Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 21:32:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975305.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_SRR975305 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975305_1.fastq.gz SRR975305_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 21:32:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975305.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	56,487,804
Mapped reads	56,288,911 / 99.65%
Unmapped reads	198,893 / 0.35%
Mapped paired reads	56,288,911 / 99.65%
Mapped reads, first in pair	28,136,089 / 49.81%
Mapped reads, second in pair	28,152,822 / 49.84%
Mapped reads, both in pair	56,201,748 / 99.49%
Mapped reads, singletons	87,163 / 0.15%
Secondary alignments	0
Supplementary alignments	111,533 / 0.2%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	33,061,021 / 58.53%
Duplication rate	43.43%
Clipped reads	34,835,391 / 61.67%

2.2. ACGT Content

Number/percentage of A's	1,330,207,811 / 25.99%
Number/percentage of C's	1,129,611,815 / 22.07%
Number/percentage of T's	1,402,024,235 / 27.39%
Number/percentage of G's	1,256,660,576 / 24.55%
Number/percentage of N's	93,970 / 0%

GC Percentage	46.62%

2.3. Coverage

Mean	1.654
Standard Deviation	24.5585

2.4. Mapping Quality

Mean Mapping Quality	55.75

2.5. Insert size

Mean	62,963.78
Standard Deviation	2,467,909.66
P25/Median/P75	146 / 184 / 234

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	29,421,272
Insertions	459,316
Mapped reads with at least one insertion	0.81%
Deletions	1,107,081
Mapped reads with at least one deletion	1.94%
Homopolymer indels	47.1%

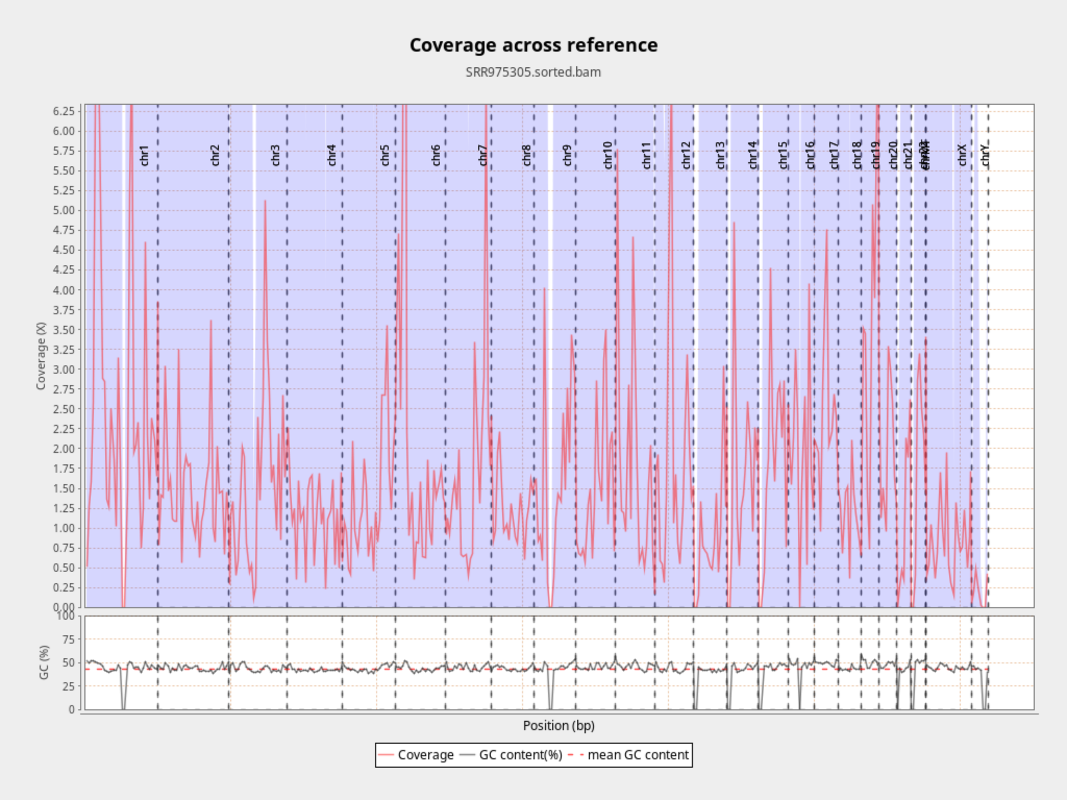
2.7. Chromosome stats

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

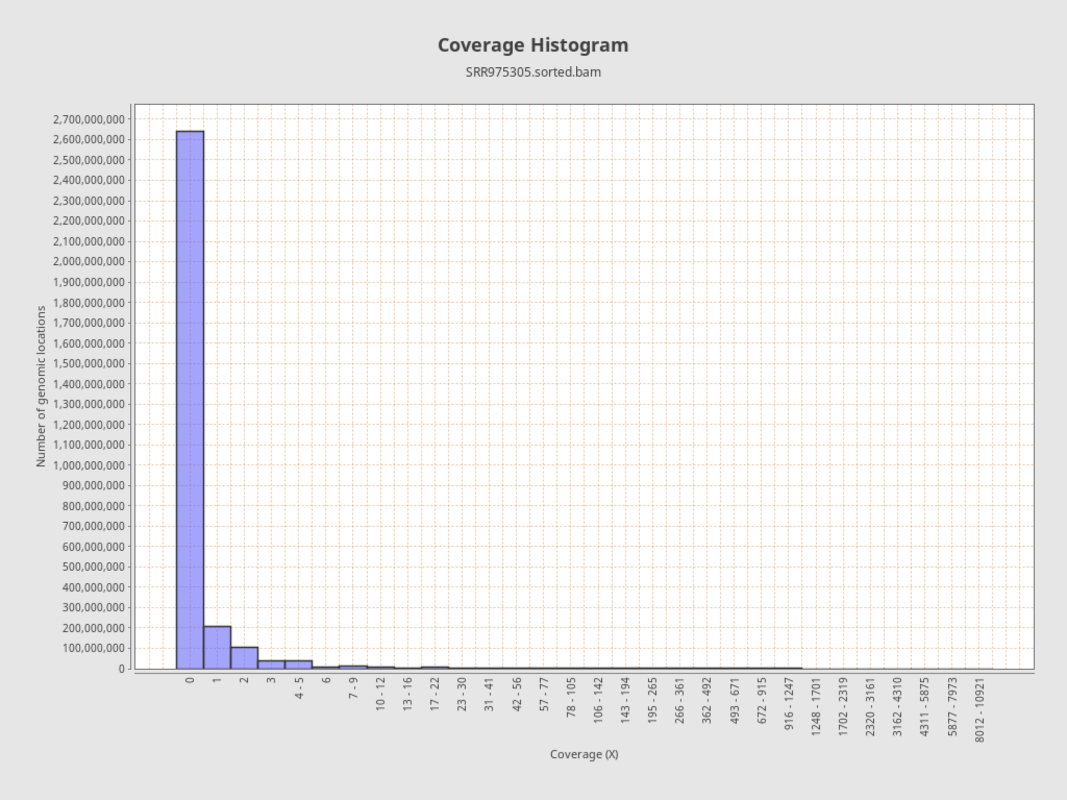
		bases	coverage	deviation
chr1	249250621	630712667	2.5304	34.0386
chr2	243199373	361156087	1.485	20.6318
chr3	198022430	315104574	1.5913	22.9544
chr4	191154276	222691333	1.165	19.7553
chr5	180915260	249376273	1.3784	19.6681
chr6	171115067	401490664	2.3463	37.2819
chr7	159138663	273998111	1.7218	28.0984
chr8	146364022	178148063	1.2172	17.4788
chr9	141213431	216062378	1.53	21.7652
chr10	135534747	204059898	1.5056	22.3397
chr11	135006516	249133631	1.8453	24.013
chr12	133851895	255546796	1.9092	24.4004
chr13	115169878	102256402	0.8879	16.1697
chr14	107349540	168935945	1.5737	22.1793
chr15	102531392	186777138	1.8217	26.1995
chr16	90354753	174364368	1.9298	25.2958
chr17	81195210	203845048	2.5106	29.3868
chr18	78077248	92998461	1.1911	19.894
chr19	59128983	219522301	3.7126	39.4901
chr20	63025520	130974575	2.0781	26.8781
chr21	48129895	52512054	1.091	19.9075
chr22	51304566	89144378	1.7376	22.0751
chrMT	16571	56613	3.4164	4.2825
chrX	155270560	130315461	0.8393	13.7936

chrY	59373566	11051382	0.1861	4.1361

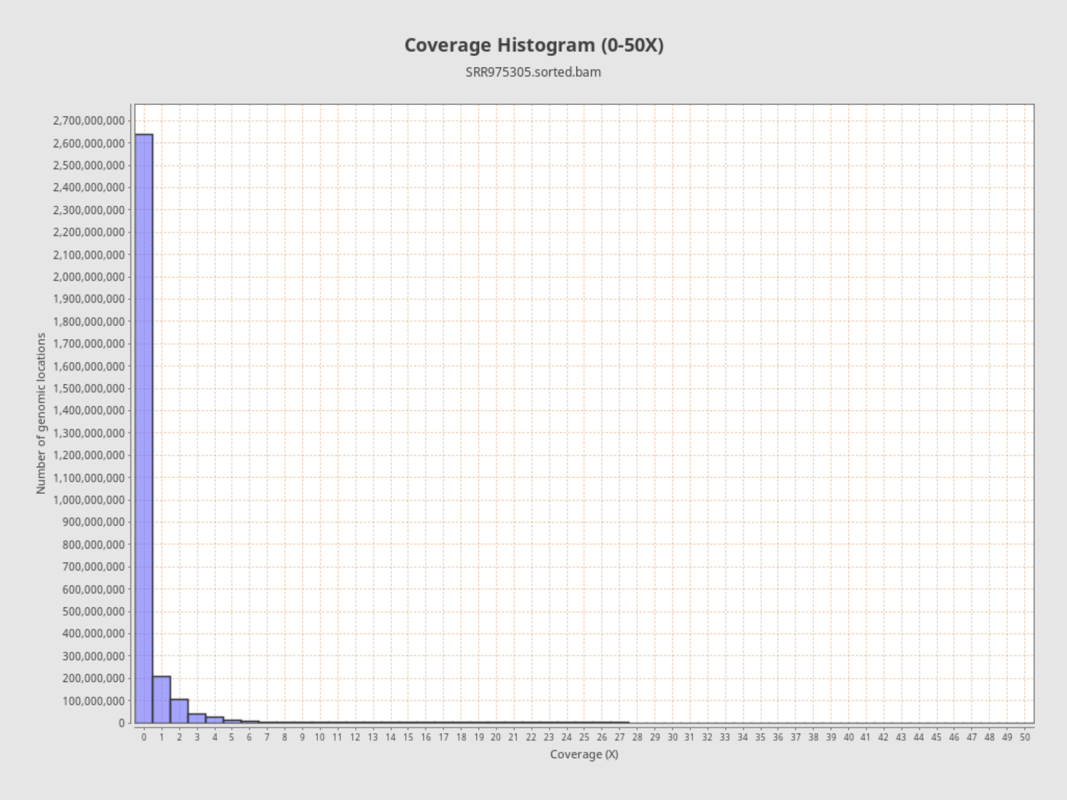
3. Results : Coverage across reference



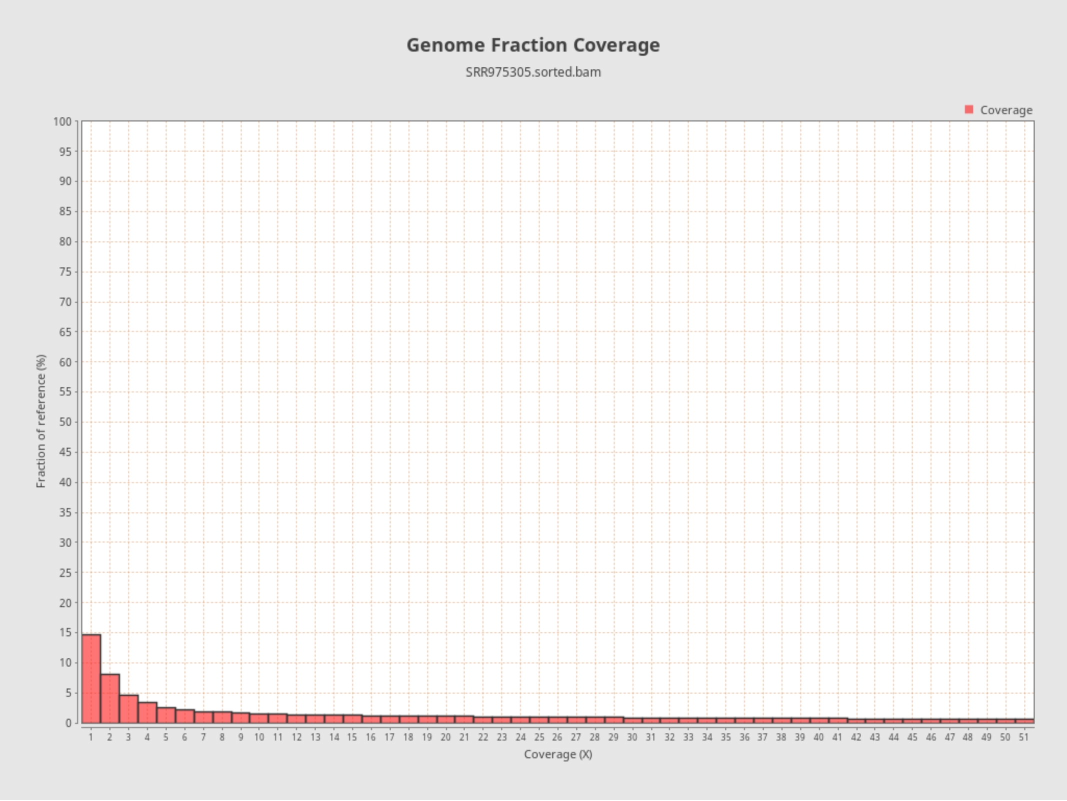
4. Results : Coverage Histogram



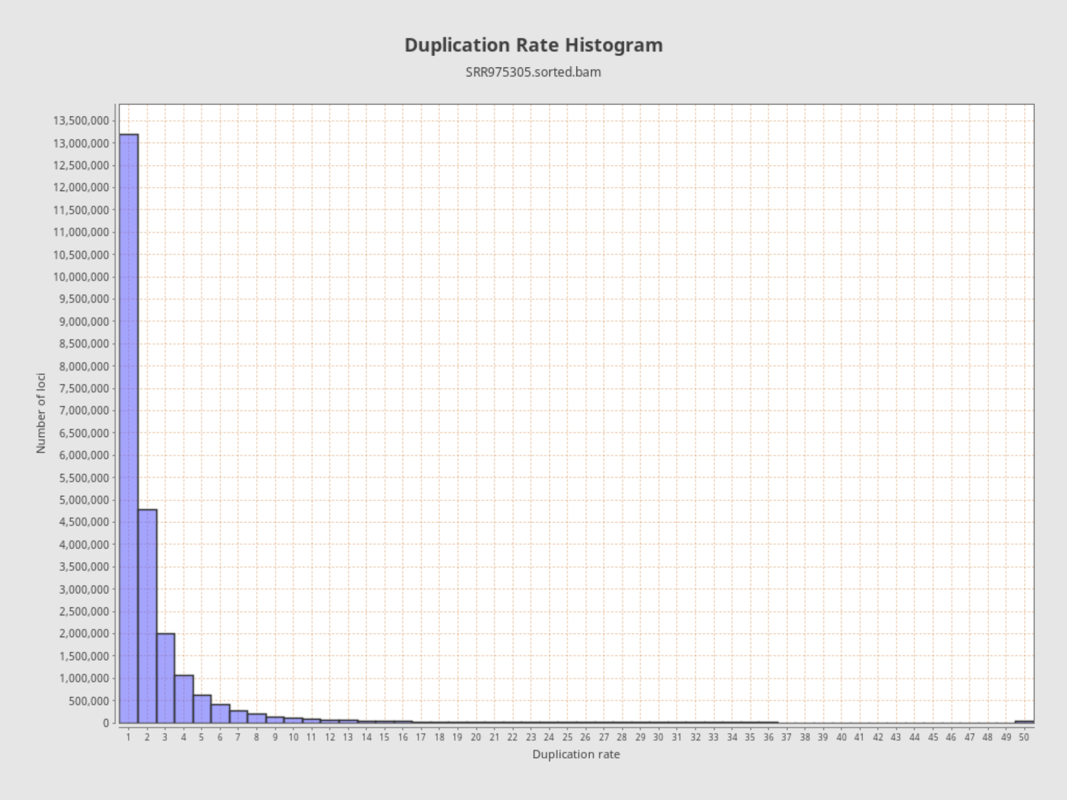
5. Results : Coverage Histogram (0-50X)



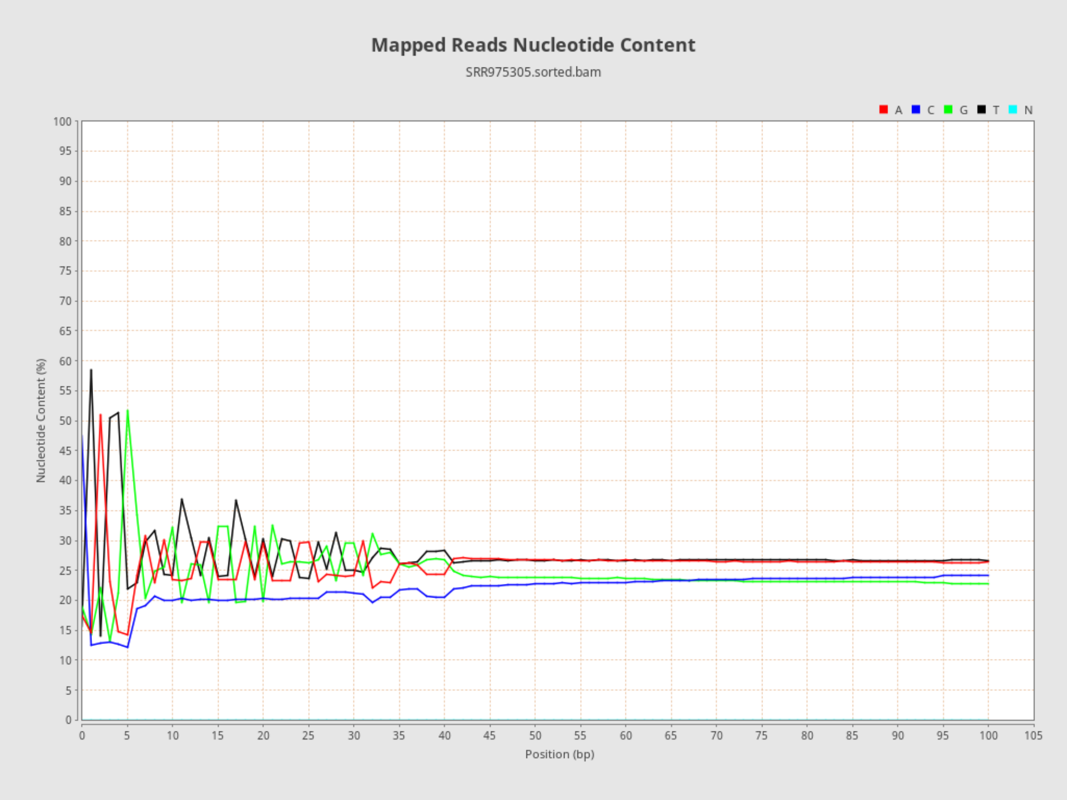
6. Results : Genome Fraction Coverage



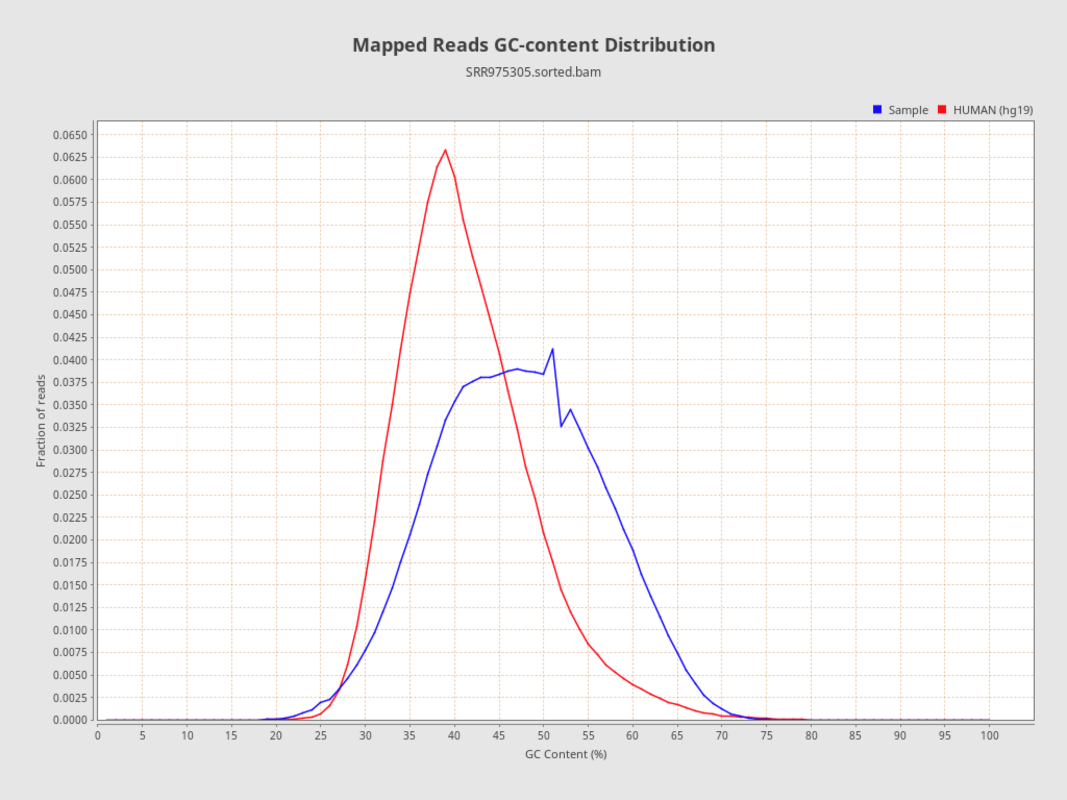
7. Results : Duplication Rate Histogram



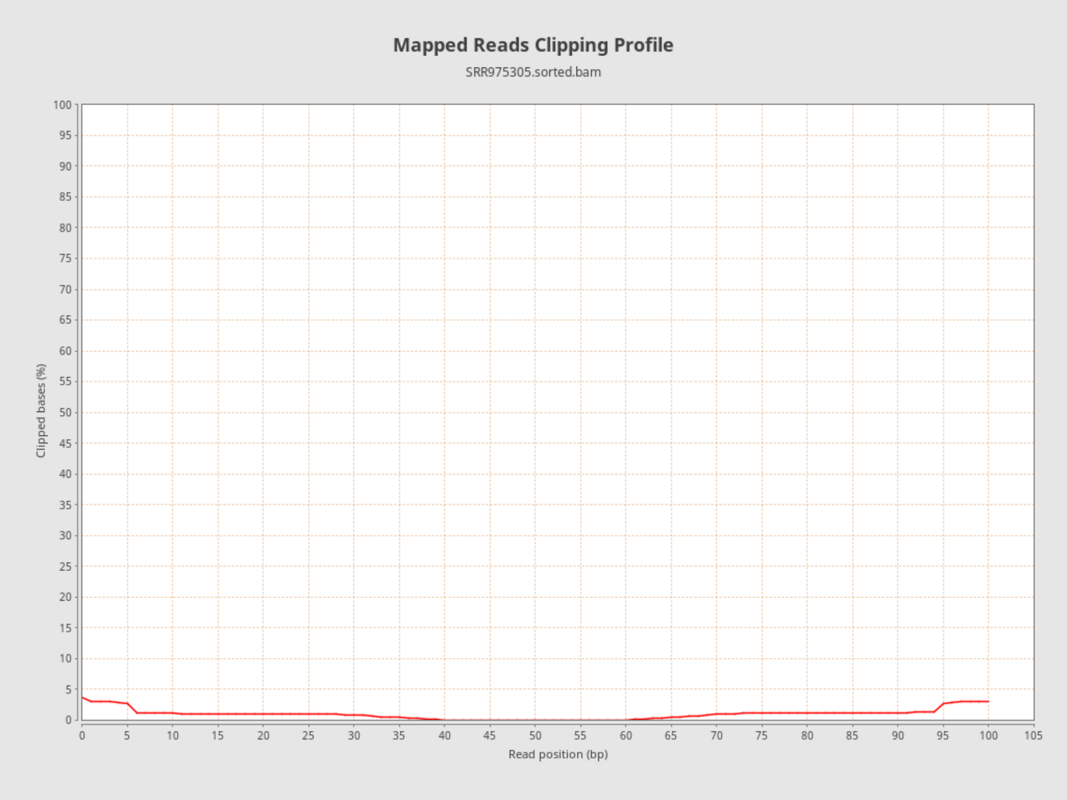
8. Results : Mapped Reads Nucleotide Content



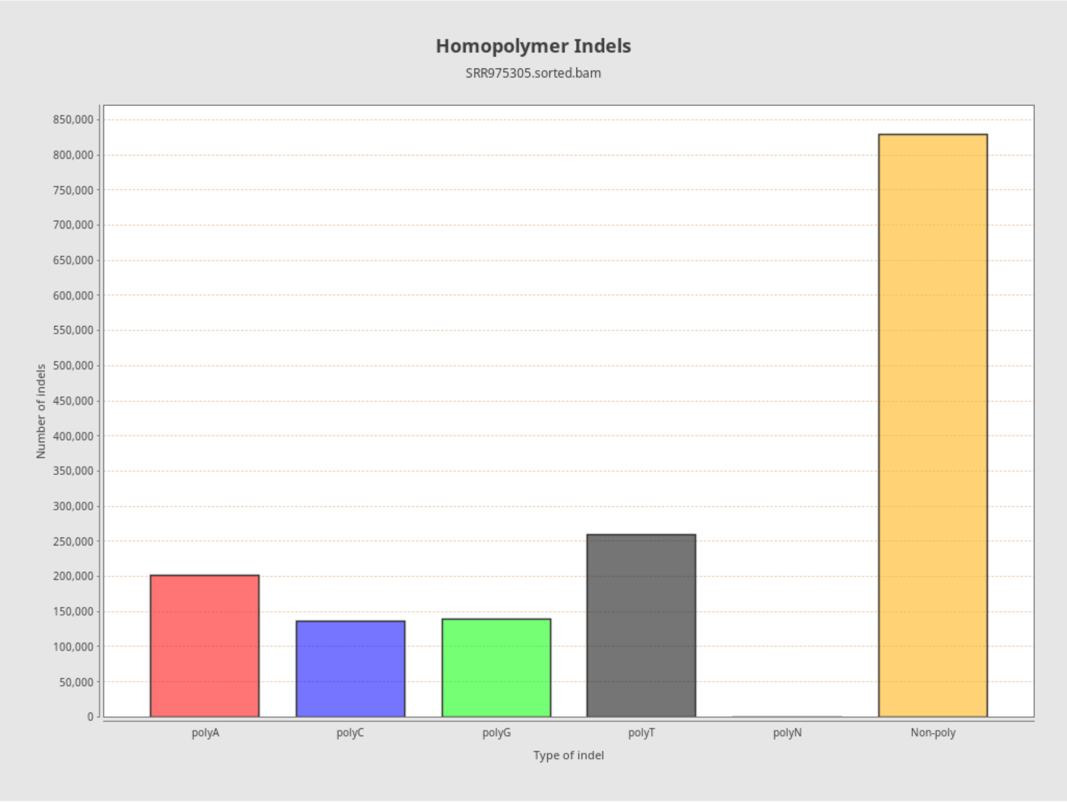
9. Results : Mapped Reads GC-content Distribution



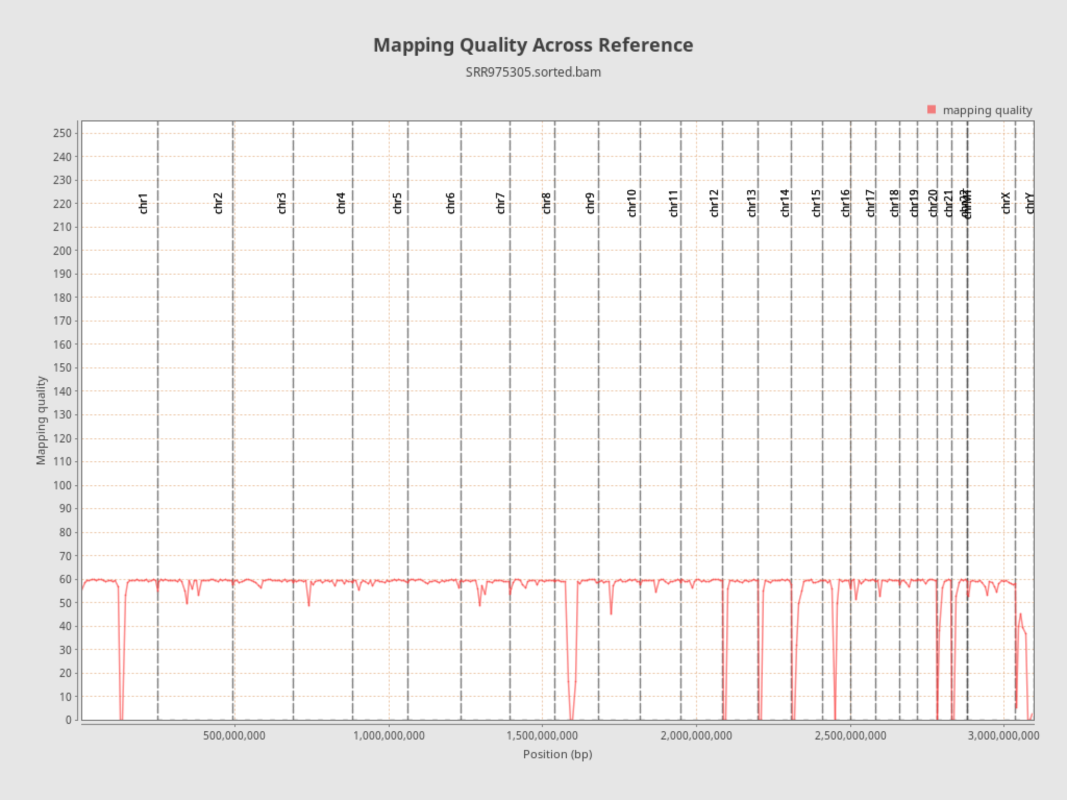
10. Results : Mapped Reads Clipping Profile



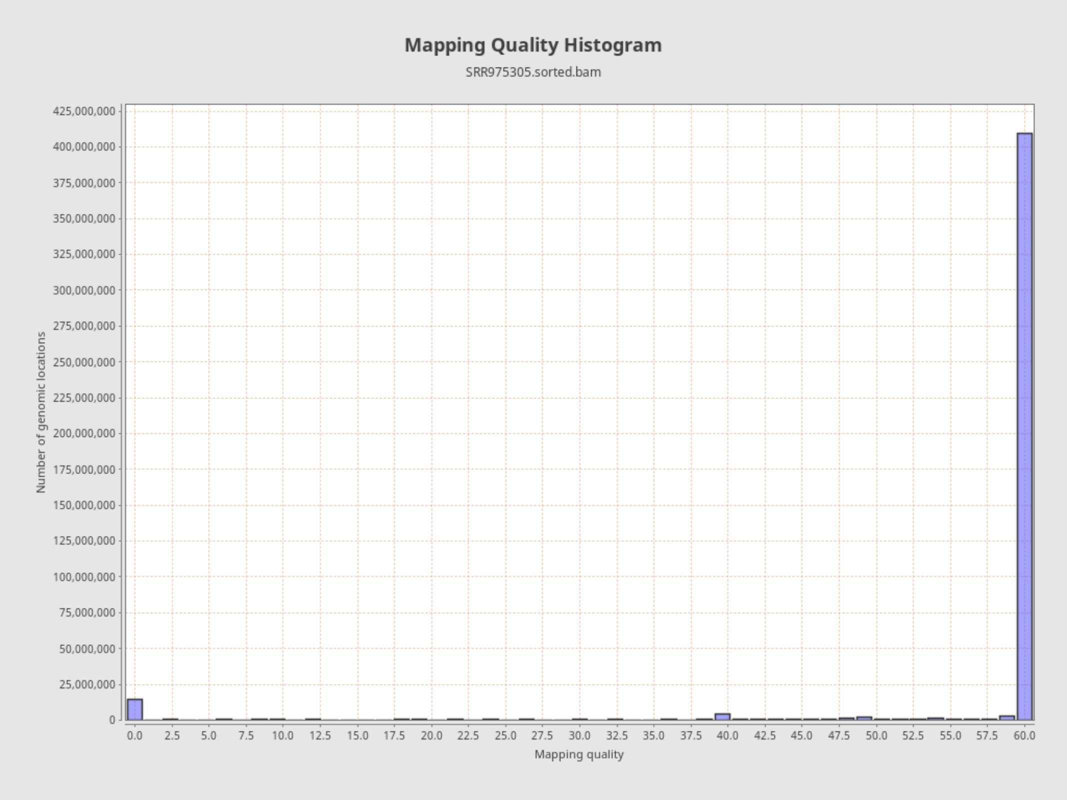
11. Results : Homopolymer Indels



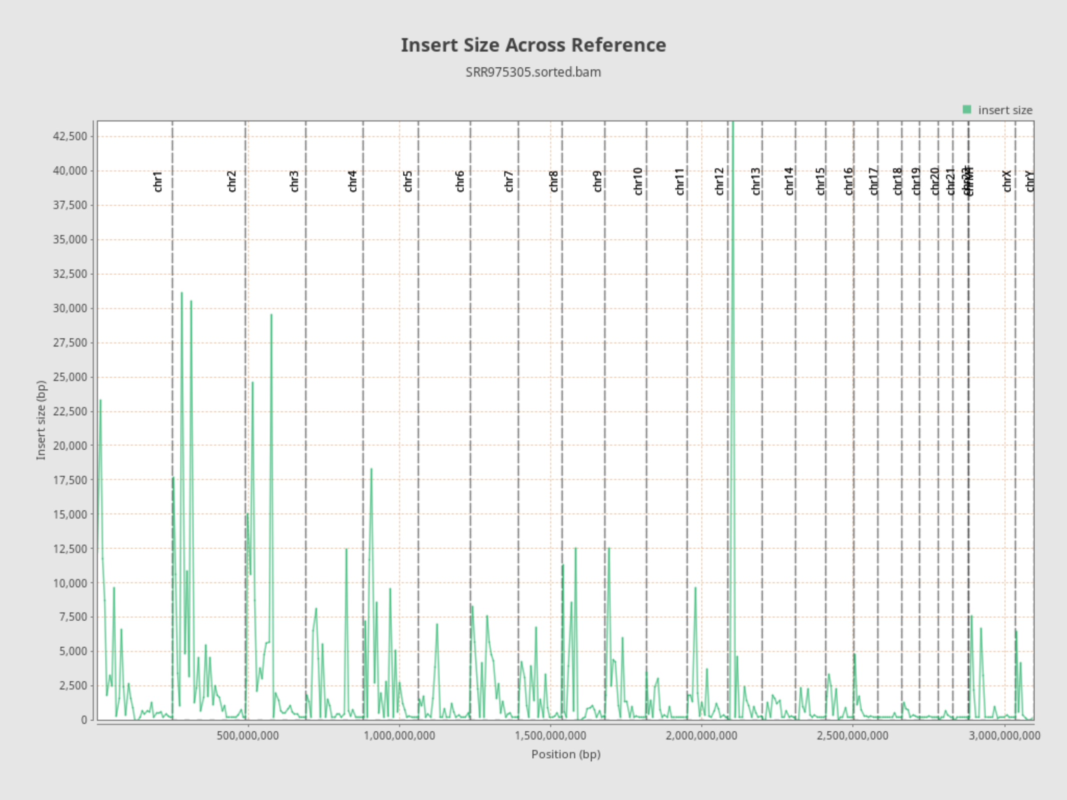
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram