Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 04:58:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975325.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_SRR975325 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975325_1.fastq.gz SRR975325_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 04:58:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975325.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,069,676
Mapped reads	4,013,006 / 98.61%
Unmapped reads	56,670 / 1.39%
Mapped paired reads	4,013,006 / 98.61%
Mapped reads, first in pair	2,005,295 / 49.27%
Mapped reads, second in pair	2,007,711 / 49.33%
Mapped reads, both in pair	3,989,906 / 98.04%
Mapped reads, singletons	23,100 / 0.57%
Secondary alignments	0
Supplementary alignments	32,378 / 0.8%
Read min/max/mean length	30 / 101 / 101.32
Duplicated reads (estimated)	441,487 / 10.85%
Duplication rate	4.14%
Clipped reads	2,458,572 / 60.41%

2.2. ACGT Content

Number/percentage of A's	109,575,654 / 29.21%
Number/percentage of C's	74,818,486 / 19.95%
Number/percentage of T's	110,537,638 / 29.47%
Number/percentage of G's	80,147,530 / 21.37%
Number/percentage of N's	7,751 / 0%

GC Percentage	41.31%

2.3. Coverage

Mean	0.1213
Standard Deviation	3.4615

2.4. Mapping Quality

Mean Mapping Quality	52.15

2.5. Insert size

Mean	112,990.25
Standard Deviation	3,178,699.67
P25/Median/P75	141 / 175 / 223

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	3,493,092
Insertions	75,655
Mapped reads with at least one insertion	1.82%
Deletions	136,198
Mapped reads with at least one deletion	3.28%
Homopolymer indels	43.19%

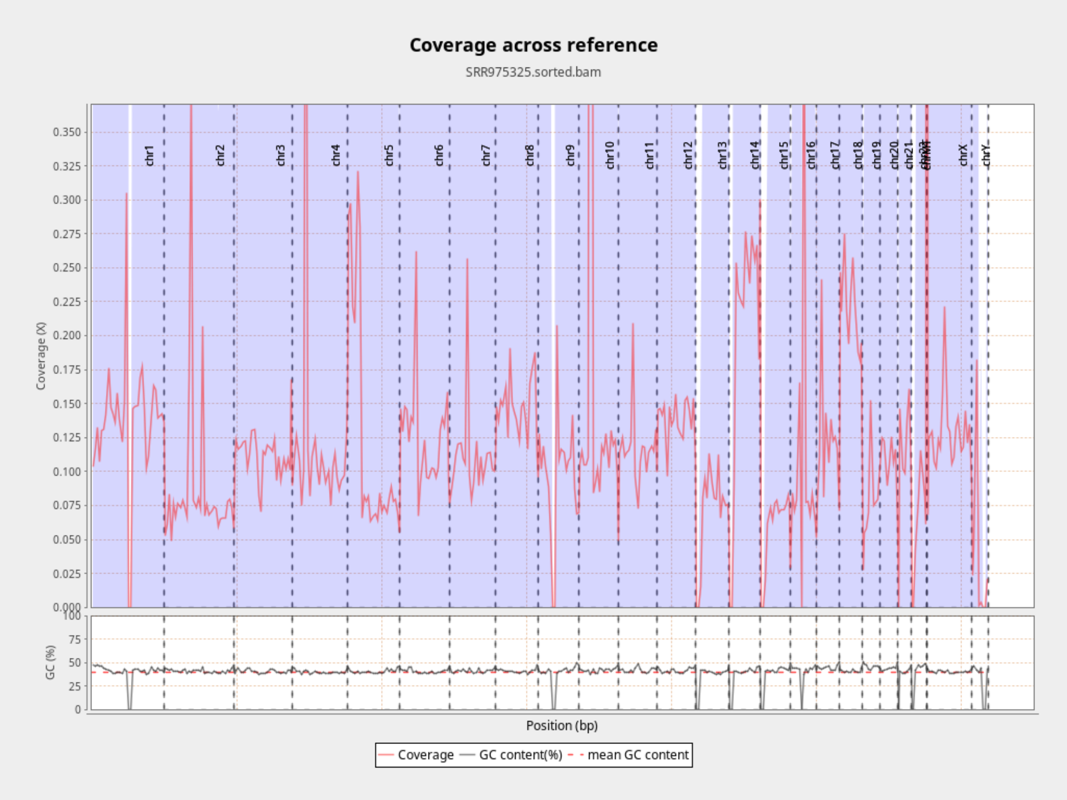
2.7. Chromosome stats

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

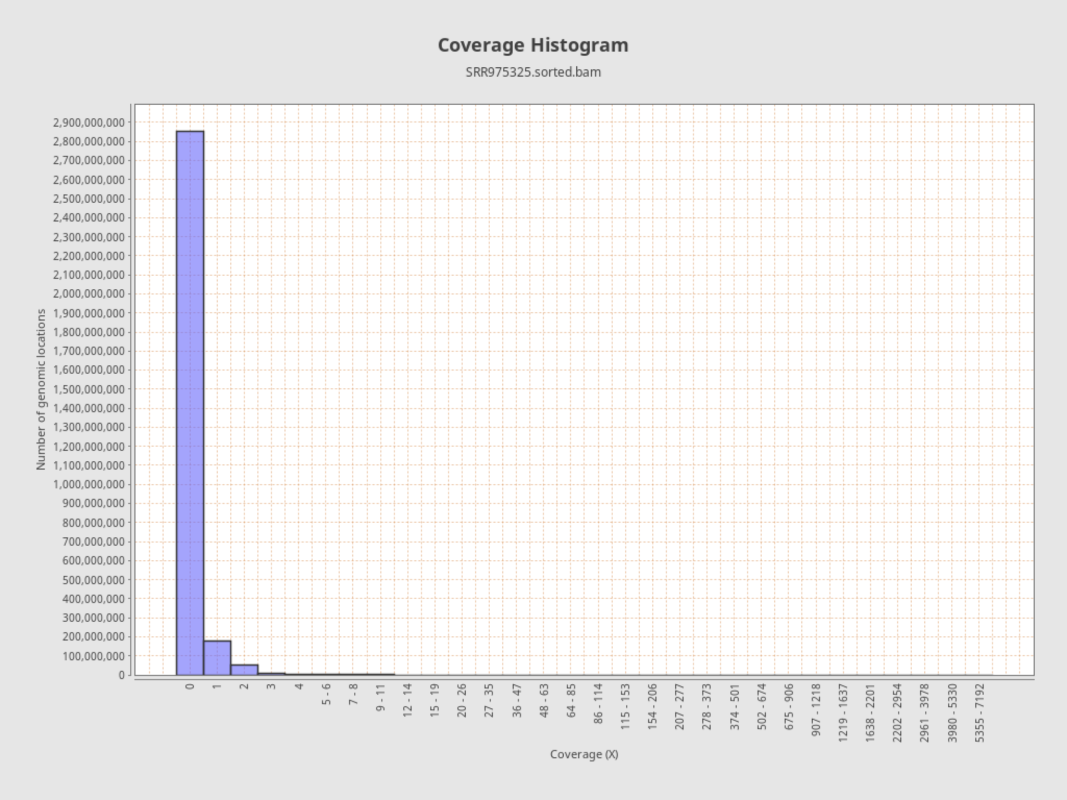
		bases	coverage	deviation
chr1	249250621	34117883	0.1369	2.4563
chr2	243199373	21436052	0.0881	2.4034
chr3	198022430	22006471	0.1111	0.9588
chr4	191154276	23592563	0.1234	2.8894
chr5	180915260	22549933	0.1246	0.5042
chr6	171115067	21448521	0.1253	1.7119
chr7	159138663	17578287	0.1105	2.218
chr8	146364022	21667967	0.148	0.7817
chr9	141213431	13777789	0.0976	2.1935
chr10	135534747	27179980	0.2005	14.2054
chr11	135006516	15685237	0.1162	1.8194
chr12	133851895	18641713	0.1393	0.4927
chr13	115169878	8225100	0.0714	0.3343
chr14	107349540	21748031	0.2026	0.6668
chr15	102531392	6004047	0.0586	0.3043
chr16	90354753	10142594	0.1123	2.7975
chr17	81195210	10073808	0.1241	2.0909
chr18	78077248	17206445	0.2204	2.7906
chr19	59128983	4669122	0.079	1.4644
chr20	63025520	6906117	0.1096	0.785
chr21	48129895	5475425	0.1138	1.0305
chr22	51304566	3378337	0.0658	0.3873
chrMT	16571	55819	3.3685	2.8189
chrX	155270560	19714352	0.127	0.8918

chrY	59373566	2078976	0.035	2.5482

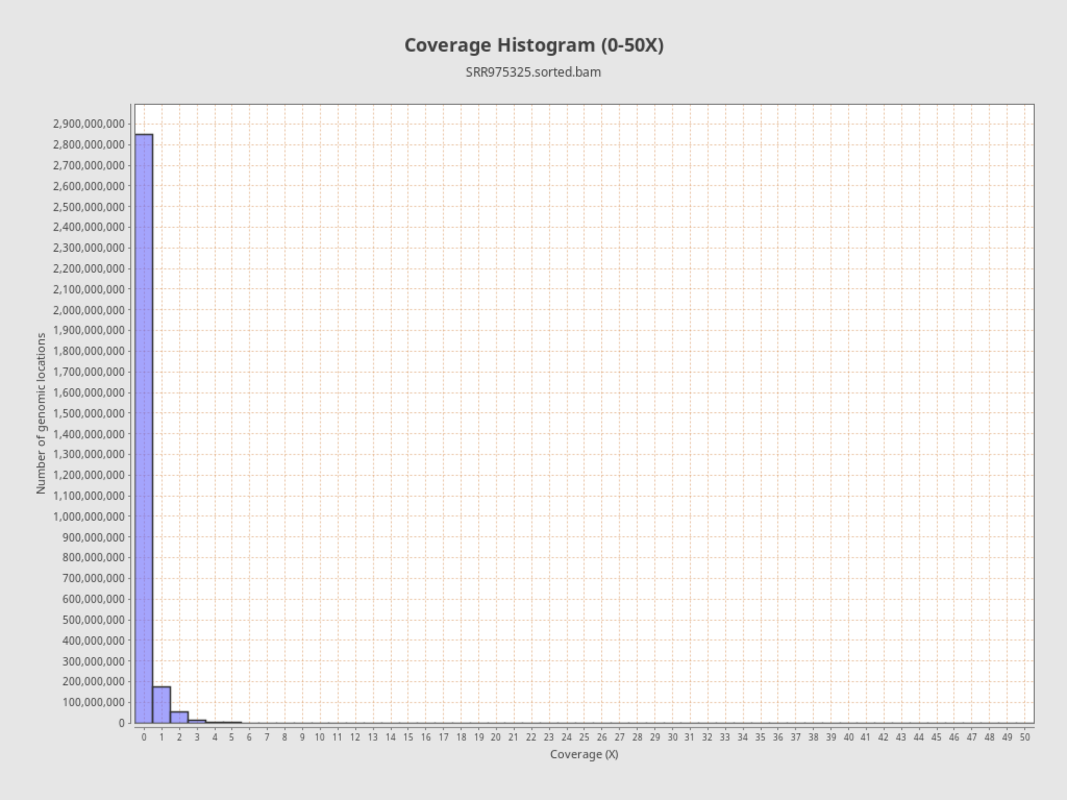
3. Results : Coverage across reference



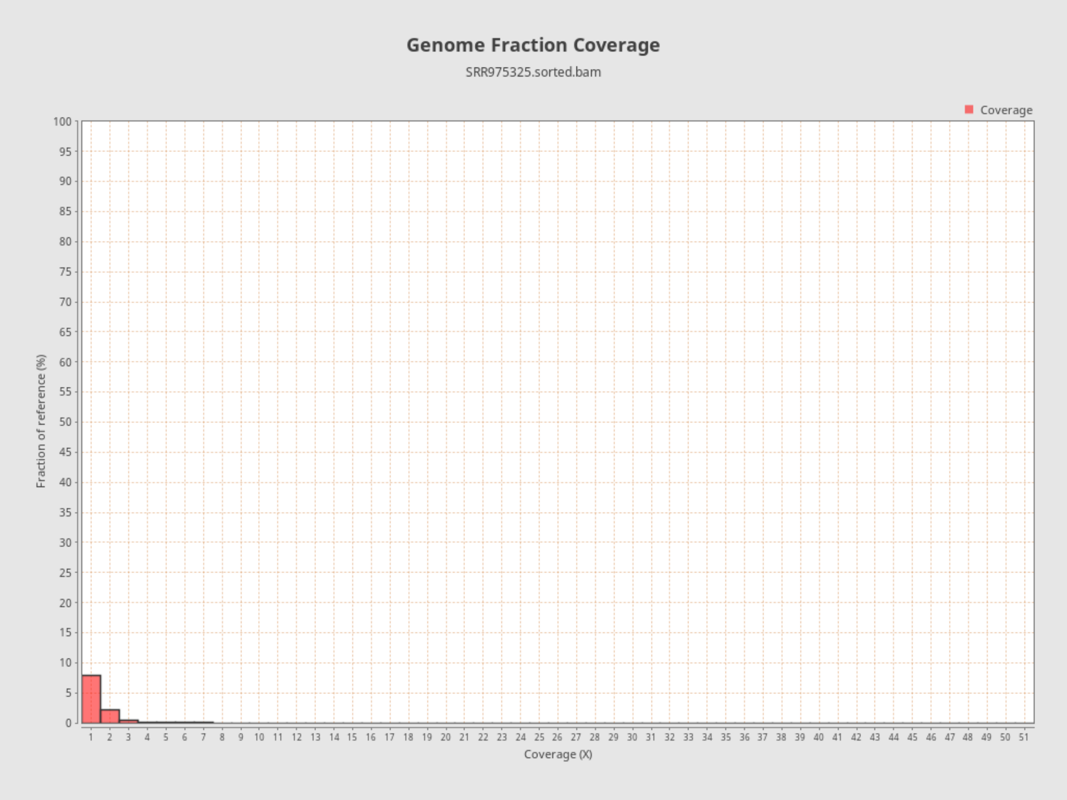
4. Results : Coverage Histogram



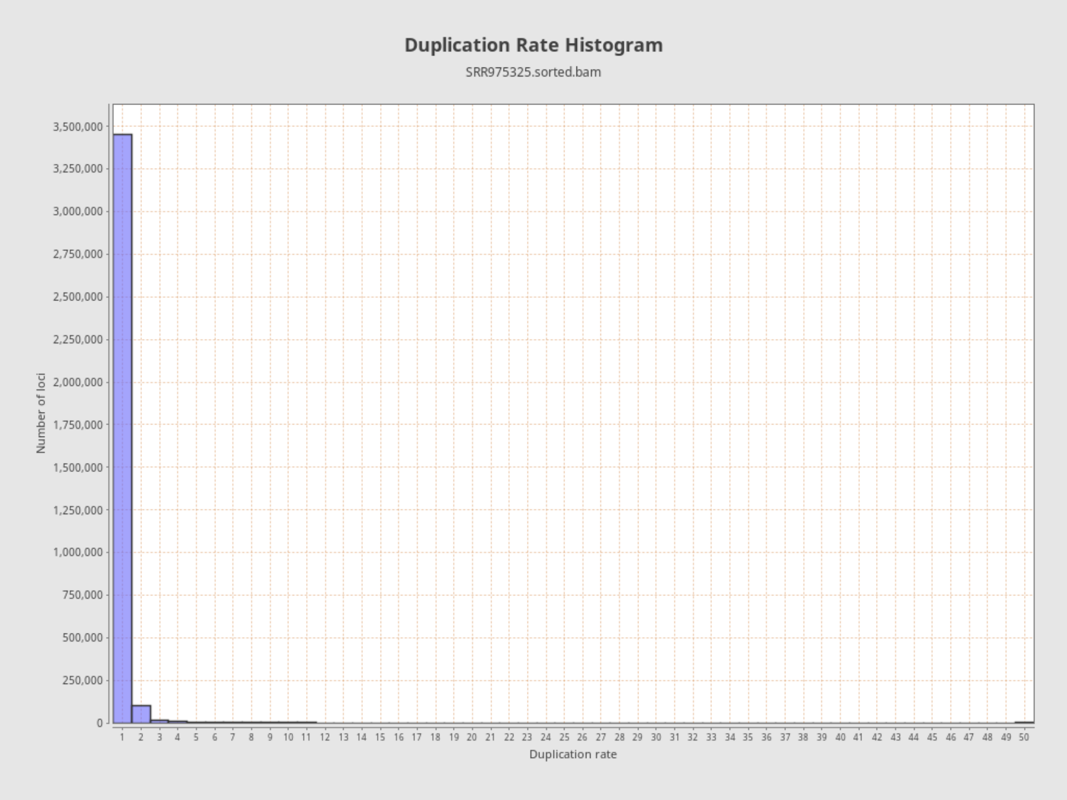
5. Results : Coverage Histogram (0-50X)



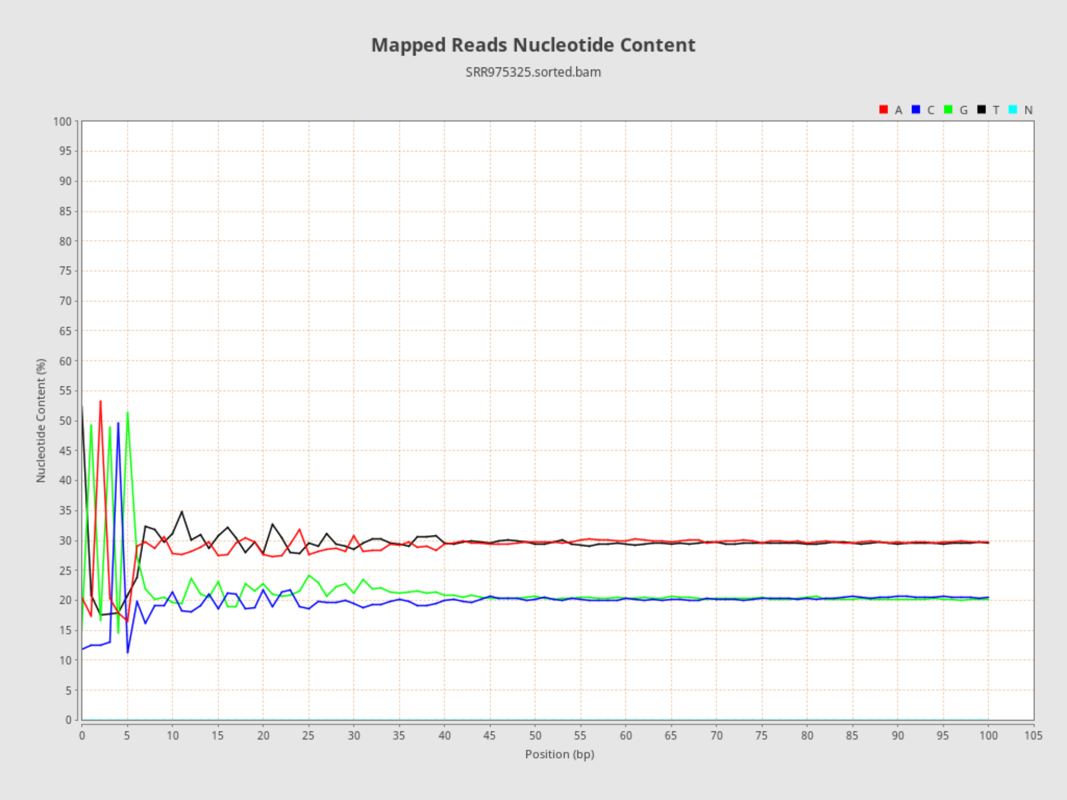
6. Results : Genome Fraction Coverage



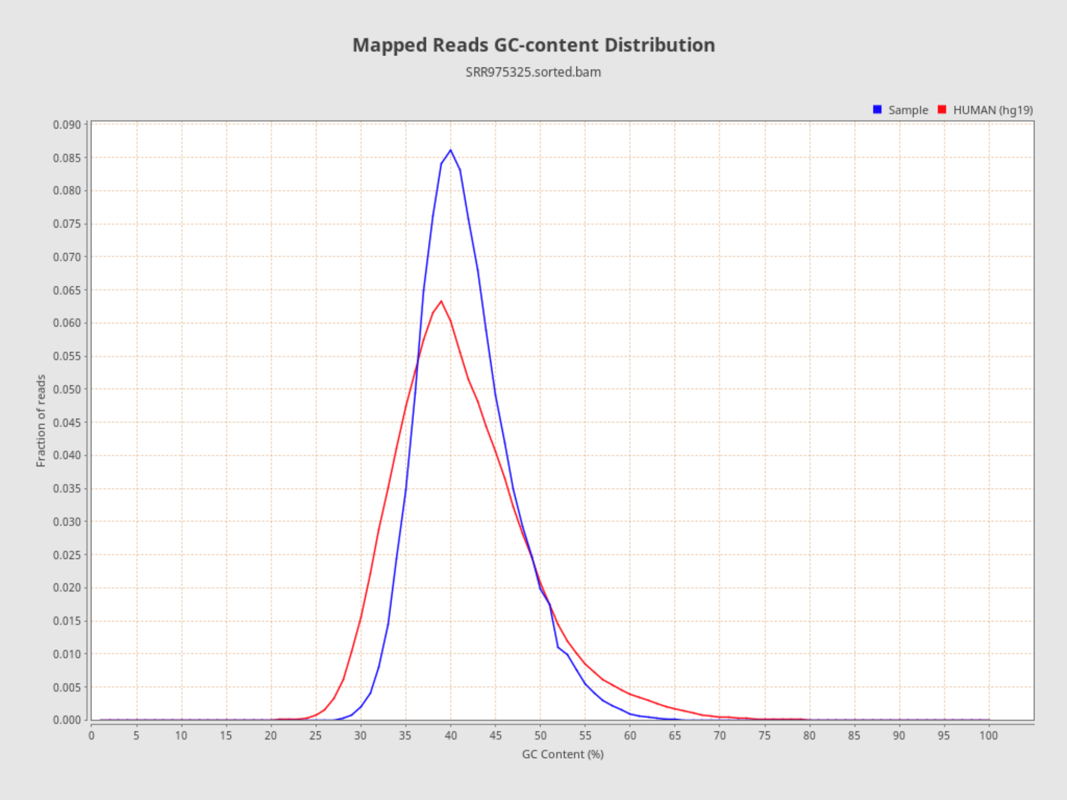
7. Results : Duplication Rate Histogram



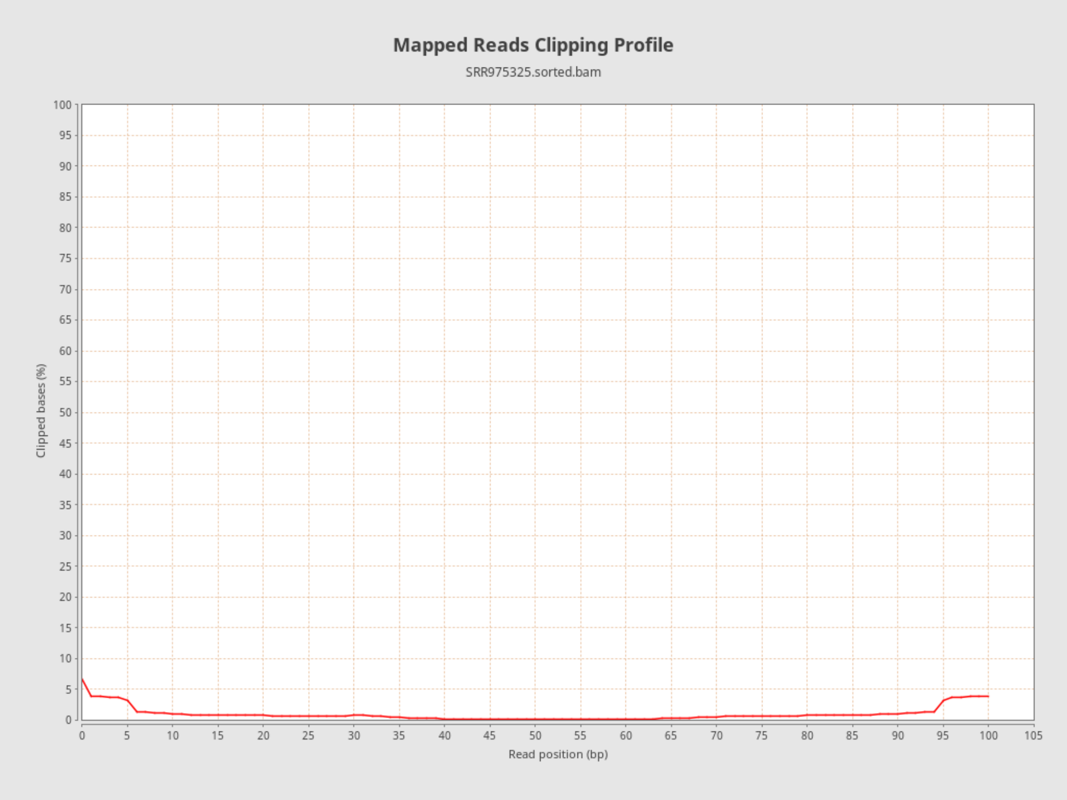
8. Results : Mapped Reads Nucleotide Content



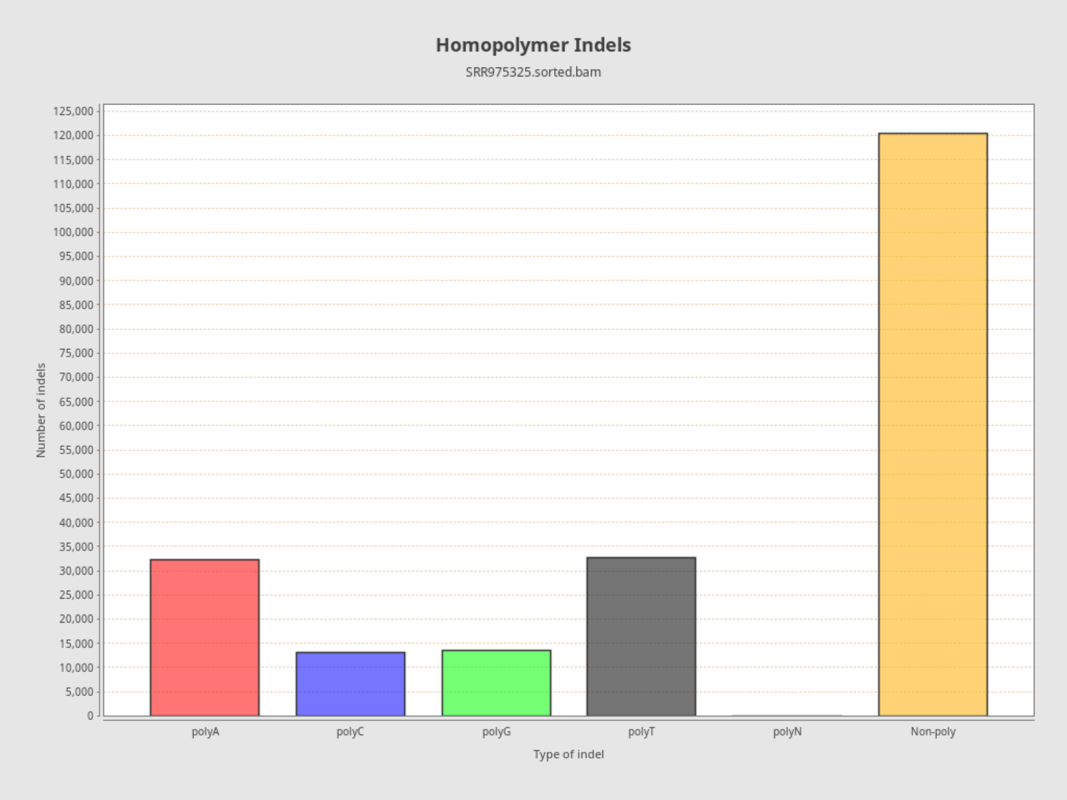
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

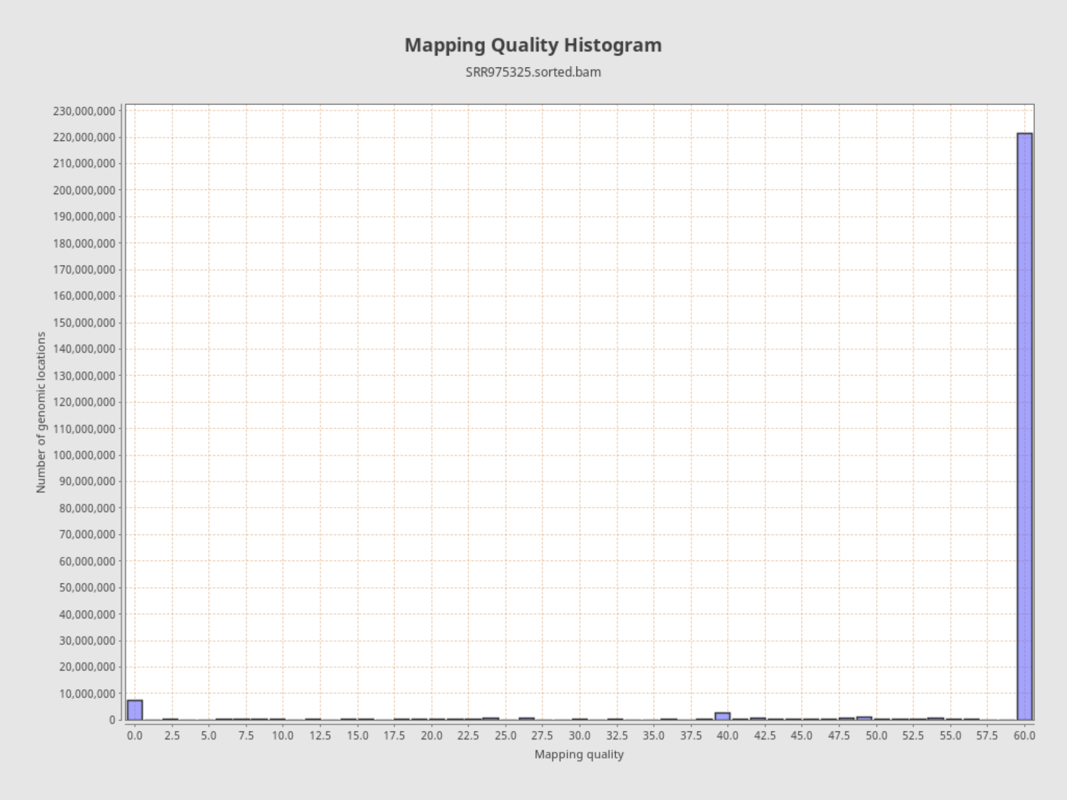


11. Results : Homopolymer Indels

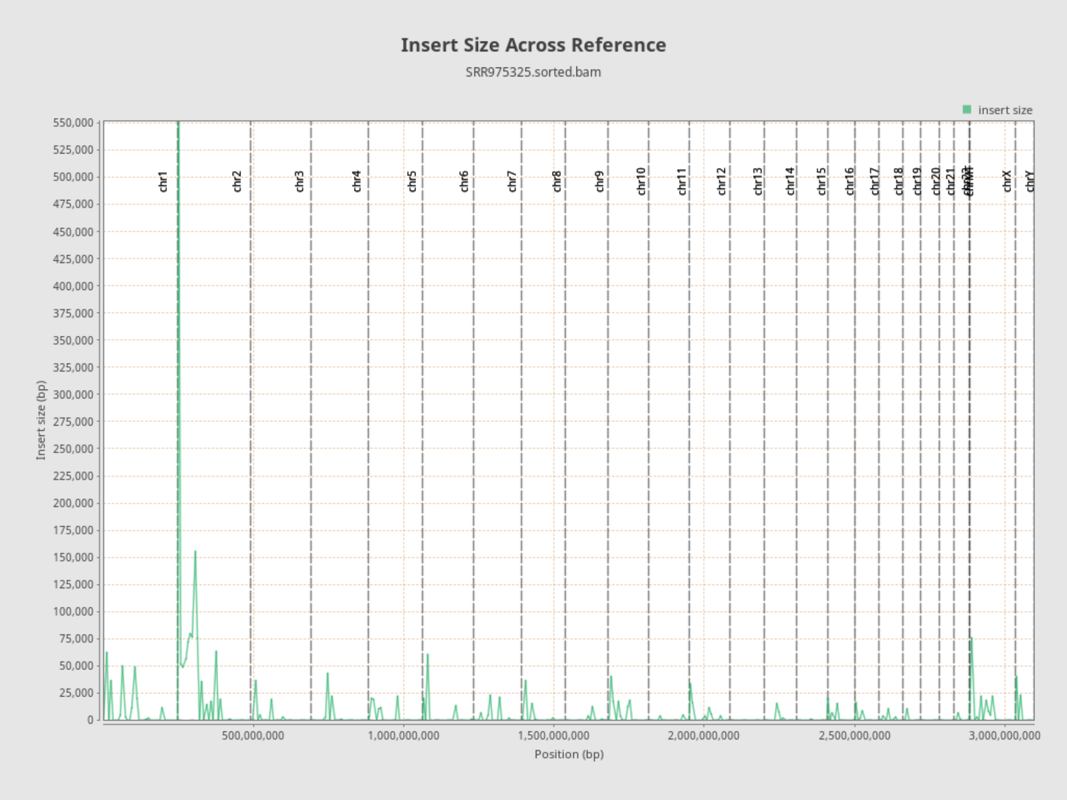


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram