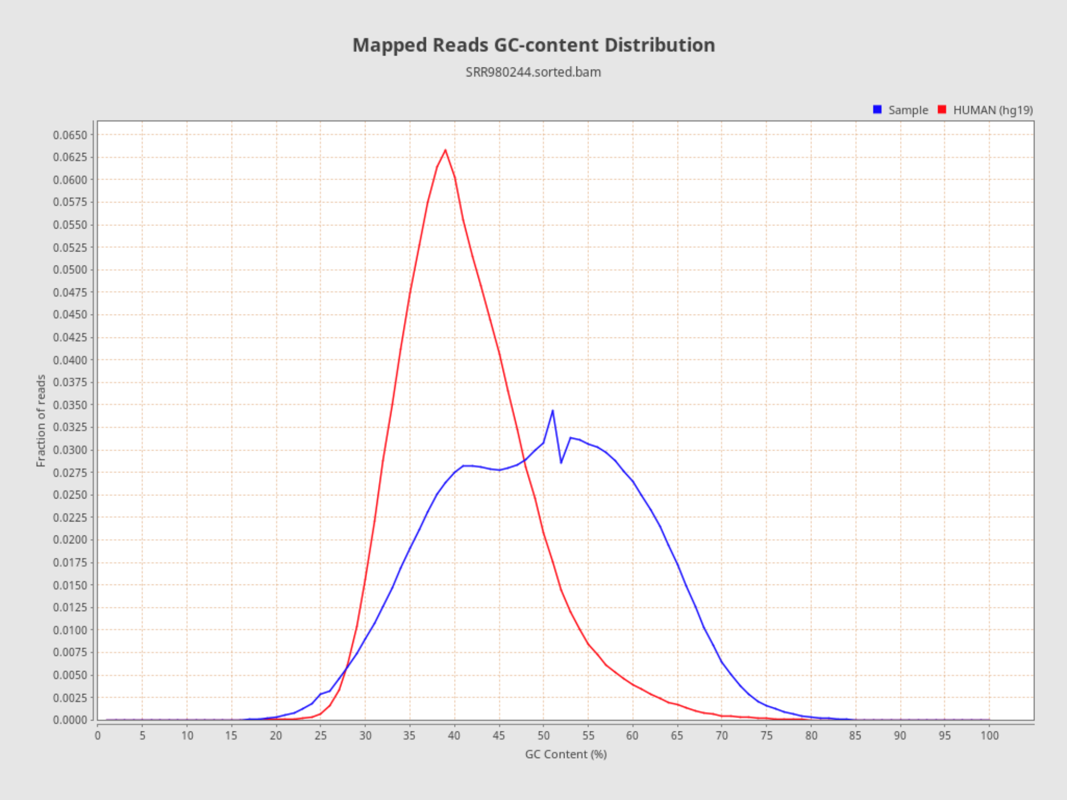
7. Results : Duplication Rate Histogram



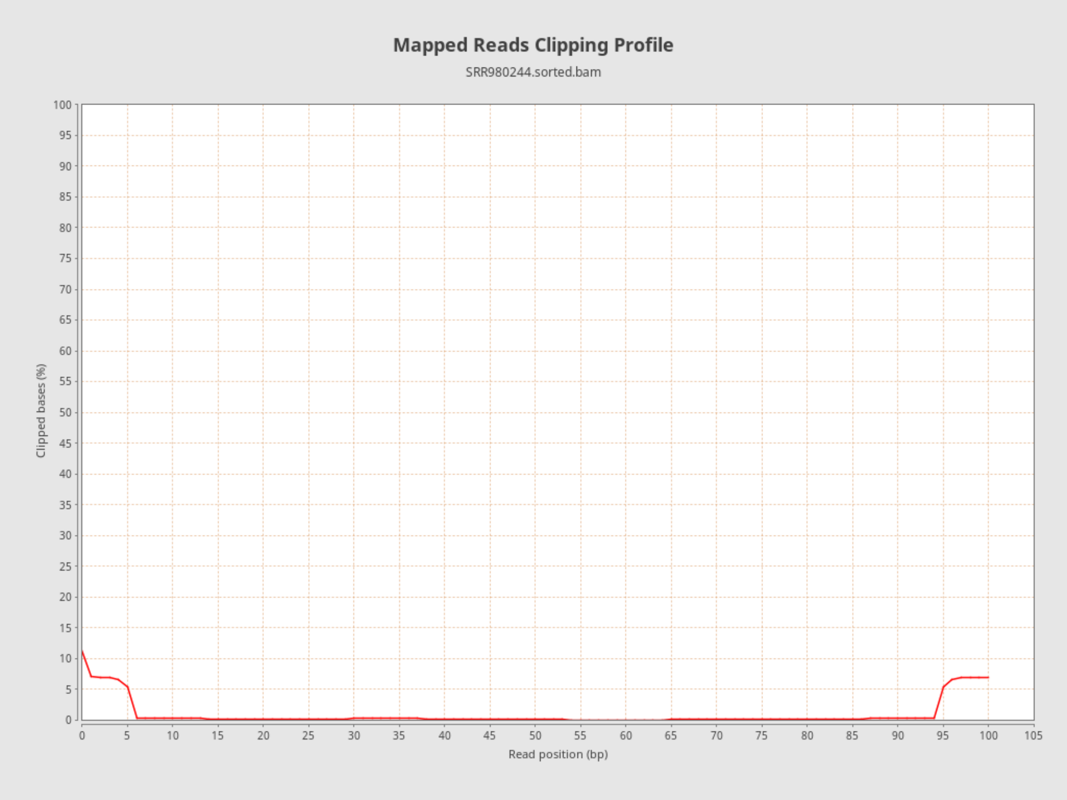
8. Results : Mapped Reads Nucleotide Content



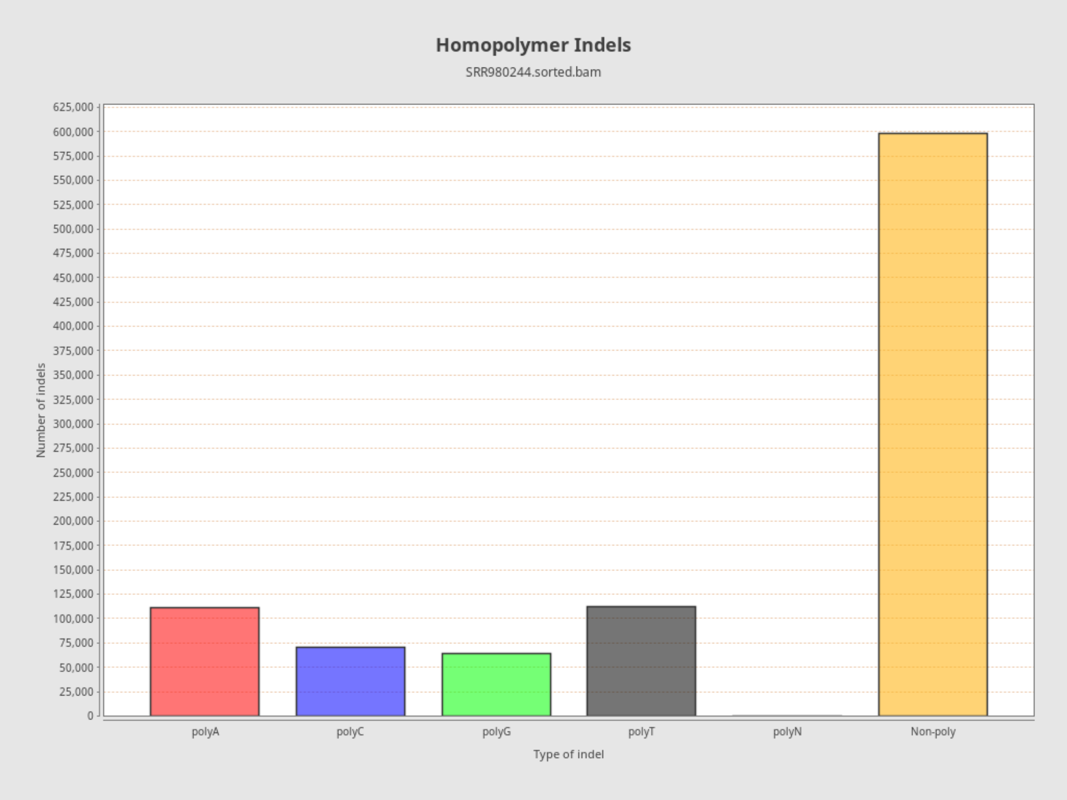
9. Results : Mapped Reads GC-content Distribution



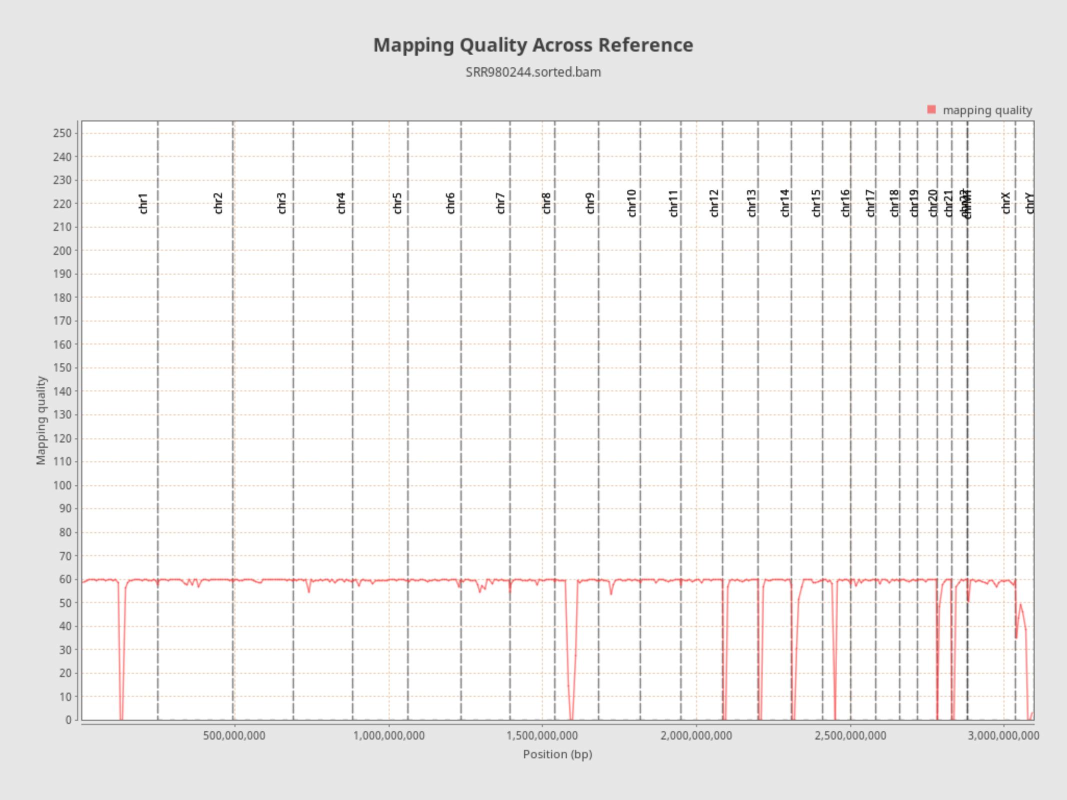
10. Results : Mapped Reads Clipping Profile



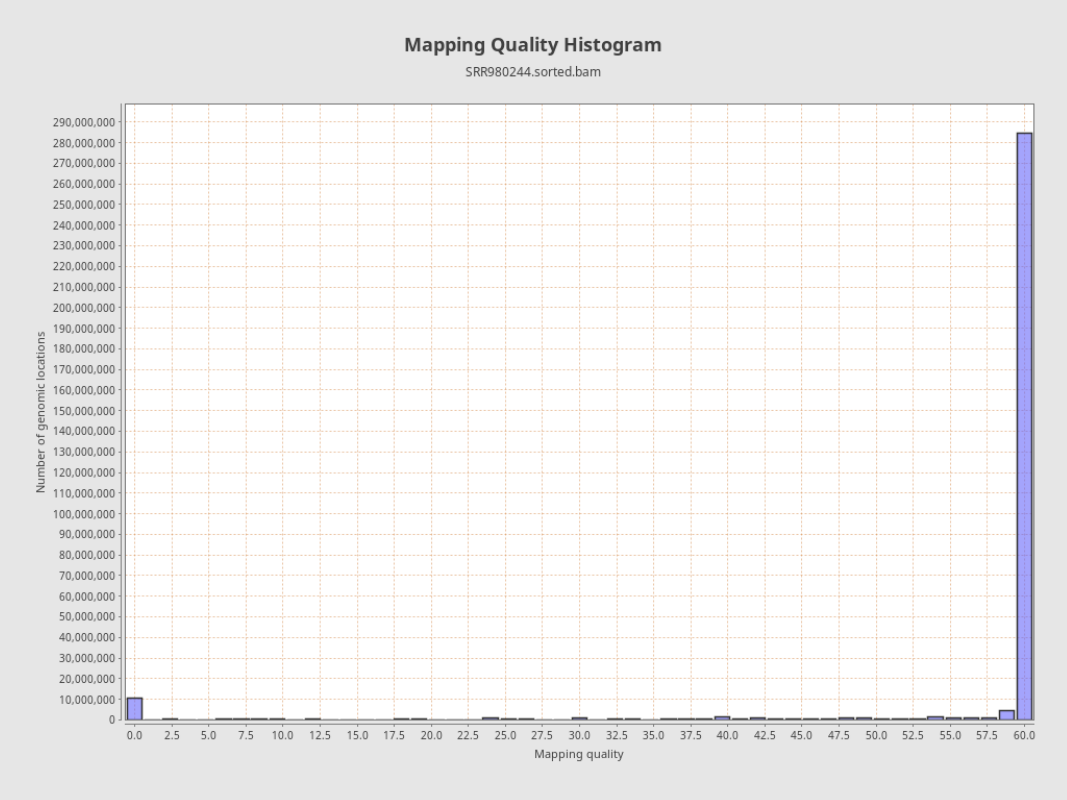
11. Results : Homopolymer Indels



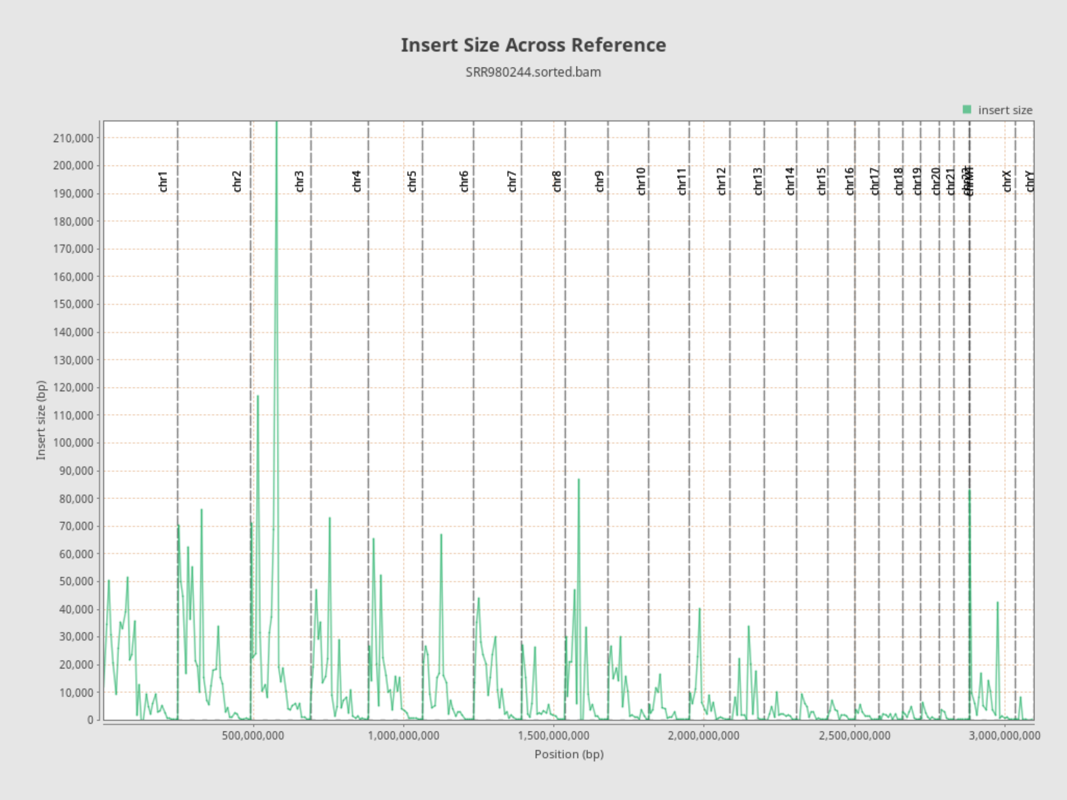
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram