Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 01:06:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975308.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_SRR975308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975308_1.fastq.gz SRR975308_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 01:06:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,115,180
Mapped reads	4,066,898 / 98.83%
Unmapped reads	48,282 / 1.17%
Mapped paired reads	4,066,898 / 98.83%
Mapped reads, first in pair	2,032,369 / 49.39%
Mapped reads, second in pair	2,034,529 / 49.44%
Mapped reads, both in pair	4,052,716 / 98.48%
Mapped reads, singletons	14,182 / 0.34%
Secondary alignments	0
Supplementary alignments	17,553 / 0.43%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	201,973 / 4.91%
Duplication rate	3.06%
Clipped reads	2,499,909 / 60.75%

2.2. ACGT Content

Number/percentage of A's	107,275,438 / 29.12%
Number/percentage of C's	71,565,304 / 19.43%
Number/percentage of T's	107,445,375 / 29.17%
Number/percentage of G's	82,101,263 / 22.29%
Number/percentage of N's	7,586 / 0%

GC Percentage	41.71%

2.3. Coverage

Mean	0.1191
Standard Deviation	1.0548

2.4. Mapping Quality

Mean Mapping Quality	52.75

2.5. Insert size

Mean	64,339
Standard Deviation	2,406,078.3
P25/Median/P75	133 / 165 / 209

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	2,750,275
Insertions	61,411
Mapped reads with at least one insertion	1.47%
Deletions	119,801
Mapped reads with at least one deletion	2.88%
Homopolymer indels	45.12%

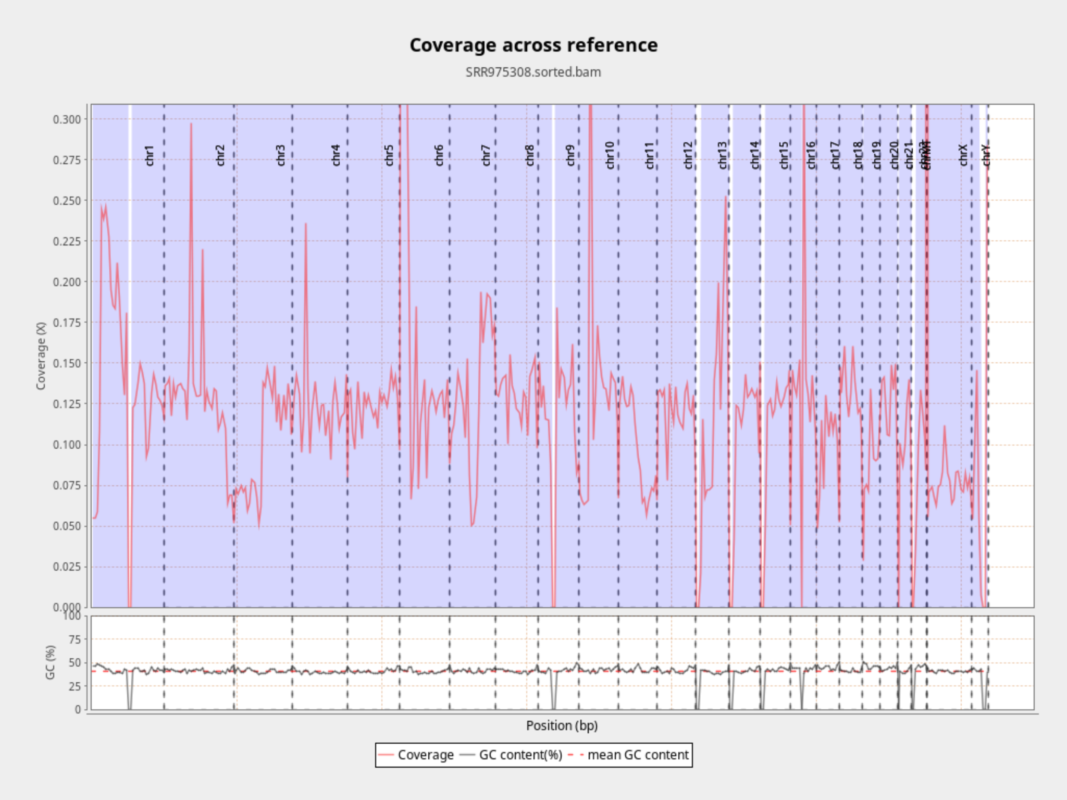
2.7. Chromosome stats

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

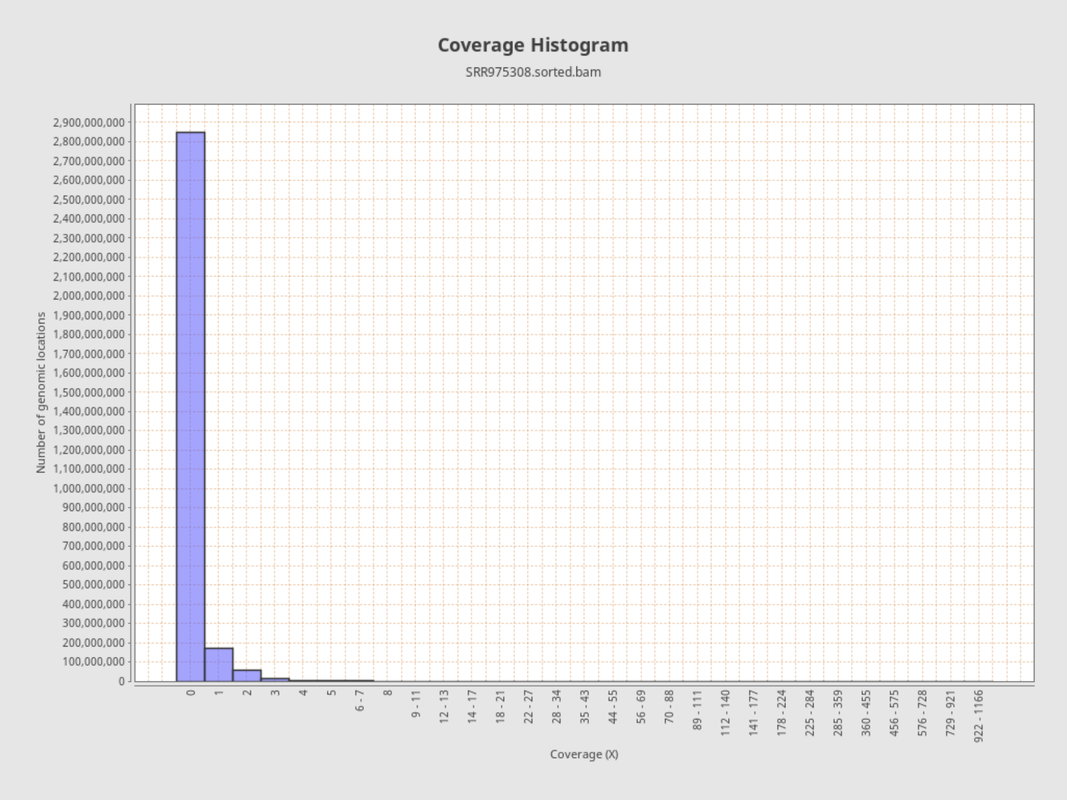
		bases	coverage	deviation
chr1	249250621	34702244	0.1392	1.0084
chr2	243199373	31619172	0.13	1.4184
chr3	198022430	19854578	0.1003	0.4304
chr4	191154276	23970820	0.1254	0.8743
chr5	180915260	22588434	0.1249	0.4708
chr6	171115067	28761513	0.1681	0.857
chr7	159138663	20691221	0.13	1.0953
chr8	146364022	19002568	0.1298	0.5928
chr9	141213431	16272071	0.1152	1.5619
chr10	135534747	17942967	0.1324	2.4056
chr11	135006516	13202927	0.0978	0.8706
chr12	133851895	16418503	0.1227	0.4635
chr13	115169878	12829426	0.1114	0.4462
chr14	107349540	11112855	0.1035	0.4686
chr15	102531392	10737226	0.1047	0.4239
chr16	90354753	12142368	0.1344	1.5887
chr17	81195210	7862519	0.0968	1.0298
chr18	78077248	10445864	0.1338	1.568
chr19	59128983	5147501	0.0871	0.6963
chr20	63025520	8019398	0.1272	0.5181
chr21	48129895	4717945	0.098	0.5799
chr22	51304566	3982858	0.0776	0.394
chrMT	16571	162012	9.7768	9.616
chrX	155270560	11723364	0.0755	0.5154

chrY	59373566	4696559	0.0791	1.6638

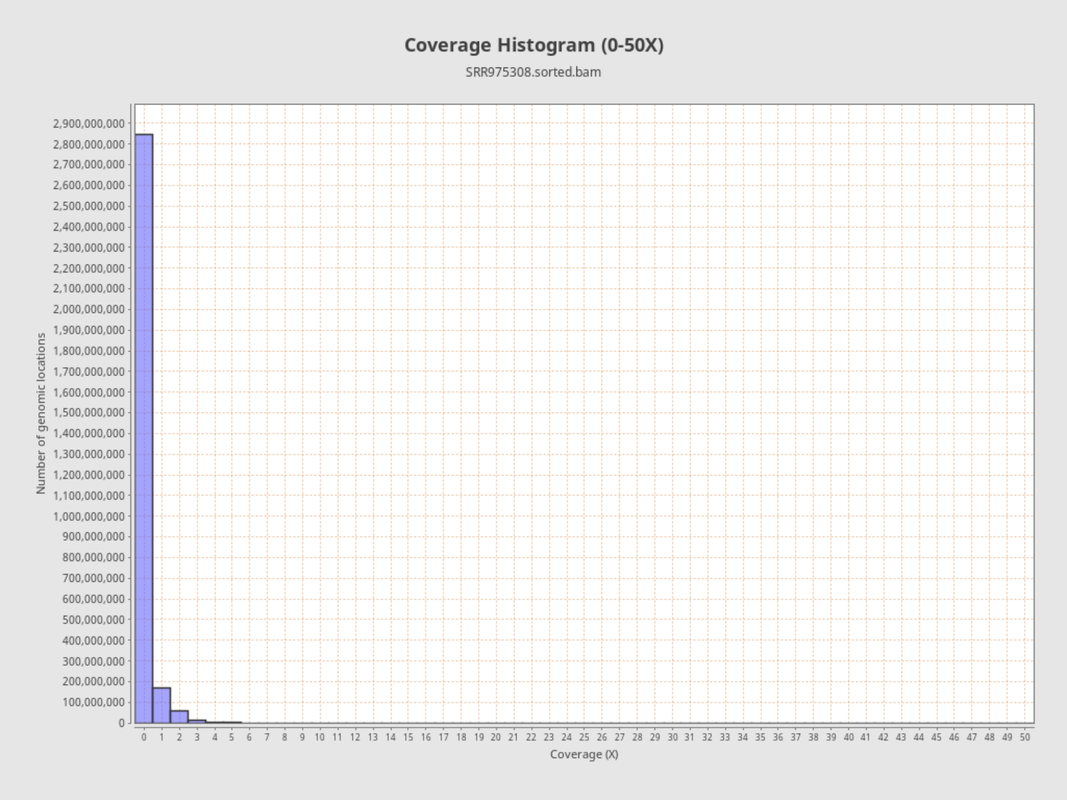
3. Results : Coverage across reference



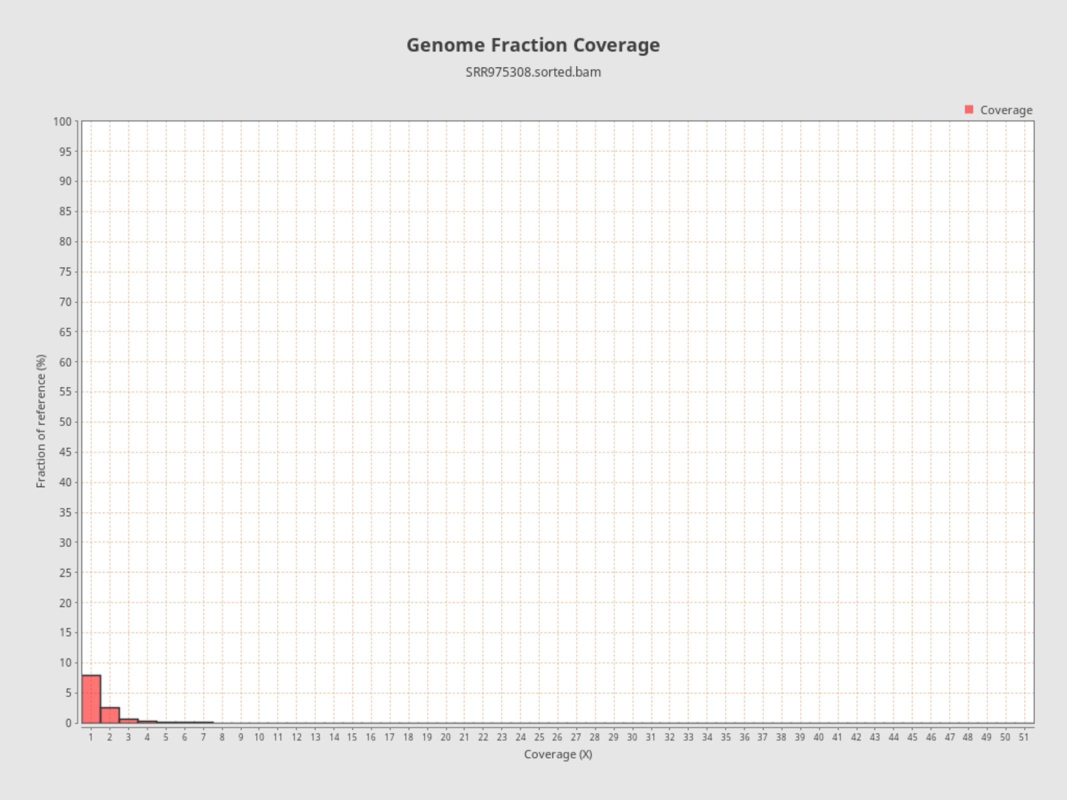
4. Results : Coverage Histogram



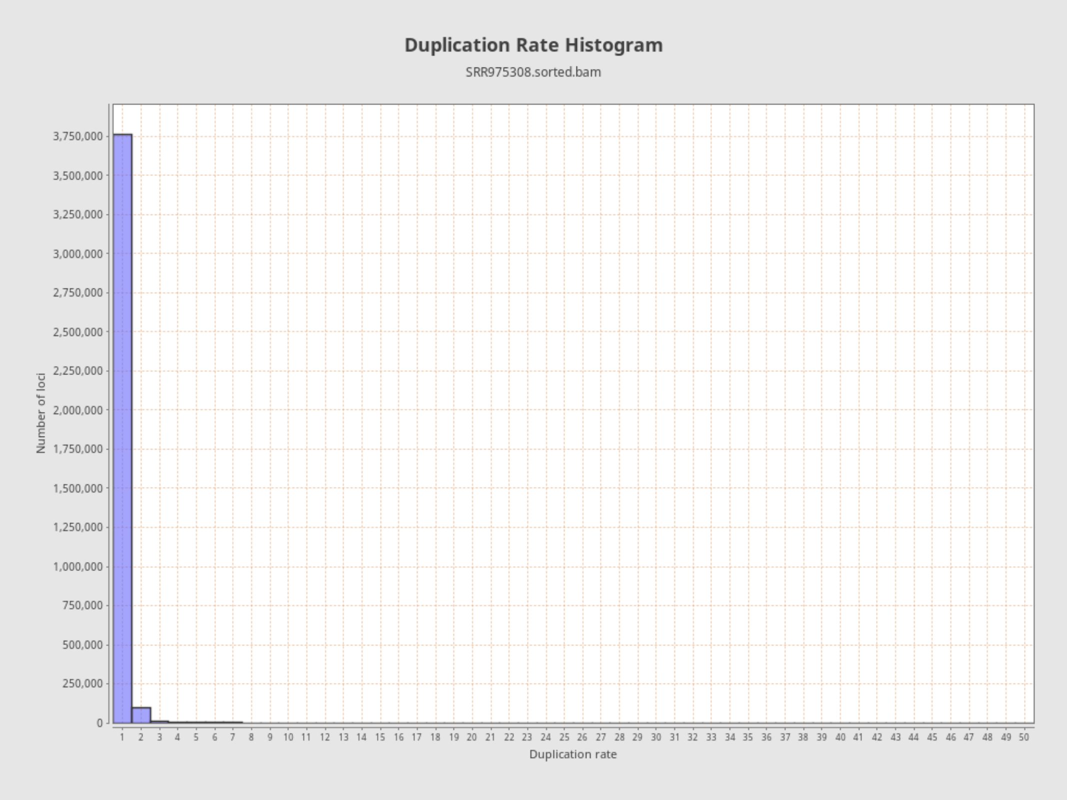
5. Results : Coverage Histogram (0-50X)



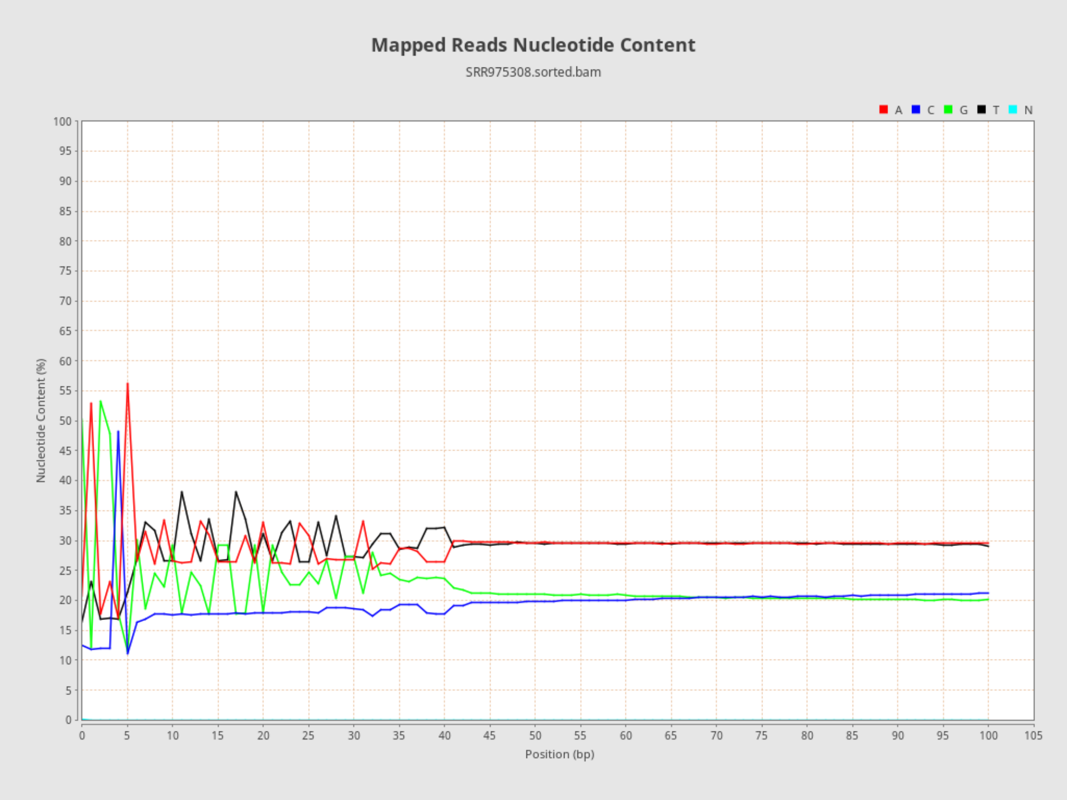
6. Results : Genome Fraction Coverage



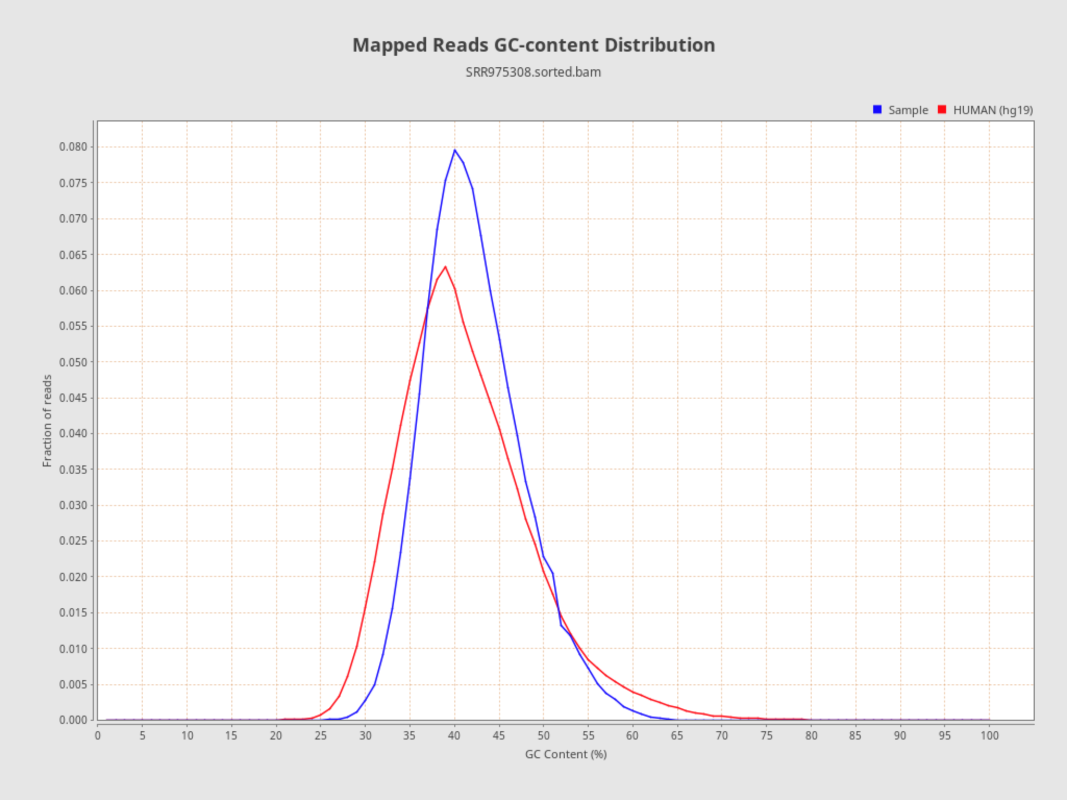
7. Results : Duplication Rate Histogram



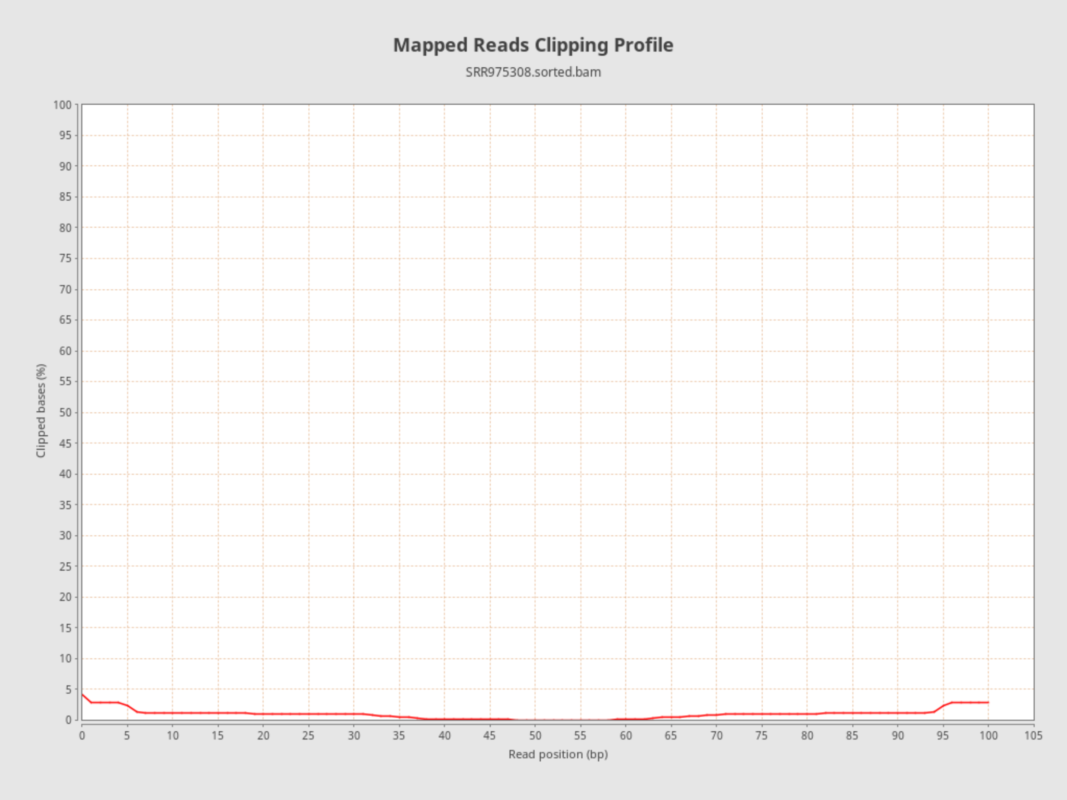
8. Results : Mapped Reads Nucleotide Content



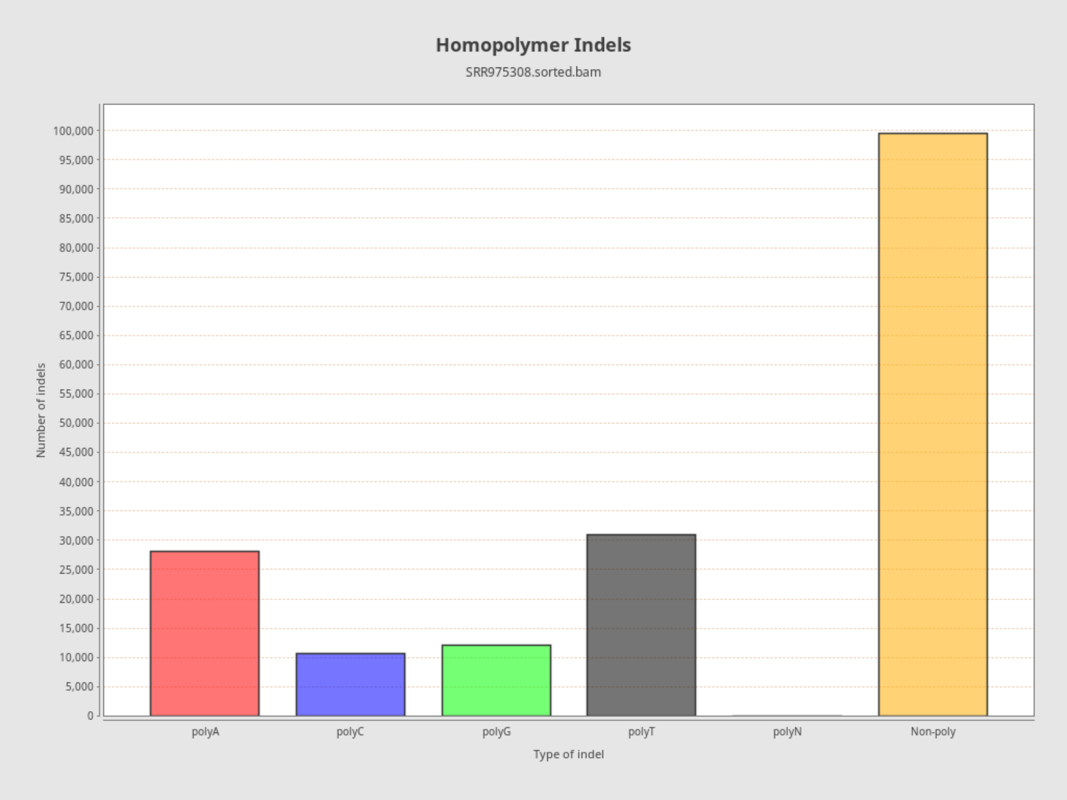
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

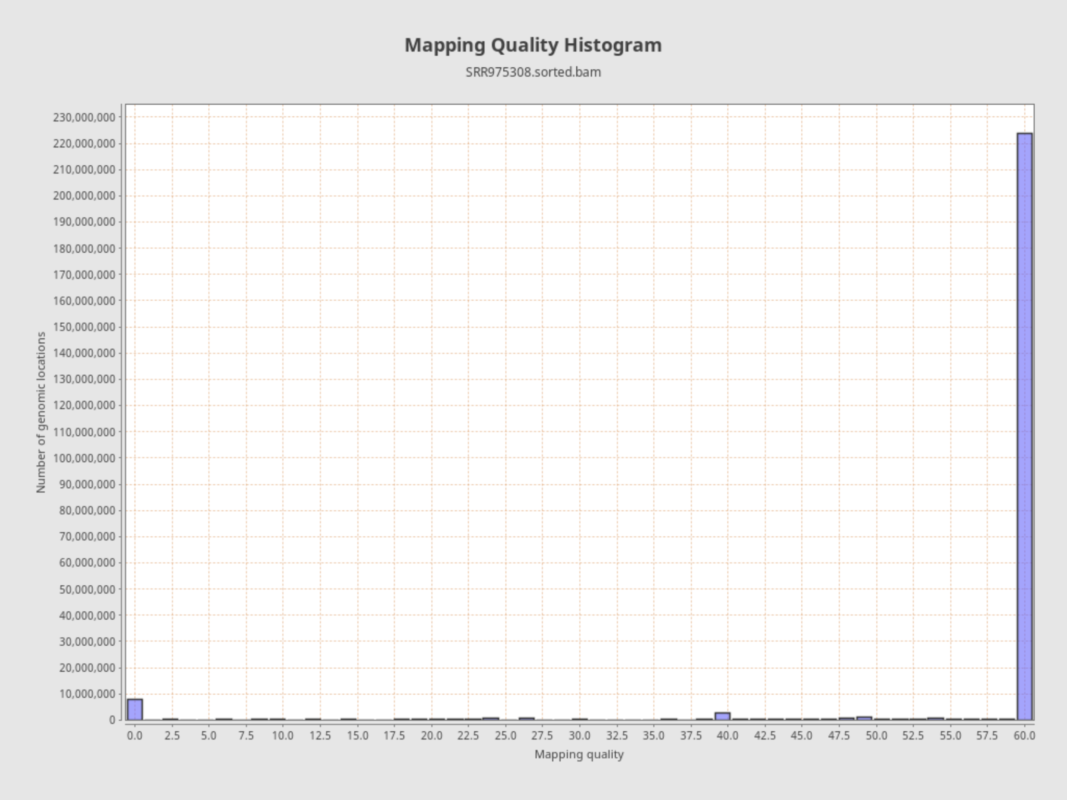


11. Results : Homopolymer Indels

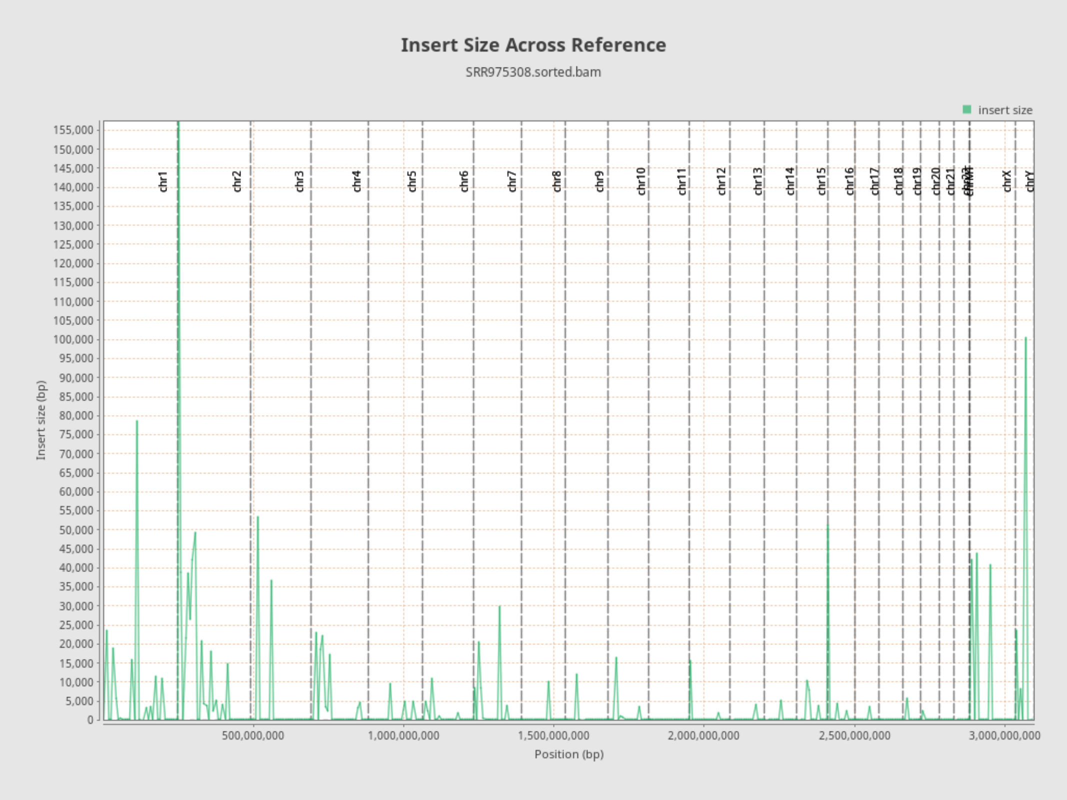


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram