Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/07 01:44:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975309.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_SRR975309 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975309_1.fastq.gz SRR975309_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 07 01:44:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975309.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	52,332,498
Mapped reads	52,070,397 / 99.5%
Unmapped reads	262,101 / 0.5%
Mapped paired reads	52,070,397 / 99.5%
Mapped reads, first in pair	26,028,497 / 49.74%
Mapped reads, second in pair	26,041,900 / 49.76%
Mapped reads, both in pair	51,984,568 / 99.34%
Mapped reads, singletons	85,829 / 0.16%
Secondary alignments	0
Supplementary alignments	105,006 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	30,078,517 / 57.48%
Duplication rate	42.24%
Clipped reads	33,099,486 / 63.25%

2.2. ACGT Content

Number/percentage of A's	1,236,772,298 / 26.24%
Number/percentage of C's	1,025,489,133 / 21.75%
Number/percentage of T's	1,295,404,253 / 27.48%
Number/percentage of G's	1,156,320,505 / 24.53%
Number/percentage of N's	81,113 / 0%

GC Percentage	46.28%

2.3. Coverage

Mean	1.5233
Standard Deviation	22.9579

2.4. Mapping Quality

Mean Mapping Quality	55.66

2.5. Insert size

Mean	37,851.1
Standard Deviation	1,913,898.09
P25/Median/P75	146 / 184 / 235

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	27,738,807
Insertions	509,610
Mapped reads with at least one insertion	0.97%
Deletions	1,083,825
Mapped reads with at least one deletion	2.05%
Homopolymer indels	45.37%

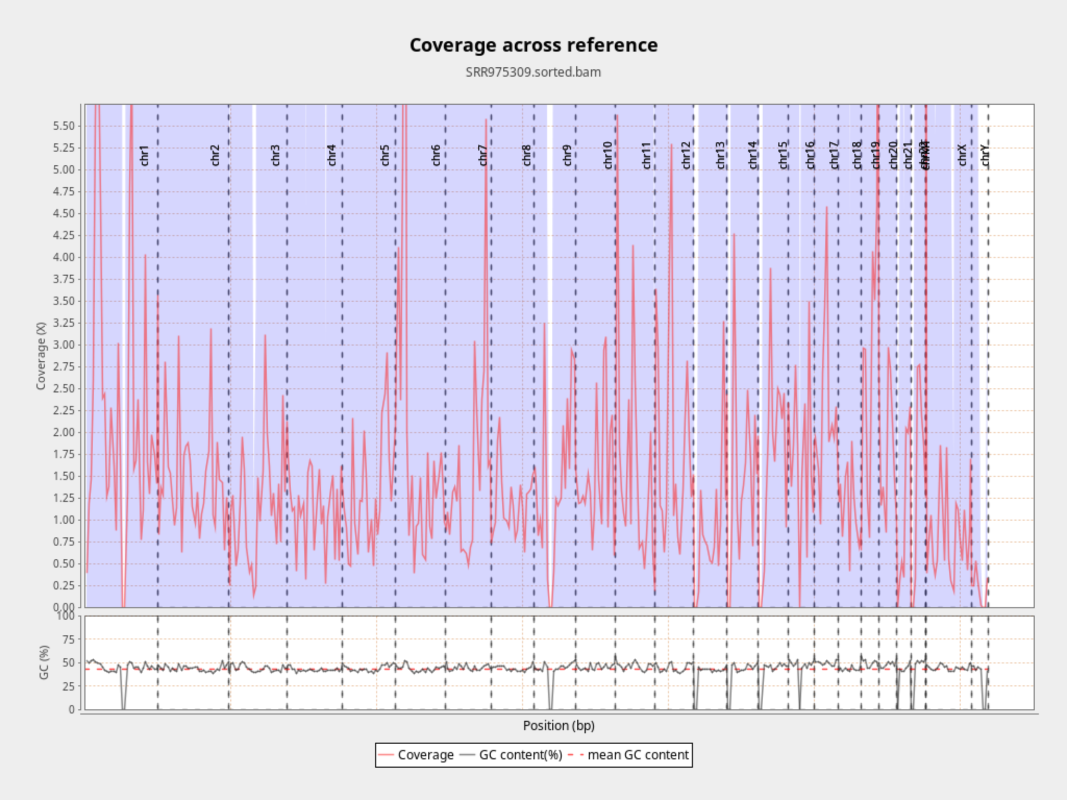
2.7. Chromosome stats

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

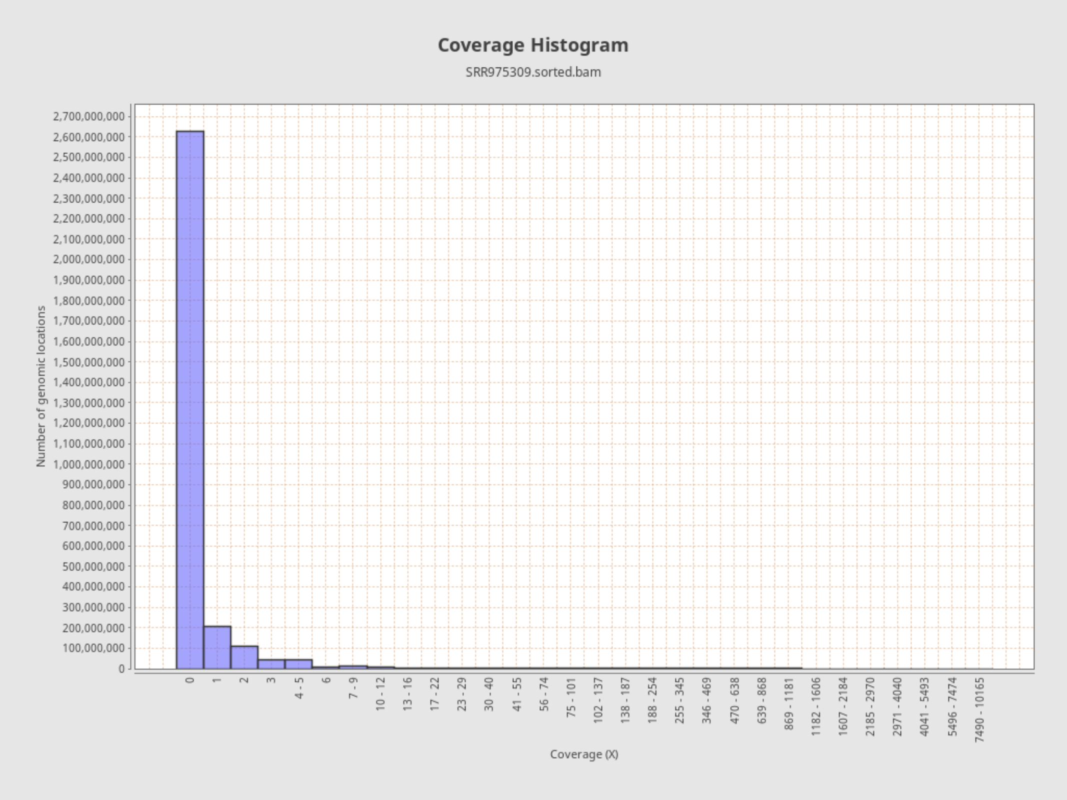
		bases	coverage	deviation
chr1	249250621	564565477	2.2651	30.7979
chr2	243199373	353048199	1.4517	20.2062
chr3	198022430	235545079	1.1895	17.802
chr4	191154276	213818680	1.1186	19.2224
chr5	180915260	238341755	1.3174	19.6725
chr6	171115067	364816852	2.132	33.2719
chr7	159138663	252240863	1.585	24.501
chr8	146364022	177677828	1.2139	17.4446
chr9	141213431	193801792	1.3724	20.982
chr10	135534747	210468723	1.5529	22.3701
chr11	135006516	228061816	1.6893	24.2877
chr12	133851895	259079801	1.9356	25.6095
chr13	115169878	103931722	0.9024	15.8472
chr14	107349540	154802955	1.442	20.7515
chr15	102531392	174952888	1.7063	23.7639
chr16	90354753	152369377	1.6863	21.3239
chr17	81195210	186040315	2.2913	30.9765
chr18	78077248	90461359	1.1586	18.3689
chr19	59128983	174738030	2.9552	32.742
chr20	63025520	115895667	1.8389	25.837
chr21	48129895	51519358	1.0704	21.608
chr22	51304566	79008591	1.54	22.4821
chrMT	16571	219726	13.2597	16.3957
chrX	155270560	128041803	0.8246	14.1763

chrY	59373566	12255079	0.2064	4.8574

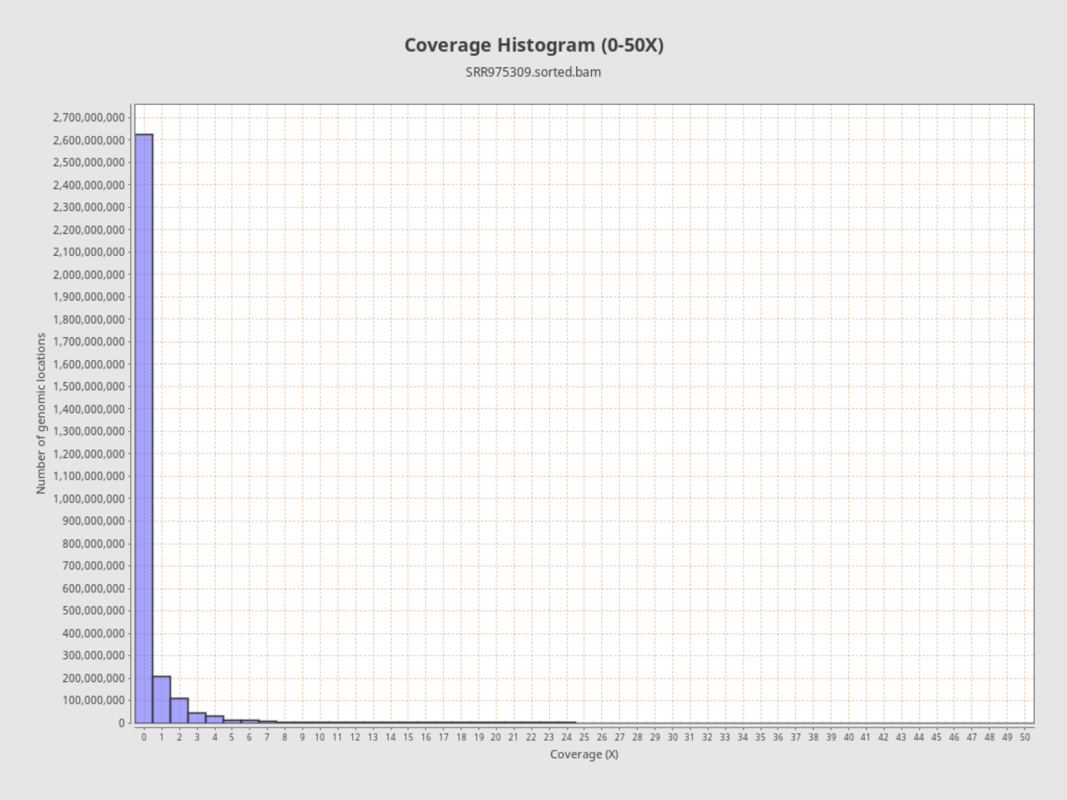
3. Results : Coverage across reference



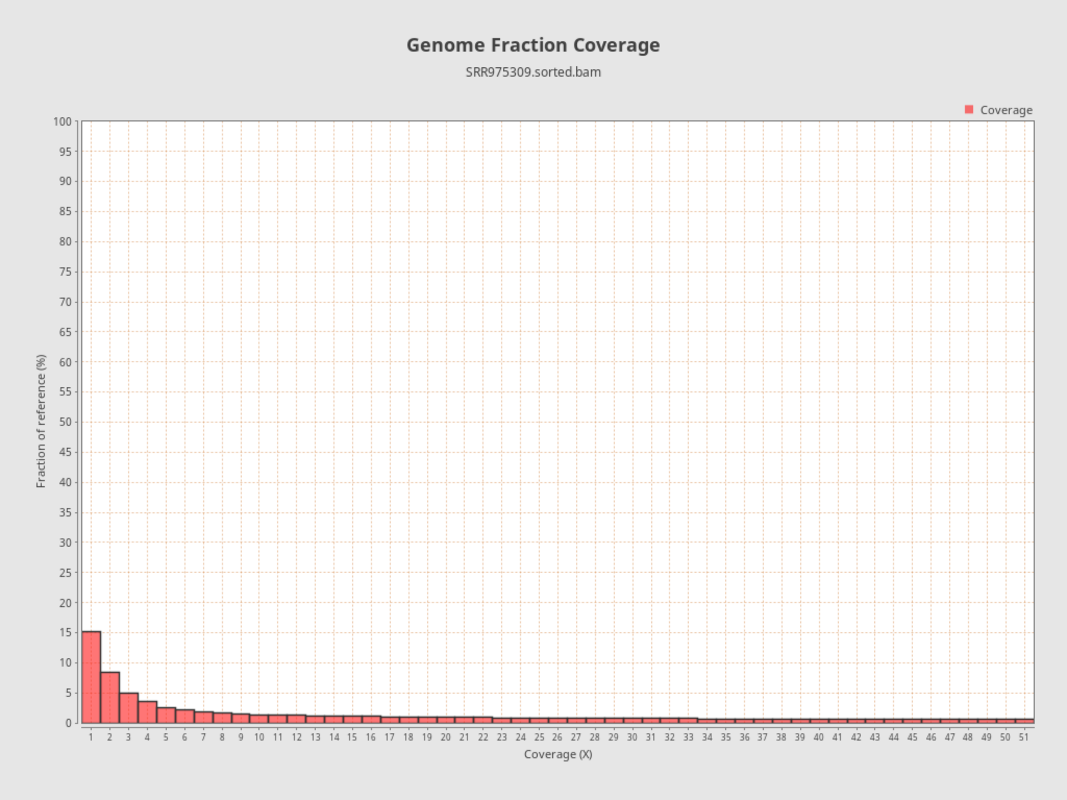
4. Results : Coverage Histogram



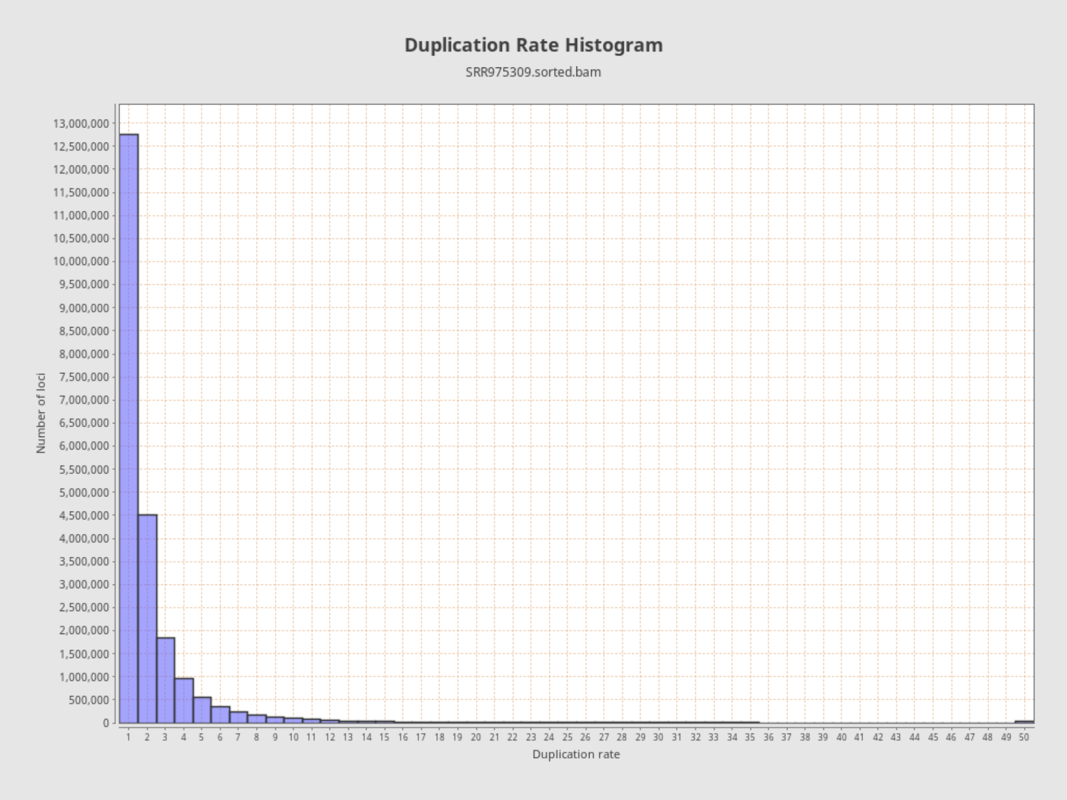
5. Results : Coverage Histogram (0-50X)



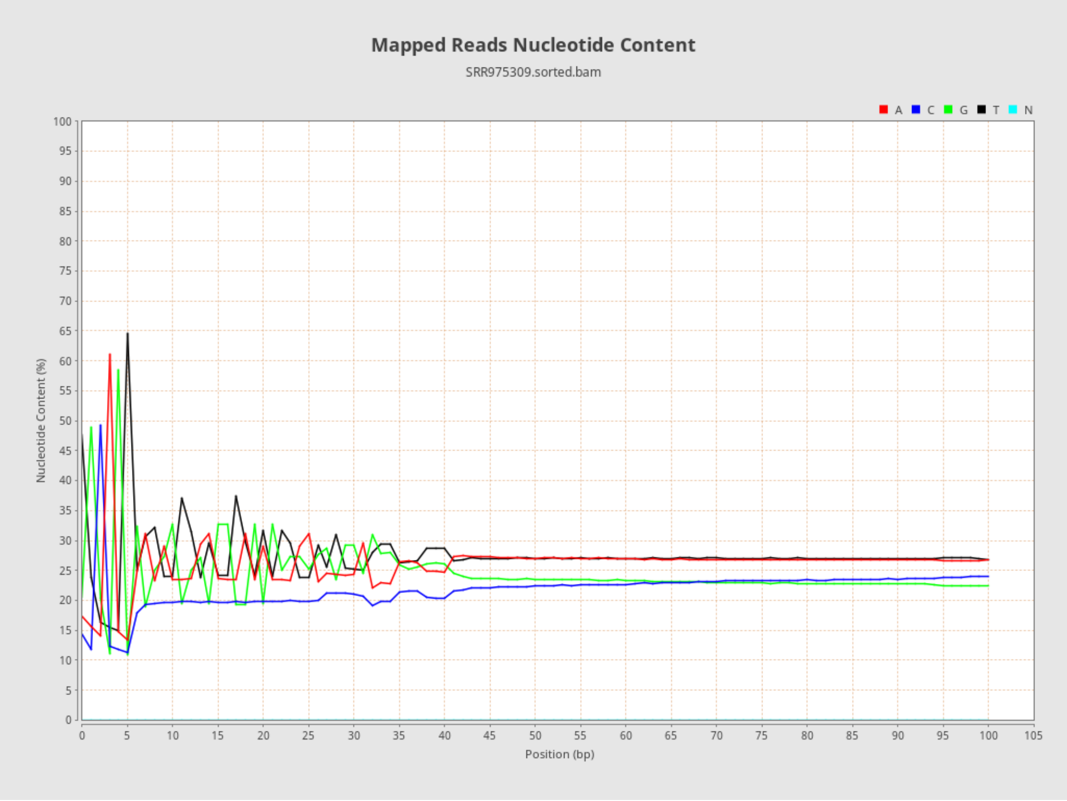
6. Results : Genome Fraction Coverage



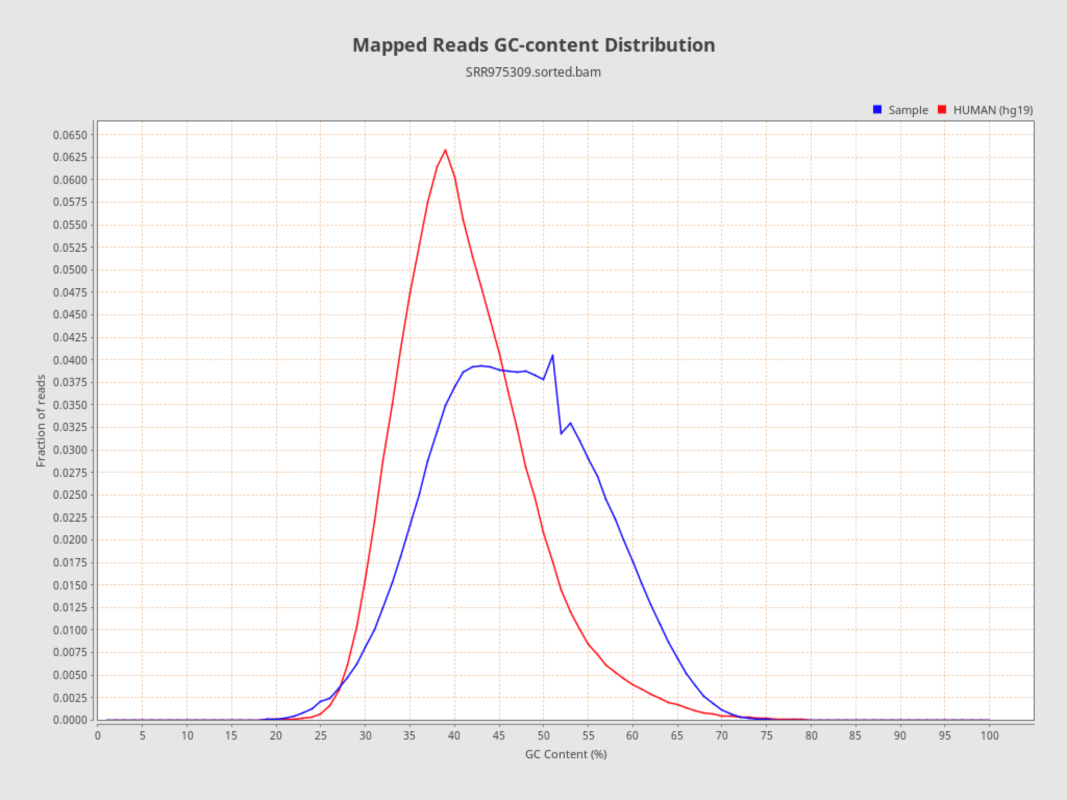
7. Results : Duplication Rate Histogram



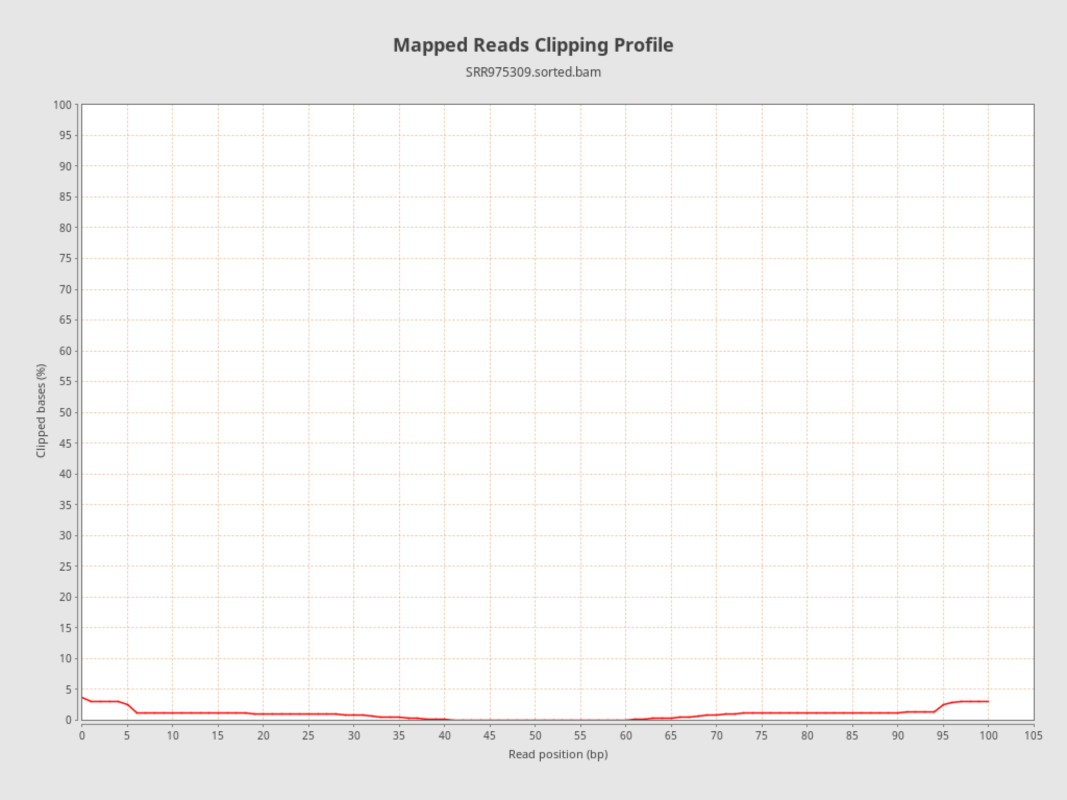
8. Results : Mapped Reads Nucleotide Content



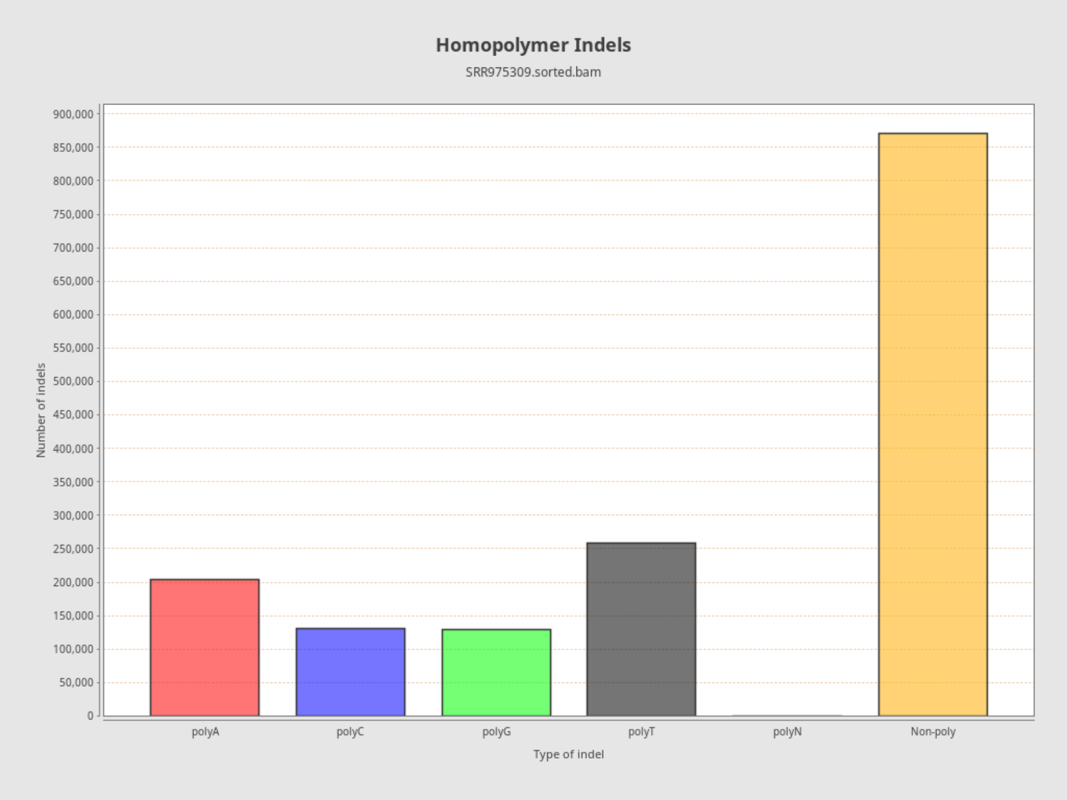
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile

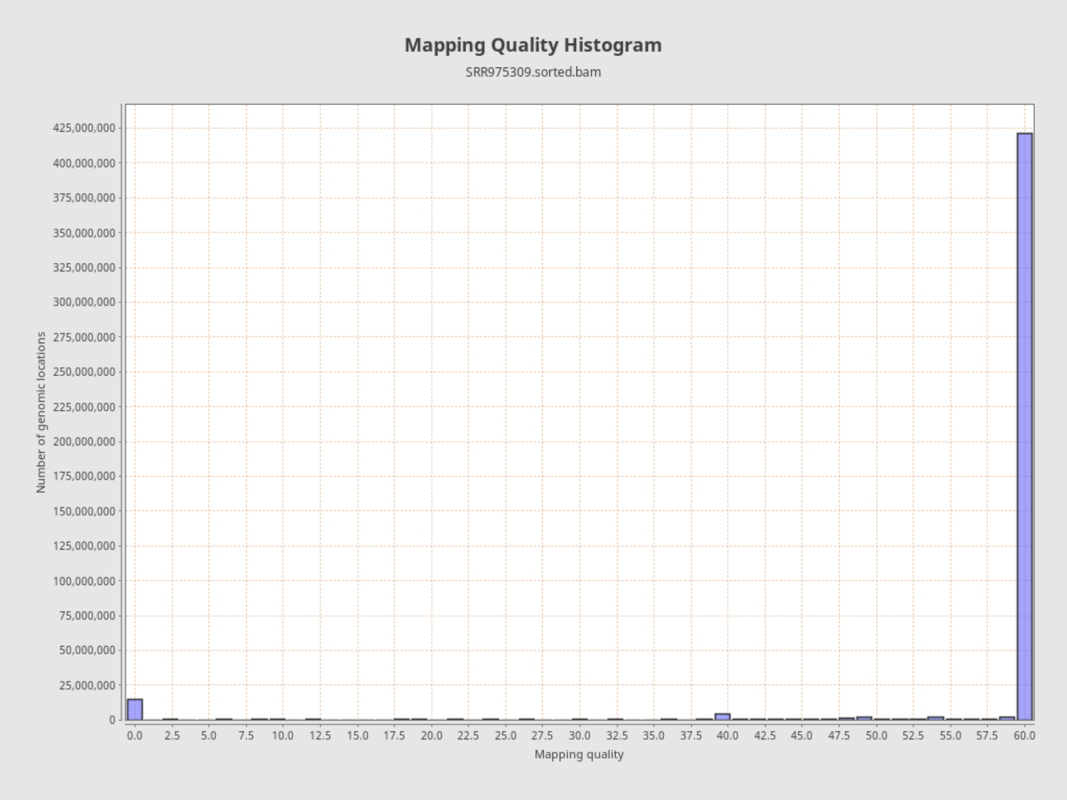


11. Results : Homopolymer Indels

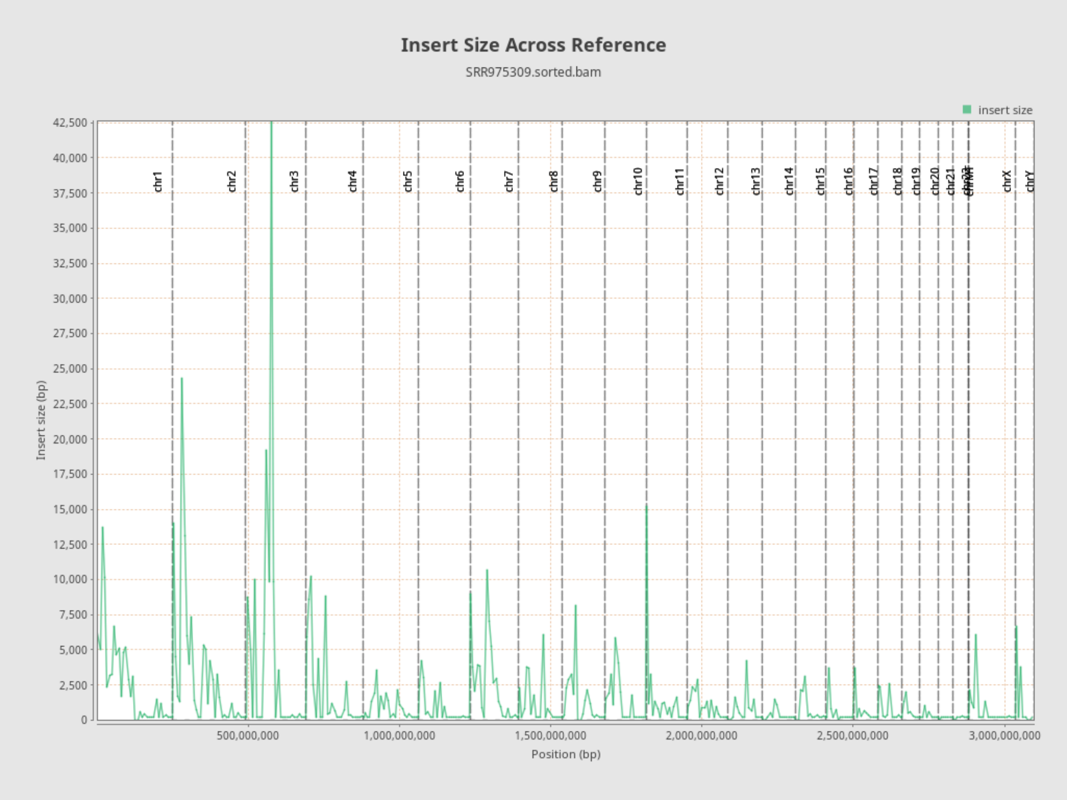


12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram