Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 23:02:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975295.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_SRR975295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975295_1.fastq.gz SRR975295_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 23:02:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,549,422
Mapped reads	48,438,374 / 99.77%
Unmapped reads	111,048 / 0.23%
Mapped paired reads	48,438,374 / 99.77%
Mapped reads, first in pair	24,210,708 / 49.87%
Mapped reads, second in pair	24,227,666 / 49.9%
Mapped reads, both in pair	48,381,092 / 99.65%
Mapped reads, singletons	57,282 / 0.12%
Secondary alignments	0
Supplementary alignments	87,025 / 0.18%
Read min/max/mean length	30 / 101 / 101.07
Duplicated reads (estimated)	27,407,938 / 56.45%
Duplication rate	43.37%
Clipped reads	28,400,851 / 58.5%

2.2. ACGT Content

Number/percentage of A's	1,191,679,756 / 26.79%
Number/percentage of C's	979,507,824 / 22.02%
Number/percentage of T's	1,207,354,066 / 27.14%
Number/percentage of G's	1,070,317,354 / 24.06%
Number/percentage of N's	138,548 / 0%

GC Percentage	46.07%

2.3. Coverage

Mean	1.4377
Standard Deviation	20.4089

2.4. Mapping Quality

Mean Mapping Quality	56.11

2.5. Insert size

Mean	77,392.98
Standard Deviation	2,753,533.58
P25/Median/P75	148 / 187 / 237

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	29,625,087
Insertions	436,862
Mapped reads with at least one insertion	0.89%
Deletions	1,128,434
Mapped reads with at least one deletion	2.3%
Homopolymer indels	48.02%

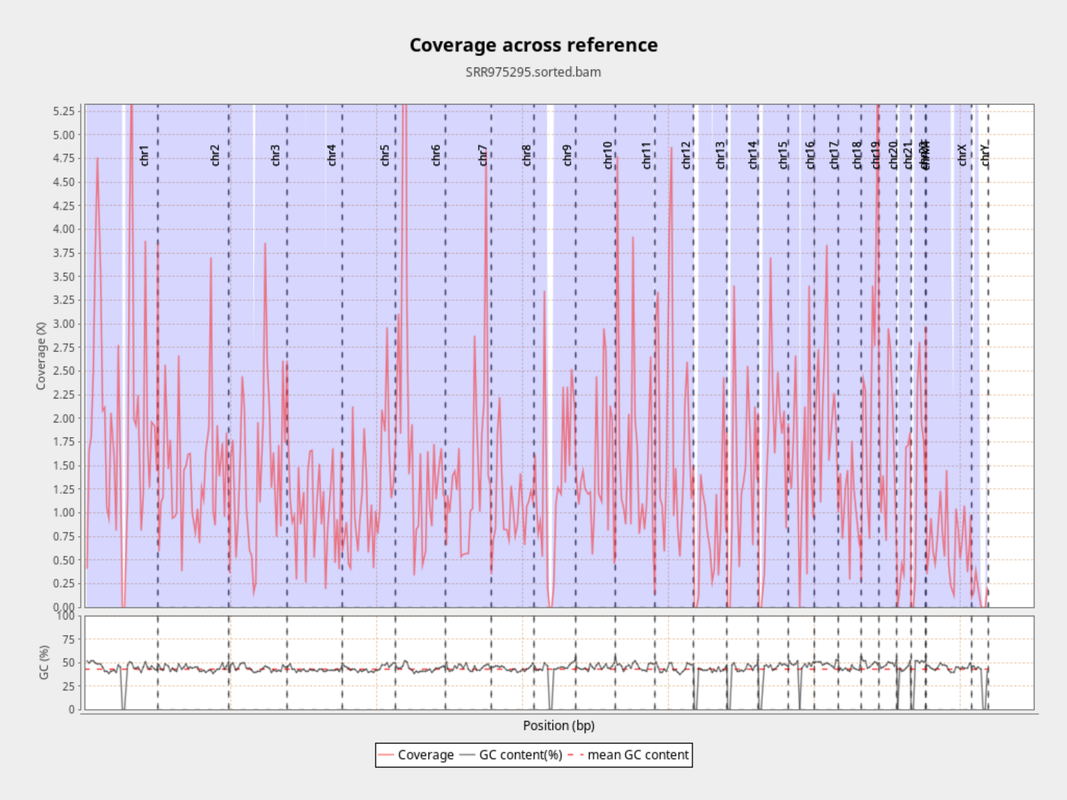
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

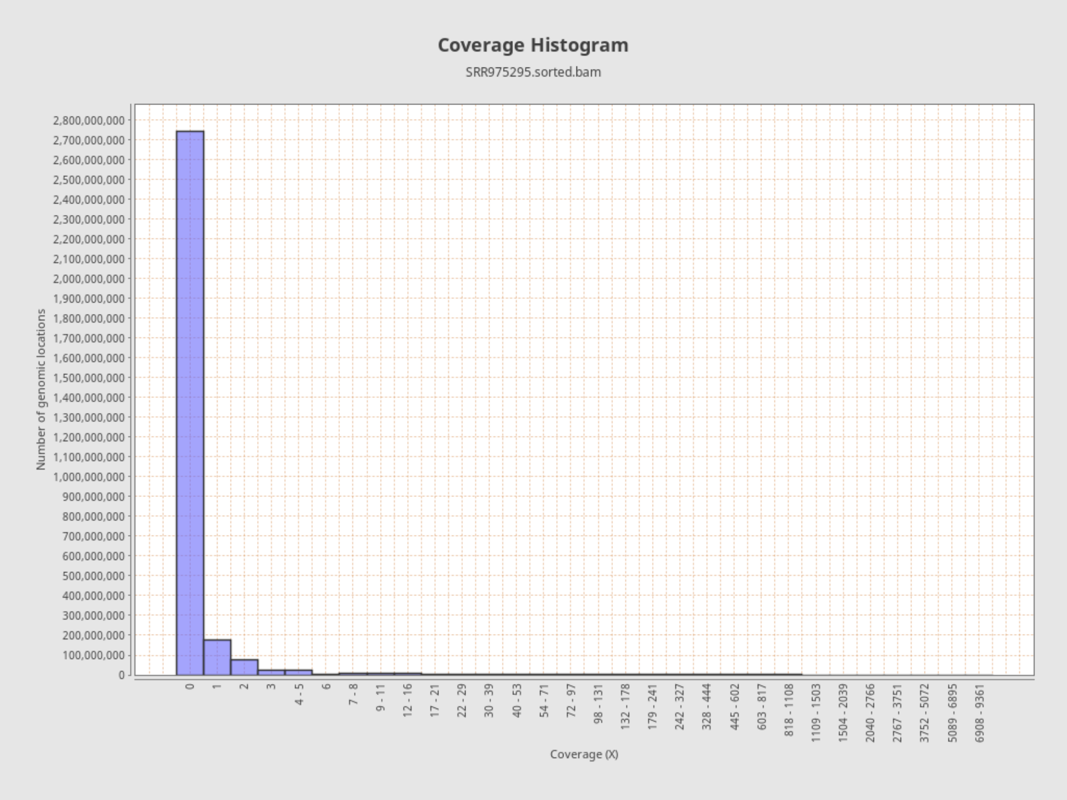
		bases	coverage	deviation
chr1	249250621	509361572	2.0436	25.6173
chr2	243199373	343221097	1.4113	18.4692
chr3	198022430	297108613	1.5004	20.0733
chr4	191154276	201294031	1.053	16.4239
chr5	180915260	217765072	1.2037	16.9618
chr6	171115067	336280124	1.9652	28.997
chr7	159138663	232126086	1.4586	21.9179
chr8	146364022	162243104	1.1085	15.7276
chr9	141213431	180216484	1.2762	18.2553
chr10	135534747	200874451	1.4821	19.645
chr11	135006516	227146835	1.6825	22.2651
chr12	133851895	252826945	1.8889	23.5516
chr13	115169878	92768232	0.8055	13.8081
chr14	107349540	143191509	1.3339	18.3462
chr15	102531392	164055288	1.6	21.7878
chr16	90354753	136019353	1.5054	19.8982
chr17	81195210	176049209	2.1682	24.6949
chr18	78077248	85177759	1.0909	16.917
chr19	59128983	148429736	2.5103	26.9188
chr20	63025520	111603383	1.7708	25.7756
chr21	48129895	43309999	0.8999	17.2637
chr22	51304566	73446218	1.4316	23.1189
chrMT	16571	49255	2.9724	5.6743
chrX	155270560	107839693	0.6945	11.4356

chrY	59373566	8179825	0.1378	3.2455

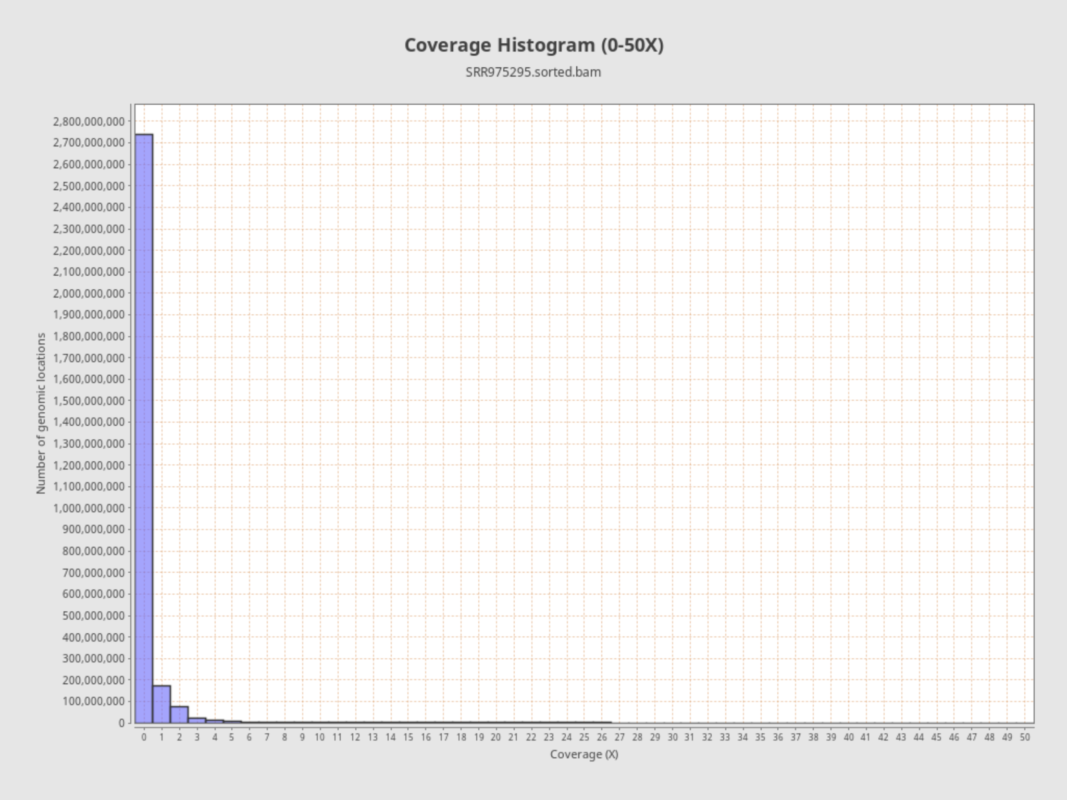
3. Results : Coverage across reference



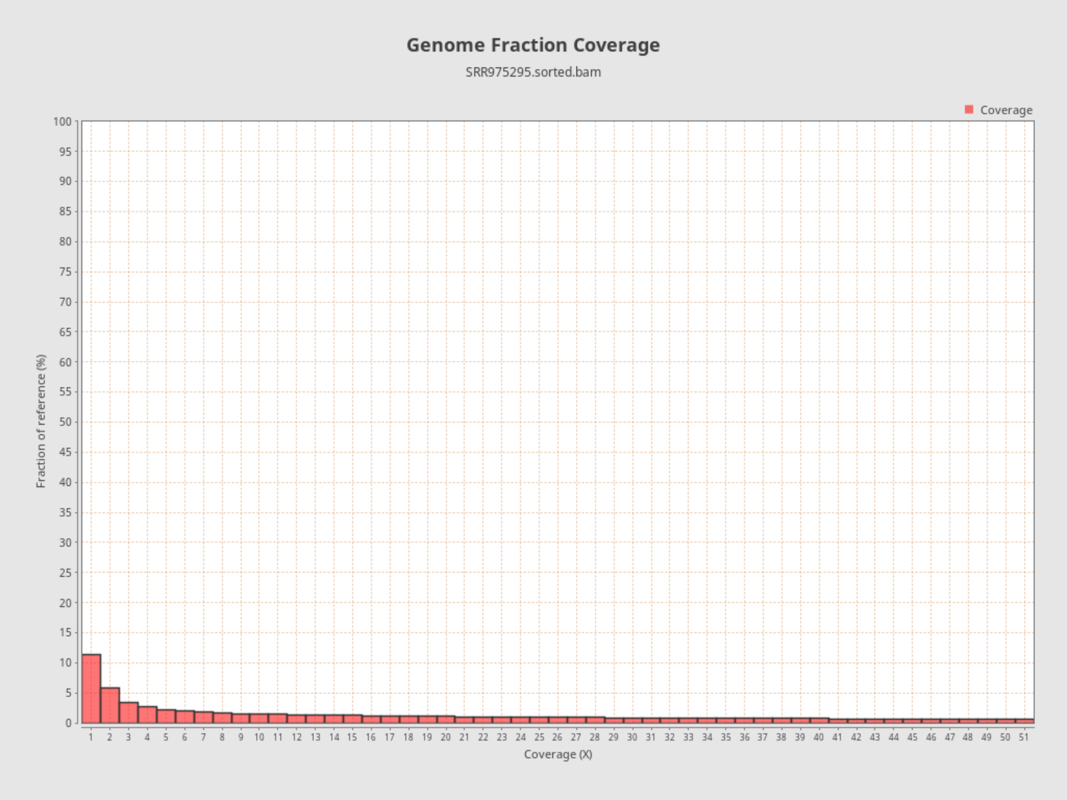
4. Results : Coverage Histogram



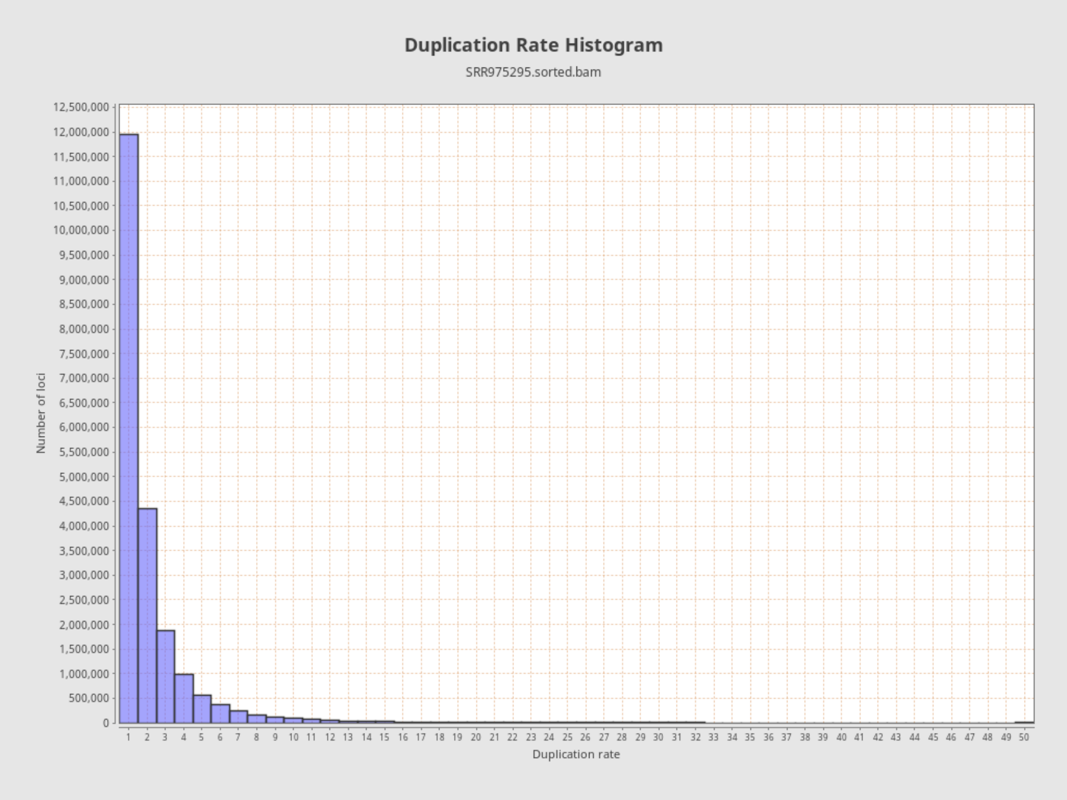
5. Results : Coverage Histogram (0-50X)



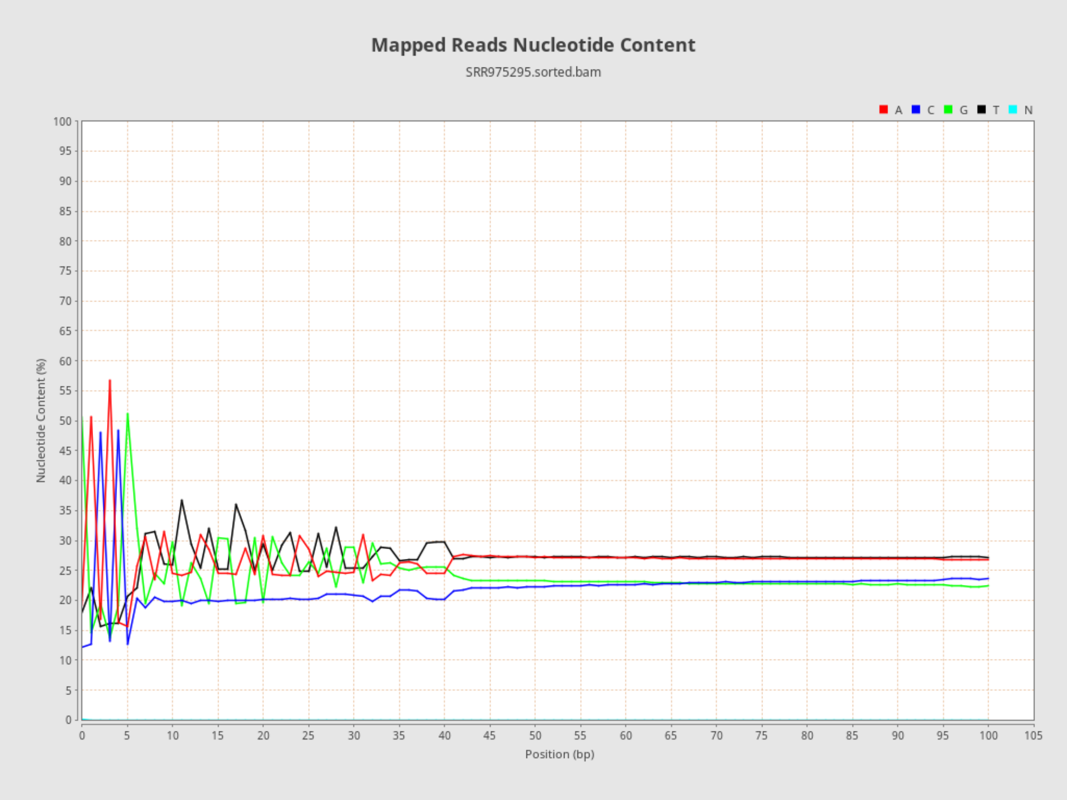
6. Results : Genome Fraction Coverage



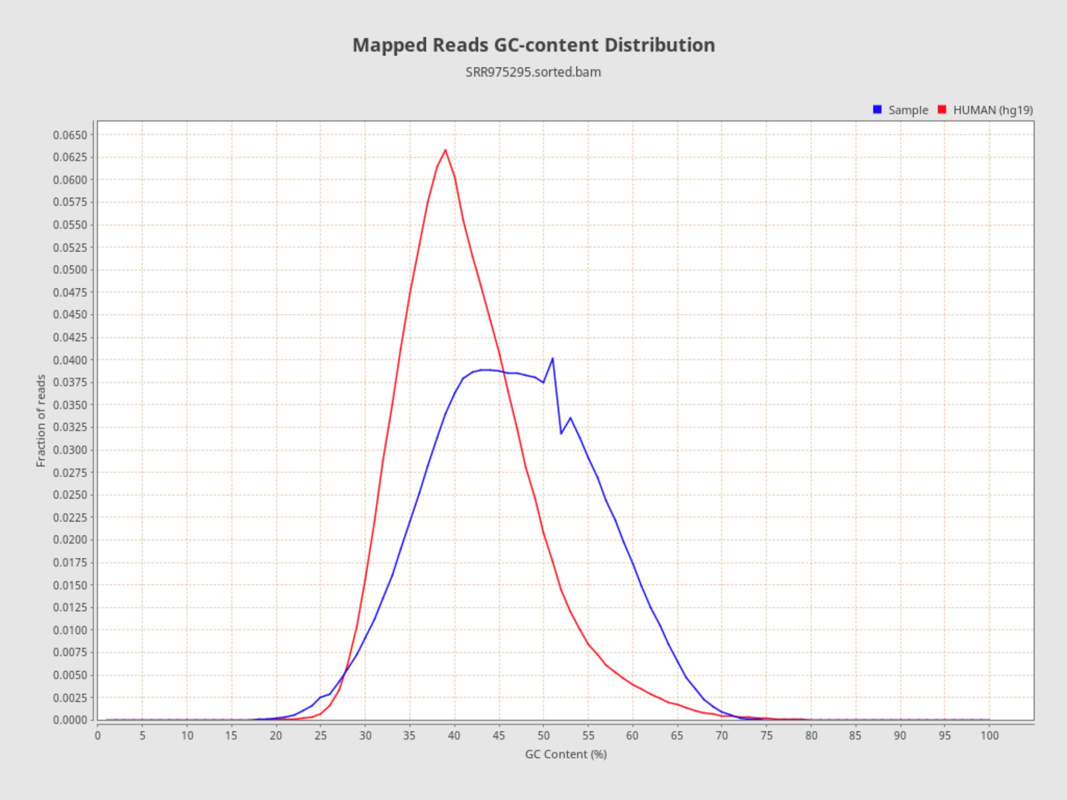
7. Results : Duplication Rate Histogram



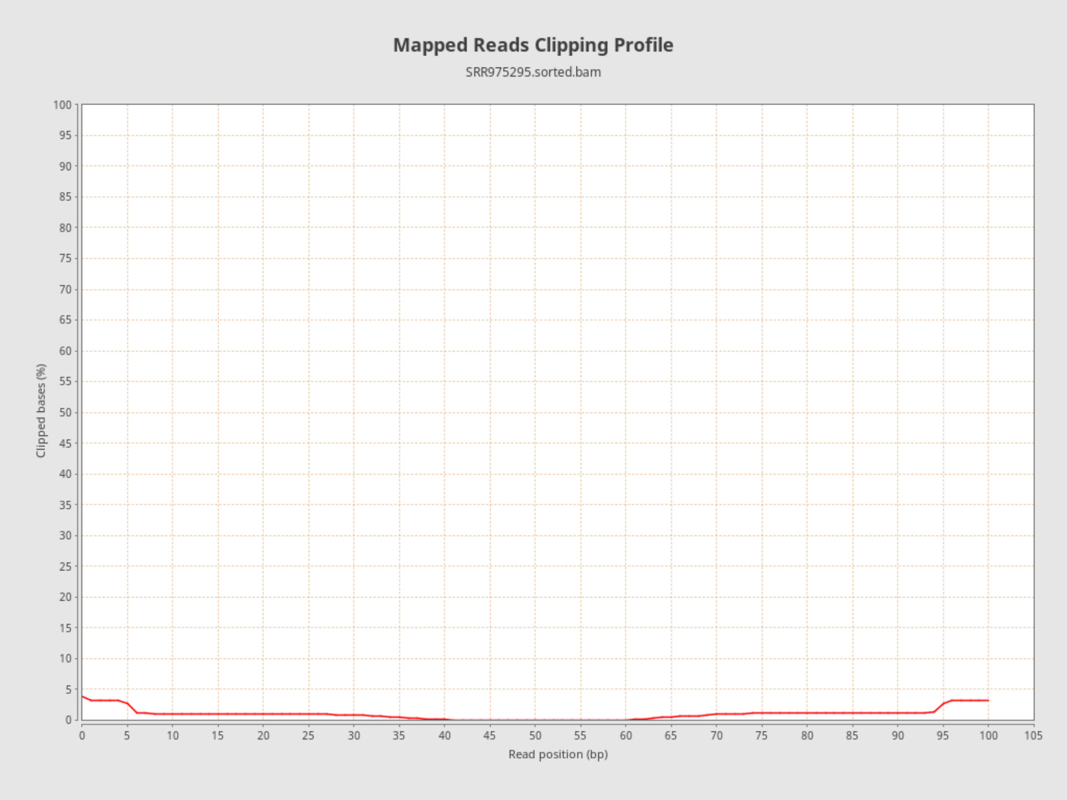
8. Results : Mapped Reads Nucleotide Content



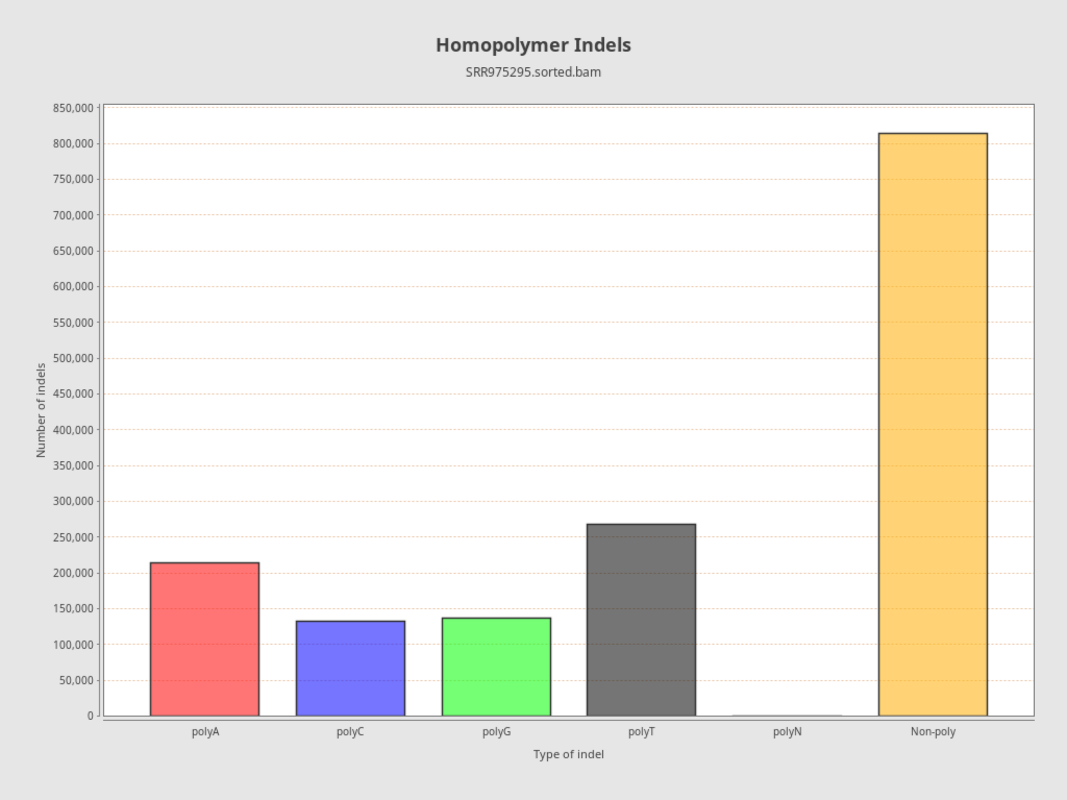
9. Results : Mapped Reads GC-content Distribution



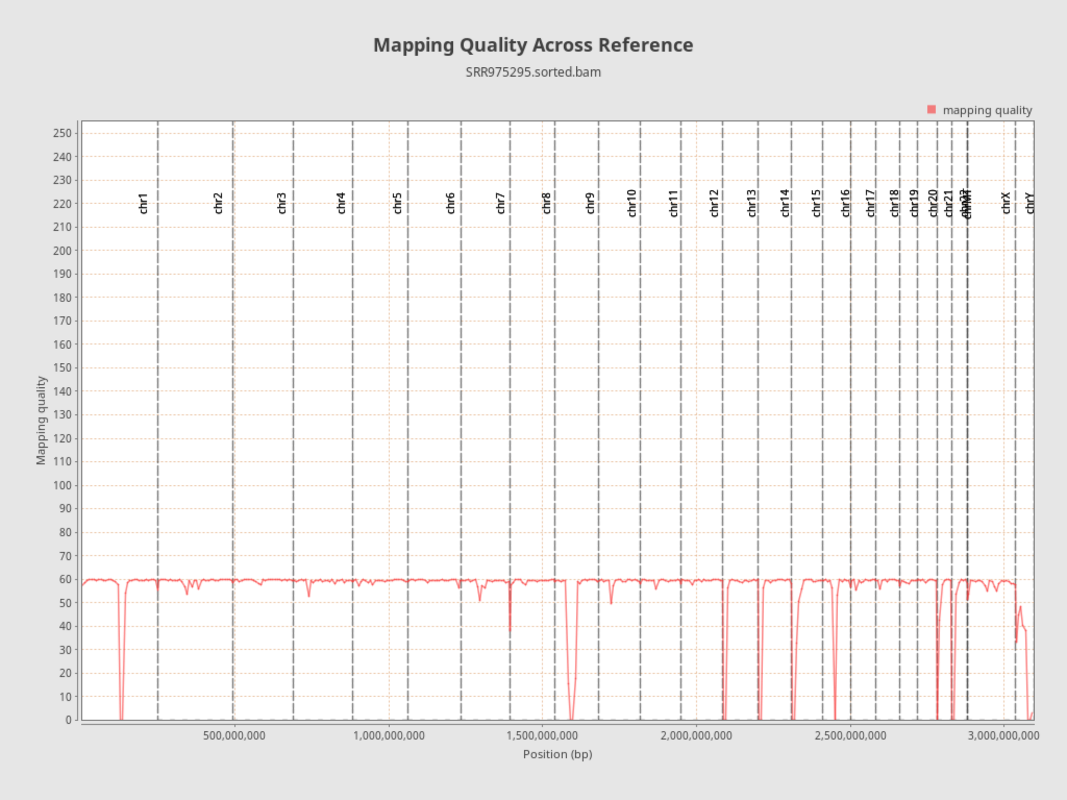
10. Results : Mapped Reads Clipping Profile



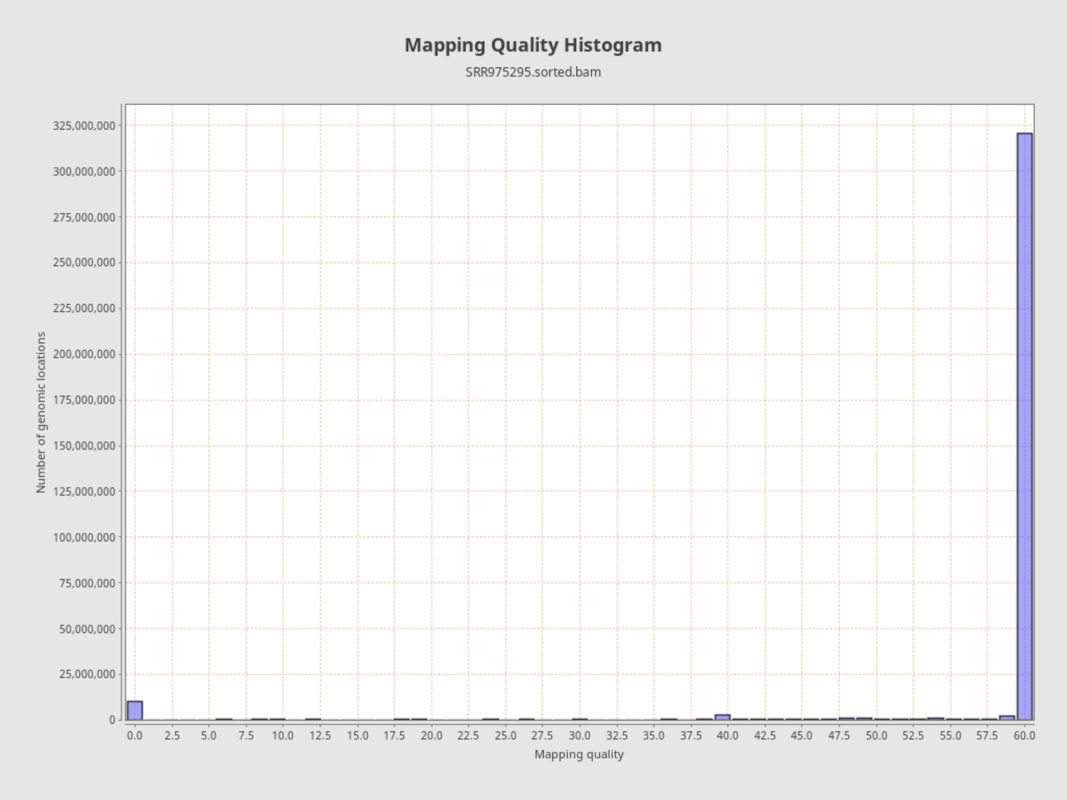
11. Results : Homopolymer Indels



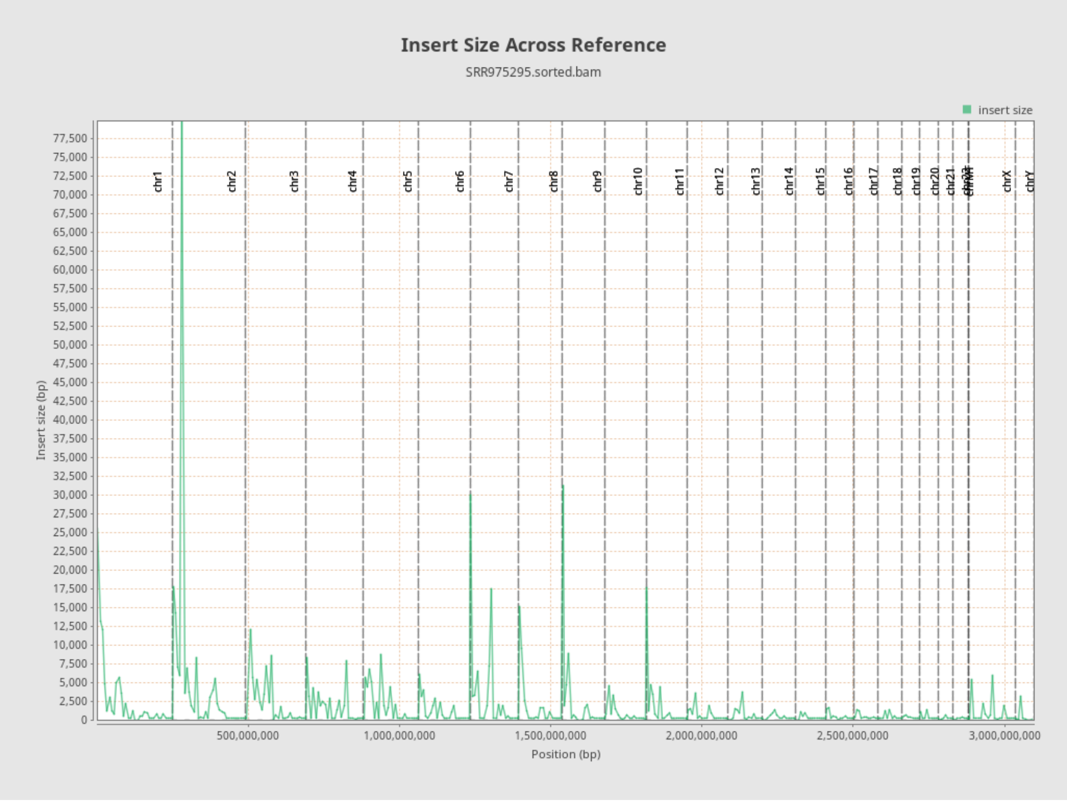
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram