Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 06:44:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975339.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_SRR975339 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975339_1.fastq.gz SRR975339_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 06:44:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975339.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,512,670
Mapped reads	4,446,496 / 98.53%
Unmapped reads	66,174 / 1.47%
Mapped paired reads	4,446,496 / 98.53%
Mapped reads, first in pair	2,222,848 / 49.26%
Mapped reads, second in pair	2,223,648 / 49.28%
Mapped reads, both in pair	4,434,424 / 98.27%
Mapped reads, singletons	12,072 / 0.27%
Secondary alignments	0
Supplementary alignments	19,004 / 0.42%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	159,352 / 3.53%
Duplication rate	2.43%
Clipped reads	2,840,676 / 62.95%

2.2. ACGT Content

Number/percentage of A's	115,372,820 / 28.62%
Number/percentage of C's	78,664,563 / 19.52%
Number/percentage of T's	120,345,331 / 29.86%
Number/percentage of G's	88,694,791 / 22%
Number/percentage of N's	8,265 / 0%

GC Percentage	41.52%

2.3. Coverage

Mean	0.1303
Standard Deviation	0.8418

2.4. Mapping Quality

Mean Mapping Quality	53.1

2.5. Insert size

Mean	86,047.69
Standard Deviation	2,828,657.94
P25/Median/P75	135 / 167 / 212

2.6. Mismatches and indels

General error rate	0.79%
Mismatches	3,064,672
Insertions	63,497
Mapped reads with at least one insertion	1.4%
Deletions	142,468
Mapped reads with at least one deletion	3.14%
Homopolymer indels	48.26%

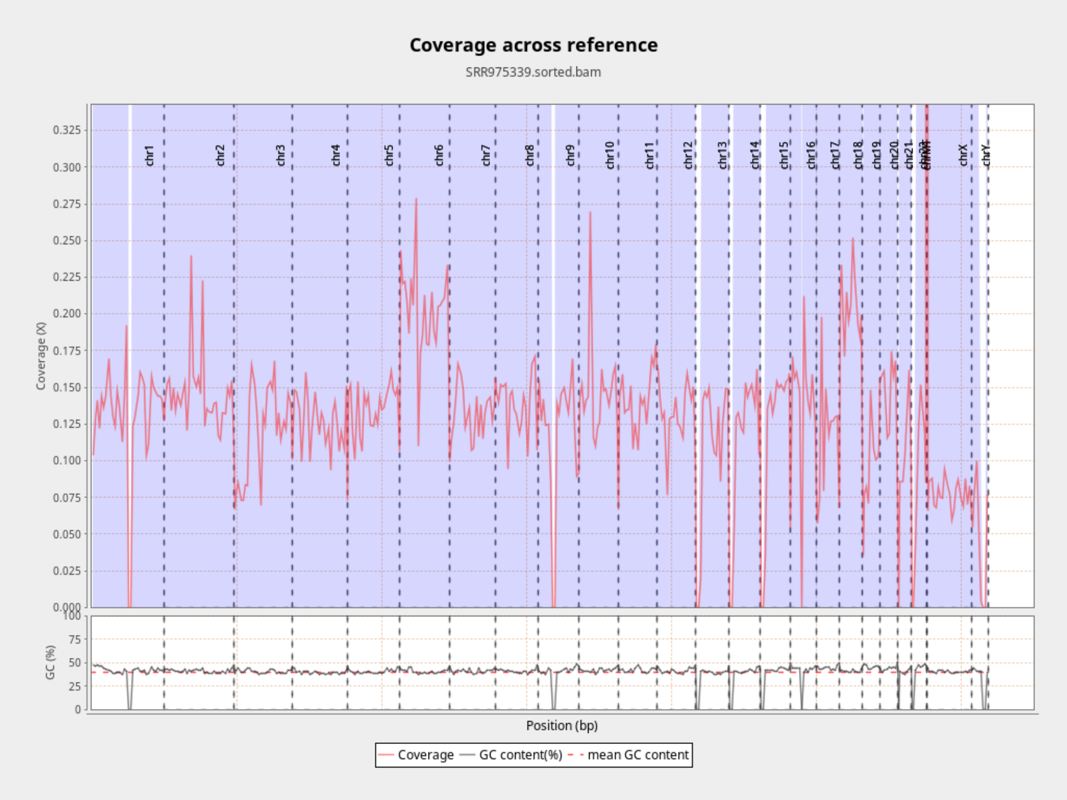
2.7. Chromosome stats

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

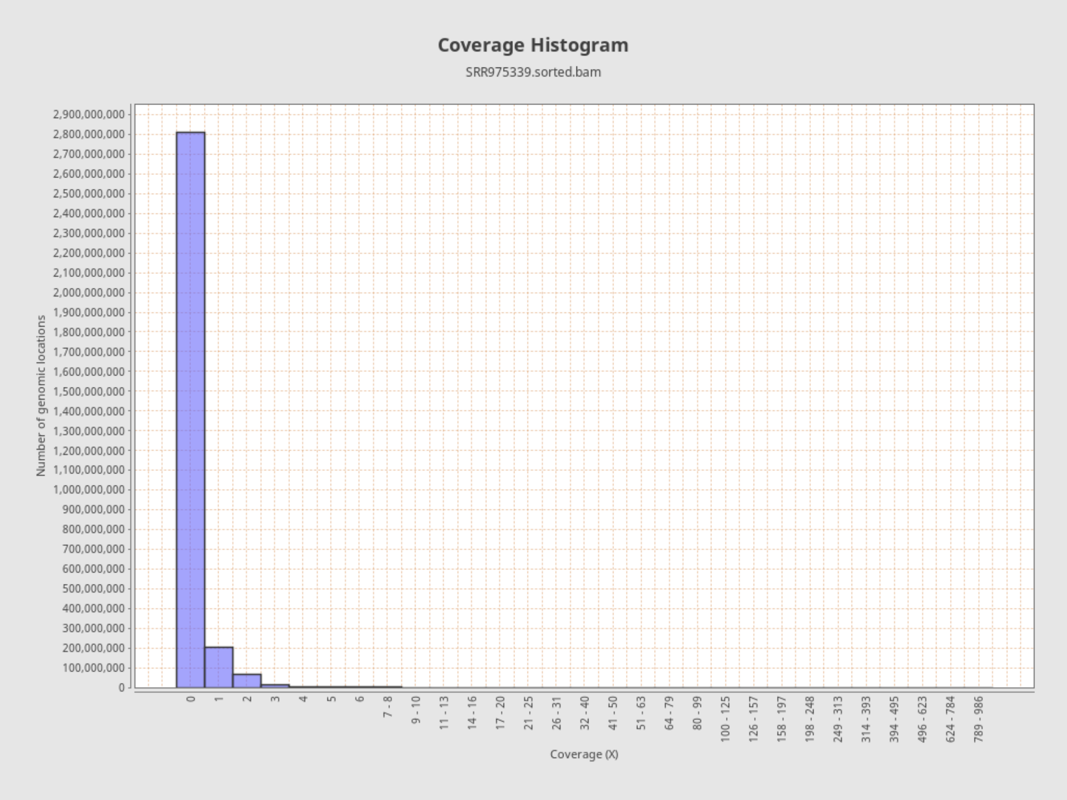
		bases	coverage	deviation
chr1	249250621	32574689	0.1307	0.967
chr2	243199373	35459410	0.1458	1.1725
chr3	198022430	23766631	0.12	0.4406
chr4	191154276	24097305	0.1261	0.5957
chr5	180915260	24600070	0.136	0.4775
chr6	171115067	34654543	0.2025	1.1292
chr7	159138663	20987171	0.1319	0.864
chr8	146364022	20136042	0.1376	0.518
chr9	141213431	16696399	0.1182	1.0234
chr10	135534747	19996429	0.1475	1.4874
chr11	135006516	18875047	0.1398	0.6965
chr12	133851895	17853989	0.1334	0.464
chr13	115169878	12304028	0.1068	0.4138
chr14	107349540	12181606	0.1135	0.4632
chr15	102531392	12061251	0.1176	0.4417
chr16	90354753	12352380	0.1367	0.9497
chr17	81195210	9447614	0.1164	1.3925
chr18	78077248	16228457	0.2079	1.2567
chr19	59128983	5660203	0.0957	0.6012
chr20	63025520	9253130	0.1468	0.503
chr21	48129895	4900068	0.1018	0.5191
chr22	51304566	4543617	0.0886	0.3955
chrMT	16571	96245	5.808	6.7737
chrX	155270560	11938145	0.0769	0.4175

chrY	59373566	2649897	0.0446	0.8823

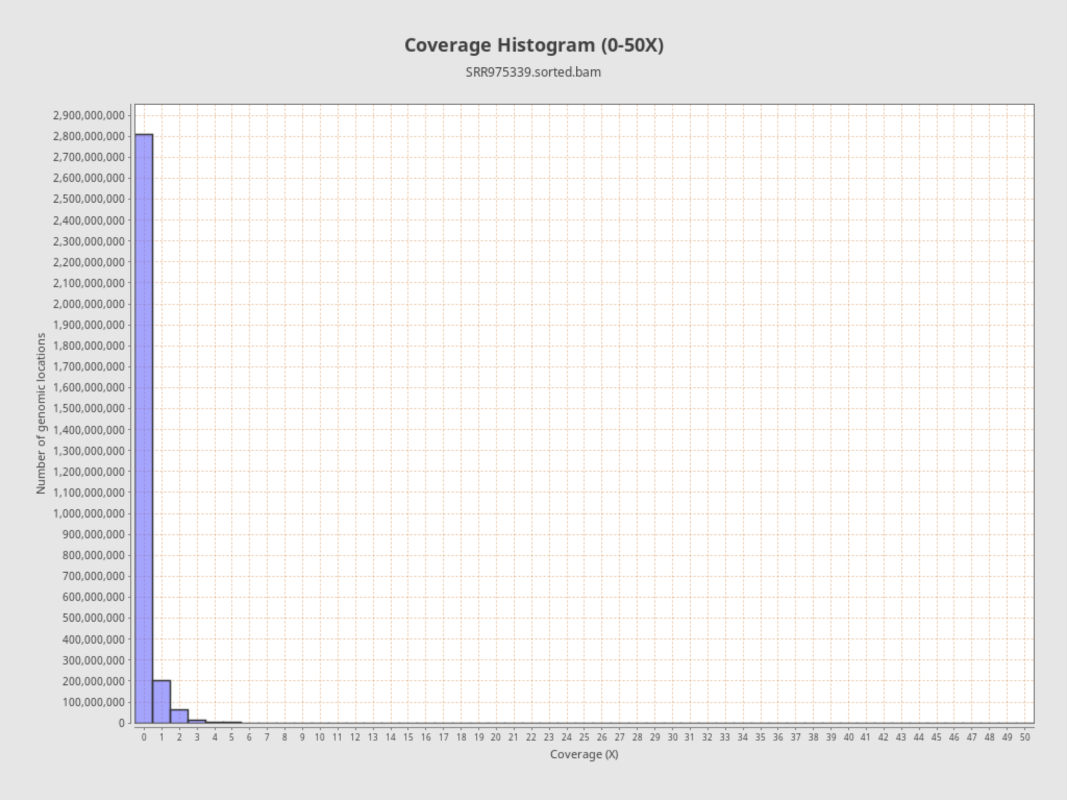
3. Results : Coverage across reference



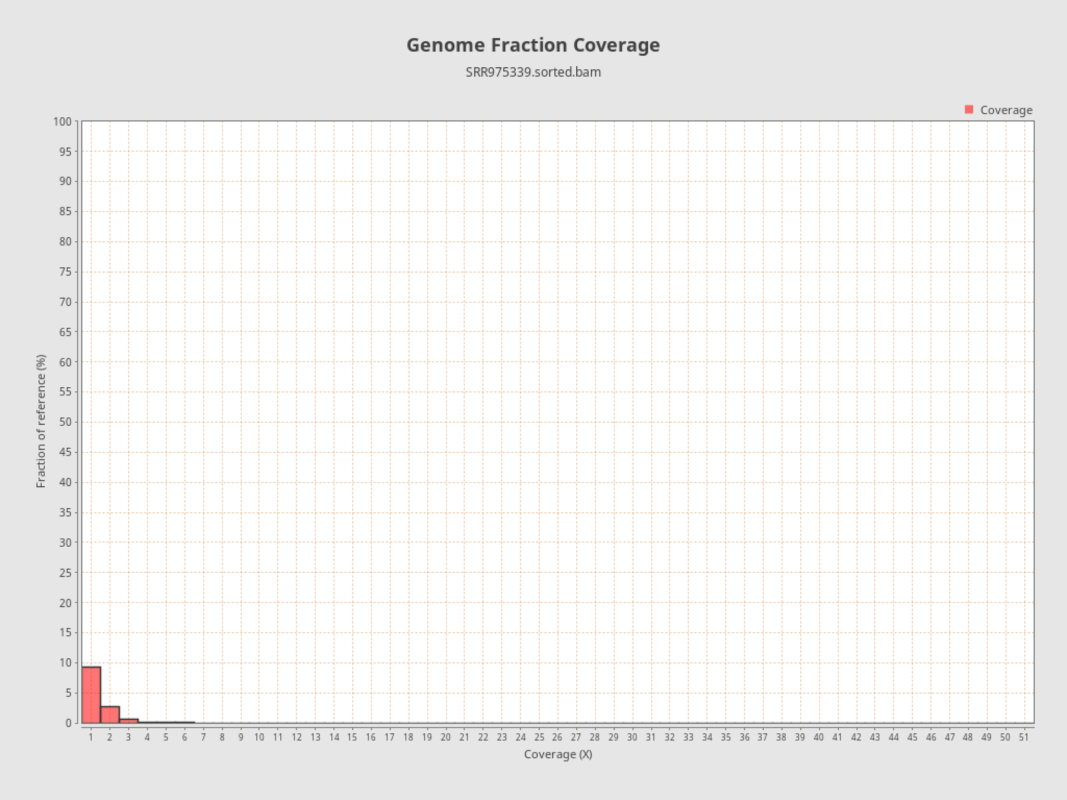
4. Results : Coverage Histogram



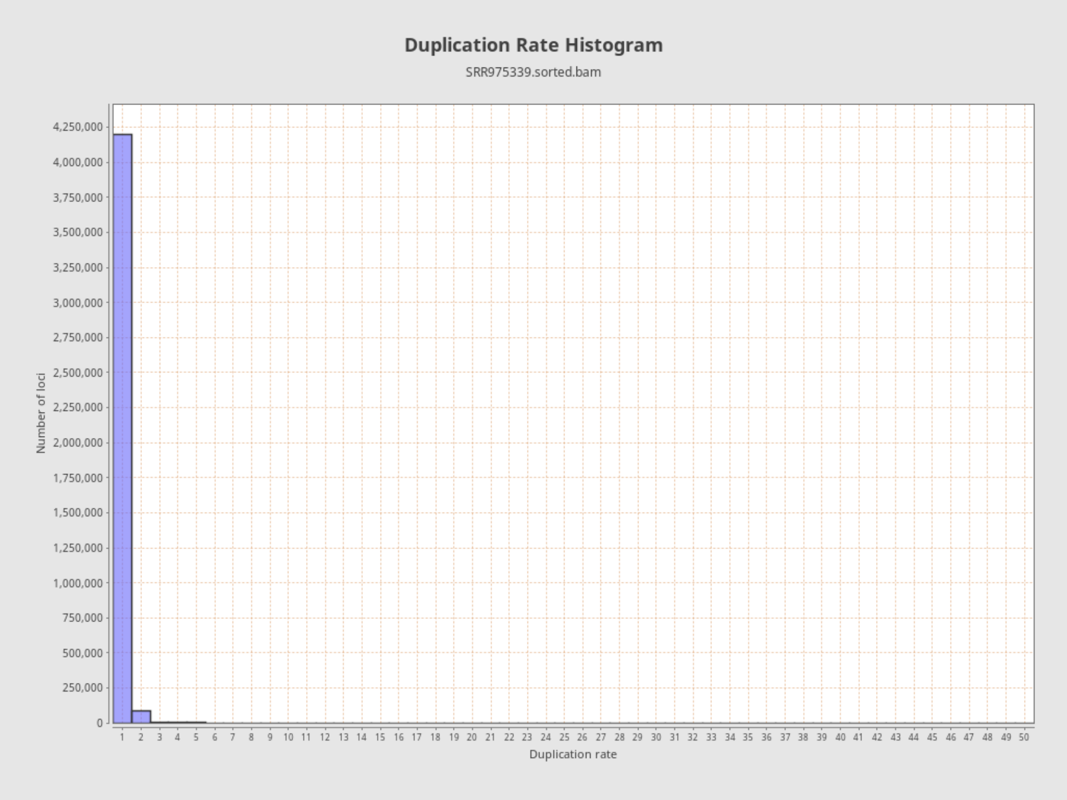
5. Results : Coverage Histogram (0-50X)



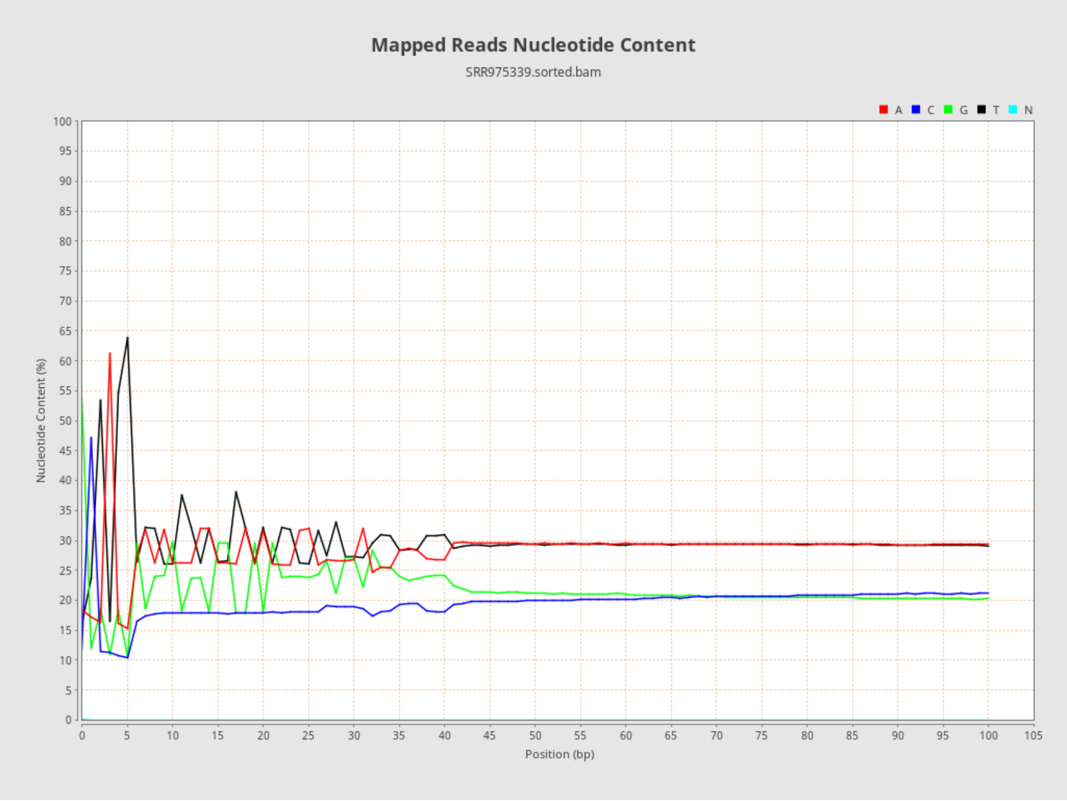
6. Results : Genome Fraction Coverage



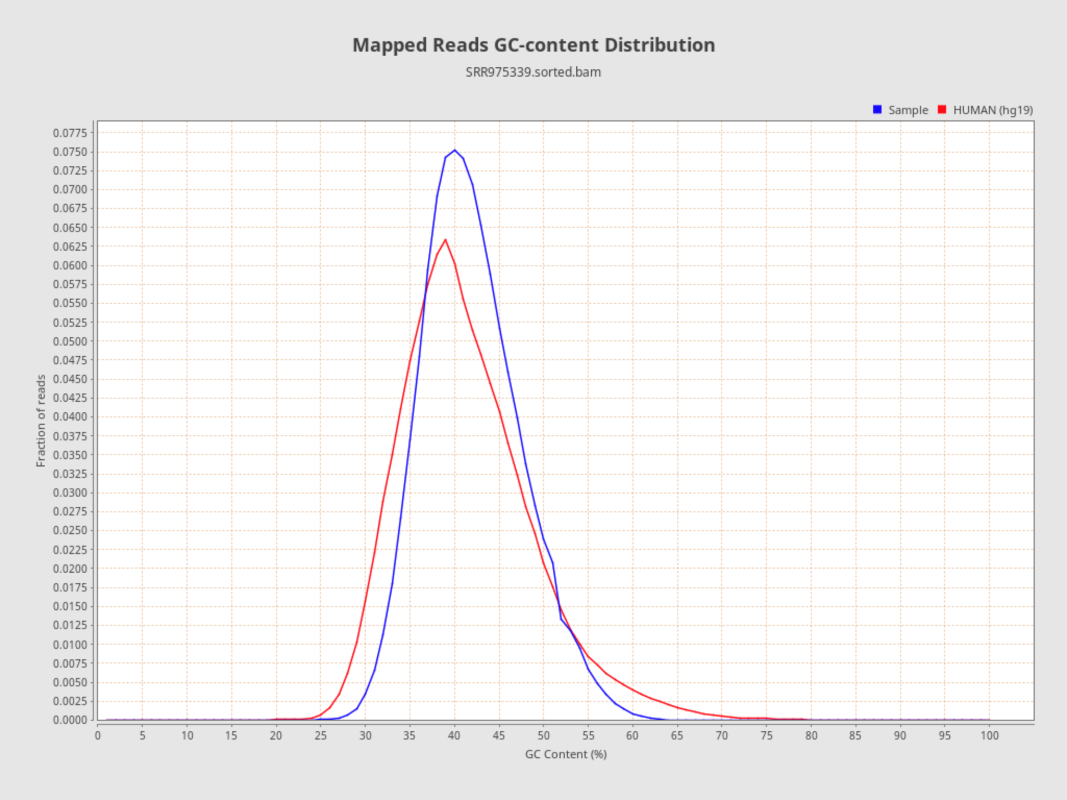
7. Results : Duplication Rate Histogram



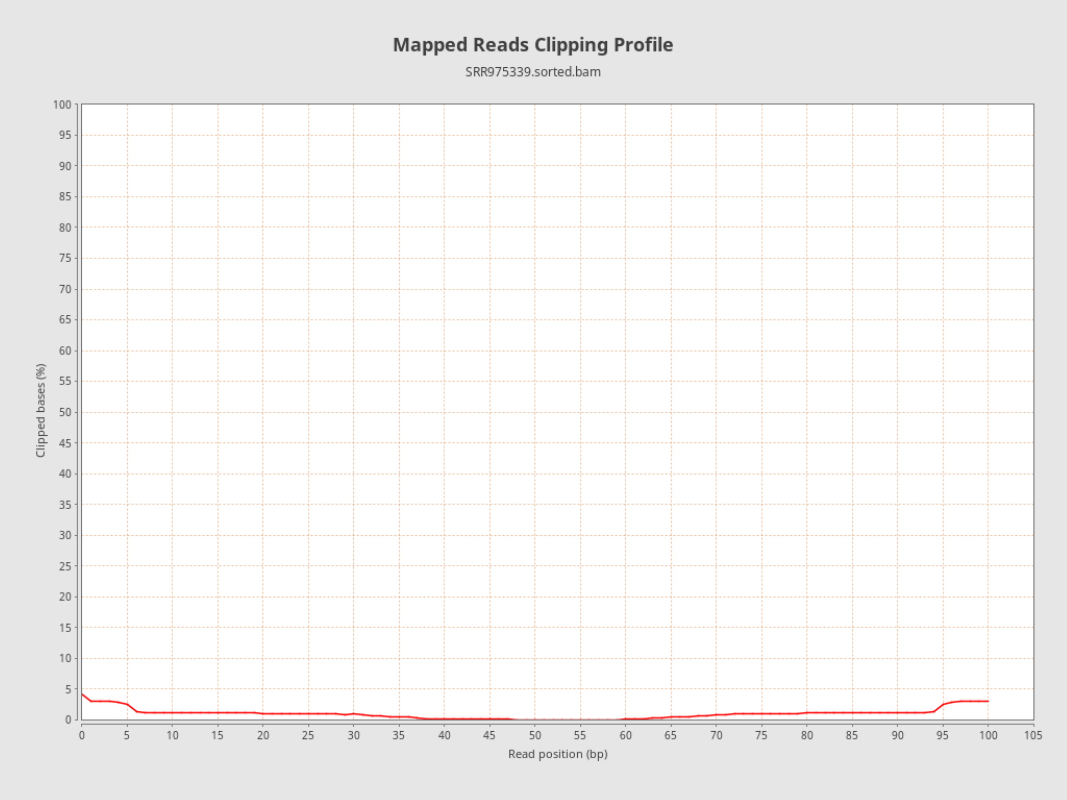
8. Results : Mapped Reads Nucleotide Content



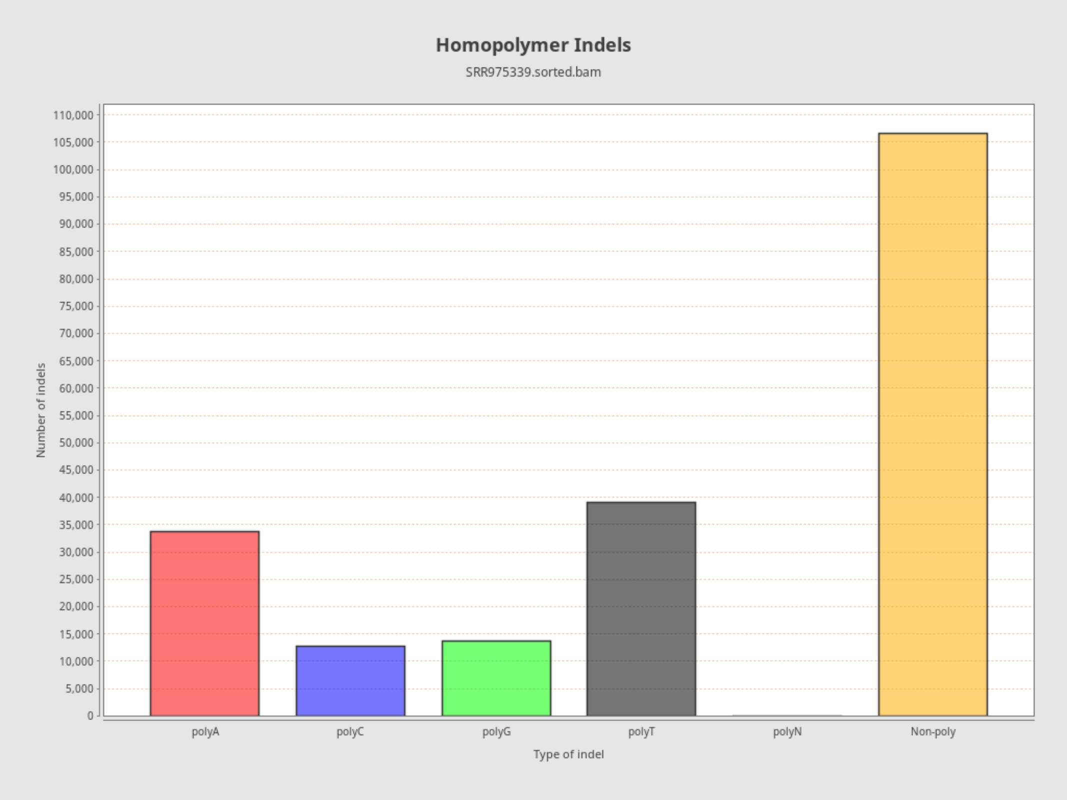
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

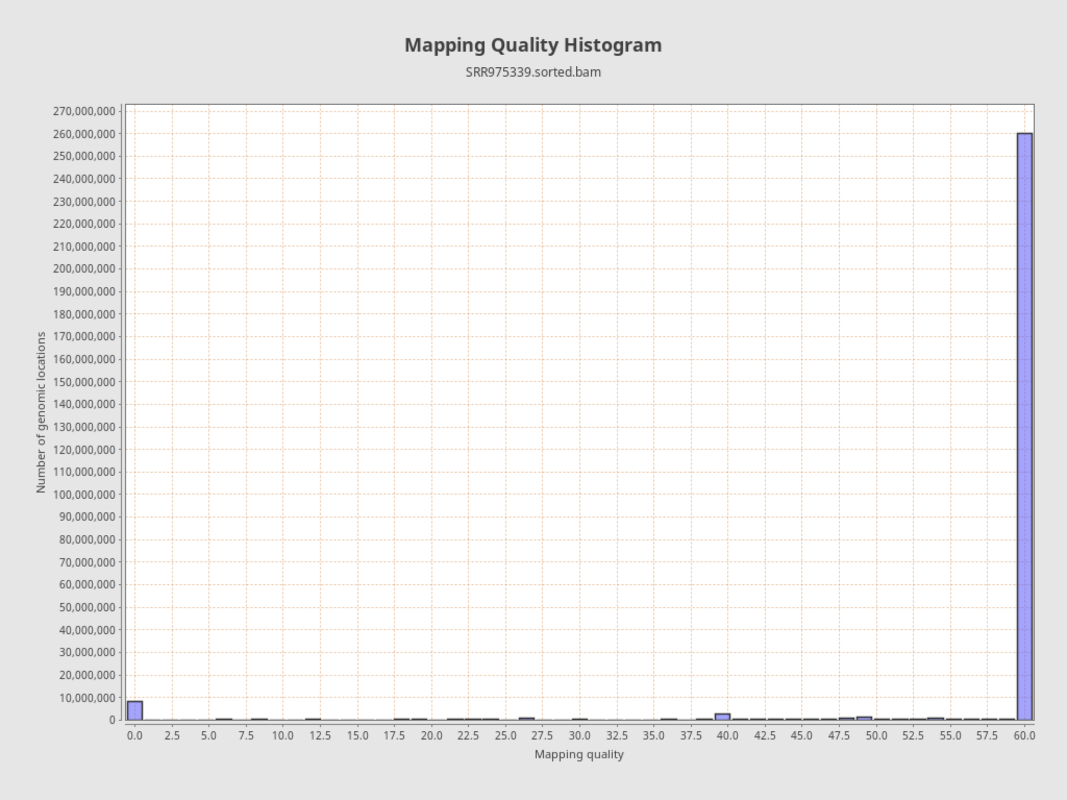


11. Results : Homopolymer Indels

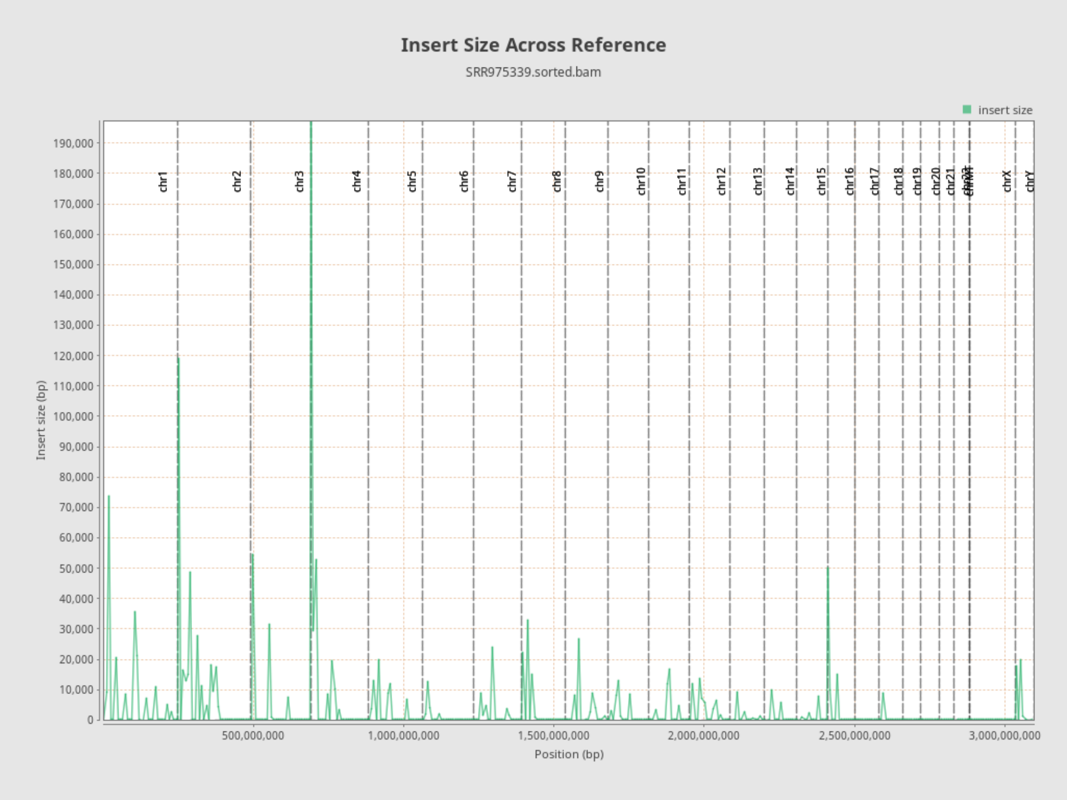


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram