Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 18:48:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975272.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_SRR975272 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975272_1.fastq.gz SRR975272_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 18:48:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975272.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,790,386
Mapped reads	5,732,341 / 99%
Unmapped reads	58,045 / 1%
Mapped paired reads	5,732,341 / 99%
Mapped reads, first in pair	2,864,954 / 49.48%
Mapped reads, second in pair	2,867,387 / 49.52%
Mapped reads, both in pair	5,713,622 / 98.67%
Mapped reads, singletons	18,719 / 0.32%
Secondary alignments	0
Supplementary alignments	27,837 / 0.48%
Read min/max/mean length	30 / 101 / 101.19
Duplicated reads (estimated)	307,642 / 5.31%
Duplication rate	2.79%
Clipped reads	3,327,983 / 57.47%

2.2. ACGT Content

Number/percentage of A's	157,682,212 / 29.54%
Number/percentage of C's	105,992,625 / 19.86%
Number/percentage of T's	156,510,434 / 29.33%
Number/percentage of G's	113,509,953 / 21.27%
Number/percentage of N's	14,570 / 0%

GC Percentage	41.13%

2.3. Coverage

Mean	0.1725
Standard Deviation	1.7958

2.4. Mapping Quality

Mean Mapping Quality	52.93

2.5. Insert size

Mean	64,370.82
Standard Deviation	2,447,267.71
P25/Median/P75	143 / 175 / 220

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	4,494,229
Insertions	88,718
Mapped reads with at least one insertion	1.52%
Deletions	184,439
Mapped reads with at least one deletion	3.15%
Homopolymer indels	46.44%

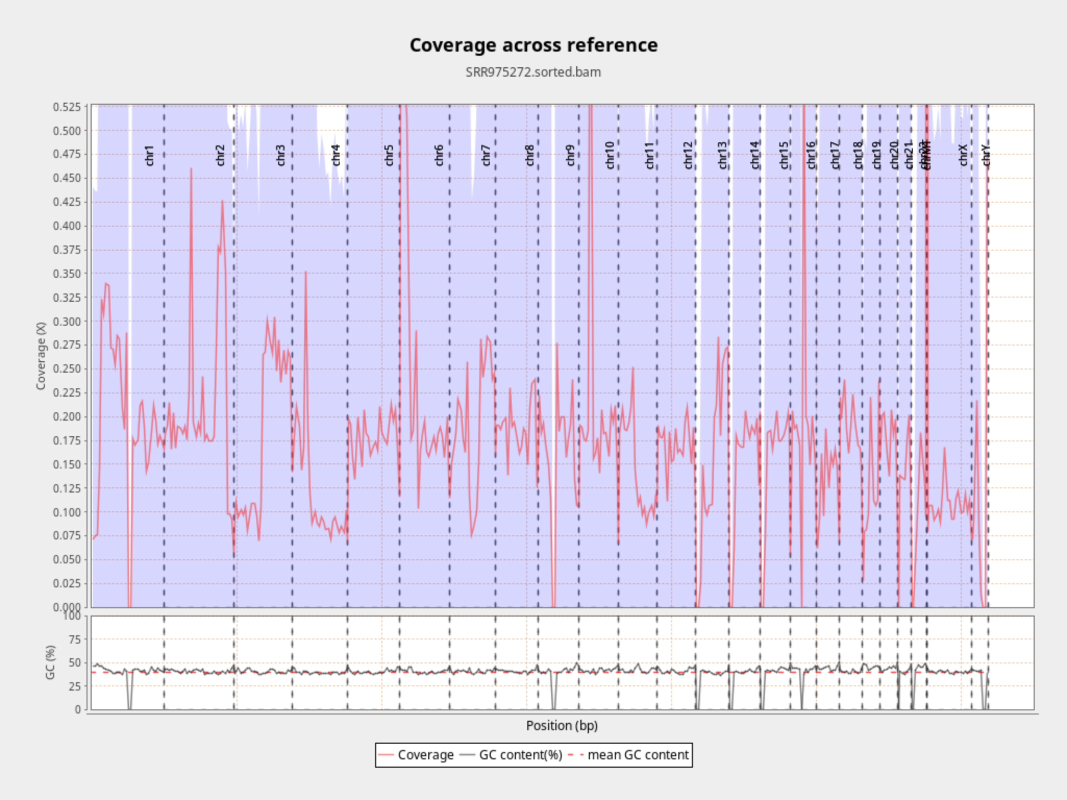
2.7. Chromosome stats

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

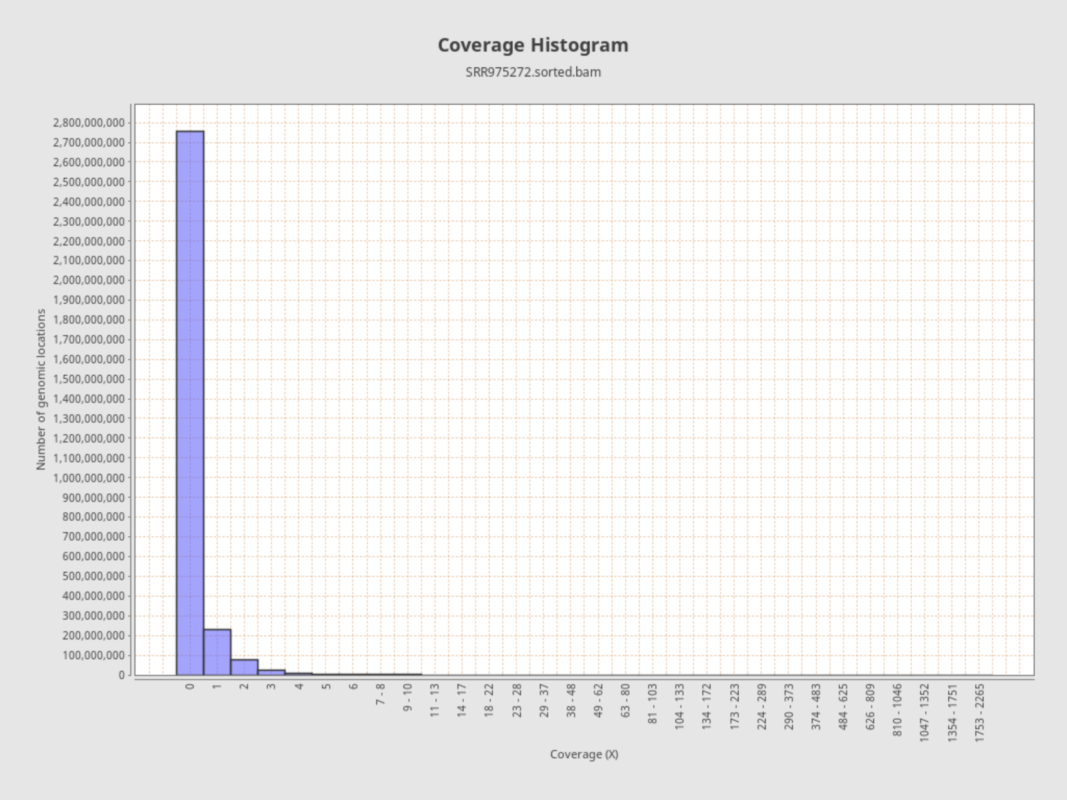
		bases	coverage	deviation
chr1	249250621	48840582	0.1959	1.9132
chr2	243199373	51816685	0.2131	1.7936
chr3	198022430	36707055	0.1854	0.6368
chr4	191154276	23660609	0.1238	1.1671
chr5	180915260	32465781	0.1795	0.5659
chr6	171115067	42327303	0.2474	1.4372
chr7	159138663	30484292	0.1916	1.9513
chr8	146364022	27445826	0.1875	0.7822
chr9	141213431	22710602	0.1608	2.6153
chr10	135534747	29120920	0.2149	4.9336
chr11	135006516	19567732	0.1449	1.7954
chr12	133851895	22959220	0.1715	0.5616
chr13	115169878	17769994	0.1543	0.5281
chr14	107349540	15829128	0.1475	0.581
chr15	102531392	15470754	0.1509	0.5223
chr16	90354753	17729301	0.1962	2.7859
chr17	81195210	10682143	0.1316	1.3862
chr18	78077248	14905203	0.1909	2.5956
chr19	59128983	6858269	0.116	1.2531
chr20	63025520	11094529	0.176	0.6303
chr21	48129895	6567478	0.1365	0.7509
chr22	51304566	5157424	0.1005	0.4324
chrMT	16571	128971	7.7829	8.0711
chrX	155270560	16566539	0.1067	0.8035

chrY	59373566	7151196	0.1204	2.4567

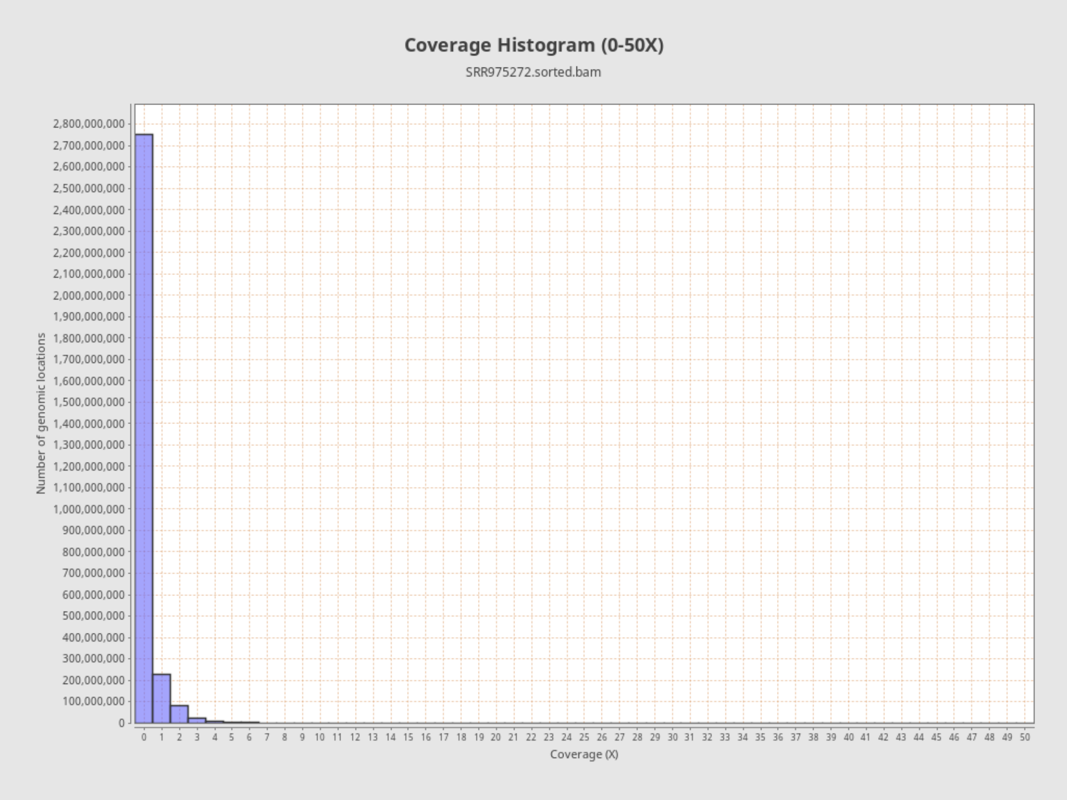
3. Results : Coverage across reference



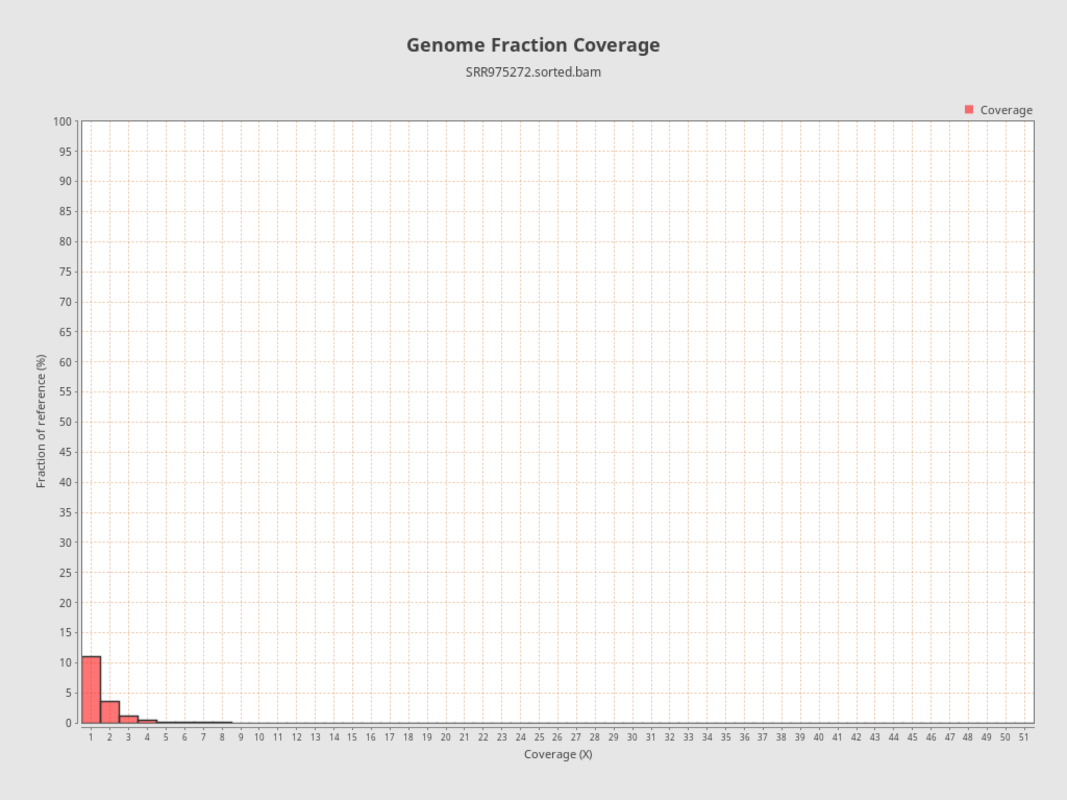
4. Results : Coverage Histogram



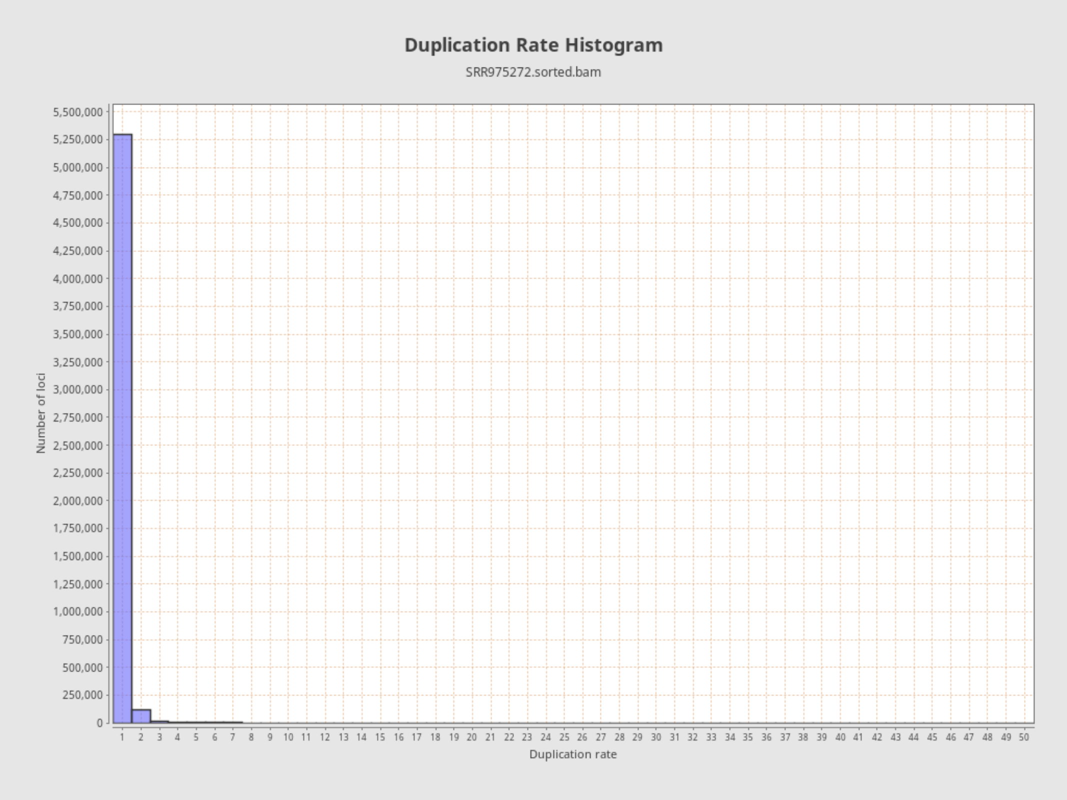
5. Results : Coverage Histogram (0-50X)



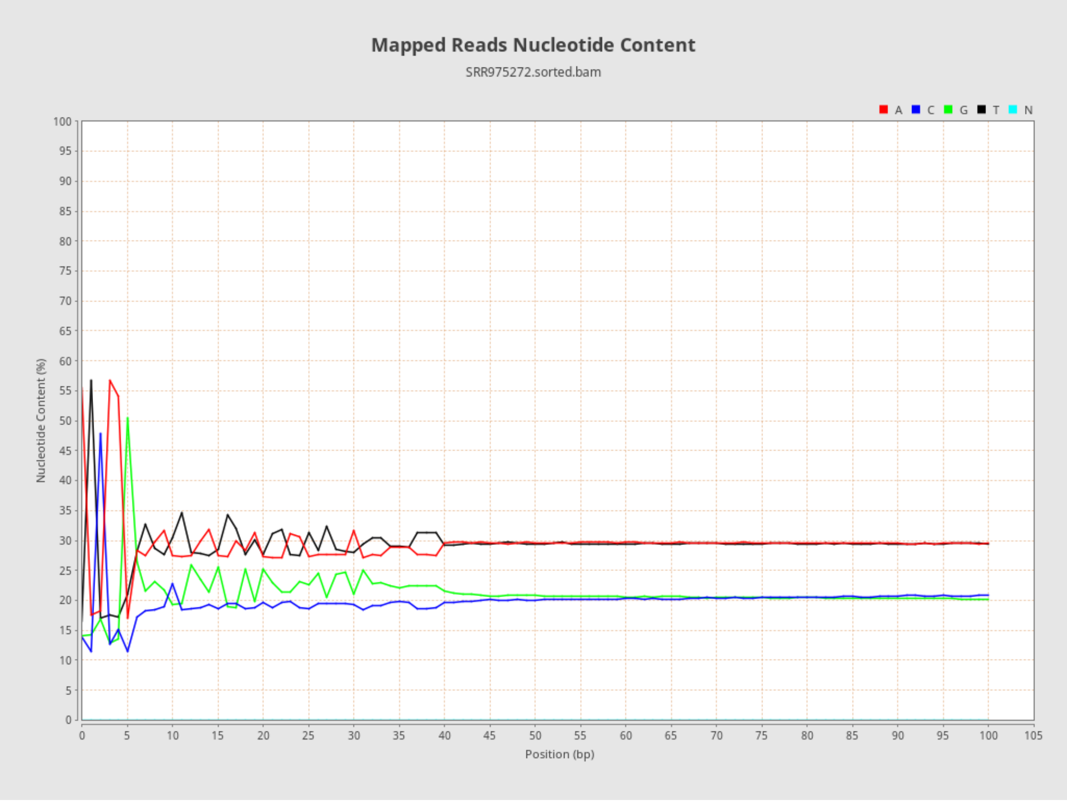
6. Results : Genome Fraction Coverage



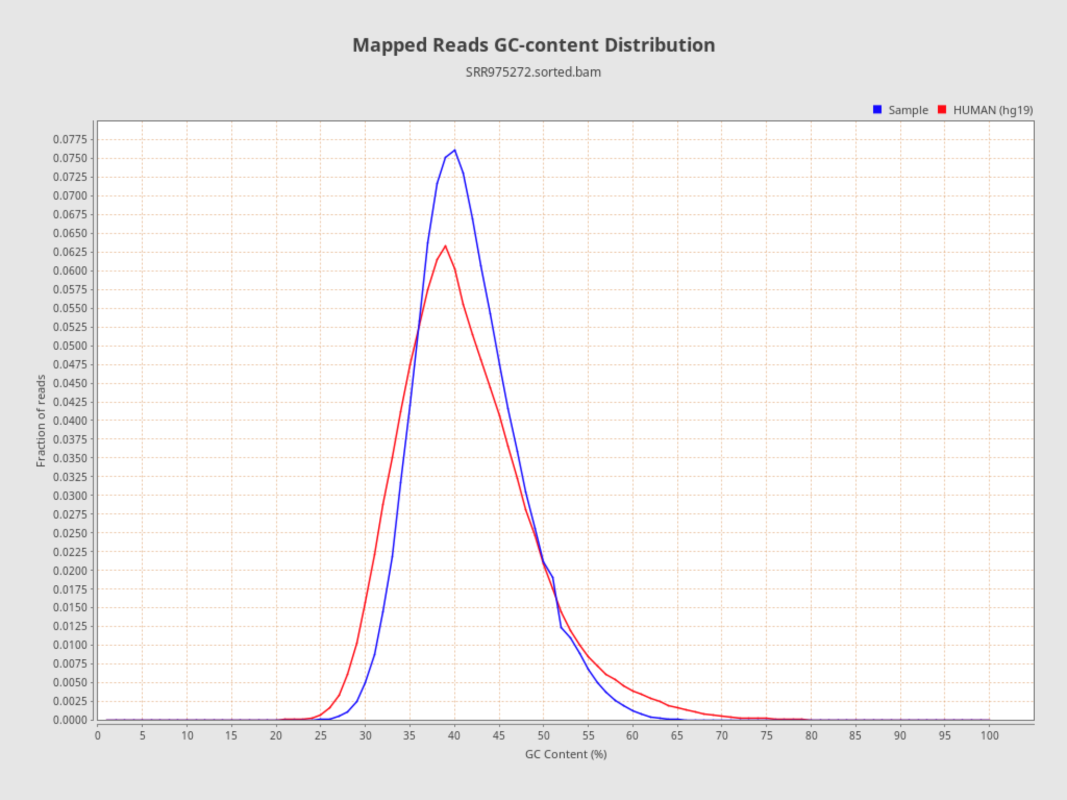
7. Results : Duplication Rate Histogram



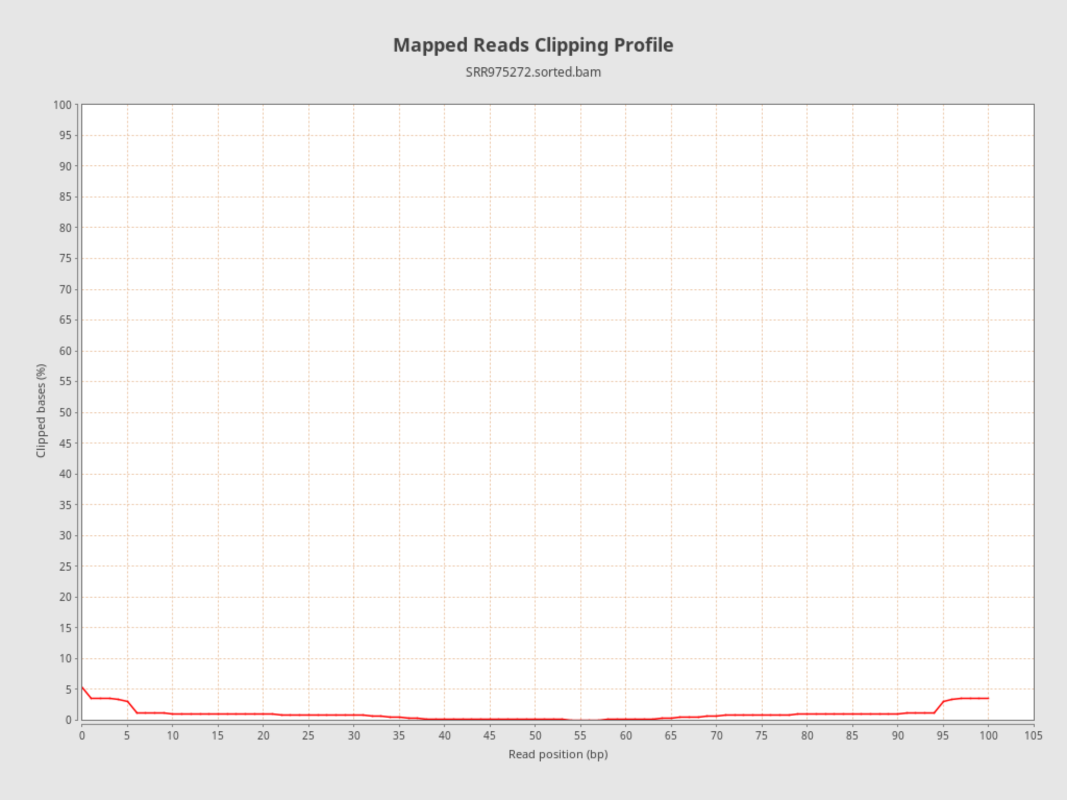
8. Results : Mapped Reads Nucleotide Content



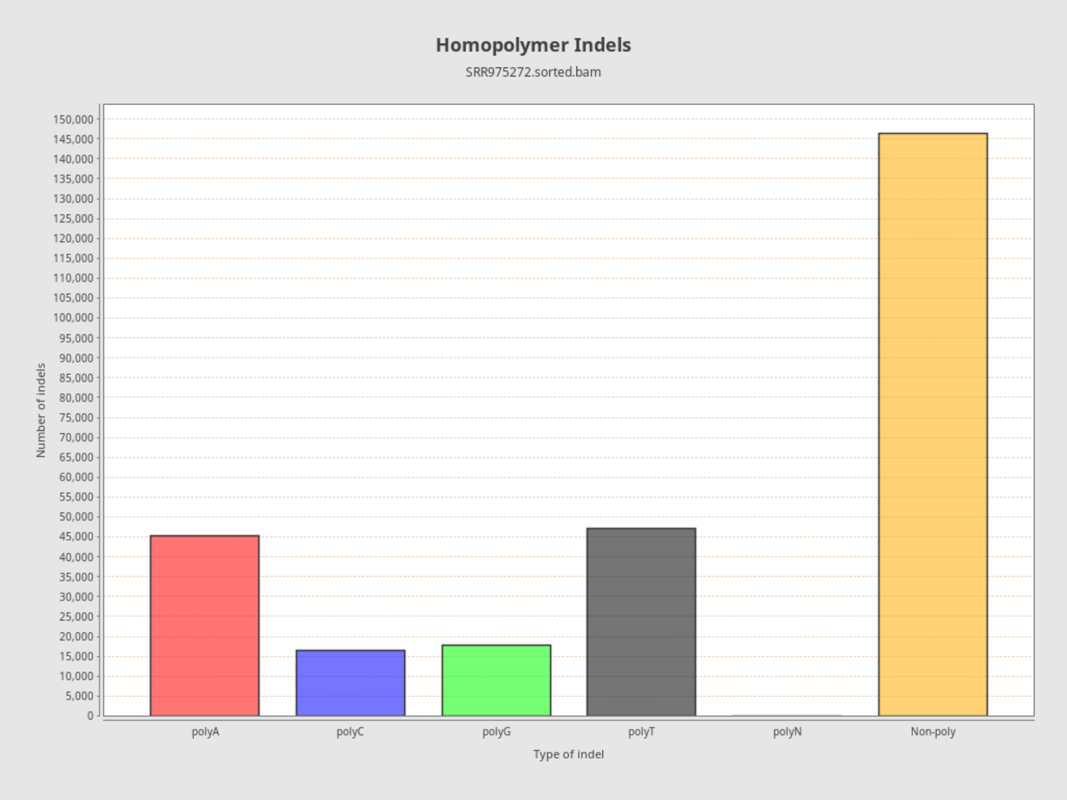
9. Results : Mapped Reads GC-content Distribution



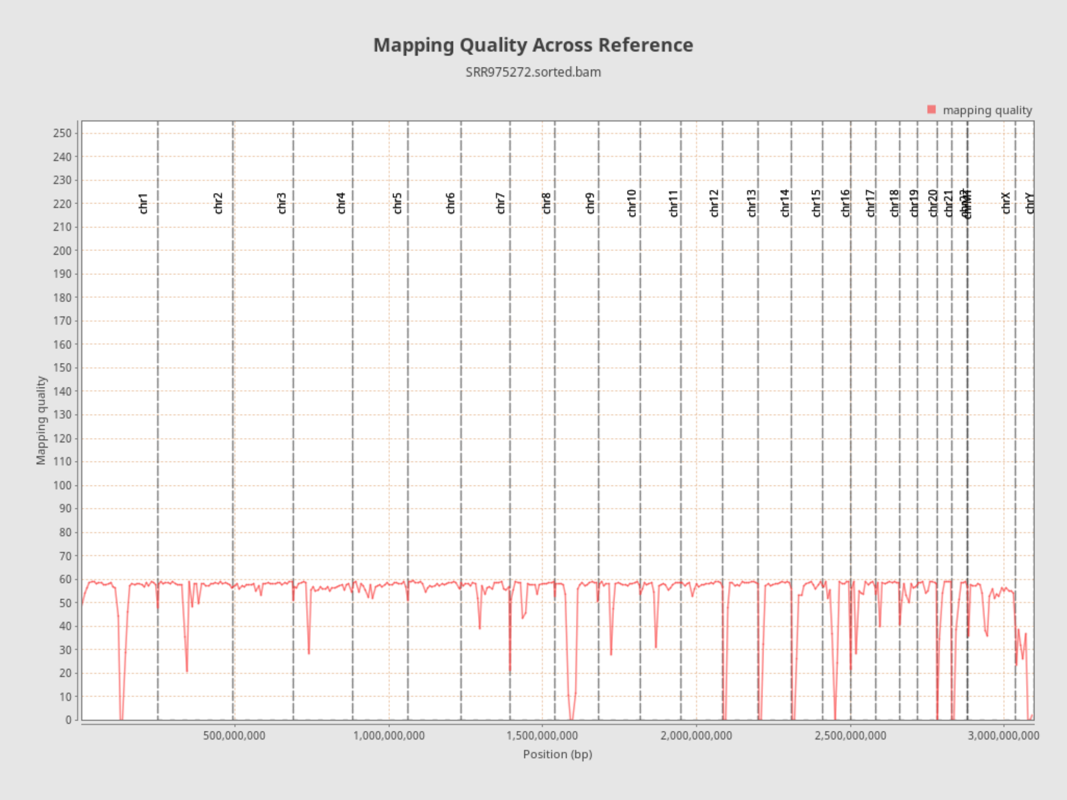
10. Results : Mapped Reads Clipping Profile



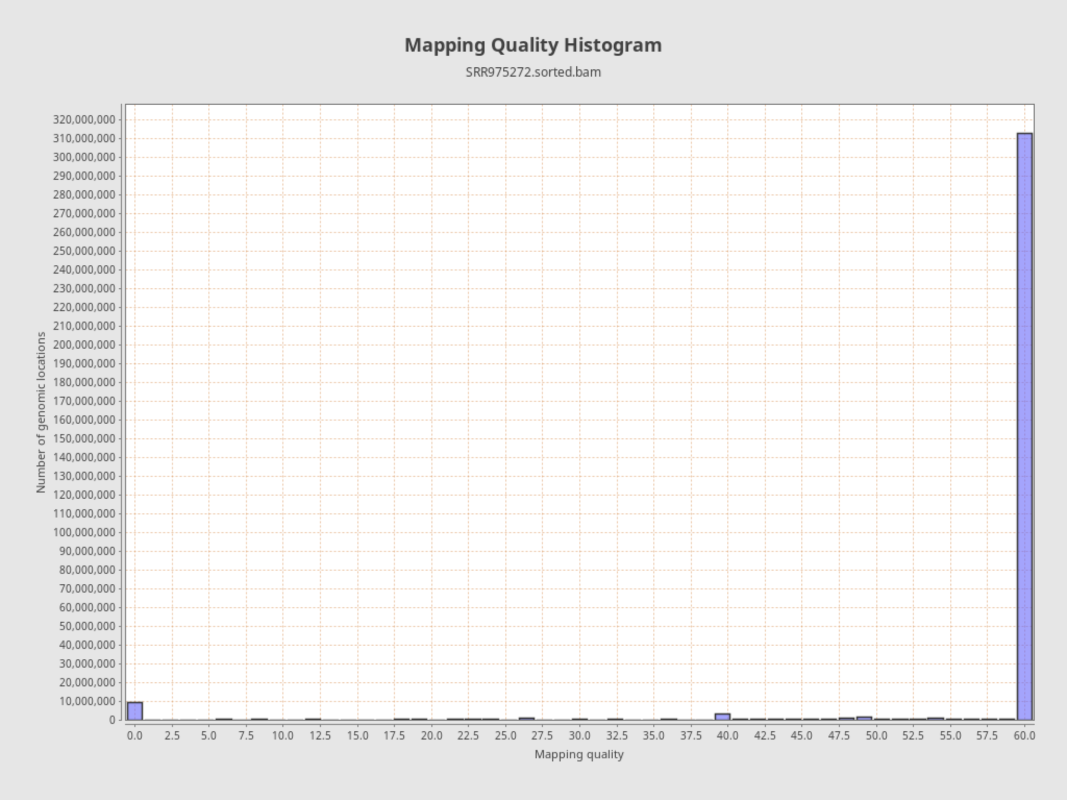
11. Results : Homopolymer Indels



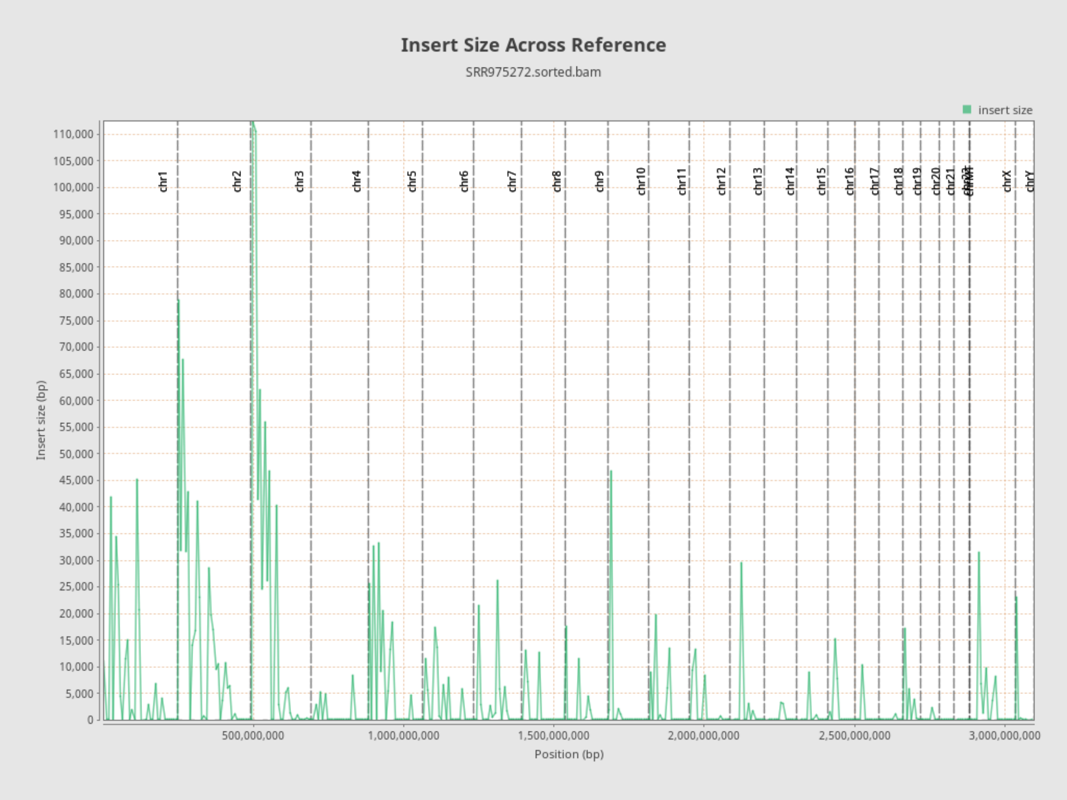
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram