Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 18:20:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975271.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_SRR975271 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975271_1.fastq.gz SRR975271_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 18:20:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975271.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,819,372
Mapped reads	48,572,589 / 99.49%
Unmapped reads	246,783 / 0.51%
Mapped paired reads	48,572,589 / 99.49%
Mapped reads, first in pair	24,354,460 / 49.89%
Mapped reads, second in pair	24,218,129 / 49.61%
Mapped reads, both in pair	48,380,282 / 99.1%
Mapped reads, singletons	192,307 / 0.39%
Secondary alignments	0
Supplementary alignments	82,914 / 0.17%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	32,473,311 / 66.52%
Duplication rate	60.05%
Clipped reads	28,131,134 / 57.62%

2.2. ACGT Content

Number/percentage of A's	1,234,405,226 / 27.14%
Number/percentage of C's	1,003,373,800 / 22.06%
Number/percentage of T's	1,245,668,267 / 27.39%
Number/percentage of G's	1,064,254,148 / 23.4%
Number/percentage of N's	988,697 / 0.02%

GC Percentage	45.46%

2.3. Coverage

Mean	1.4699
Standard Deviation	23.5445

2.4. Mapping Quality

Mean Mapping Quality	56.22

2.5. Insert size

Mean	85,006.82
Standard Deviation	2,909,308.72
P25/Median/P75	188 / 230 / 279

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	38,488,395
Insertions	474,487
Mapped reads with at least one insertion	0.97%
Deletions	1,163,006
Mapped reads with at least one deletion	2.36%
Homopolymer indels	47.52%

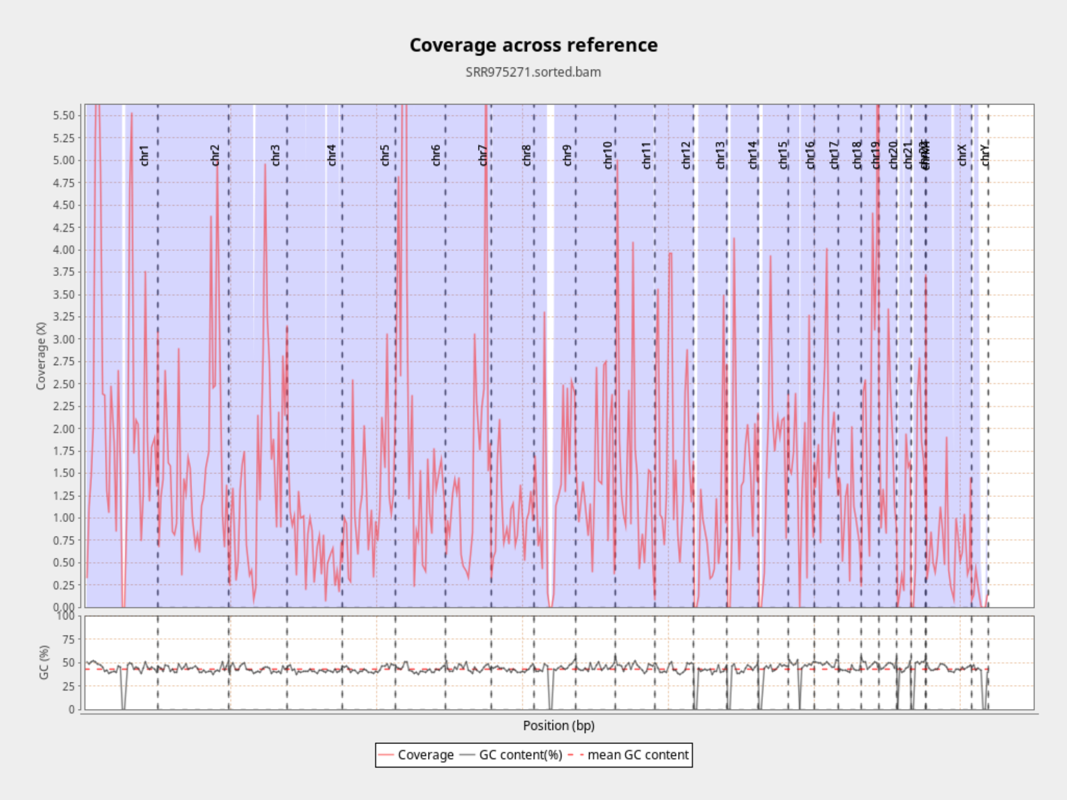
2.7. Chromosome stats

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

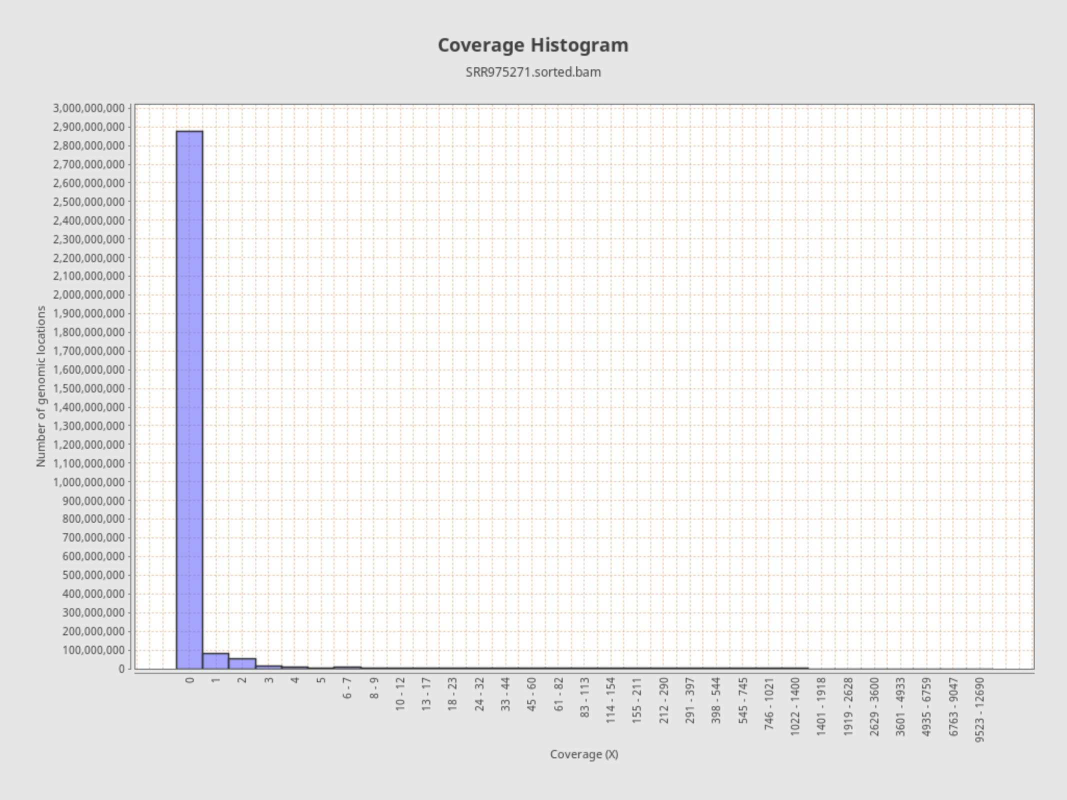
		bases	coverage	deviation
chr1	249250621	545430673	2.1883	29.9446
chr2	243199373	392248731	1.6129	23.7195
chr3	198022430	309194882	1.5614	23.1632
chr4	191154276	133302029	0.6974	13.6045
chr5	180915260	219447997	1.213	19.5399
chr6	171115067	412113479	2.4084	39.1403
chr7	159138663	251050823	1.5776	26.7569
chr8	146364022	150064239	1.0253	16.0075
chr9	141213431	183959304	1.3027	19.8892
chr10	135534747	201348024	1.4856	22.4508
chr11	135006516	211787586	1.5687	23.0444
chr12	133851895	245994523	1.8378	23.7606
chr13	115169878	98491551	0.8552	19.7236
chr14	107349540	148635689	1.3846	20.8175
chr15	102531392	167862527	1.6372	23.647
chr16	90354753	131880895	1.4596	21.44
chr17	81195210	157998174	1.9459	26.552
chr18	78077248	82840403	1.061	18.1525
chr19	59128983	174058379	2.9437	35.3237
chr20	63025520	108112915	1.7154	25.6202
chr21	48129895	40649194	0.8446	20.4474
chr22	51304566	72263351	1.4085	21.4477
chrMT	16571	61848	3.7323	12.0723
chrX	155270560	103623460	0.6674	12.8113

chrY	59373566	7905640	0.1332	5.2211

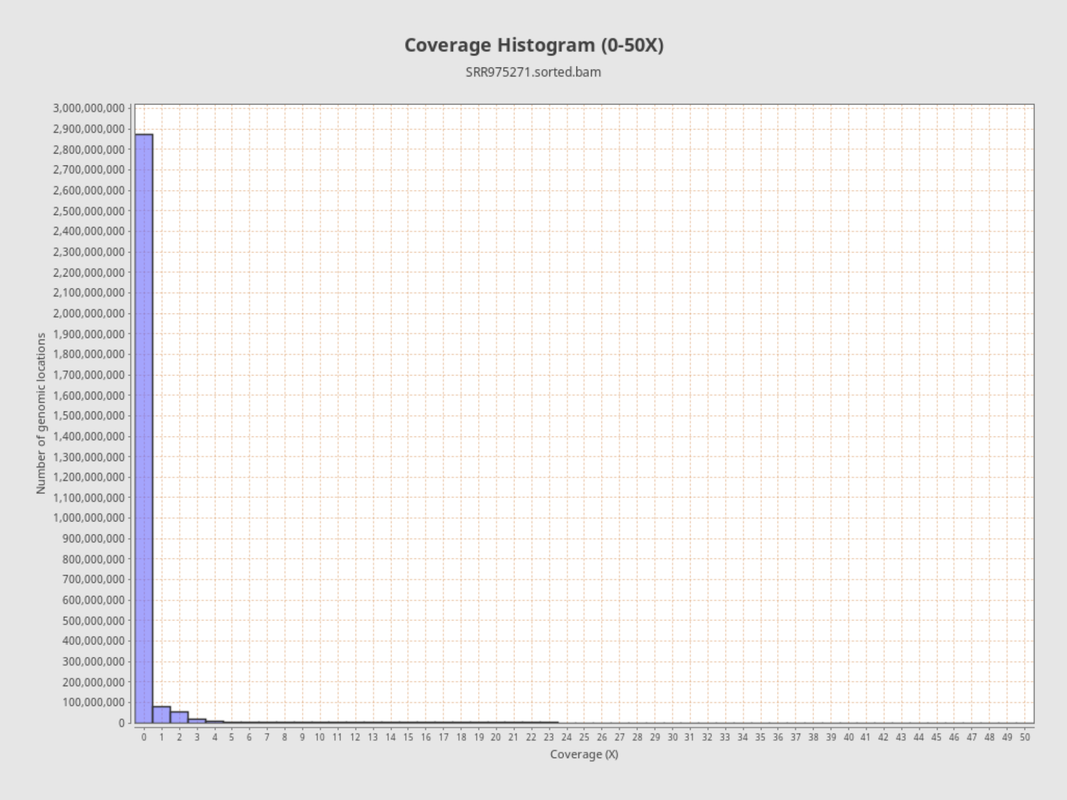
3. Results : Coverage across reference



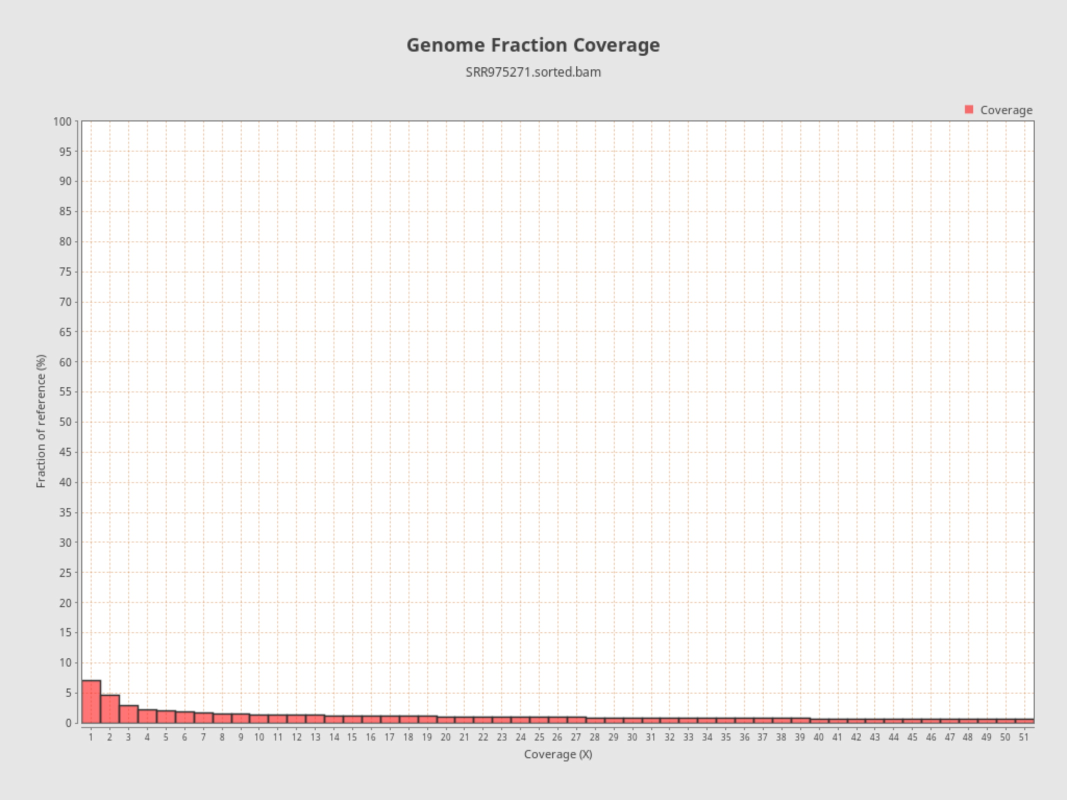
4. Results : Coverage Histogram



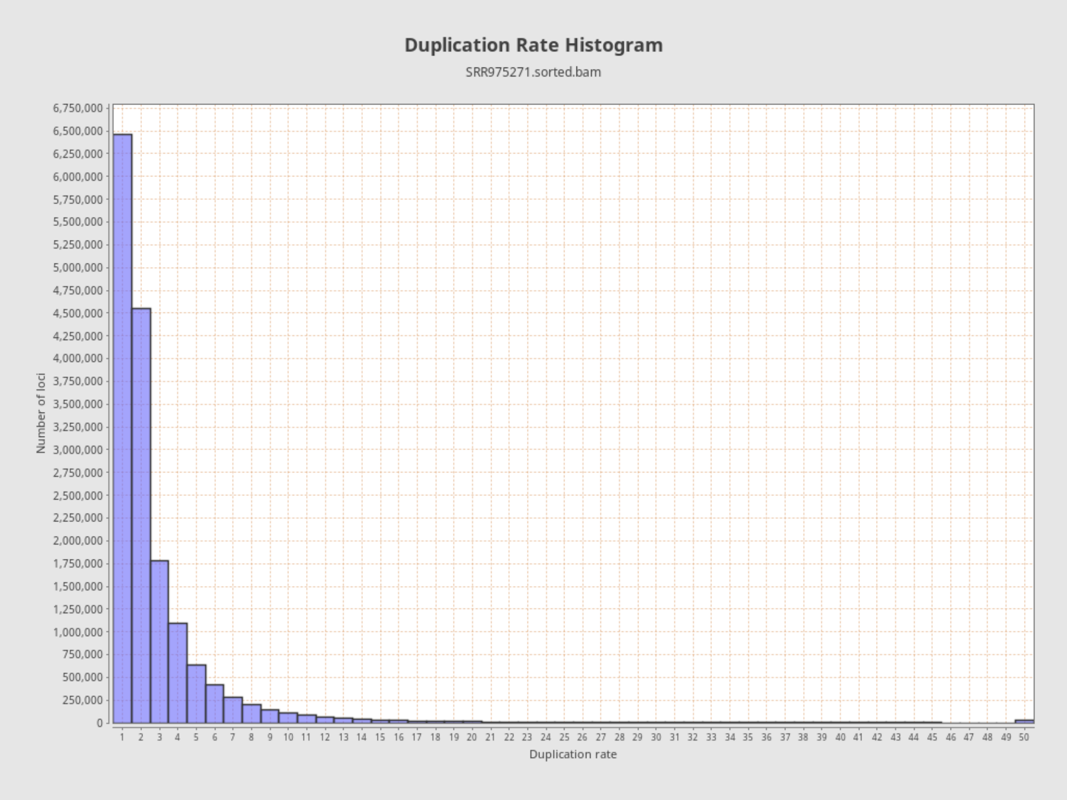
5. Results : Coverage Histogram (0-50X)



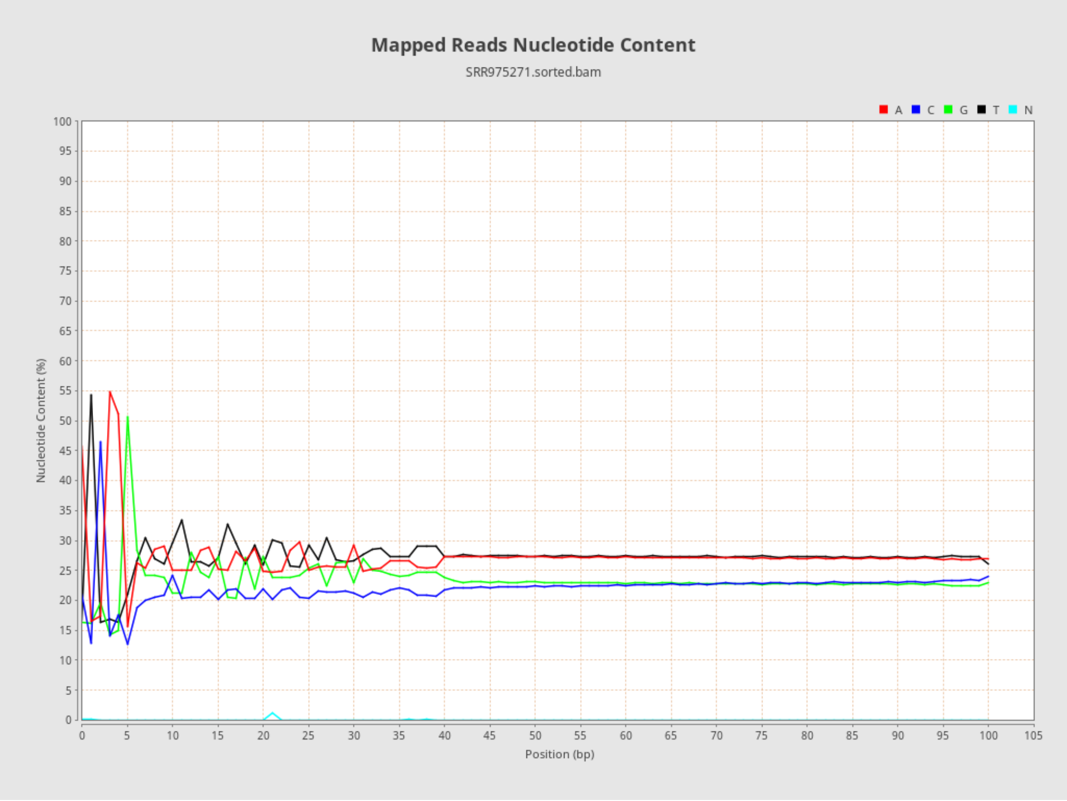
6. Results : Genome Fraction Coverage



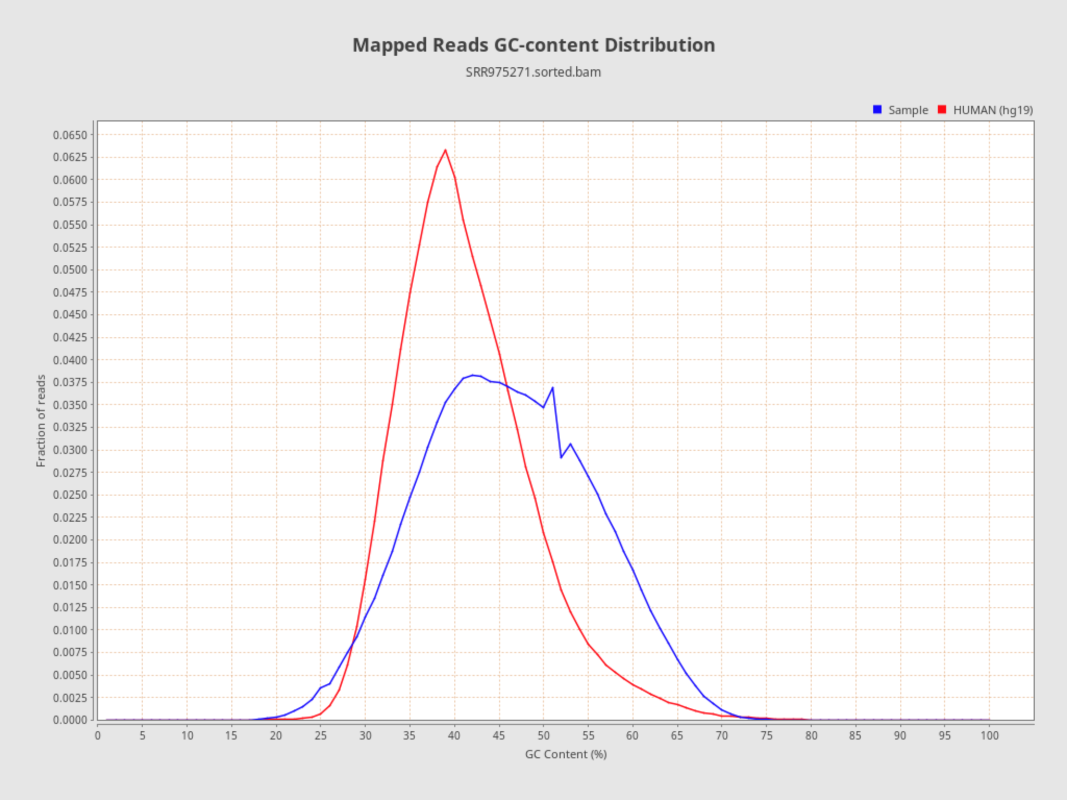
7. Results : Duplication Rate Histogram



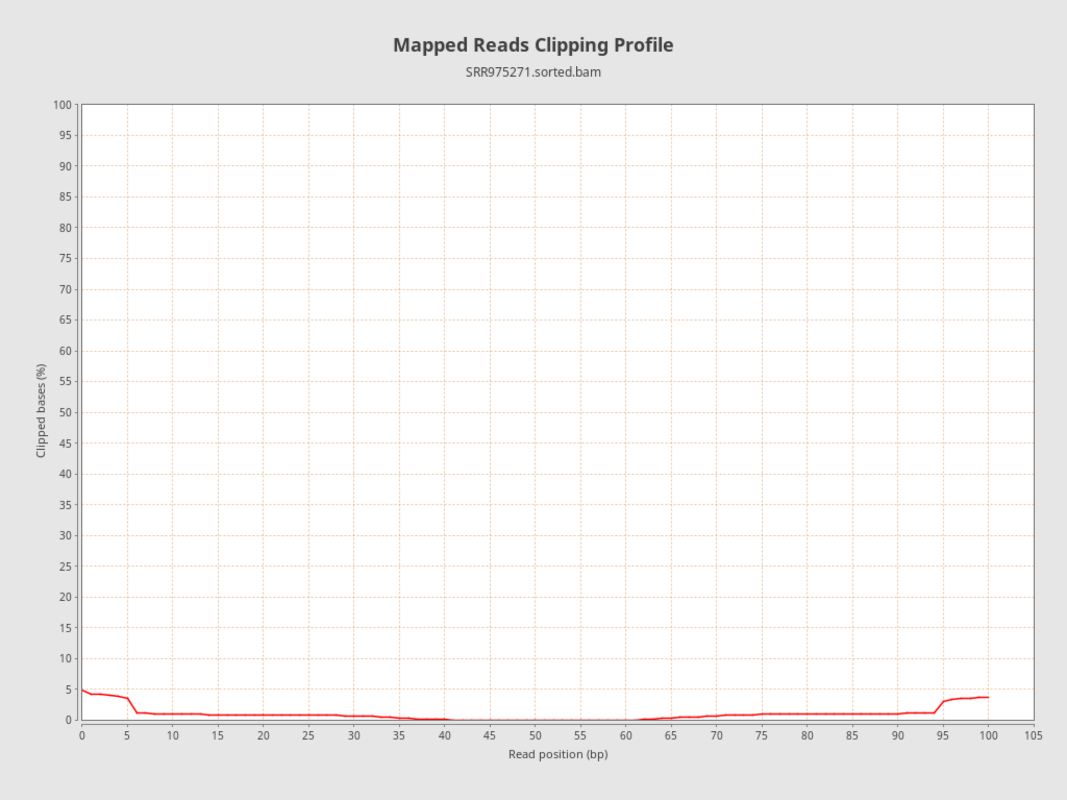
8. Results : Mapped Reads Nucleotide Content



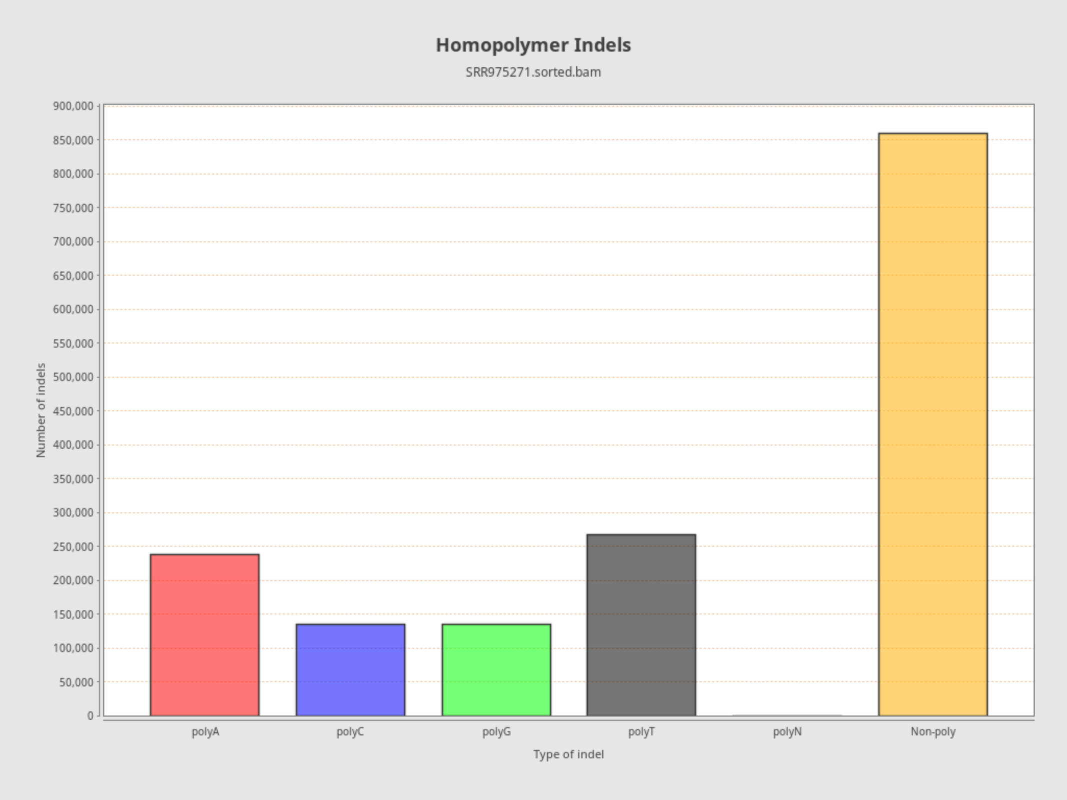
9. Results : Mapped Reads GC-content Distribution



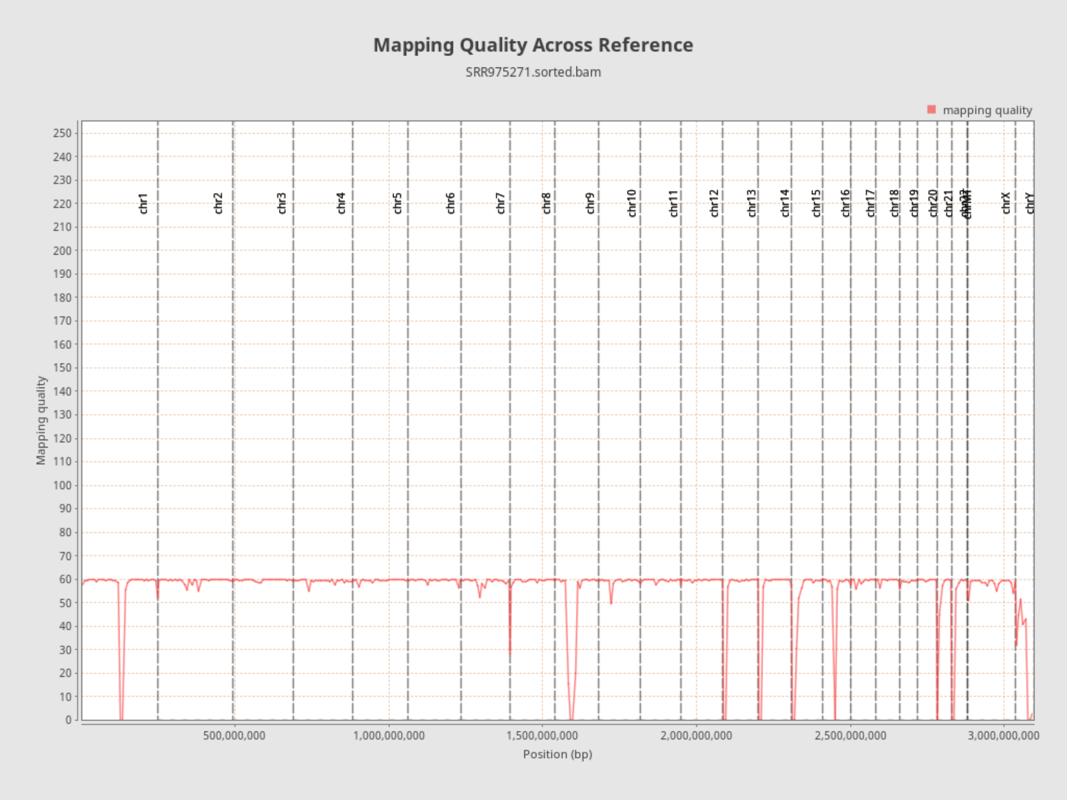
10. Results : Mapped Reads Clipping Profile



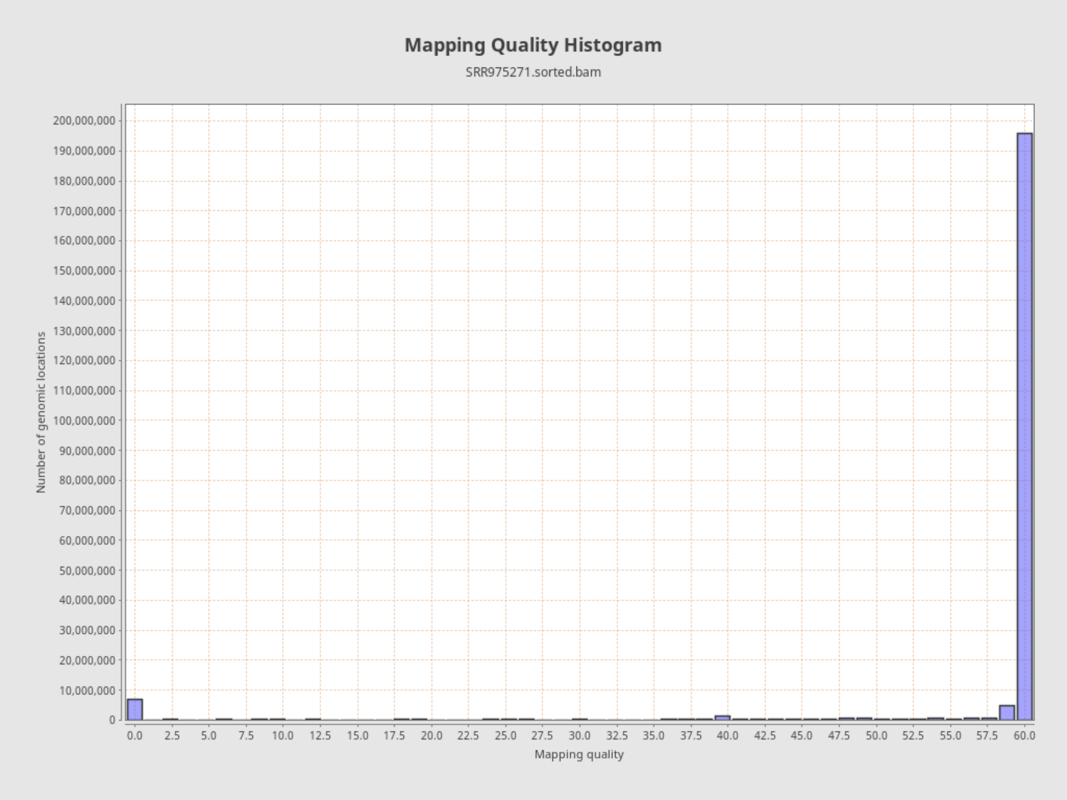
11. Results : Homopolymer Indels



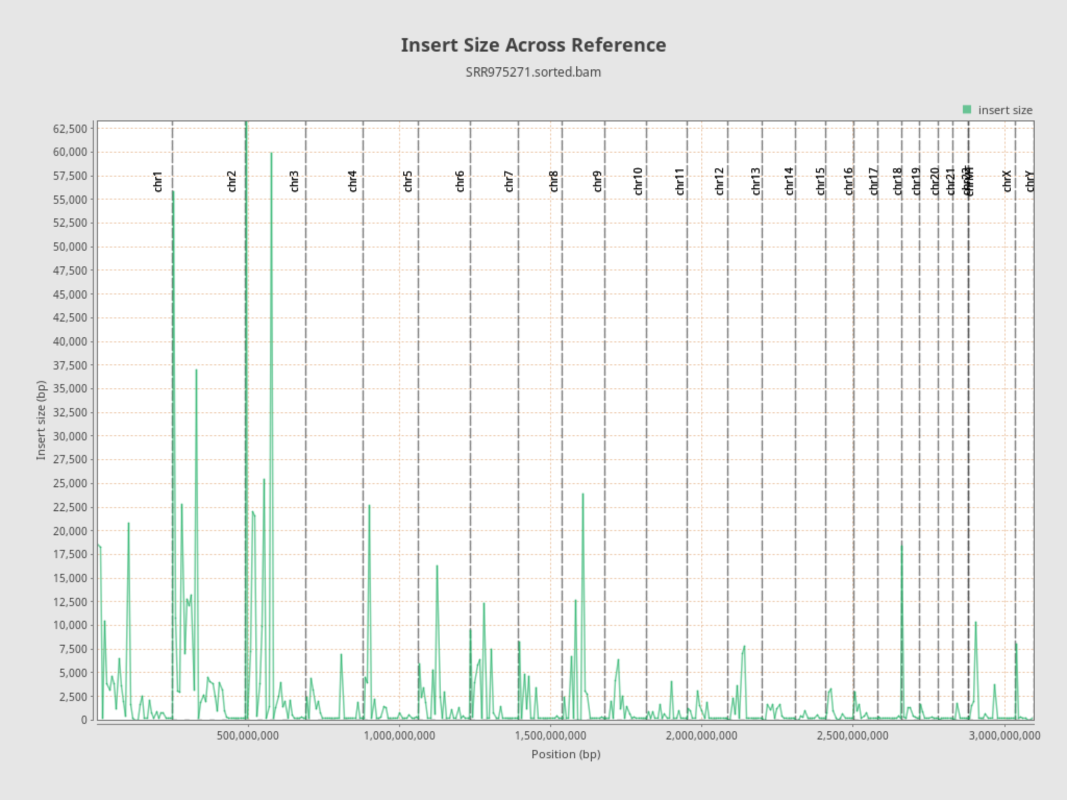
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram