Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 22:26:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975254.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_SRR975254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975254_1.fastq.gz SRR975254_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 22:26:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	148,961,592
Mapped reads	148,340,632 / 99.58%
Unmapped reads	620,960 / 0.42%
Mapped paired reads	148,340,632 / 99.58%
Mapped reads, first in pair	74,149,815 / 49.78%
Mapped reads, second in pair	74,190,817 / 49.81%
Mapped reads, both in pair	148,093,766 / 99.42%
Mapped reads, singletons	246,866 / 0.17%
Secondary alignments	0
Supplementary alignments	269,807 / 0.18%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	99,877,488 / 67.05%
Duplication rate	46.35%
Clipped reads	92,492,353 / 62.09%

2.2. ACGT Content

Number/percentage of A's	3,529,702,464 / 26.16%
Number/percentage of C's	3,035,180,285 / 22.49%
Number/percentage of T's	3,646,196,357 / 27.02%
Number/percentage of G's	3,282,415,182 / 24.33%
Number/percentage of N's	366,948 / 0%

GC Percentage	46.82%

2.3. Coverage

Mean	4.3605
Standard Deviation	58.8315

2.4. Mapping Quality

Mean Mapping Quality	55.69

2.5. Insert size

Mean	78,379.25
Standard Deviation	2,760,639.24
P25/Median/P75	144 / 181 / 230

2.6. Mismatches and indels

General error rate	0.7%
Mismatches	92,468,558
Insertions	1,464,848
Mapped reads with at least one insertion	0.98%
Deletions	3,421,303
Mapped reads with at least one deletion	2.27%
Homopolymer indels	46.51%

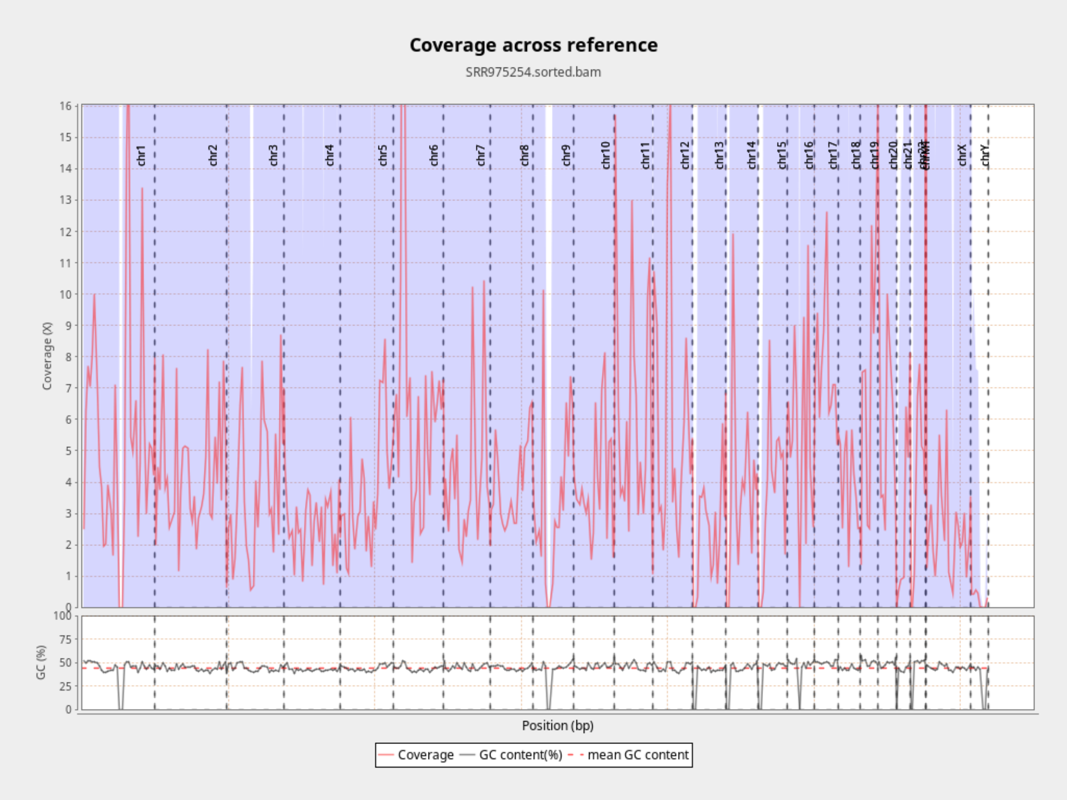
2.7. Chromosome stats

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

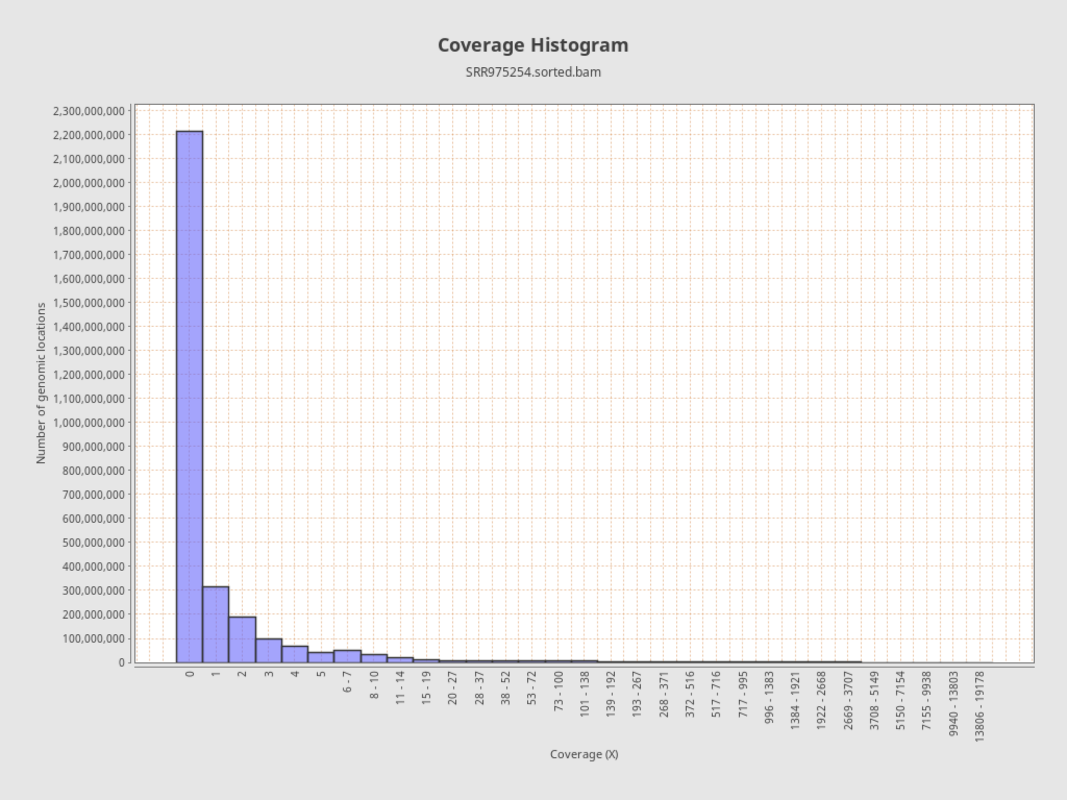
		bases	coverage	deviation
chr1	249250621	1387622909	5.5672	69.7708
chr2	243199373	1030961223	4.2392	53.2091
chr3	198022430	737613480	3.7249	50.928
chr4	191154276	496127711	2.5954	40.5369
chr5	180915260	677357746	3.7441	50.9608
chr6	171115067	1211632314	7.0808	88.4556
chr7	159138663	651732522	4.0954	59.6915
chr8	146364022	580582987	3.9667	50.6147
chr9	141213431	482764700	3.4187	46.5172
chr10	135534747	545199323	4.0226	53.8421
chr11	135006516	845460389	6.2624	73.5306
chr12	133851895	796161080	5.9481	72.2569
chr13	115169878	276660250	2.4022	36.8701
chr14	107349540	399693223	3.7233	53.162
chr15	102531392	374087792	3.6485	50.3096
chr16	90354753	504875448	5.5877	71.0604
chr17	81195210	631253546	7.7745	78.1808
chr18	78077248	307491133	3.9383	57.0382
chr19	59128983	445370607	7.5322	78.1854
chr20	63025520	375955926	5.9651	72.0815
chr21	48129895	145477050	3.0226	46.7417
chr22	51304566	206244486	4.02	55.6883
chrMT	16571	502246	30.3087	34.2503
chrX	155270560	372376627	2.3982	37.5116

chrY	59373566	15476670	0.2607	5.6636

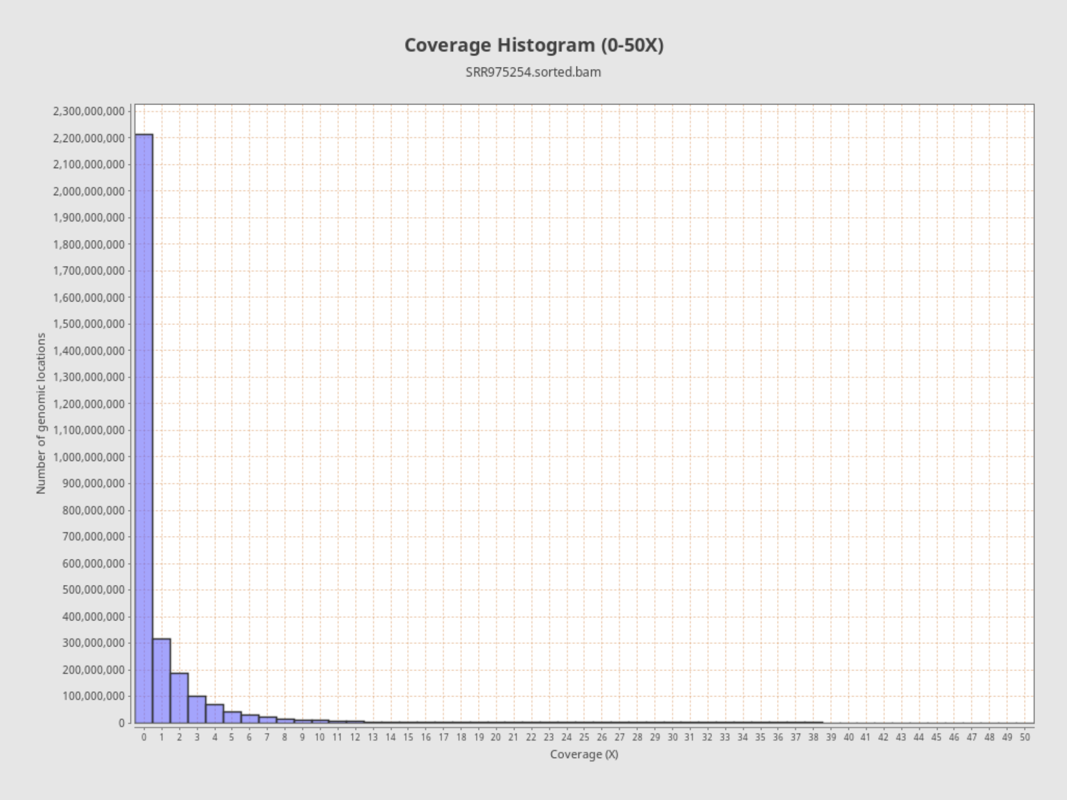
3. Results : Coverage across reference



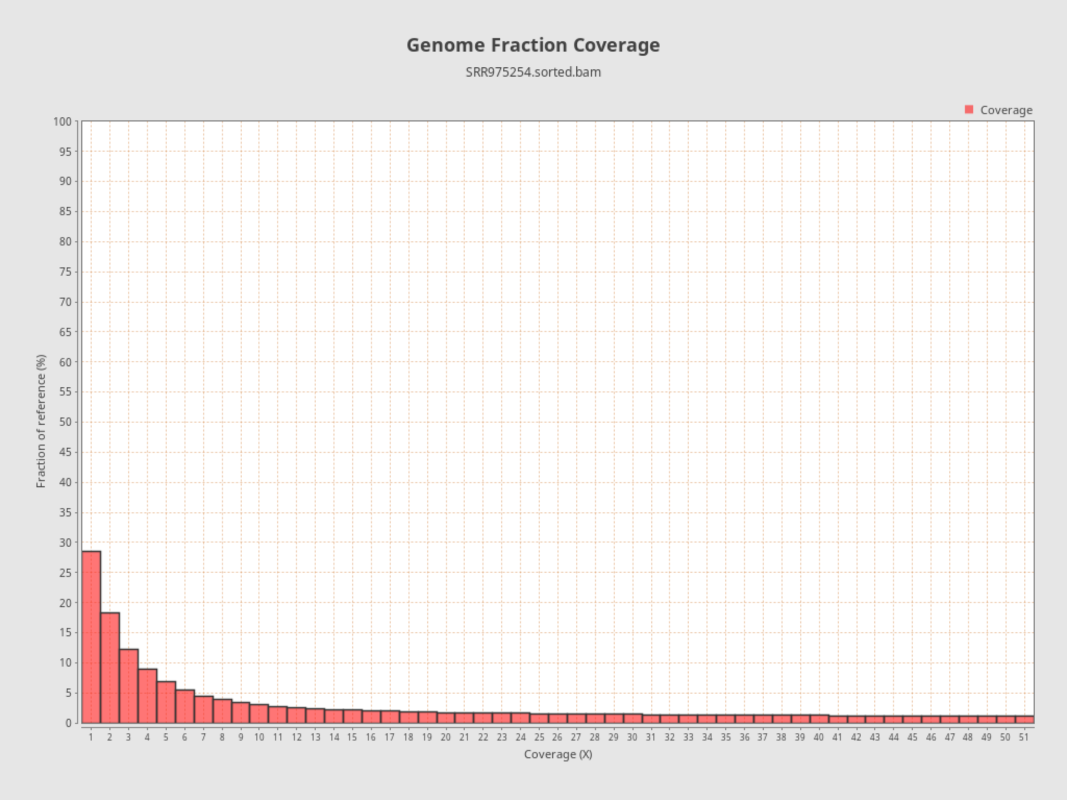
4. Results : Coverage Histogram



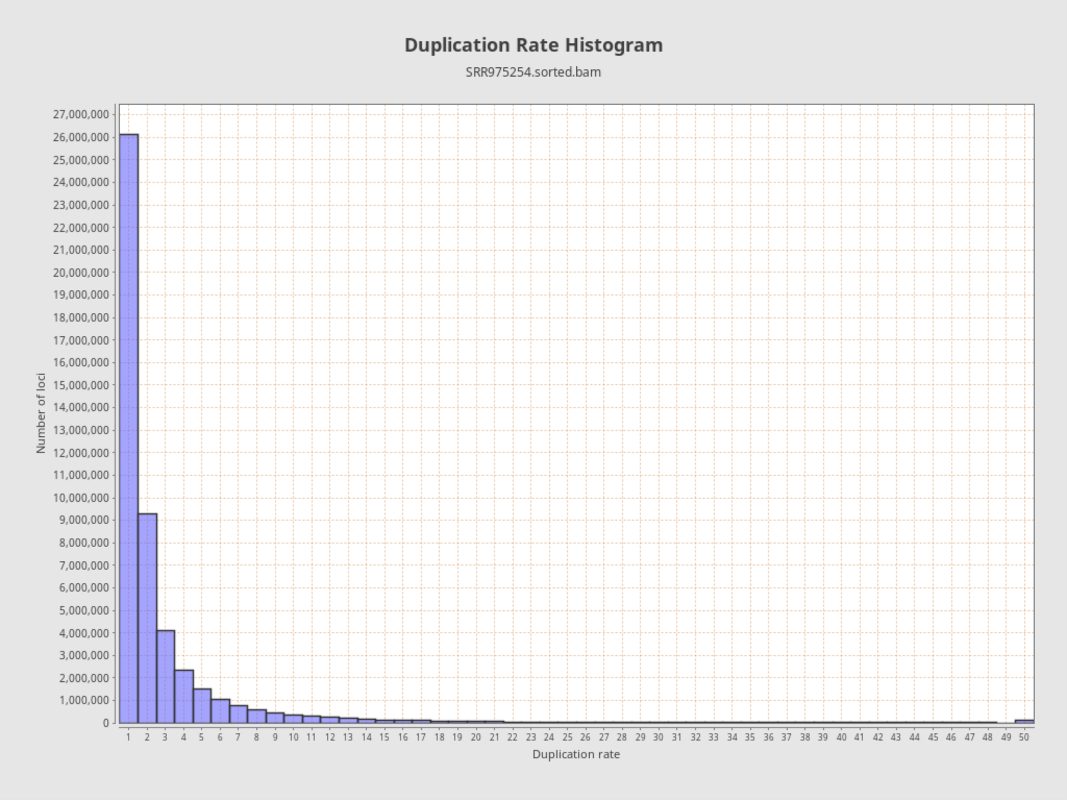
5. Results : Coverage Histogram (0-50X)



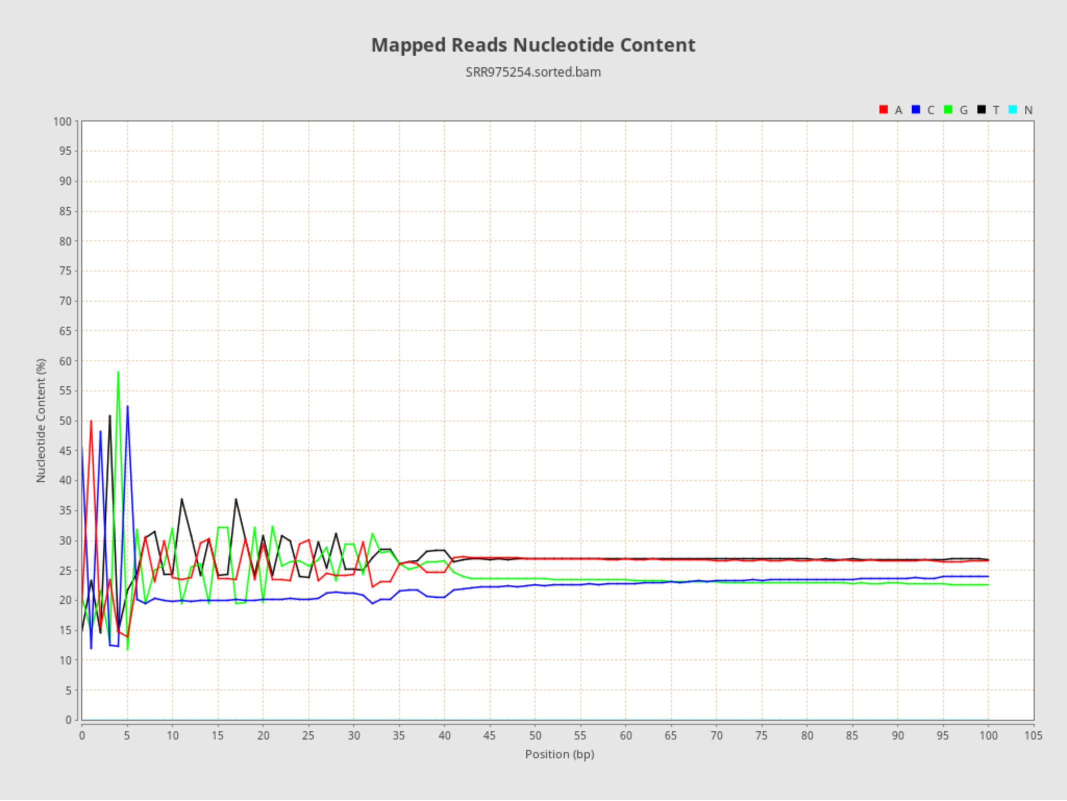
6. Results : Genome Fraction Coverage



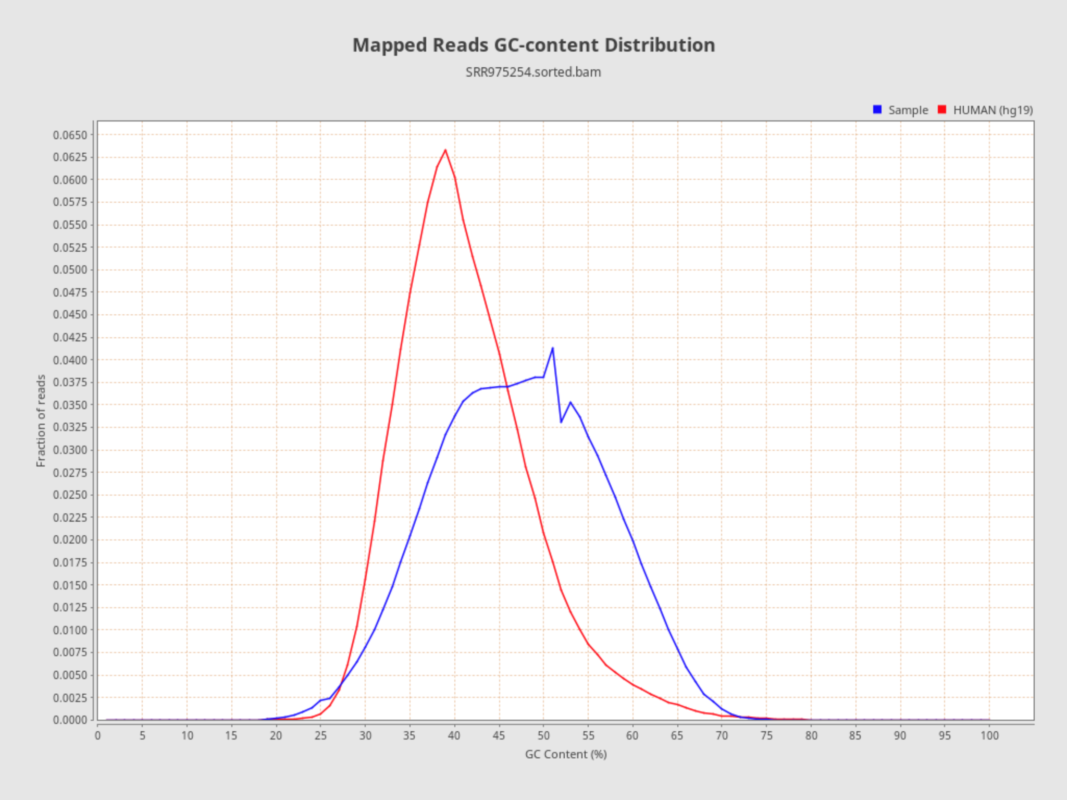
7. Results : Duplication Rate Histogram



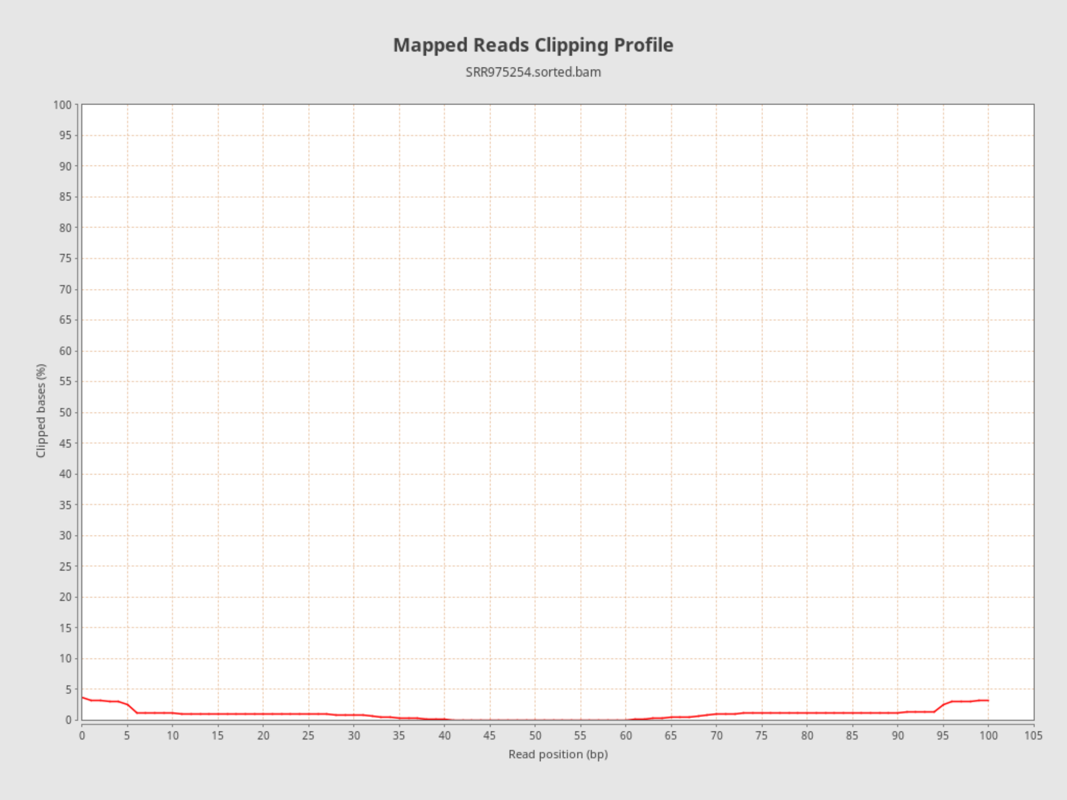
8. Results : Mapped Reads Nucleotide Content



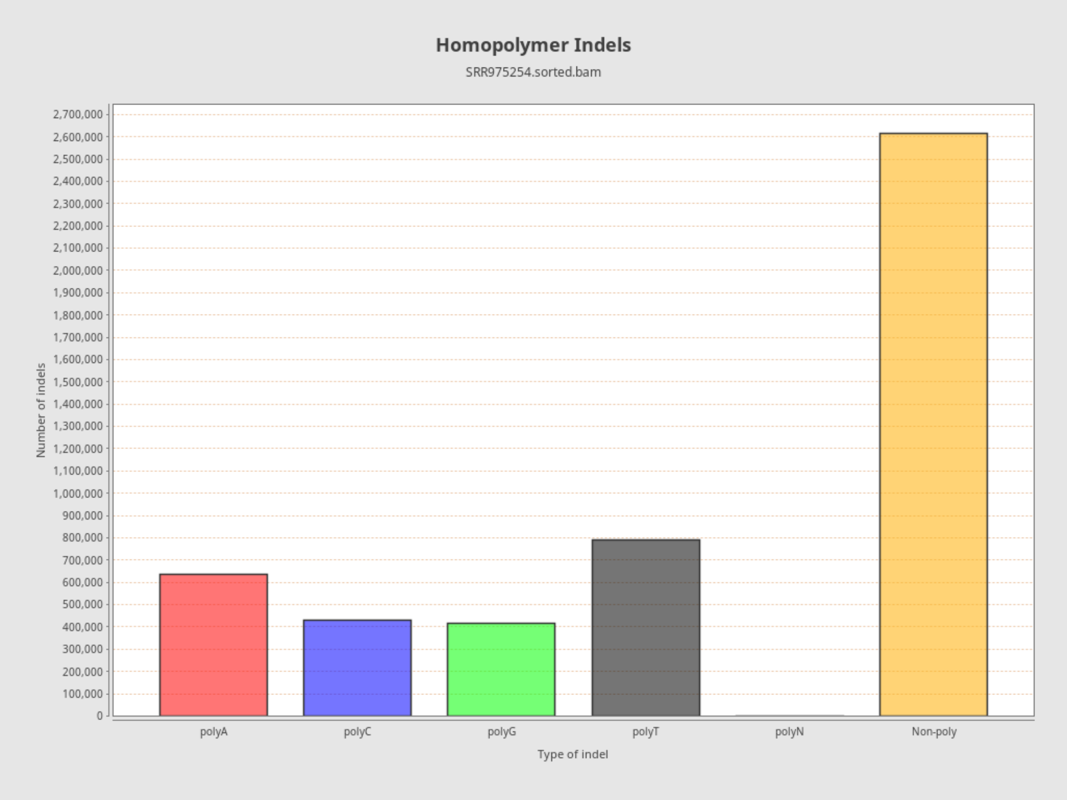
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

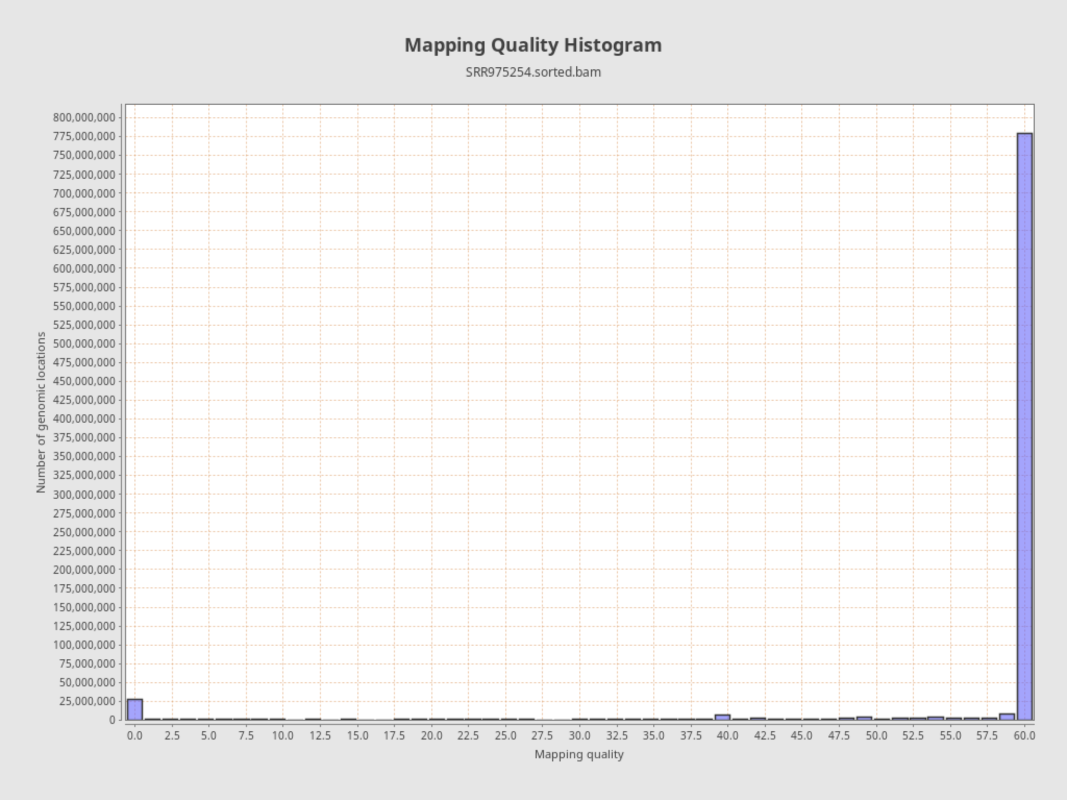


11. Results : Homopolymer Indels

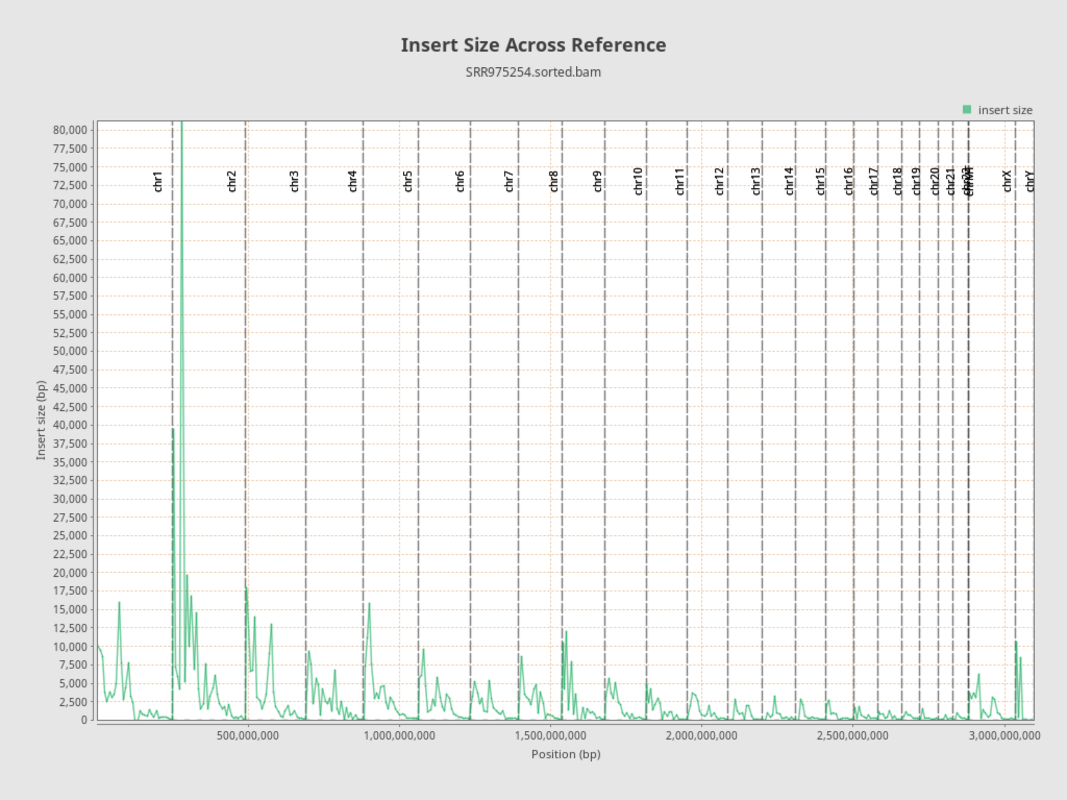


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram