Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 15:37:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975251.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_SRR975251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975251_1.fastq.gz SRR975251_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 15:37:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,258,236
Mapped reads	3,230,369 / 99.14%
Unmapped reads	27,867 / 0.86%
Mapped paired reads	3,230,369 / 99.14%
Mapped reads, first in pair	1,614,800 / 49.56%
Mapped reads, second in pair	1,615,569 / 49.58%
Mapped reads, both in pair	3,222,080 / 98.89%
Mapped reads, singletons	8,289 / 0.25%
Secondary alignments	0
Supplementary alignments	8,561 / 0.26%
Read min/max/mean length	30 / 101 / 101.11
Duplicated reads (estimated)	118,130 / 3.63%
Duplication rate	2.1%
Clipped reads	1,888,527 / 57.96%

2.2. ACGT Content

Number/percentage of A's	88,000,594 / 29.44%
Number/percentage of C's	57,519,429 / 19.25%
Number/percentage of T's	90,905,118 / 30.42%
Number/percentage of G's	62,448,934 / 20.89%
Number/percentage of N's	3,878 / 0%

GC Percentage	40.14%

2.3. Coverage

Mean	0.0966
Standard Deviation	0.9937

2.4. Mapping Quality

Mean Mapping Quality	52.87

2.5. Insert size

Mean	41,974.99
Standard Deviation	1,947,922.74
P25/Median/P75	139 / 171 / 215

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	2,254,566
Insertions	46,335
Mapped reads with at least one insertion	1.41%
Deletions	91,746
Mapped reads with at least one deletion	2.79%
Homopolymer indels	46.36%

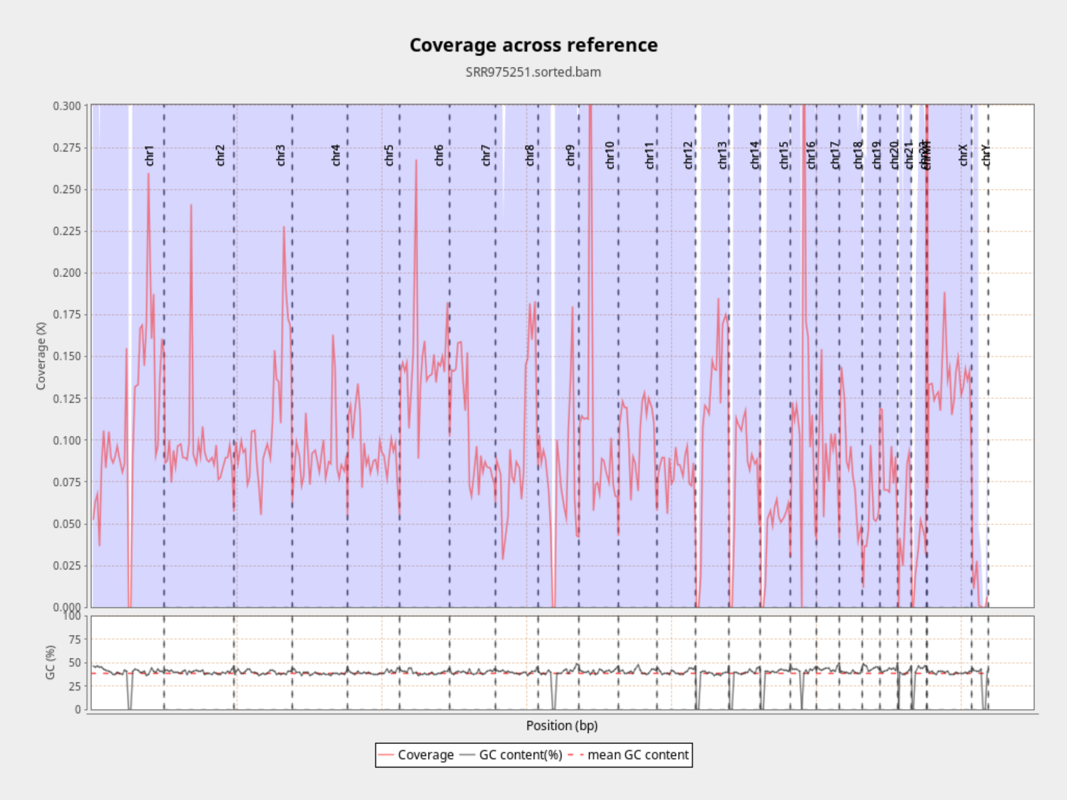
2.7. Chromosome stats

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

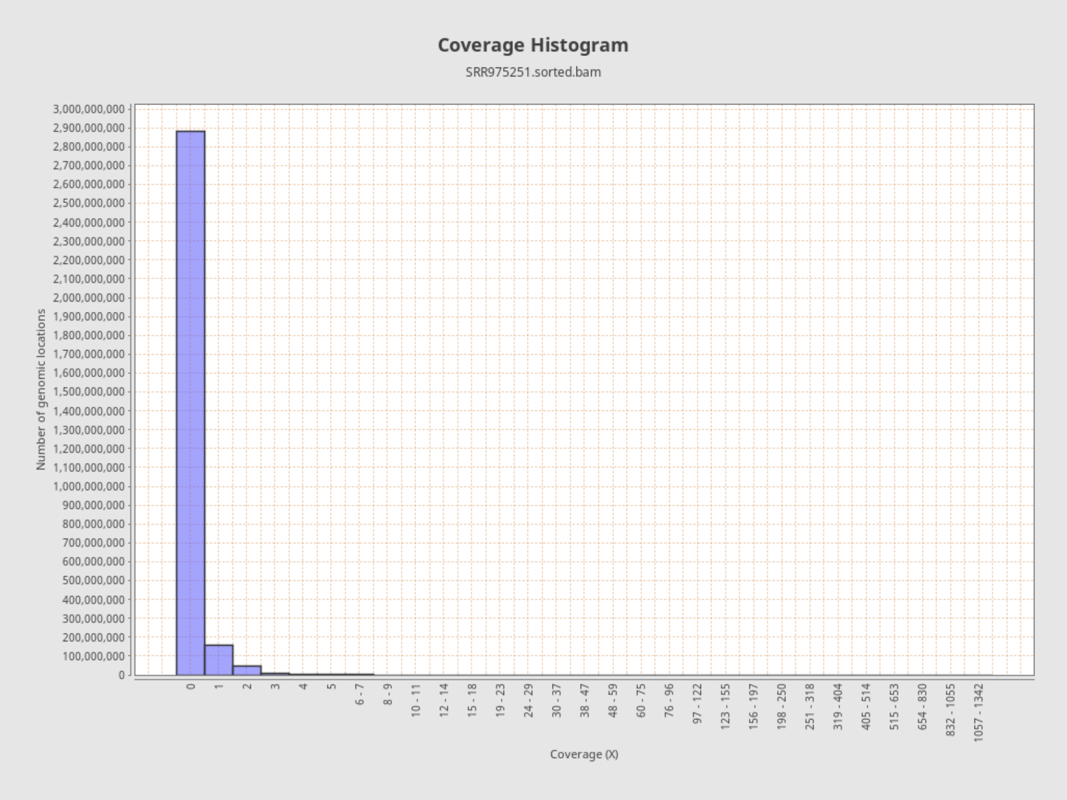
		bases	coverage	deviation
chr1	249250621	27134828	0.1089	1.0102
chr2	243199373	22902101	0.0942	0.9551
chr3	198022430	22329575	0.1128	0.4529
chr4	191154276	17564985	0.0919	0.4888
chr5	180915260	17207453	0.0951	0.3781
chr6	171115067	25107103	0.1467	1.4368
chr7	159138663	16747863	0.1052	1.3007
chr8	146364022	14302354	0.0977	0.4389
chr9	141213431	10894048	0.0771	0.8926
chr10	135534747	14176948	0.1046	2.7459
chr11	135006516	13938826	0.1032	0.7383
chr12	133851895	10942162	0.0817	0.3496
chr13	115169878	13582177	0.1179	0.431
chr14	107349540	8490487	0.0791	0.3544
chr15	102531392	4620883	0.0451	0.2569
chr16	90354753	11249806	0.1245	1.6835
chr17	81195210	7502929	0.0924	1.1195
chr18	78077248	6636314	0.085	1.113
chr19	59128983	3061560	0.0518	0.5632
chr20	63025520	5345121	0.0848	0.3644
chr21	48129895	2532957	0.0526	0.3024
chr22	51304566	1588625	0.031	0.2135
chrMT	16571	16739	1.0101	1.2143
chrX	155270560	20663747	0.1331	0.5957

chrY	59373566	484638	0.0082	0.3219

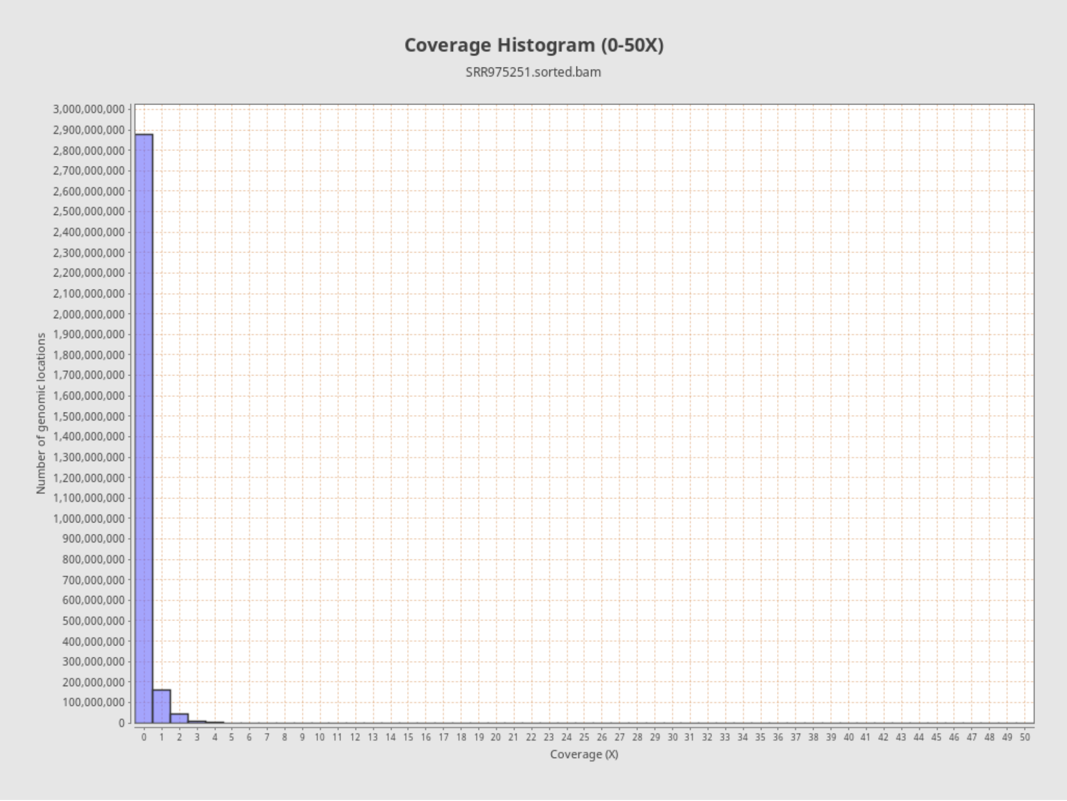
3. Results : Coverage across reference



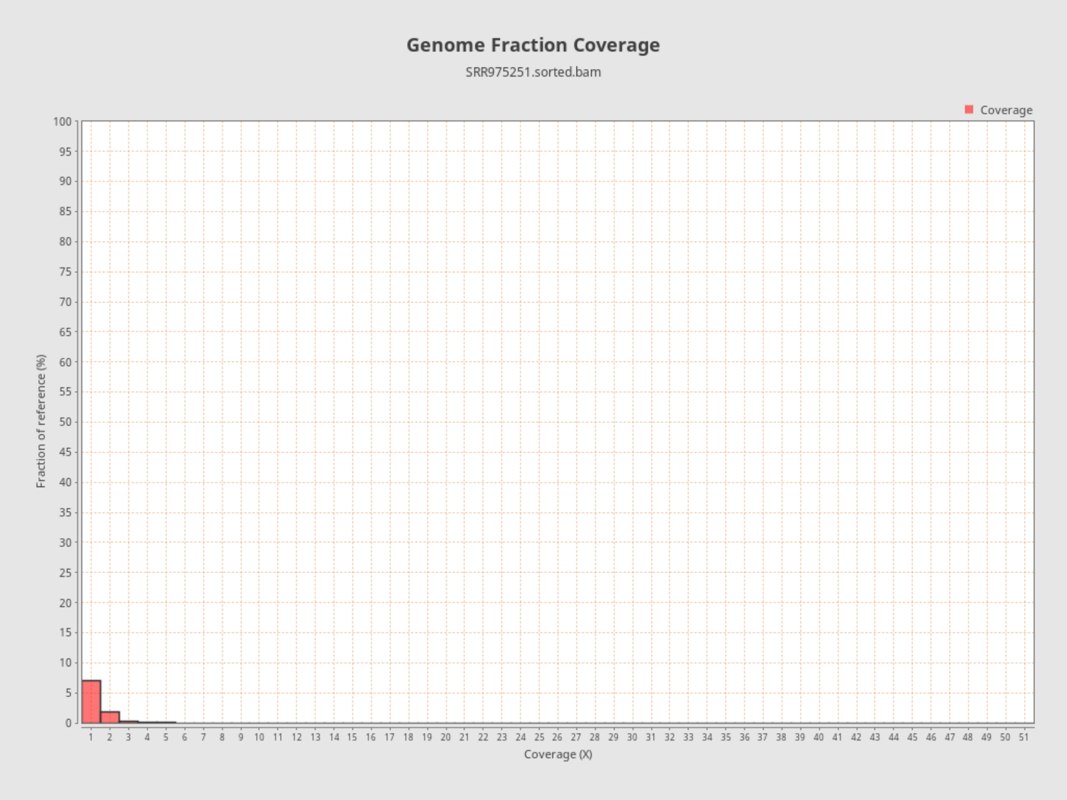
4. Results : Coverage Histogram



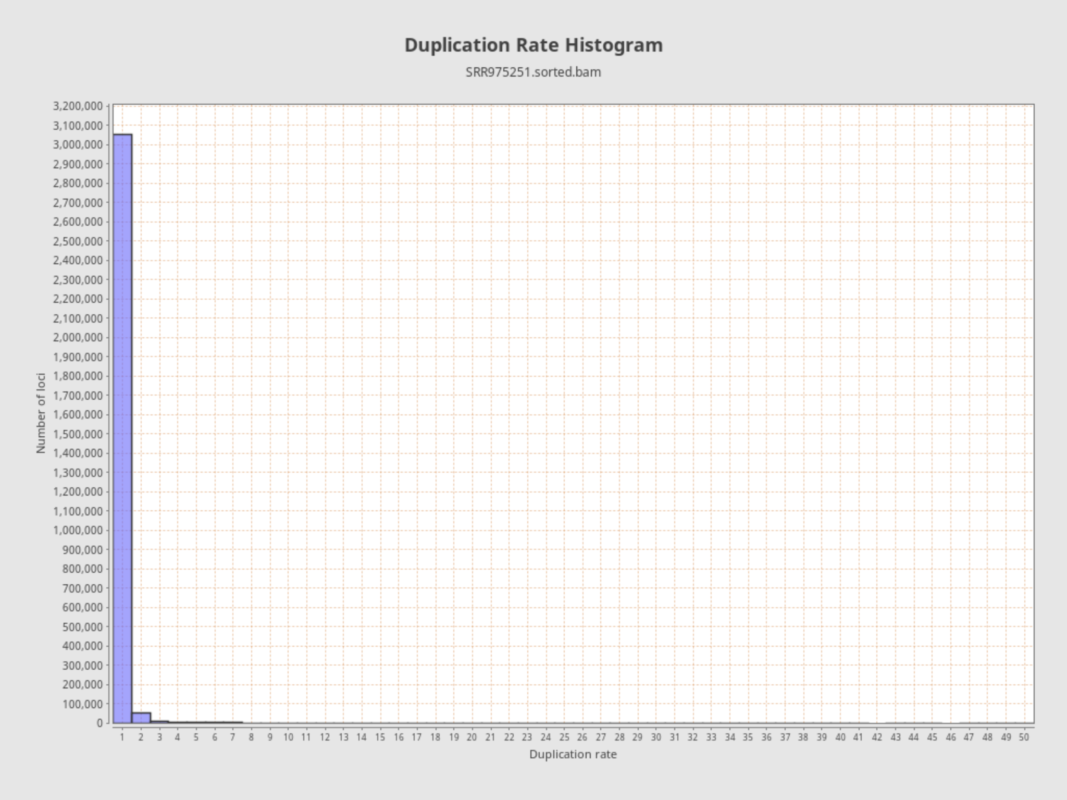
5. Results : Coverage Histogram (0-50X)



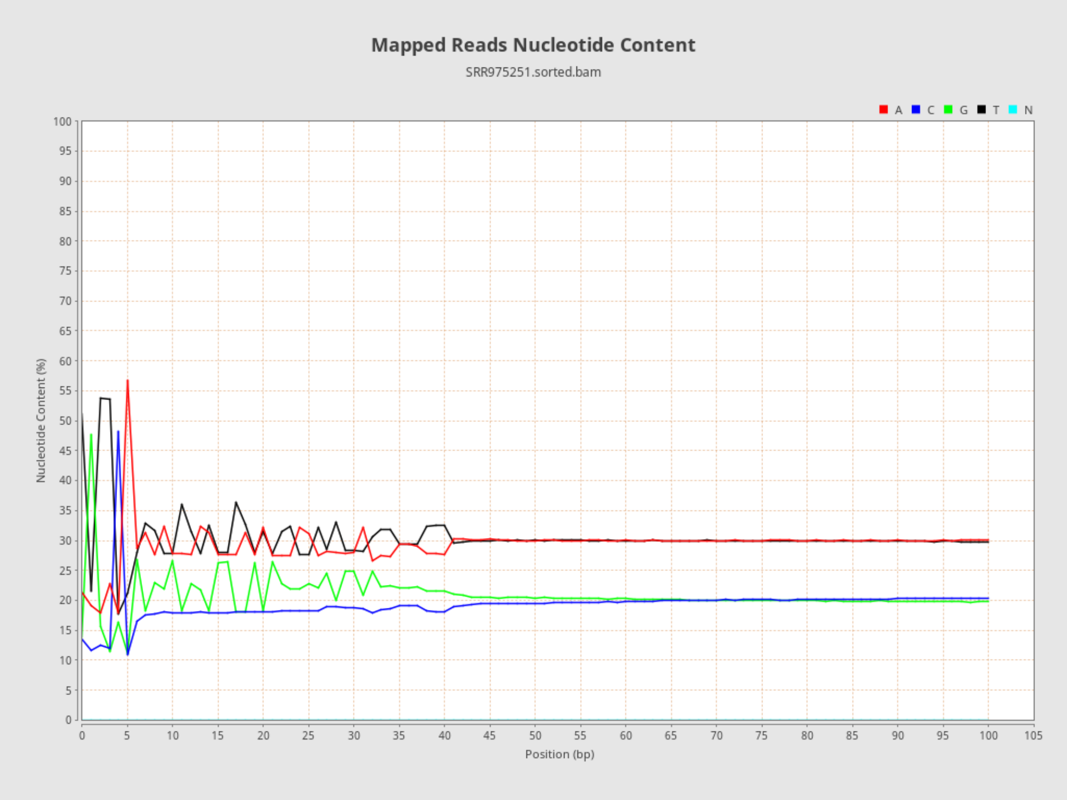
6. Results : Genome Fraction Coverage



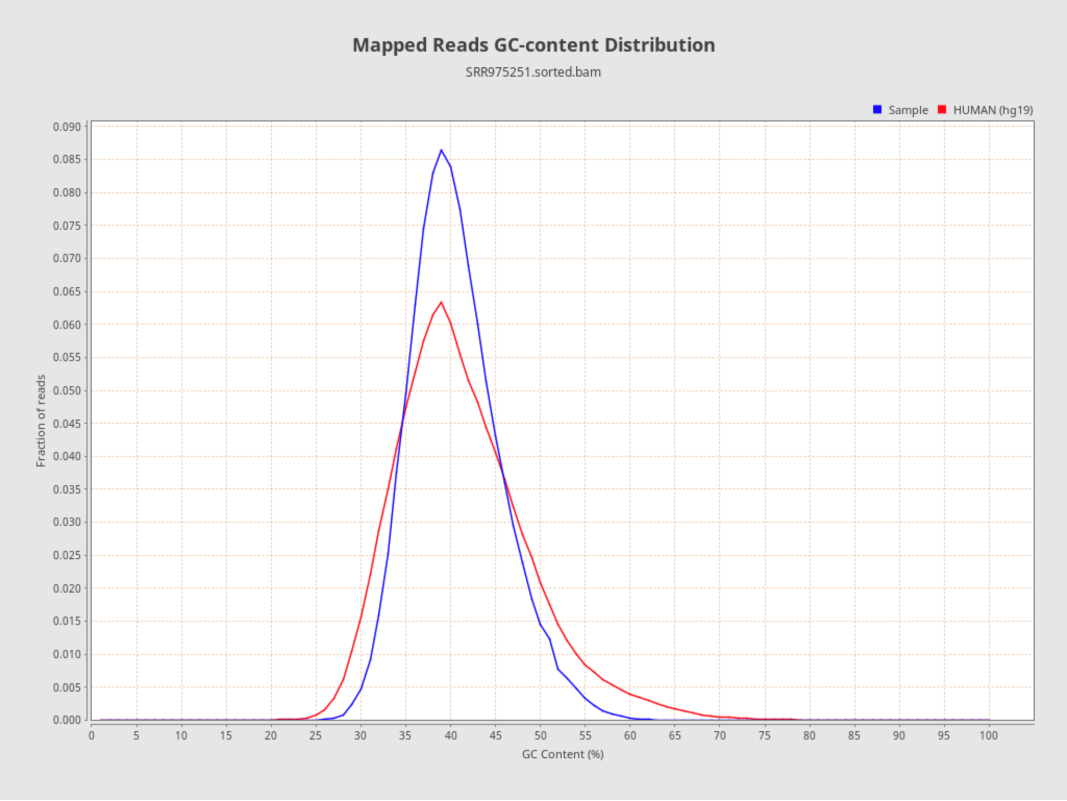
7. Results : Duplication Rate Histogram



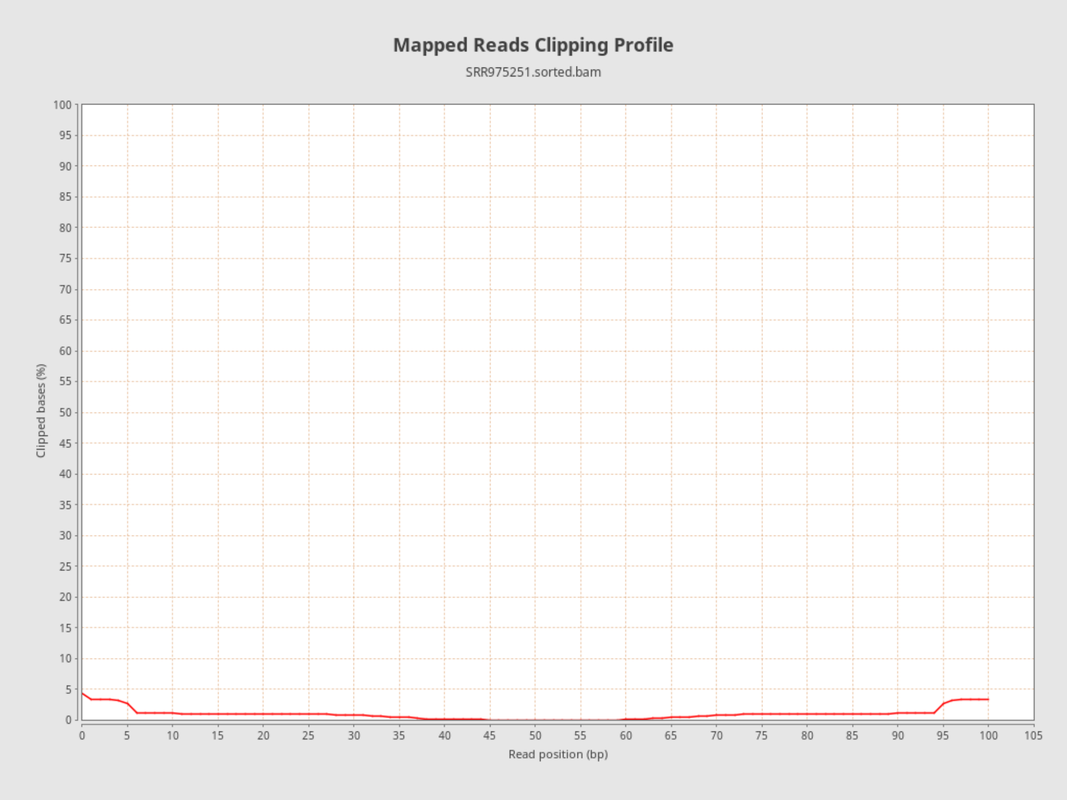
8. Results : Mapped Reads Nucleotide Content



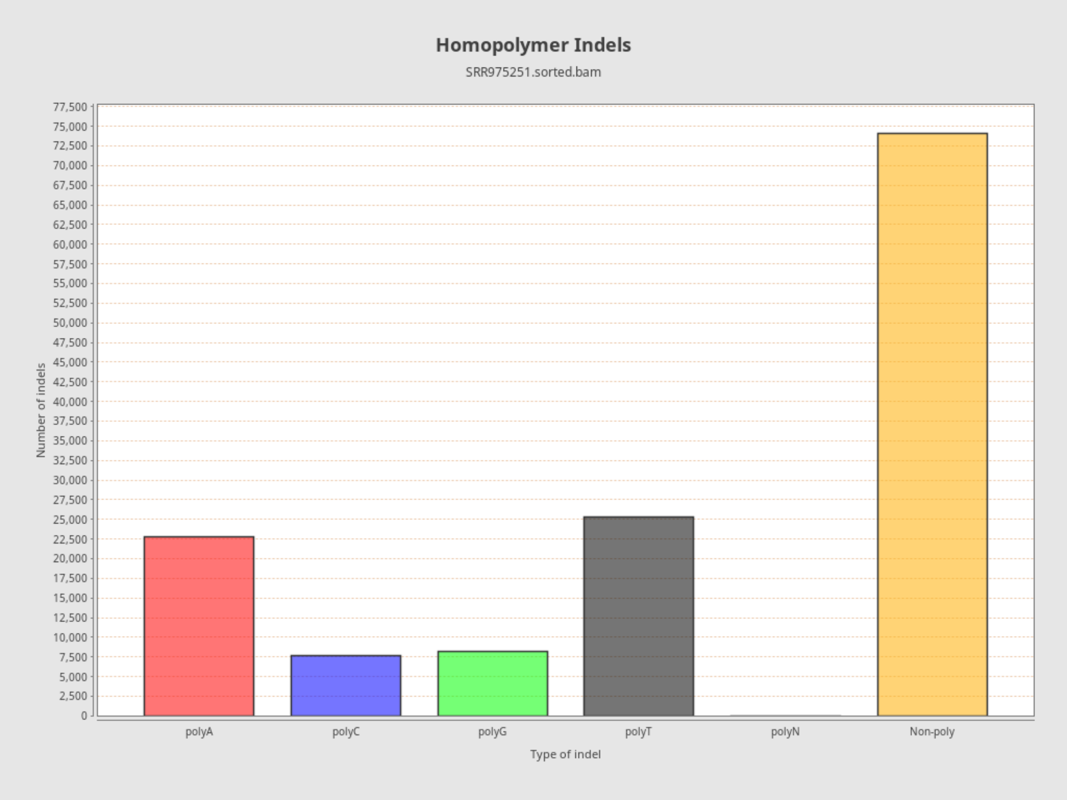
9. Results : Mapped Reads GC-content Distribution



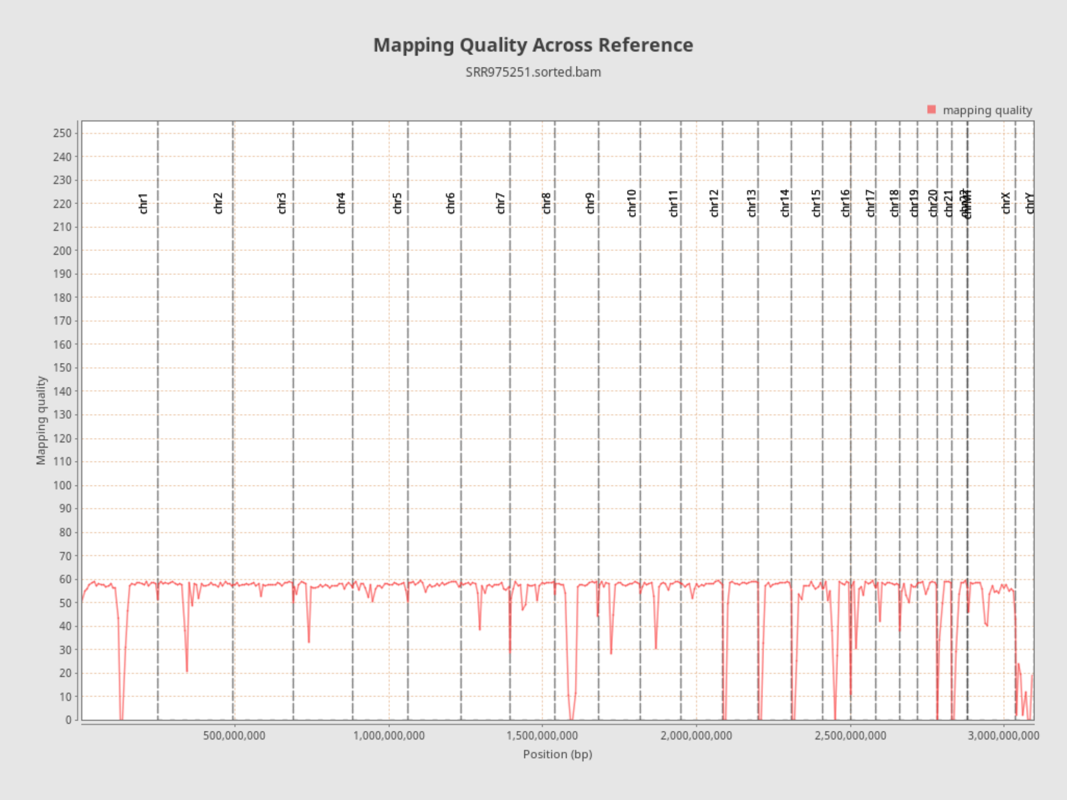
10. Results : Mapped Reads Clipping Profile



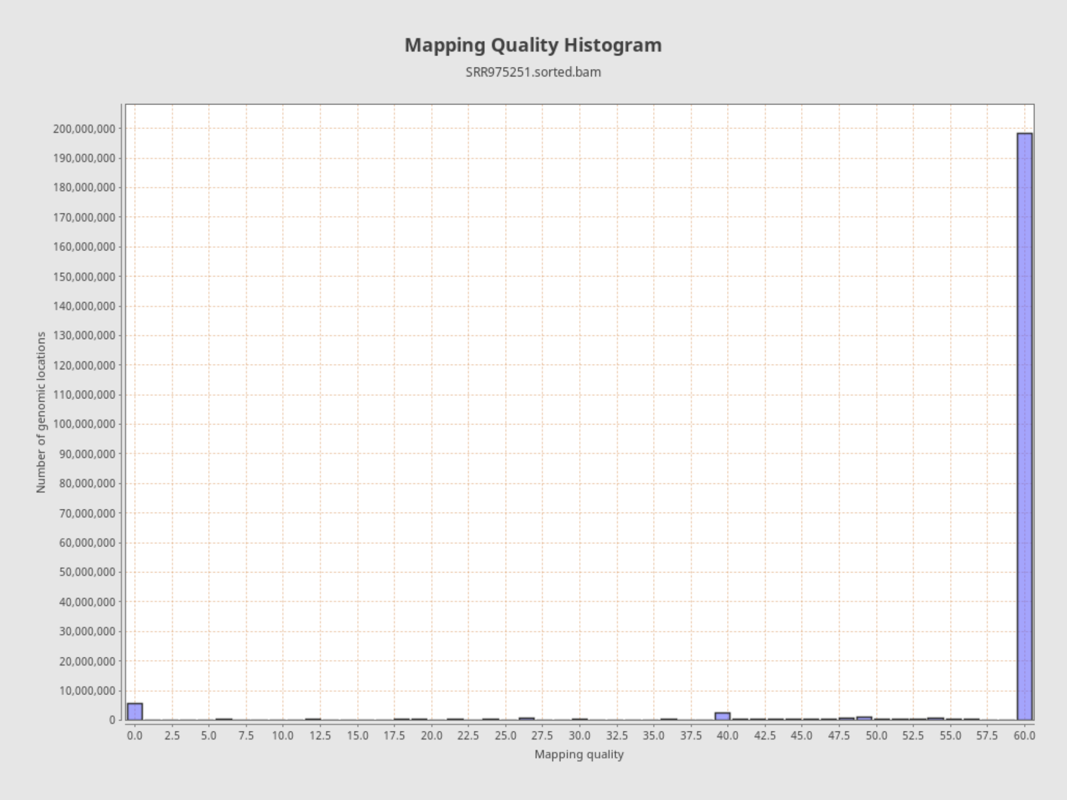
11. Results : Homopolymer Indels



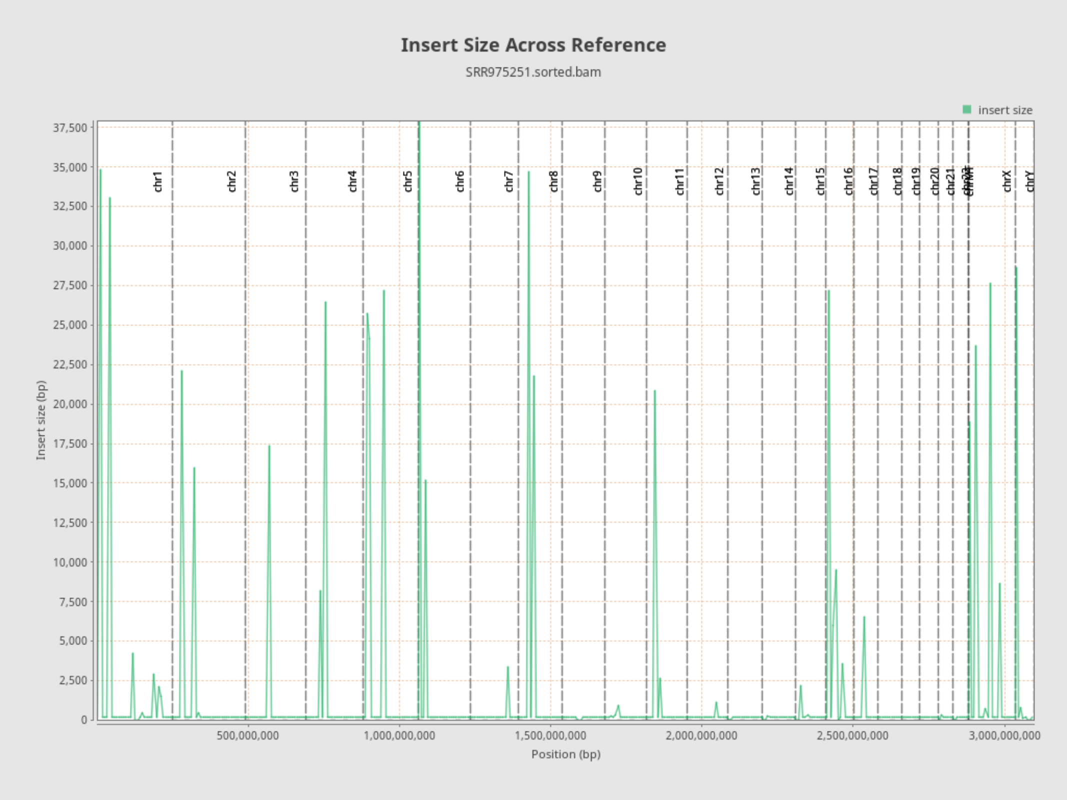
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram