Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 15:46:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975253.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_SRR975253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975253_1.fastq.gz SRR975253_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 15:46:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,657,586
Mapped reads	5,597,008 / 98.93%
Unmapped reads	60,578 / 1.07%
Mapped paired reads	5,597,008 / 98.93%
Mapped reads, first in pair	2,797,597 / 49.45%
Mapped reads, second in pair	2,799,411 / 49.48%
Mapped reads, both in pair	5,582,590 / 98.67%
Mapped reads, singletons	14,418 / 0.25%
Secondary alignments	0
Supplementary alignments	16,757 / 0.3%
Read min/max/mean length	30 / 101 / 101.12
Duplicated reads (estimated)	275,097 / 4.86%
Duplication rate	2.64%
Clipped reads	3,323,477 / 58.74%

2.2. ACGT Content

Number/percentage of A's	154,200,039 / 29.86%
Number/percentage of C's	99,674,612 / 19.3%
Number/percentage of T's	153,824,597 / 29.79%
Number/percentage of G's	108,735,040 / 21.05%
Number/percentage of N's	7,568 / 0%

GC Percentage	40.35%

2.3. Coverage

Mean	0.1669
Standard Deviation	1.7741

2.4. Mapping Quality

Mean Mapping Quality	52.78

2.5. Insert size

Mean	53,709.63
Standard Deviation	2,225,721.37
P25/Median/P75	138 / 171 / 218

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	3,712,061
Insertions	83,903
Mapped reads with at least one insertion	1.48%
Deletions	153,987
Mapped reads with at least one deletion	2.7%
Homopolymer indels	46.52%

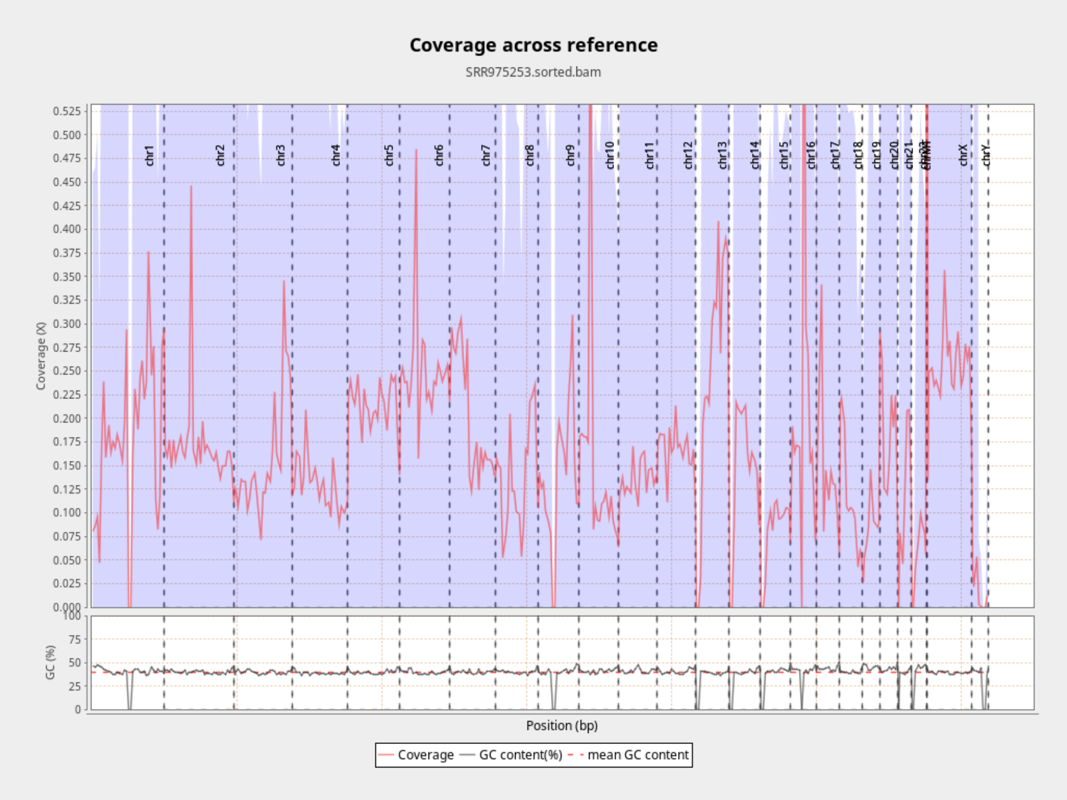
2.7. Chromosome stats

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

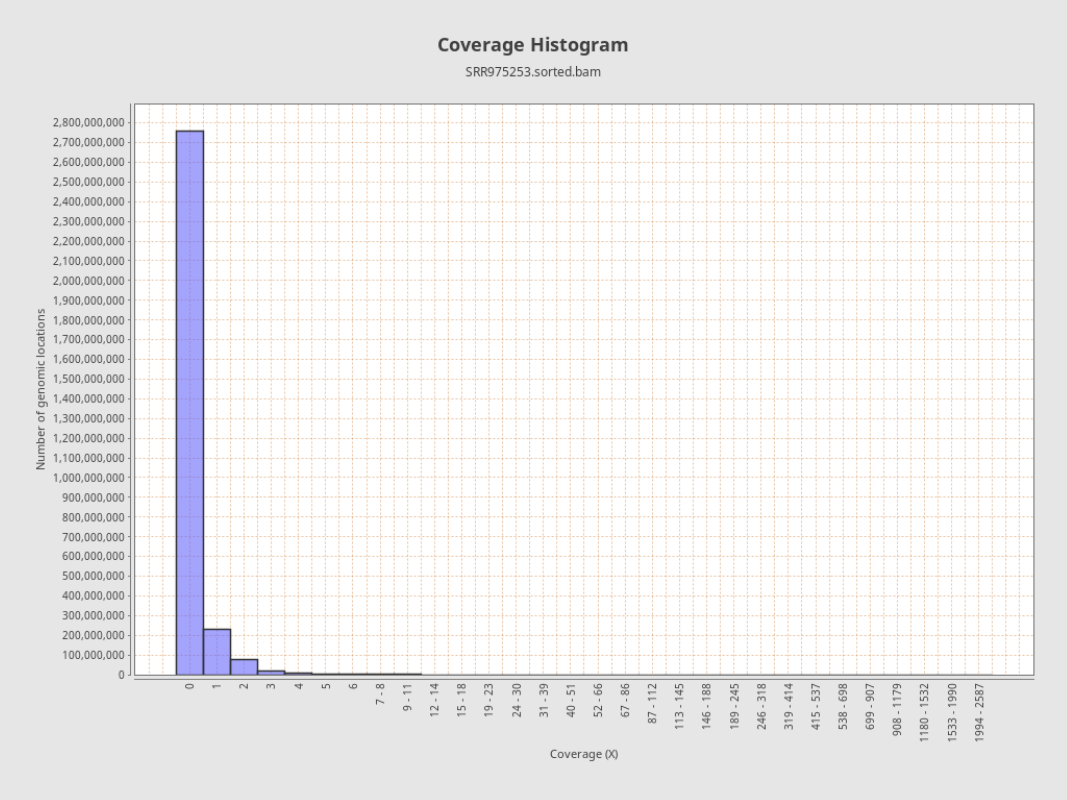
		bases	coverage	deviation
chr1	249250621	43867716	0.176	1.8506
chr2	243199373	41793678	0.1718	1.6556
chr3	198022430	31000302	0.1565	0.5945
chr4	191154276	24827583	0.1299	0.754
chr5	180915260	39051920	0.2159	0.6122
chr6	171115067	42842082	0.2504	2.6163
chr7	159138663	31979659	0.201	2.3247
chr8	146364022	20170480	0.1378	0.6065
chr9	141213431	20079421	0.1422	1.3904
chr10	135534747	21008700	0.155	4.9613
chr11	135006516	18254979	0.1352	1.2392
chr12	133851895	22618589	0.169	0.534
chr13	115169878	28587028	0.2482	0.6875
chr14	107349540	15588545	0.1452	0.5203
chr15	102531392	8118754	0.0792	0.3589
chr16	90354753	19036627	0.2107	3.3425
chr17	81195210	12559976	0.1547	2.1924
chr18	78077248	9035763	0.1157	1.8273
chr19	59128983	5007311	0.0847	1.0029
chr20	63025520	12028721	0.1909	0.5916
chr21	48129895	5819971	0.1209	0.508
chr22	51304566	3033660	0.0591	0.3157
chrMT	16571	24688	1.4898	1.6445
chrX	155270560	39421389	0.2539	0.9851

chrY	59373566	934635	0.0157	0.6139

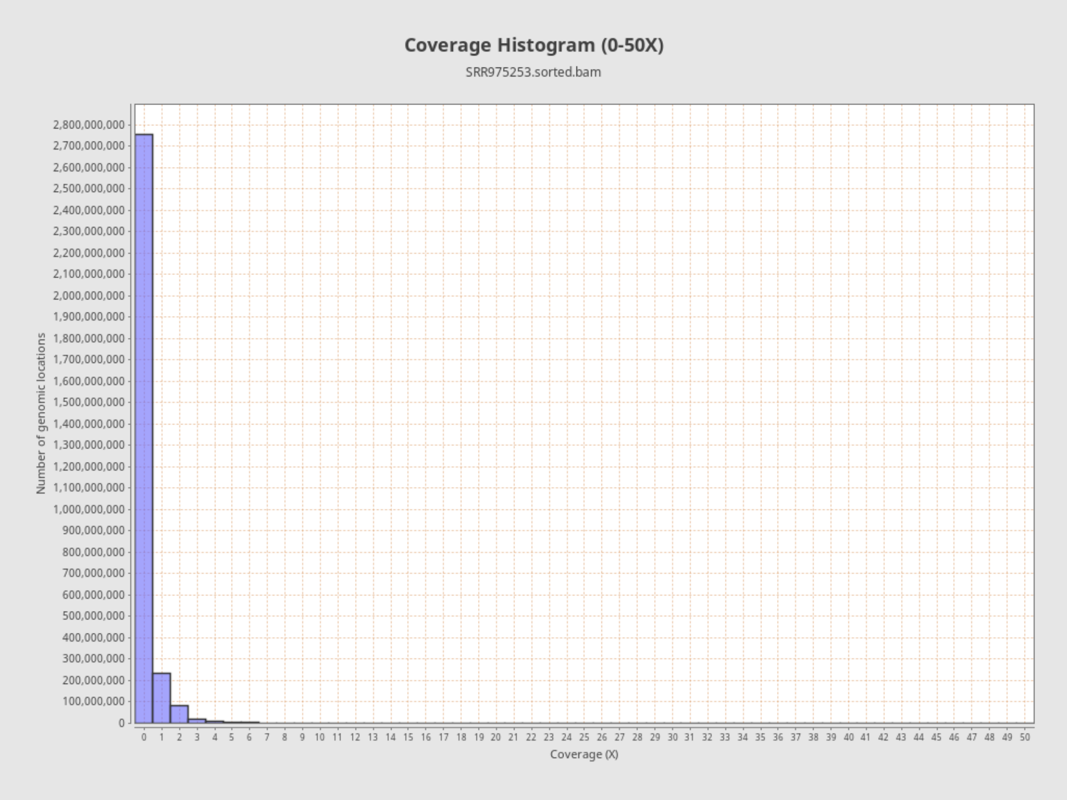
3. Results : Coverage across reference



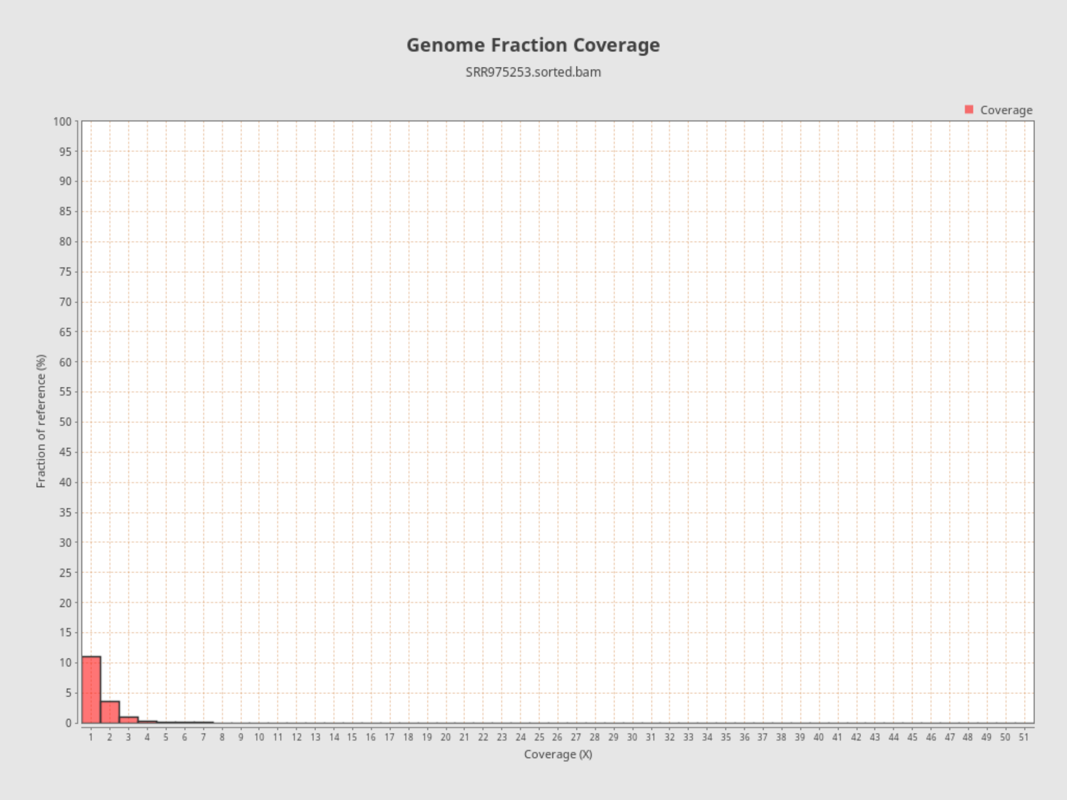
4. Results : Coverage Histogram



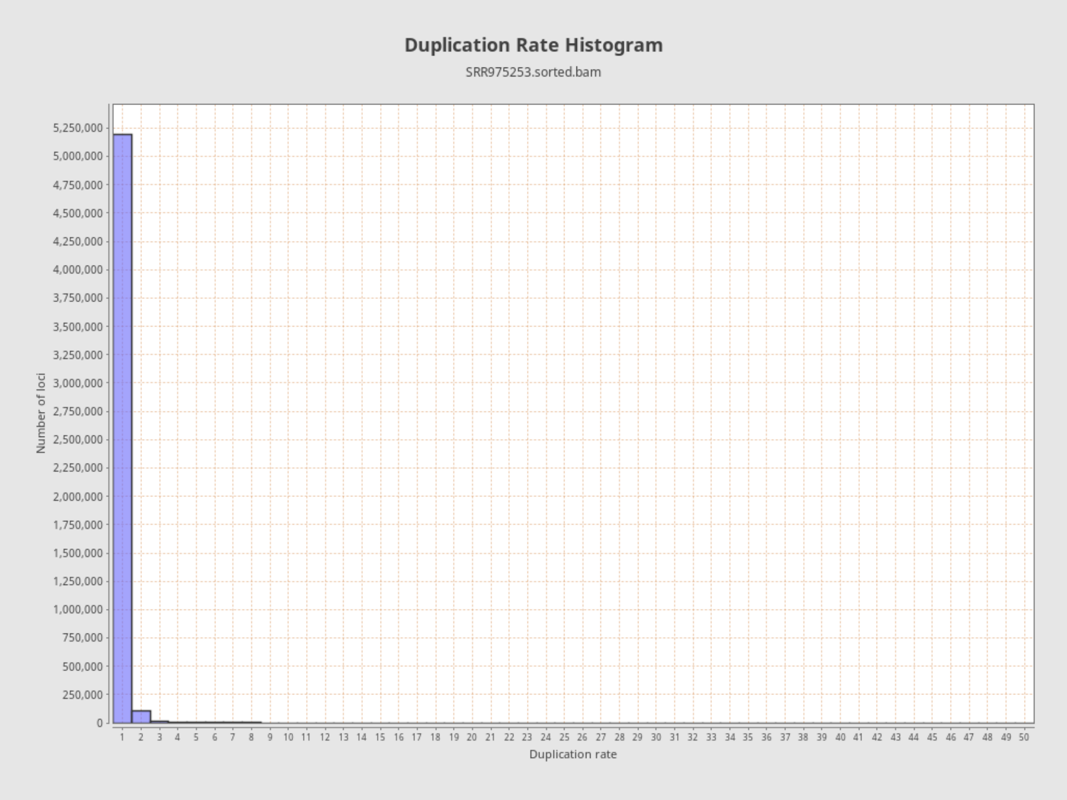
5. Results : Coverage Histogram (0-50X)



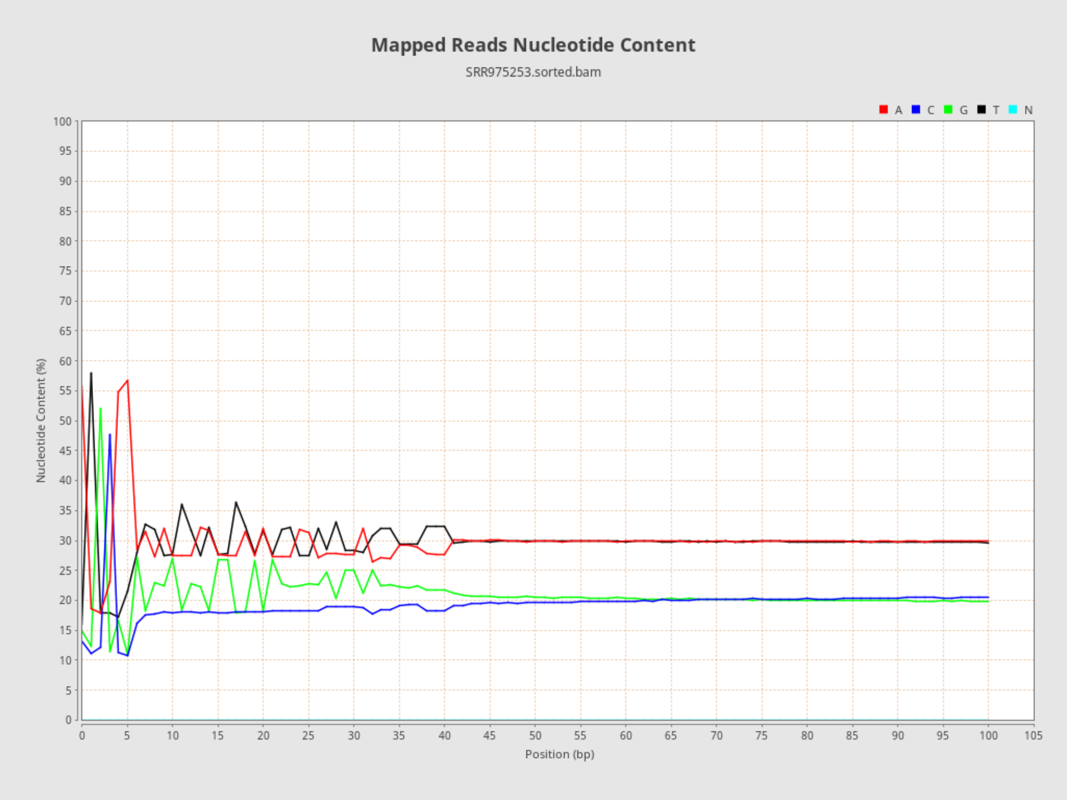
6. Results : Genome Fraction Coverage



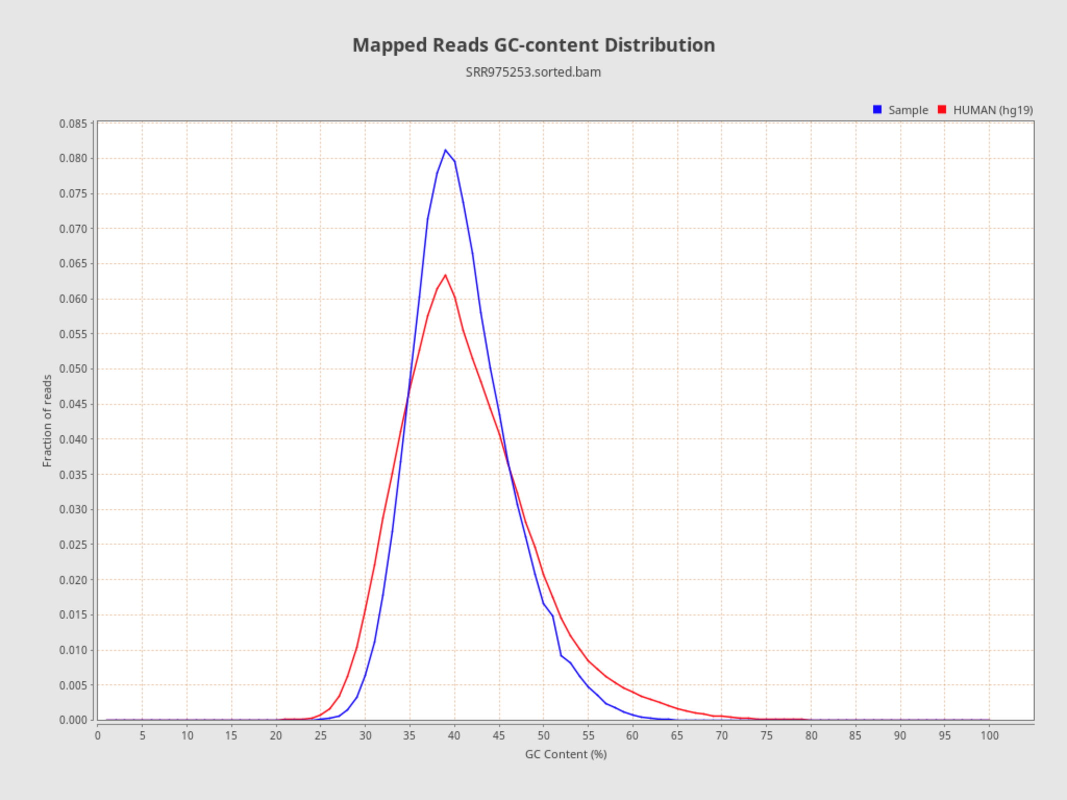
7. Results : Duplication Rate Histogram



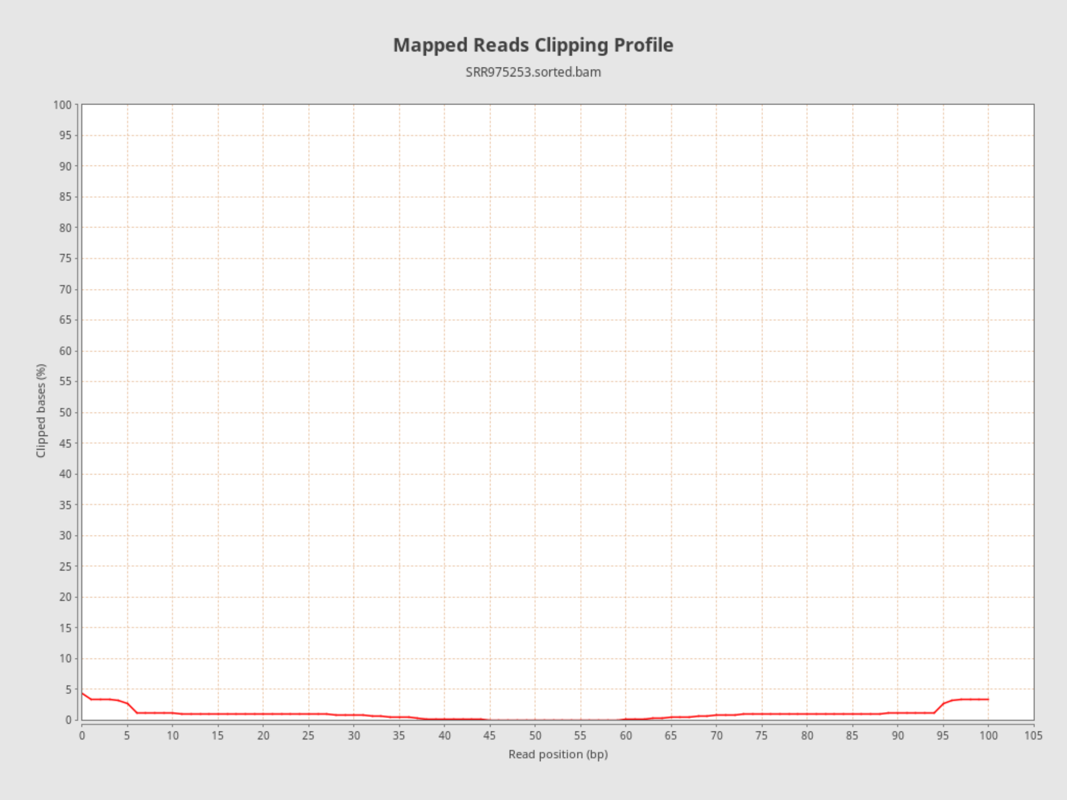
8. Results : Mapped Reads Nucleotide Content



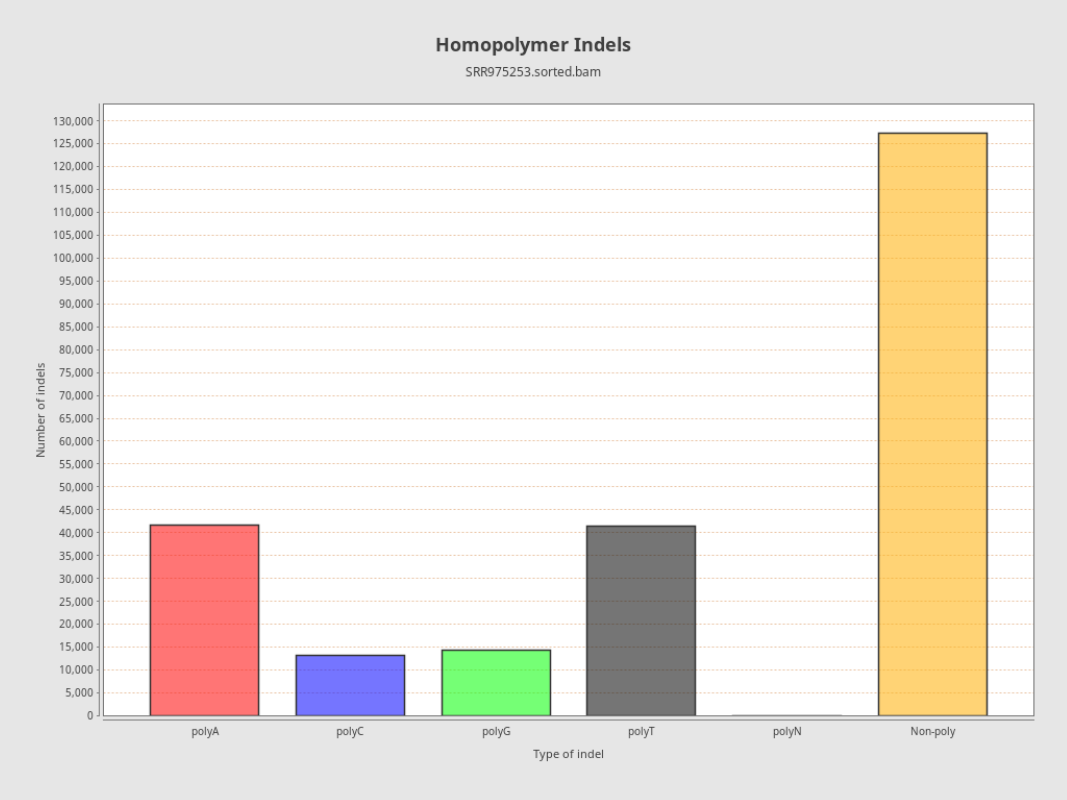
9. Results : Mapped Reads GC-content Distribution



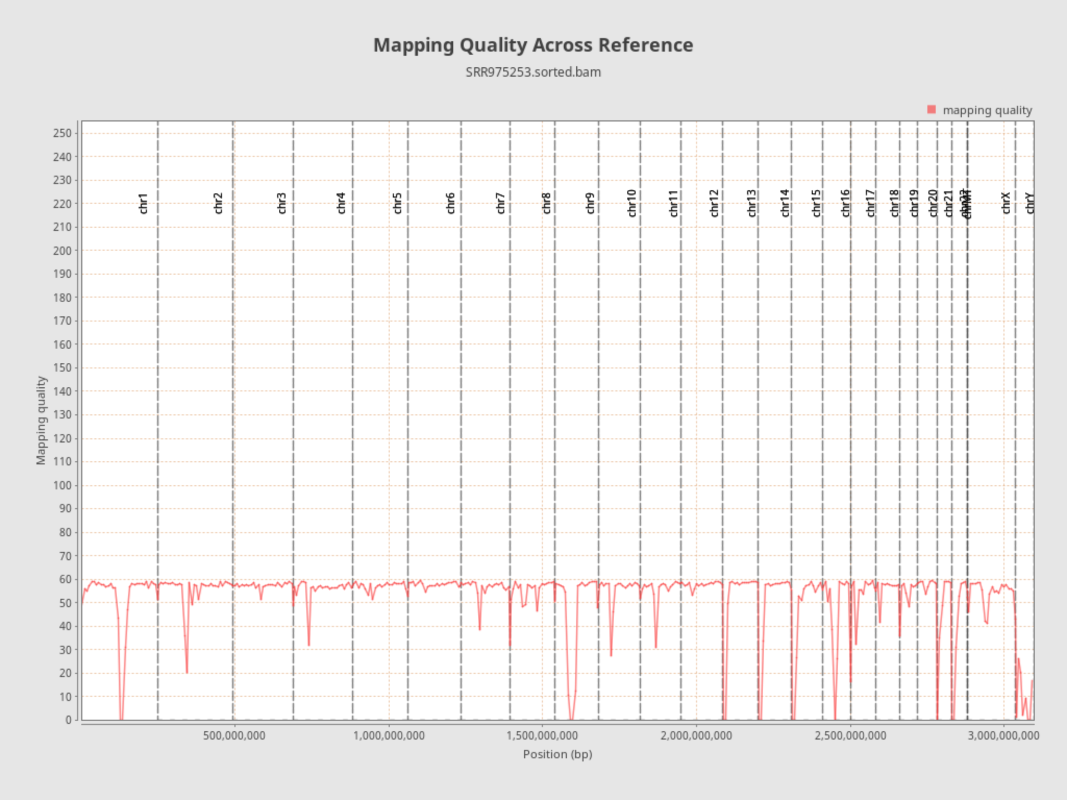
10. Results : Mapped Reads Clipping Profile



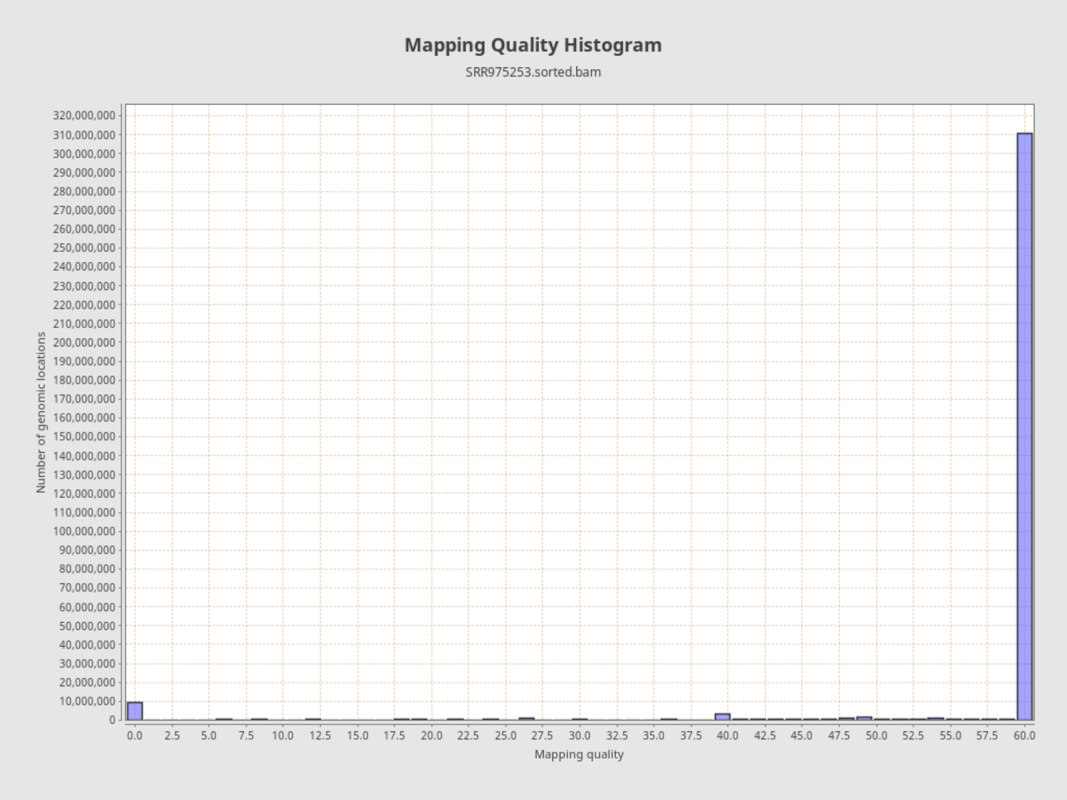
11. Results : Homopolymer Indels



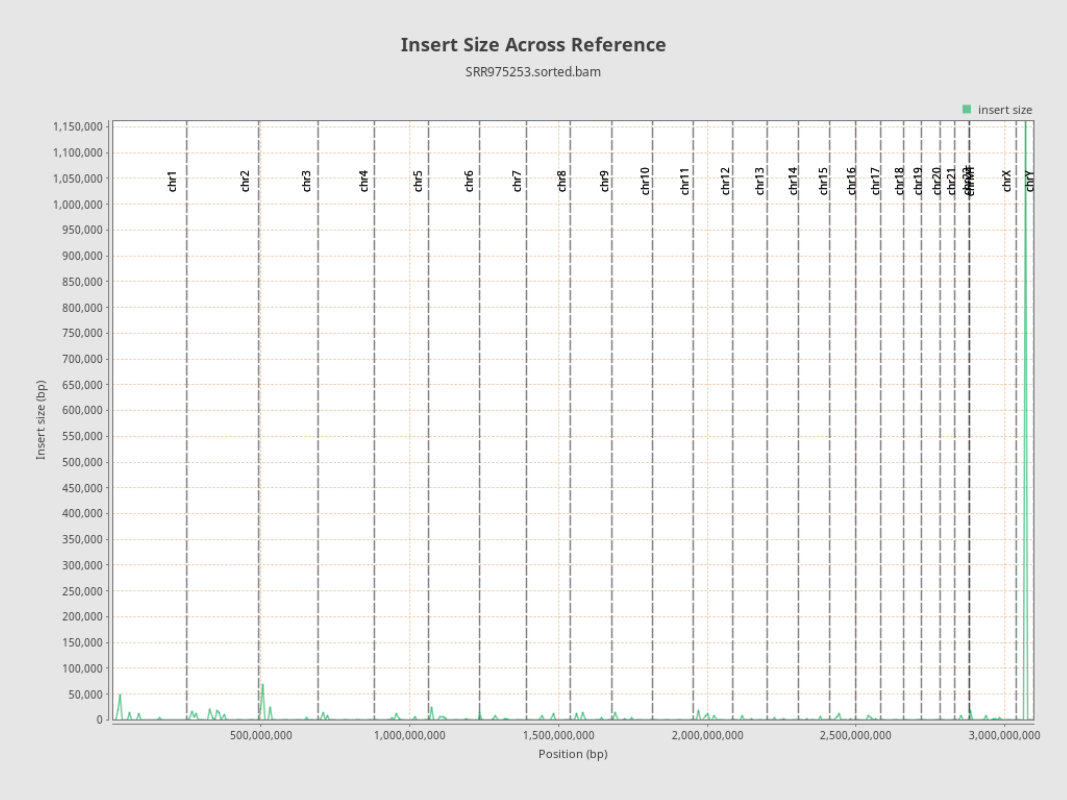
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram