Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 09:42:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975273.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_SRR975273 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975273_1.fastq.gz SRR975273_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 09:42:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975273.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	64,890,198
Mapped reads	64,752,123 / 99.79%
Unmapped reads	138,075 / 0.21%
Mapped paired reads	64,752,123 / 99.79%
Mapped reads, first in pair	32,390,455 / 49.92%
Mapped reads, second in pair	32,361,668 / 49.87%
Mapped reads, both in pair	64,689,702 / 99.69%
Mapped reads, singletons	62,421 / 0.1%
Secondary alignments	0
Supplementary alignments	109,429 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	39,511,744 / 60.89%
Duplication rate	46.5%
Clipped reads	35,521,120 / 54.74%

2.2. ACGT Content

Number/percentage of A's	1,610,463,944 / 26.76%
Number/percentage of C's	1,327,979,419 / 22.07%
Number/percentage of T's	1,643,868,674 / 27.31%
Number/percentage of G's	1,435,762,961 / 23.86%
Number/percentage of N's	263,310 / 0%

GC Percentage	45.92%

2.3. Coverage

Mean	1.9448
Standard Deviation	26.3035

2.4. Mapping Quality

Mean Mapping Quality	56.12

2.5. Insert size

Mean	80,758.99
Standard Deviation	2,805,924.86
P25/Median/P75	150 / 187 / 235

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	38,560,992
Insertions	682,527
Mapped reads with at least one insertion	1.04%
Deletions	1,520,712
Mapped reads with at least one deletion	2.31%
Homopolymer indels	46.52%

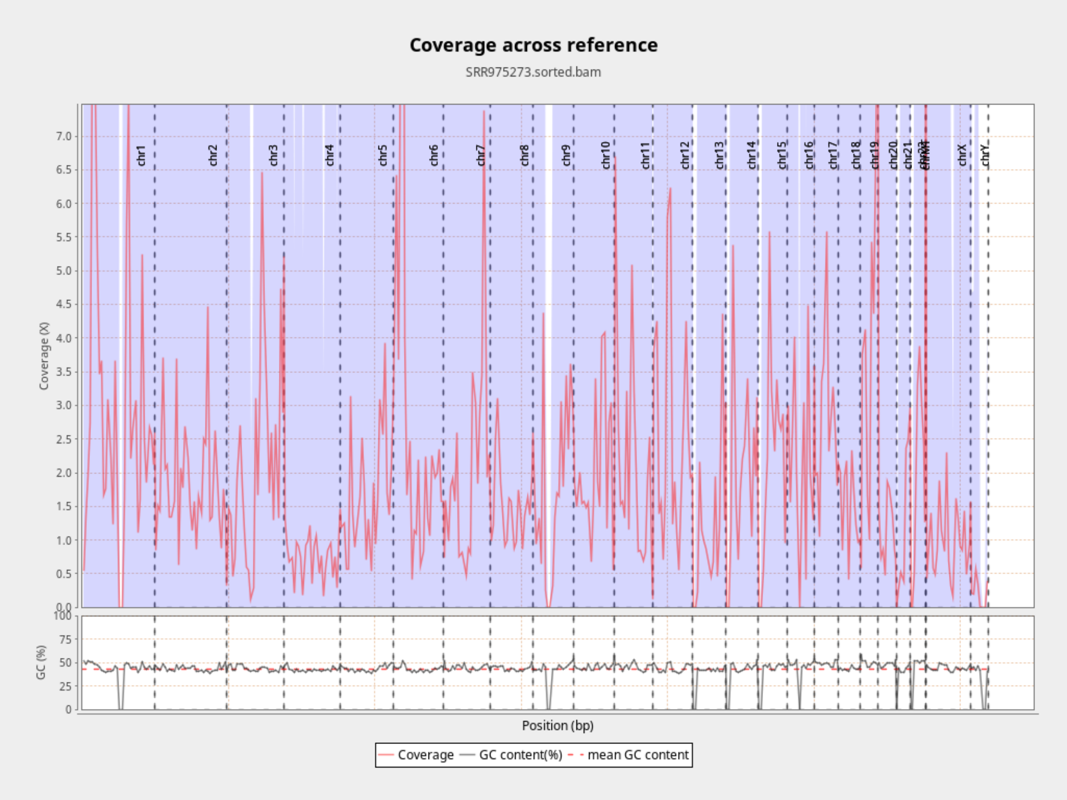
2.7. Chromosome stats

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

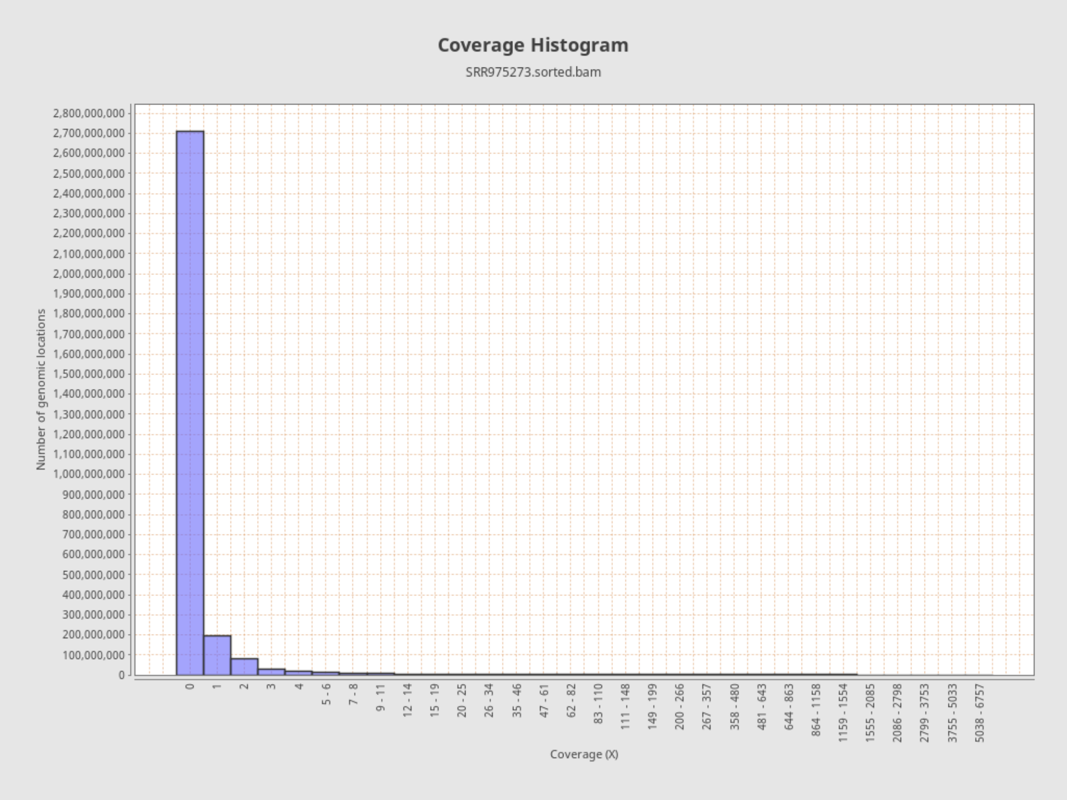
		bases	coverage	deviation
chr1	249250621	732376894	2.9383	34.7762
chr2	243199373	451849697	1.8579	23.9095
chr3	198022430	415562232	2.0986	27.8383
chr4	191154276	141375930	0.7396	12.9122
chr5	180915260	301878461	1.6686	22.6465
chr6	171115067	540427256	3.1583	41.1602
chr7	159138663	321270526	2.0188	27.5603
chr8	146364022	217957394	1.4891	20.4867
chr9	141213431	252032889	1.7848	24.2019
chr10	135534747	276084593	2.037	25.445
chr11	135006516	287307927	2.1281	27.0057
chr12	133851895	341757742	2.5533	29.1571
chr13	115169878	133095369	1.1556	20.2464
chr14	107349540	206388079	1.9226	25.6959
chr15	102531392	224359078	2.1882	27.1037
chr16	90354753	194301748	2.1504	26.4448
chr17	81195210	228573339	2.8151	29.298
chr18	78077248	117953207	1.5107	22.8935
chr19	59128983	231986927	3.9234	37.6588
chr20	63025520	71965910	1.1419	19.2478
chr21	48129895	61370266	1.2751	20.6291
chr22	51304566	104539578	2.0376	24.8391
chrMT	16571	169558	10.2322	19.5418
chrX	155270560	153127179	0.9862	15.7407

chrY	59373566	12780910	0.2153	5.2399

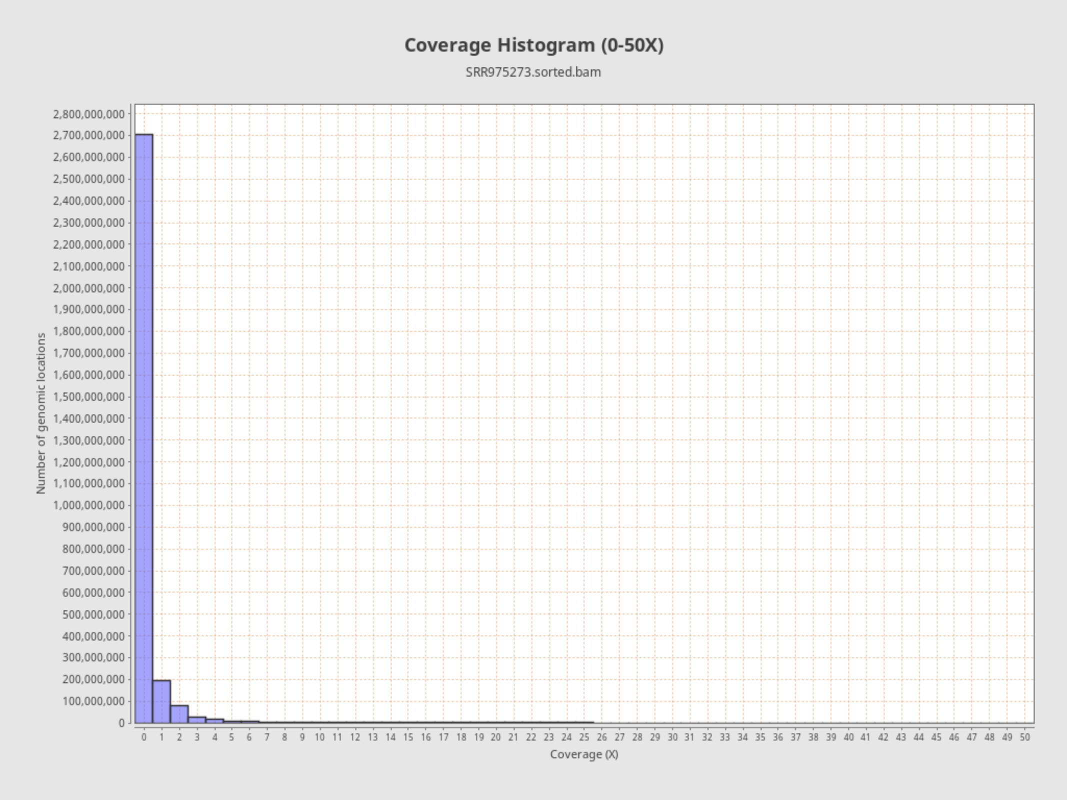
3. Results : Coverage across reference



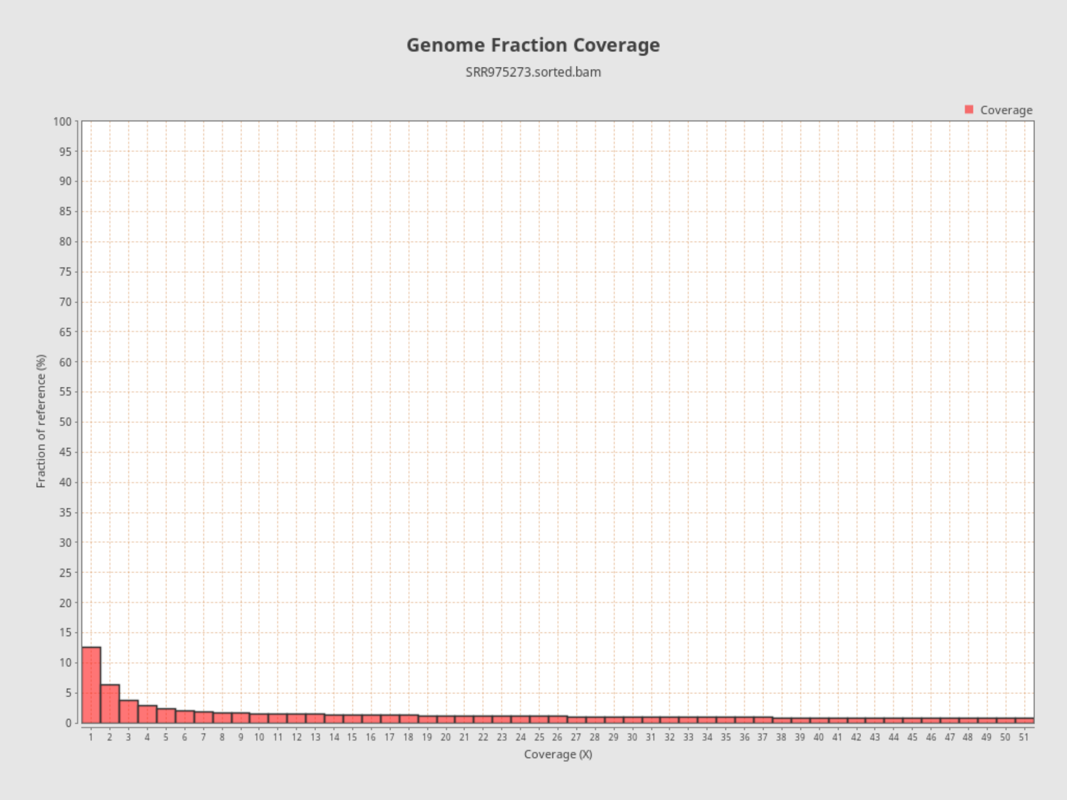
4. Results : Coverage Histogram



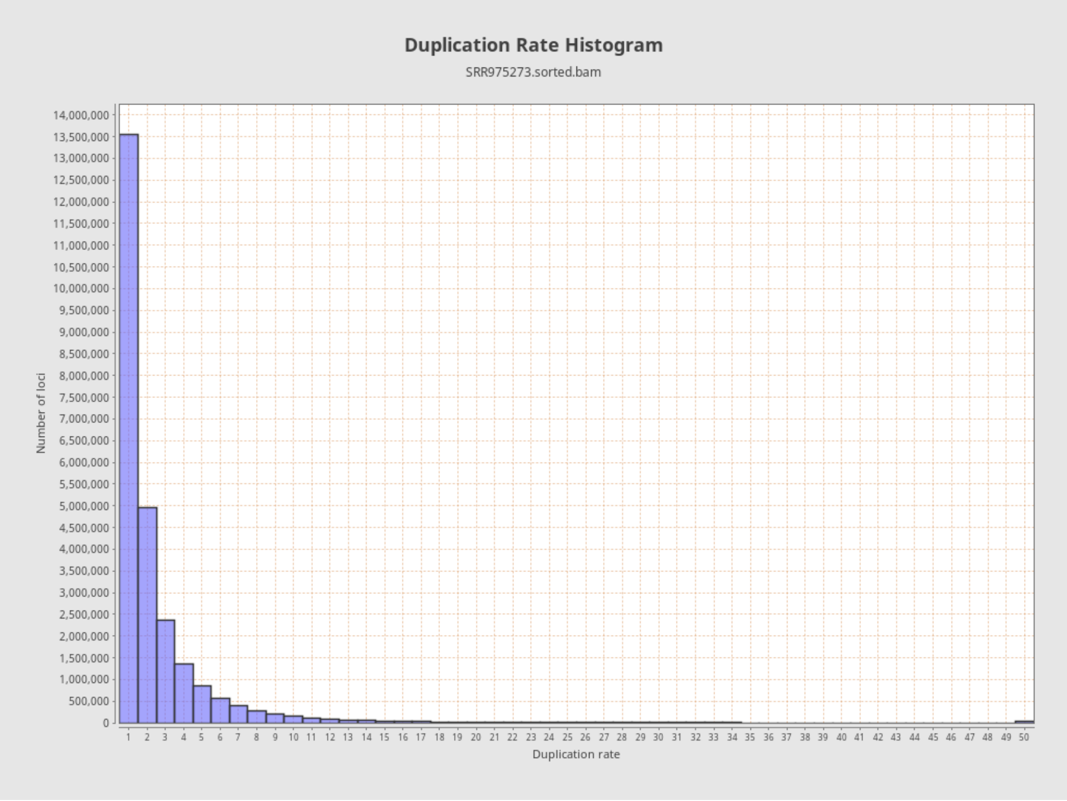
5. Results : Coverage Histogram (0-50X)



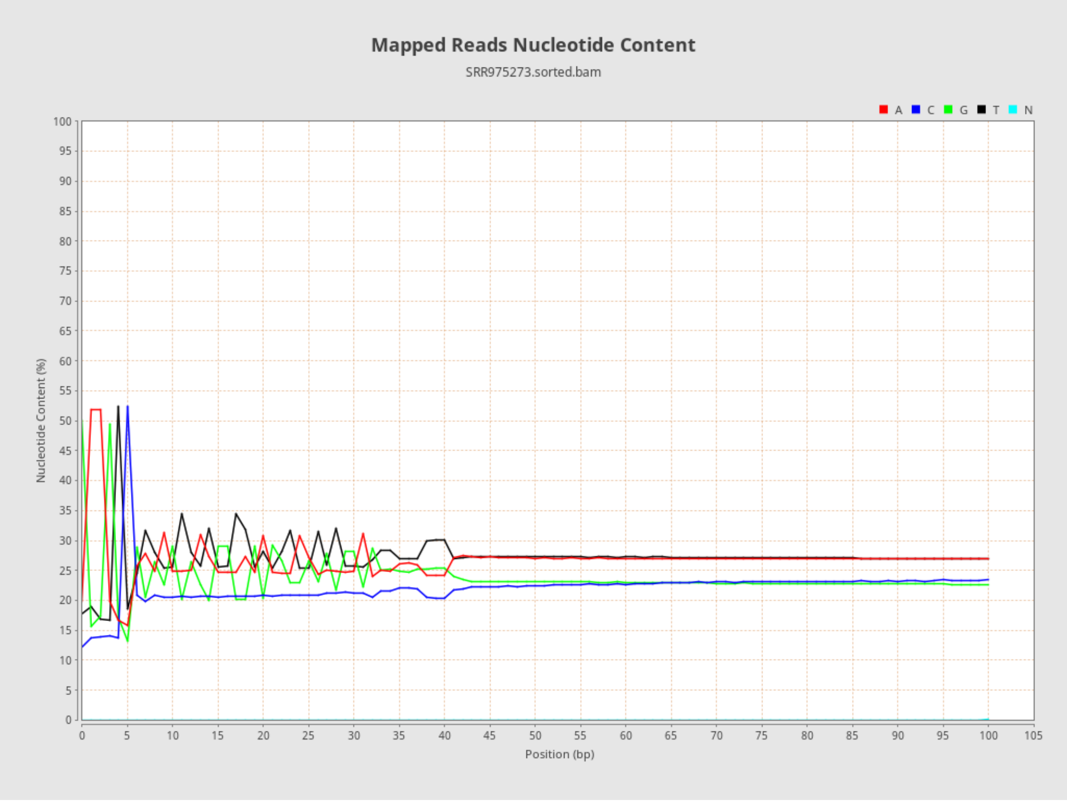
6. Results : Genome Fraction Coverage



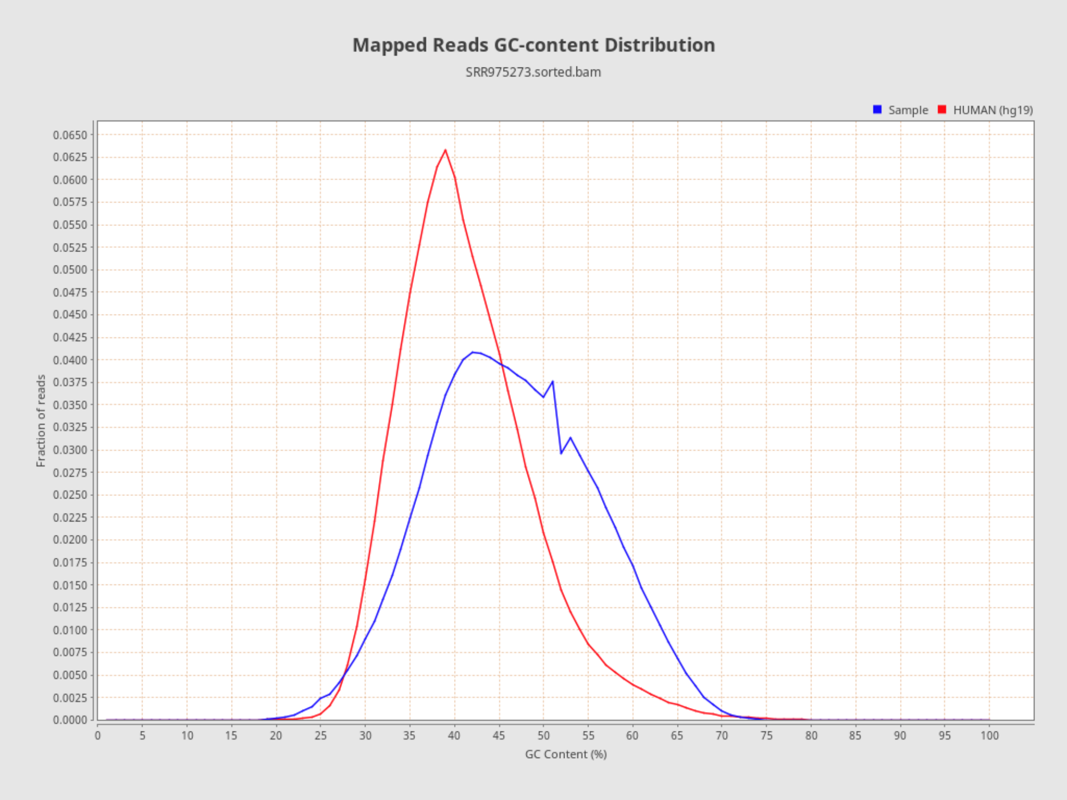
7. Results : Duplication Rate Histogram



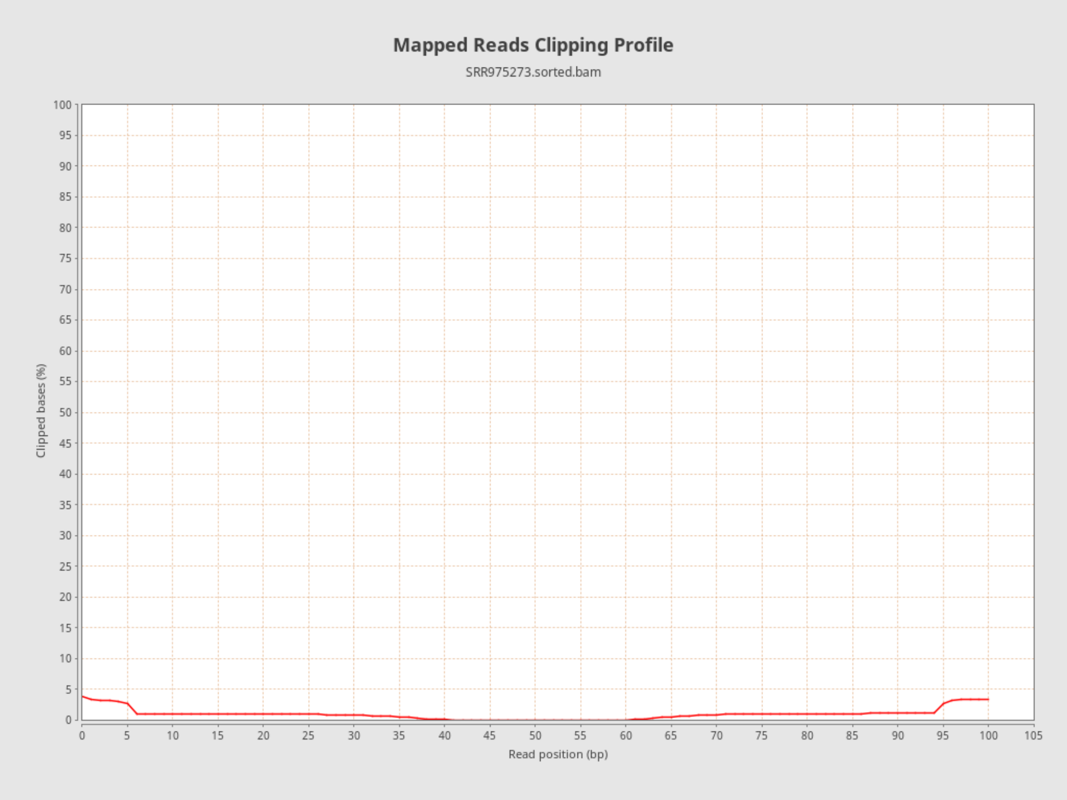
8. Results : Mapped Reads Nucleotide Content



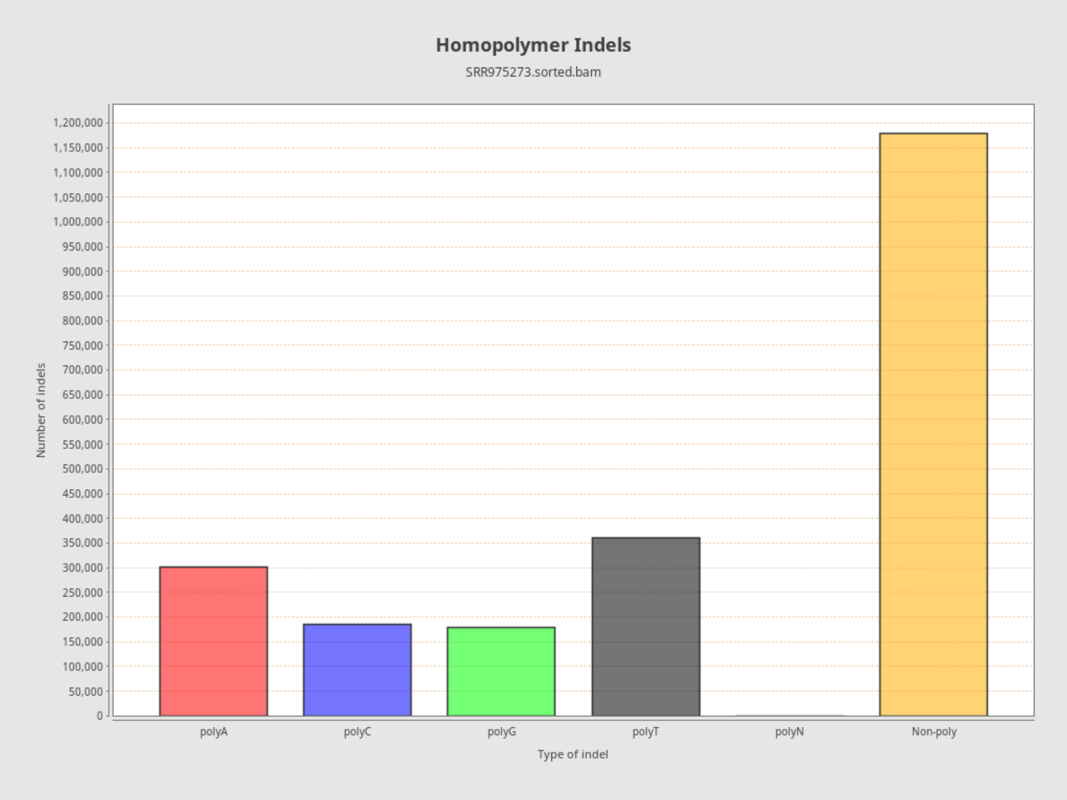
9. Results : Mapped Reads GC-content Distribution



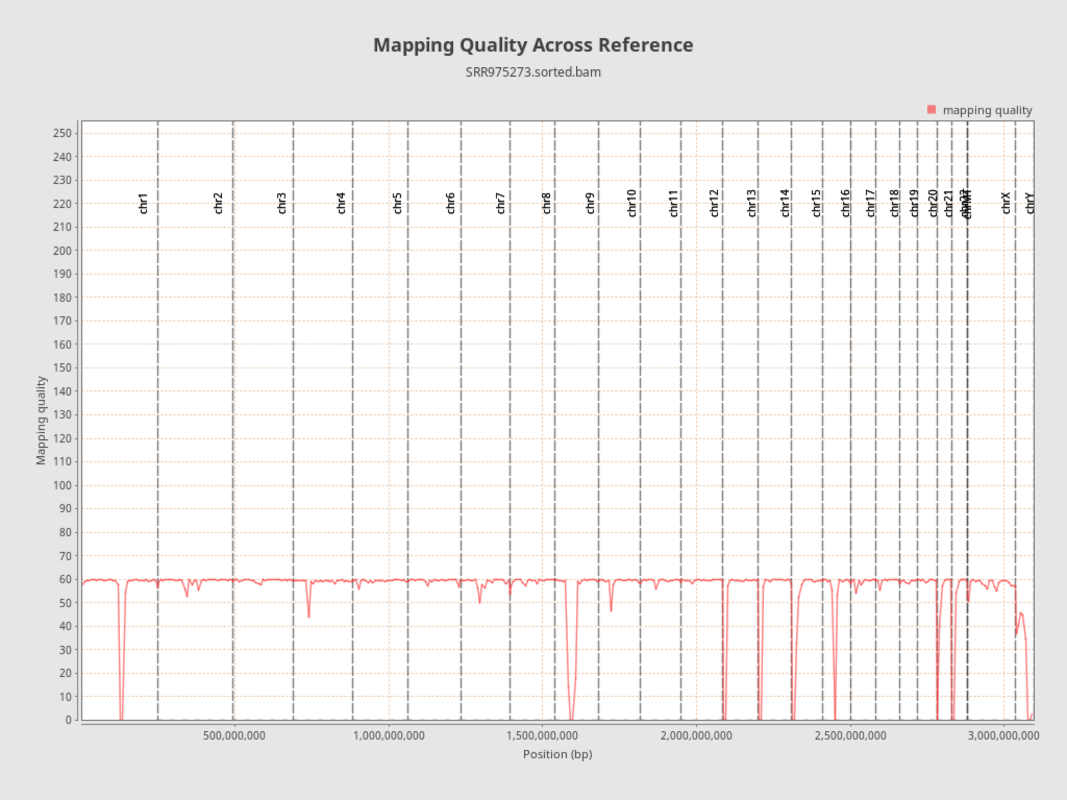
10. Results : Mapped Reads Clipping Profile



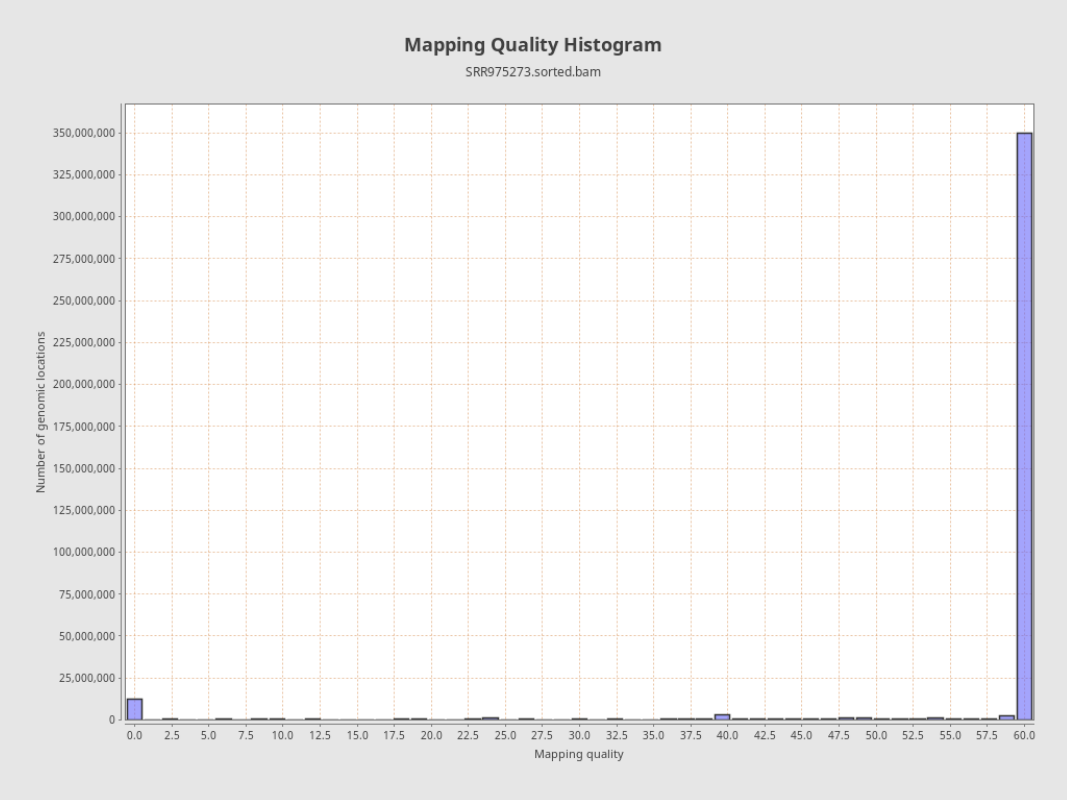
11. Results : Homopolymer Indels



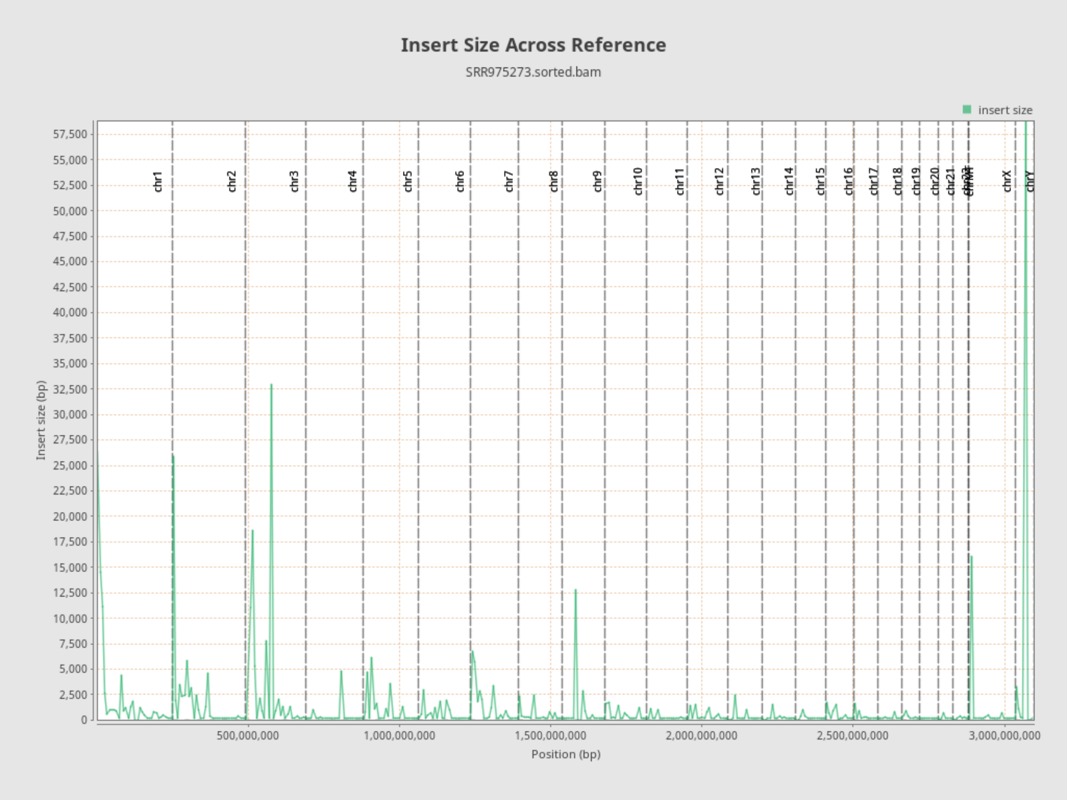
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram