Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 05:35:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975330.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_SRR975330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975330_1.fastq.gz SRR975330_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 05:35:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975330.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,585,008
Mapped reads	2,386,901 / 66.58%
Unmapped reads	1,198,107 / 33.42%
Mapped paired reads	2,386,901 / 66.58%
Mapped reads, first in pair	1,193,048 / 33.28%
Mapped reads, second in pair	1,193,853 / 33.3%
Mapped reads, both in pair	2,363,068 / 65.92%
Mapped reads, singletons	23,833 / 0.66%
Secondary alignments	0
Supplementary alignments	13,520 / 0.38%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	125,154 / 3.49%
Duplication rate	2.88%
Clipped reads	1,473,723 / 41.11%

2.2. ACGT Content

Number/percentage of A's	63,967,512 / 29.39%
Number/percentage of C's	42,611,919 / 19.58%
Number/percentage of T's	65,444,857 / 30.07%
Number/percentage of G's	45,627,415 / 20.96%
Number/percentage of N's	4,962 / 0%

GC Percentage	40.54%

2.3. Coverage

Mean	0.0703
Standard Deviation	0.9155

2.4. Mapping Quality

Mean Mapping Quality	52.52

2.5. Insert size

Mean	60,800.62
Standard Deviation	2,346,963.17
P25/Median/P75	135 / 167 / 212

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	1,674,756
Insertions	37,069
Mapped reads with at least one insertion	1.51%
Deletions	67,042
Mapped reads with at least one deletion	2.75%
Homopolymer indels	44.71%

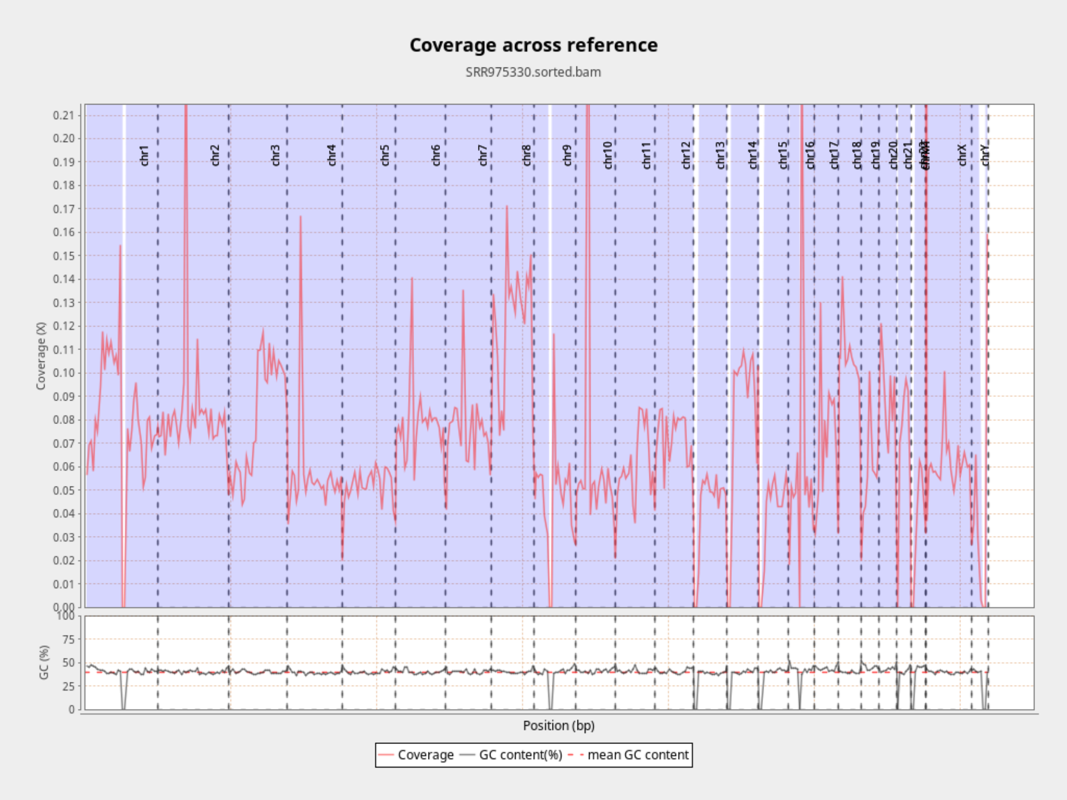
2.7. Chromosome stats

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

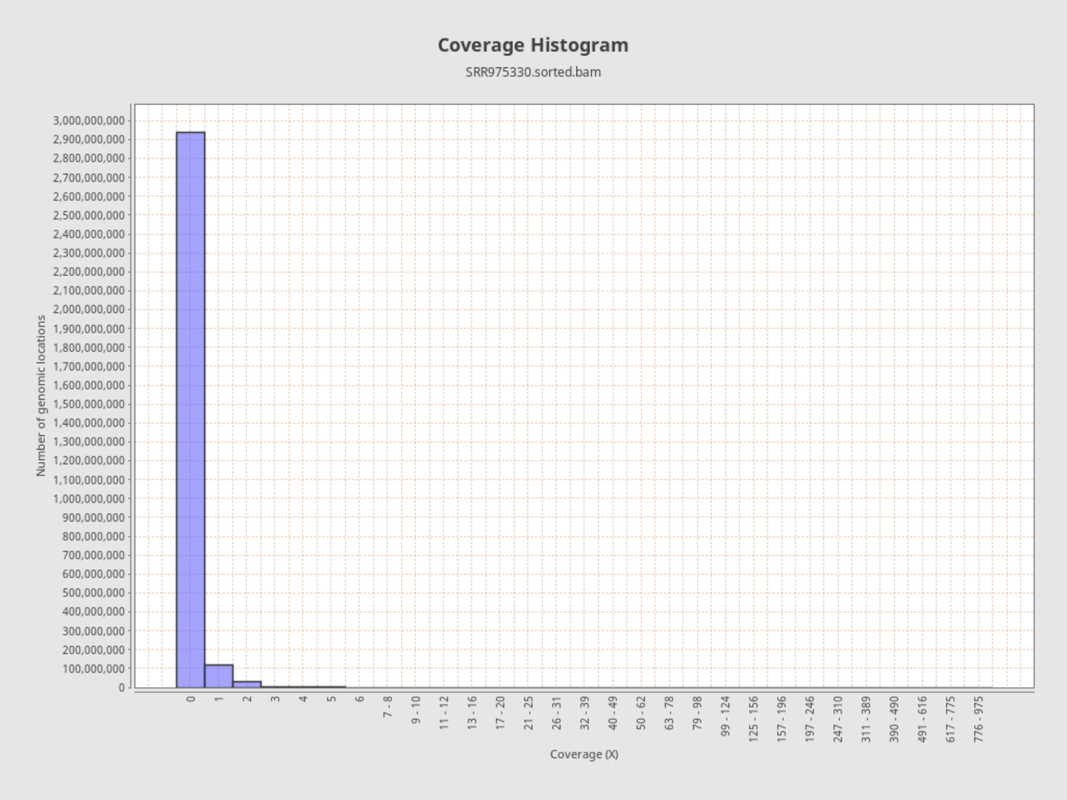
		bases	coverage	deviation
chr1	249250621	19956187	0.0801	0.9871
chr2	243199373	20668105	0.085	1.2172
chr3	198022430	16178019	0.0817	0.4318
chr4	191154276	10829242	0.0567	0.6972
chr5	180915260	9547482	0.0528	0.2824
chr6	171115067	13419714	0.0784	0.7288
chr7	159138663	12099866	0.076	1.1434
chr8	146364022	17899426	0.1223	0.6351
chr9	141213431	6644461	0.0471	1.2714
chr10	135534747	8927409	0.0659	2.1397
chr11	135006516	8219011	0.0609	0.4708
chr12	133851895	9708924	0.0725	0.336
chr13	115169878	4846676	0.0421	0.2465
chr14	107349540	8712535	0.0812	0.3756
chr15	102531392	4045625	0.0395	0.2423
chr16	90354753	5480454	0.0607	1.275
chr17	81195210	5834650	0.0719	1.264
chr18	78077248	8319218	0.1066	1.5223
chr19	59128983	3370848	0.057	0.5117
chr20	63025520	5564350	0.0883	0.4014
chr21	48129895	3558777	0.0739	0.4014
chr22	51304566	1883536	0.0367	0.2437
chrMT	16571	89998	5.4311	6.9504
chrX	155270560	9573758	0.0617	0.419

chrY	59373566	2399304	0.0404	0.8541

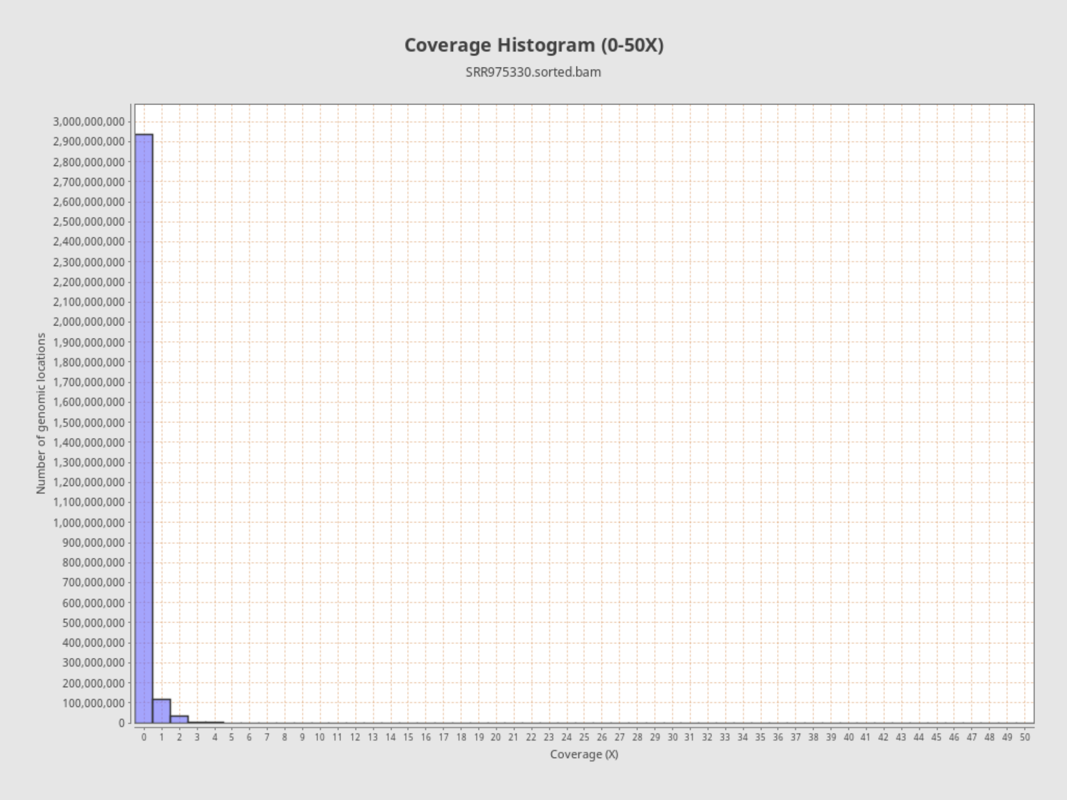
3. Results : Coverage across reference



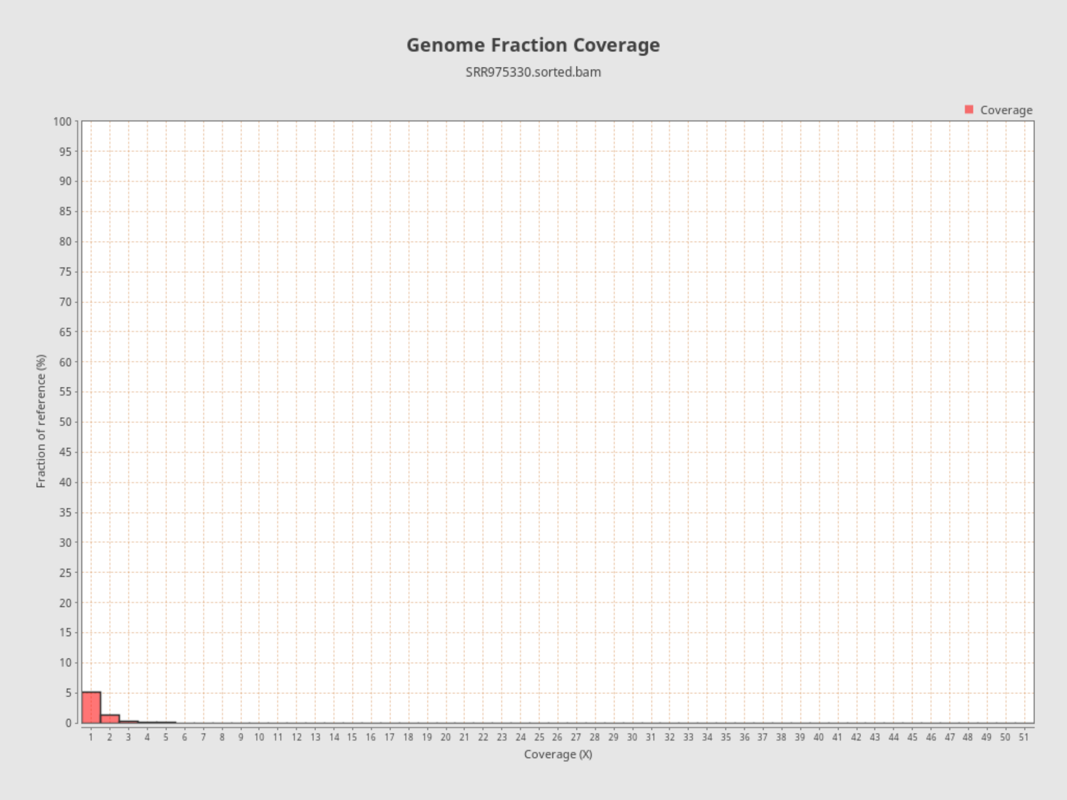
4. Results : Coverage Histogram



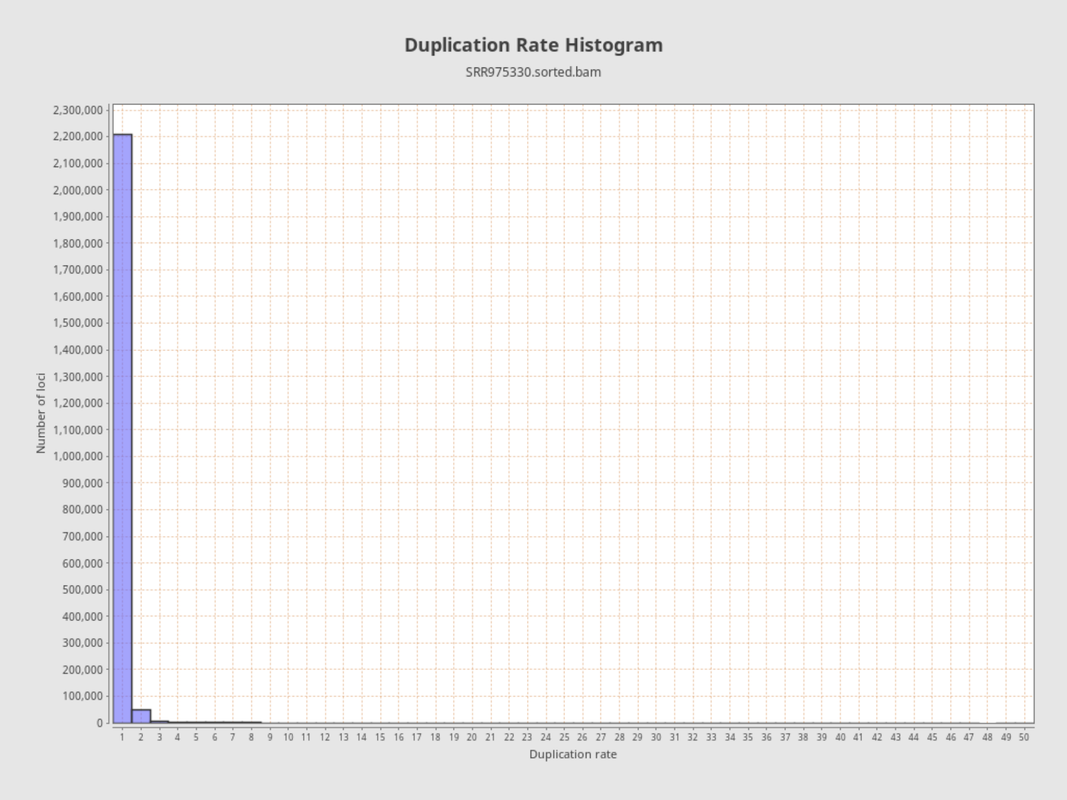
5. Results : Coverage Histogram (0-50X)



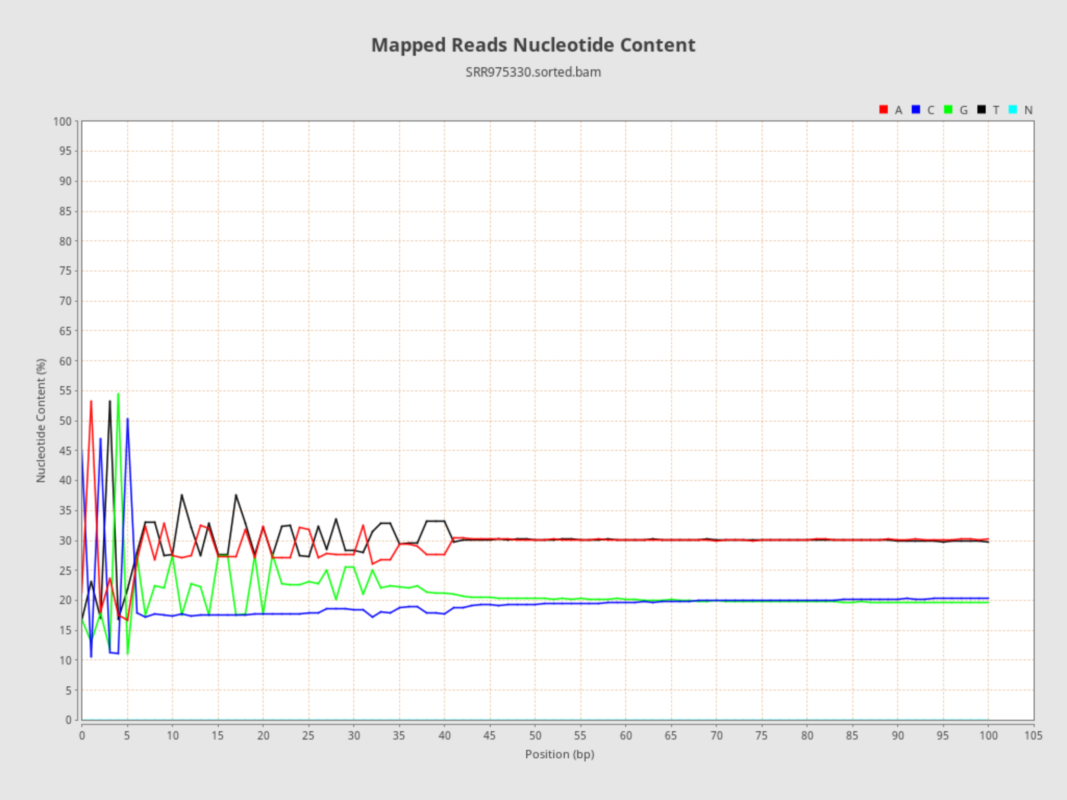
6. Results : Genome Fraction Coverage



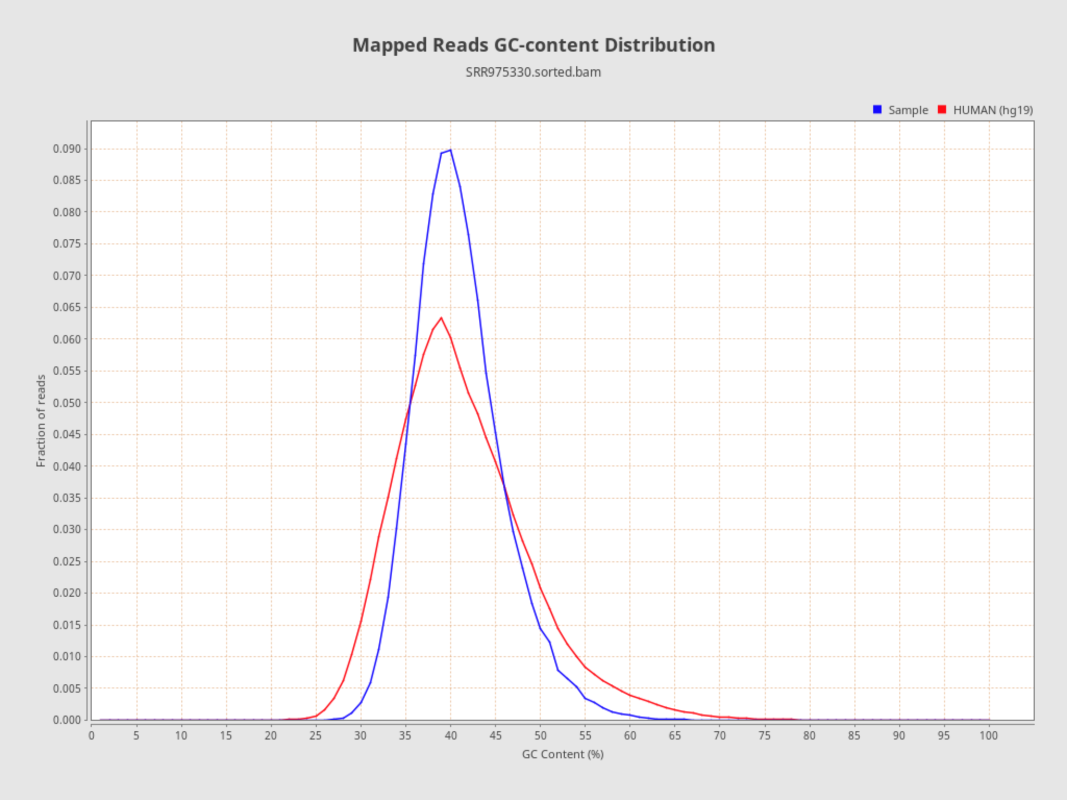
7. Results : Duplication Rate Histogram



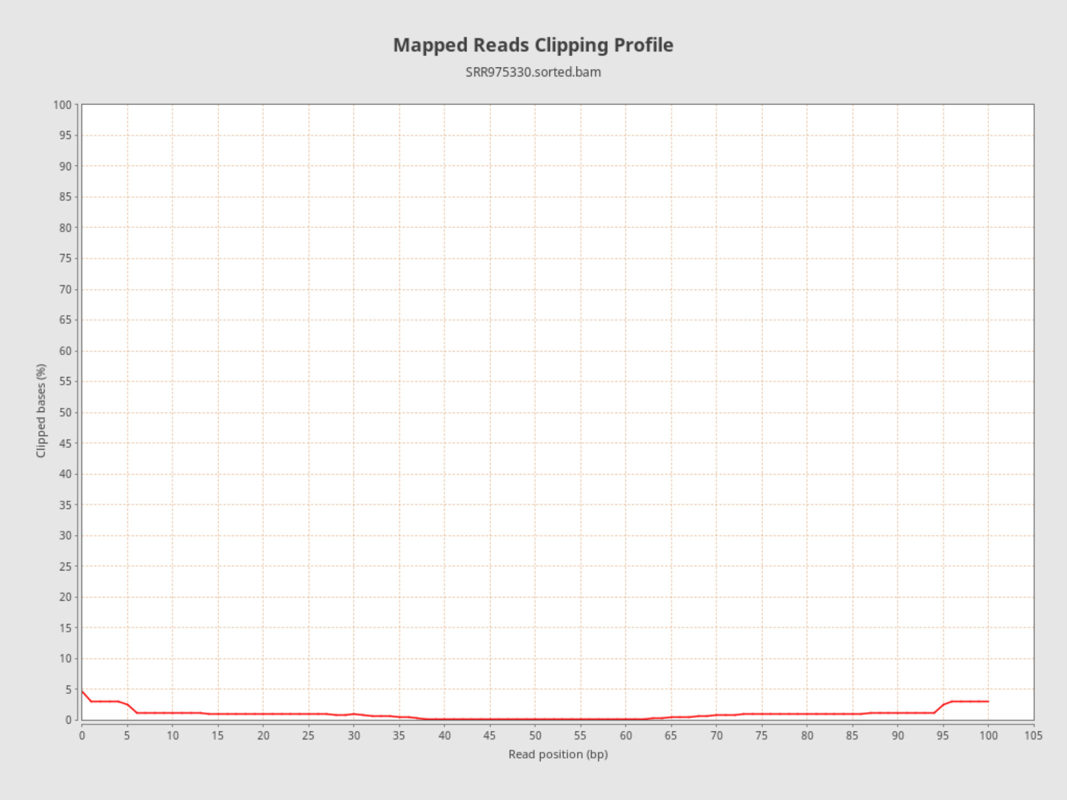
8. Results : Mapped Reads Nucleotide Content



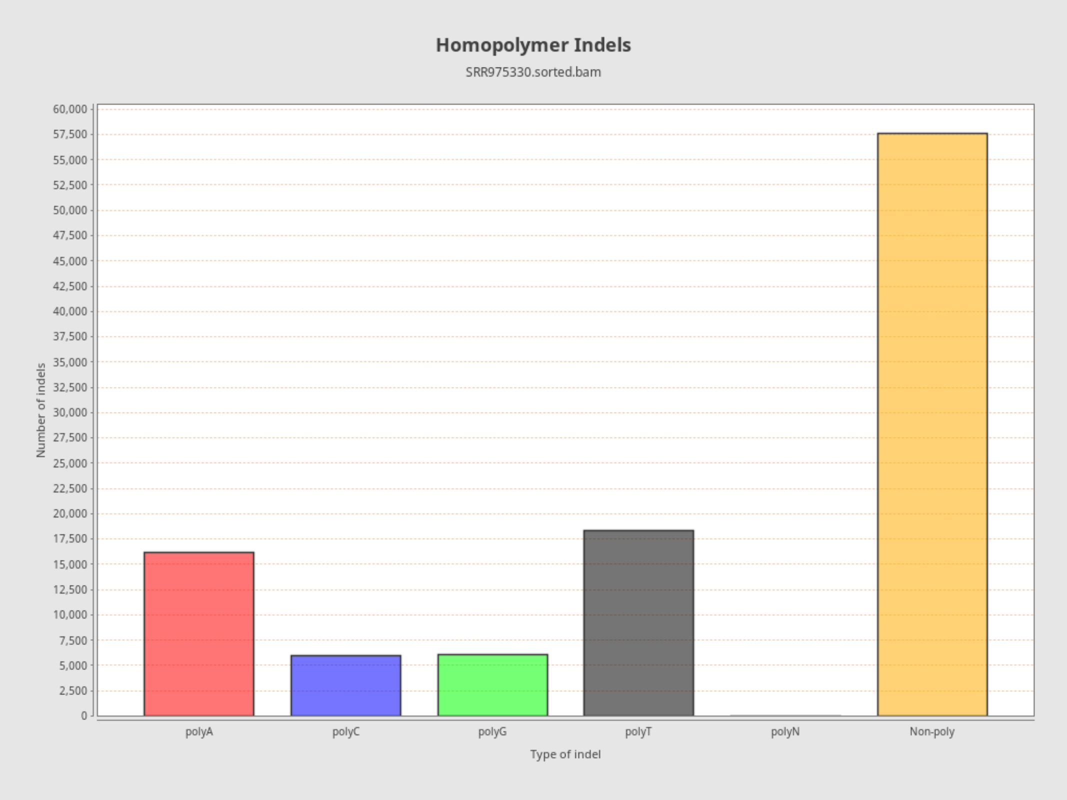
9. Results : Mapped Reads GC-content Distribution



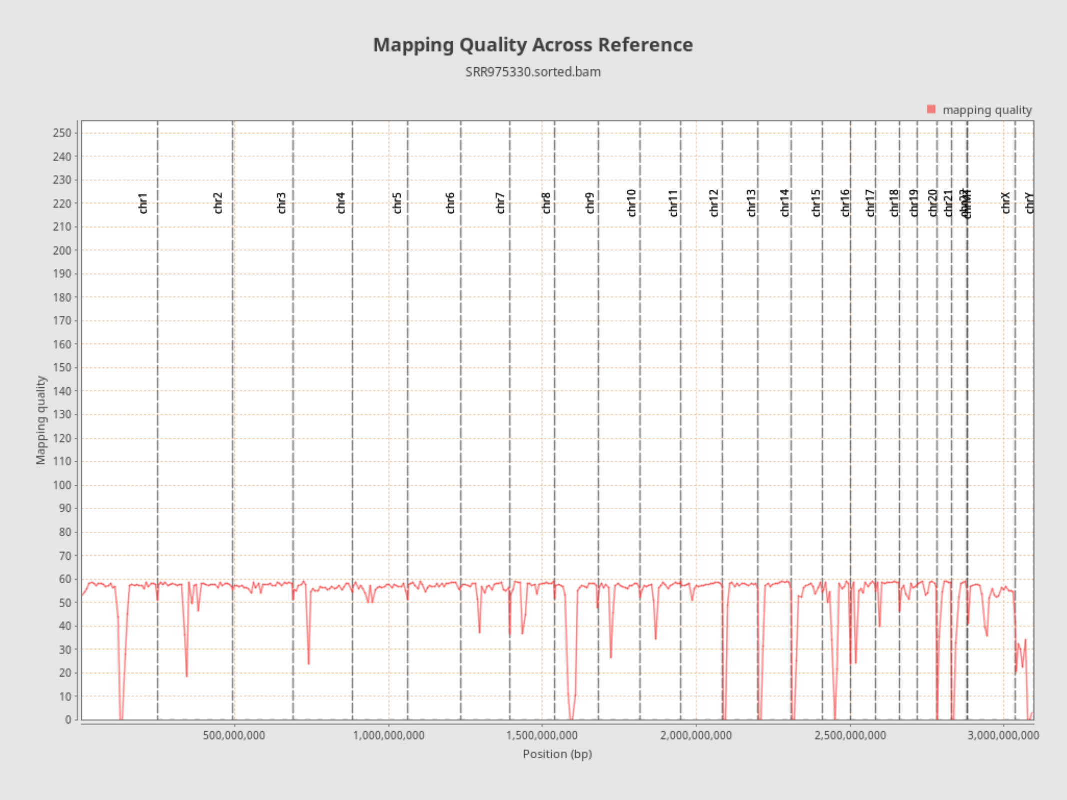
10. Results : Mapped Reads Clipping Profile



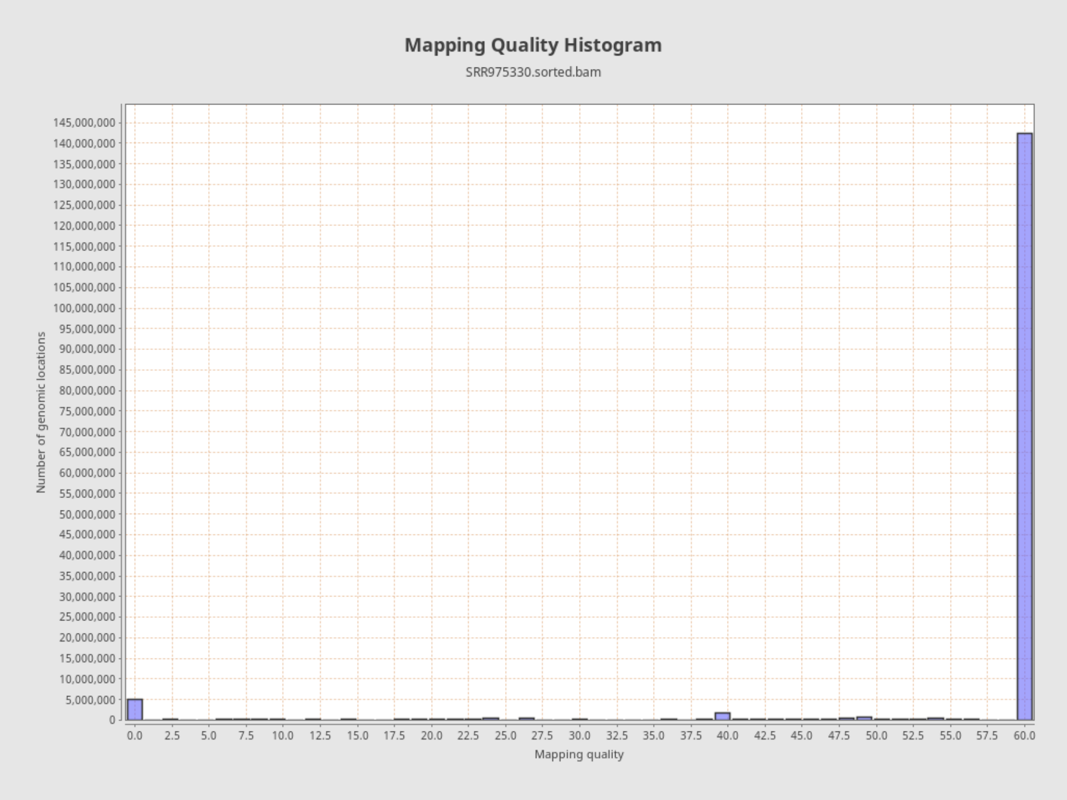
11. Results : Homopolymer Indels



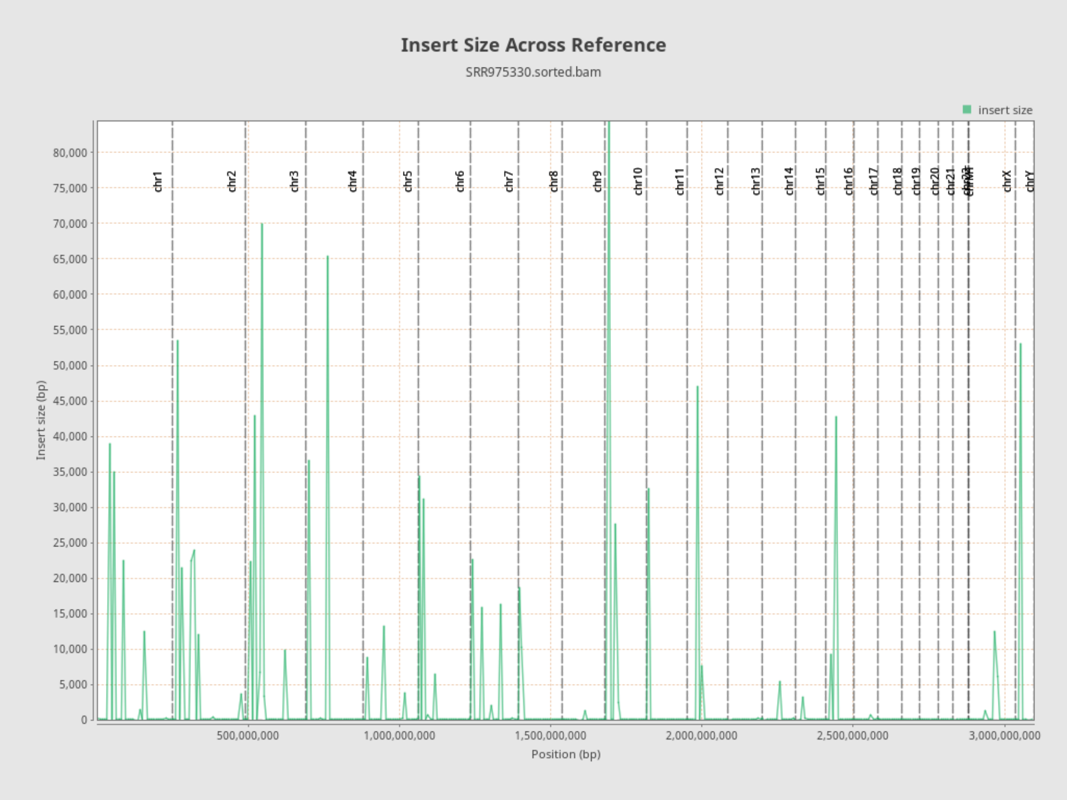
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram