Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/06 19:32:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975275.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_SRR975275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975275_1.fastq.gz SRR975275_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 06 19:32:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975275.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	54,051,448
Mapped reads	53,901,893 / 99.72%
Unmapped reads	149,555 / 0.28%
Mapped paired reads	53,901,893 / 99.72%
Mapped reads, first in pair	26,947,080 / 49.85%
Mapped reads, second in pair	26,954,813 / 49.87%
Mapped reads, both in pair	53,844,292 / 99.62%
Mapped reads, singletons	57,601 / 0.11%
Secondary alignments	0
Supplementary alignments	118,733 / 0.22%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	31,352,608 / 58.01%
Duplication rate	43.57%
Clipped reads	33,182,411 / 61.39%

2.2. ACGT Content

Number/percentage of A's	1,278,200,900 / 25.87%
Number/percentage of C's	1,104,700,473 / 22.36%
Number/percentage of T's	1,332,178,111 / 26.96%
Number/percentage of G's	1,225,605,861 / 24.81%
Number/percentage of N's	154,152 / 0%

GC Percentage	47.16%

2.3. Coverage

Mean	1.5966
Standard Deviation	22.8913

2.4. Mapping Quality

Mean Mapping Quality	55.89

2.5. Insert size

Mean	42,519.78
Standard Deviation	2,049,446.75
P25/Median/P75	149 / 187 / 237

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	31,851,357
Insertions	505,690
Mapped reads with at least one insertion	0.93%
Deletions	1,218,852
Mapped reads with at least one deletion	2.23%
Homopolymer indels	46.1%

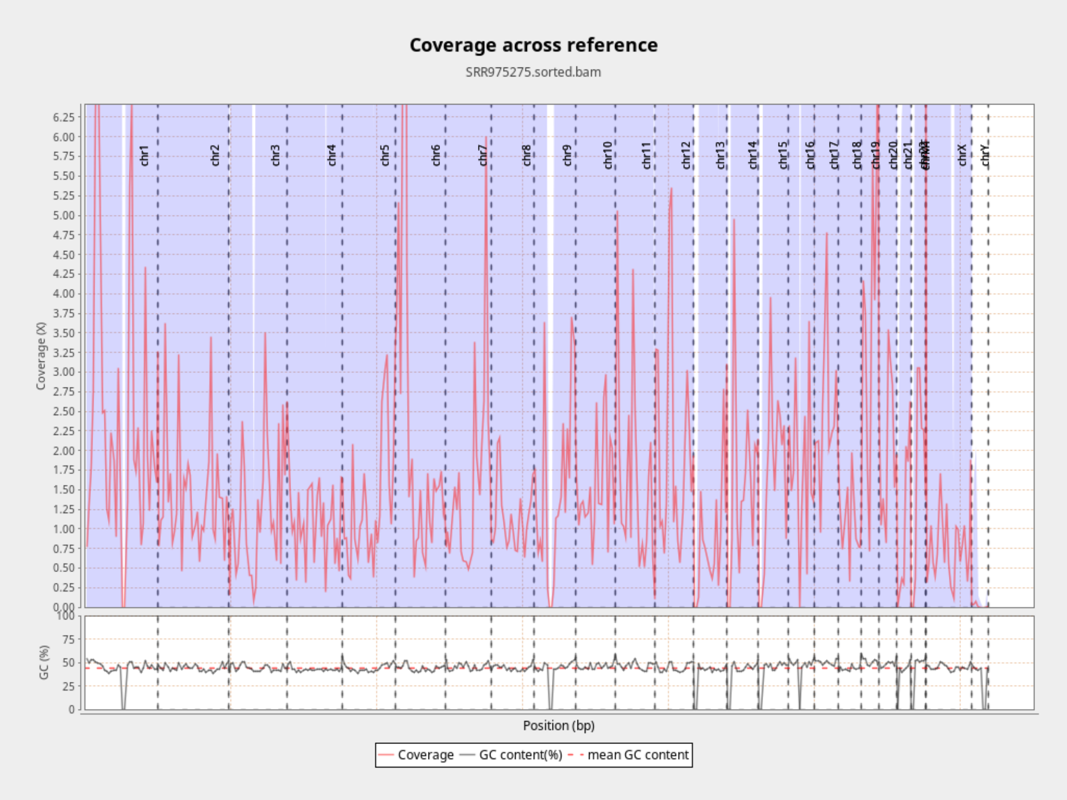
2.7. Chromosome stats

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

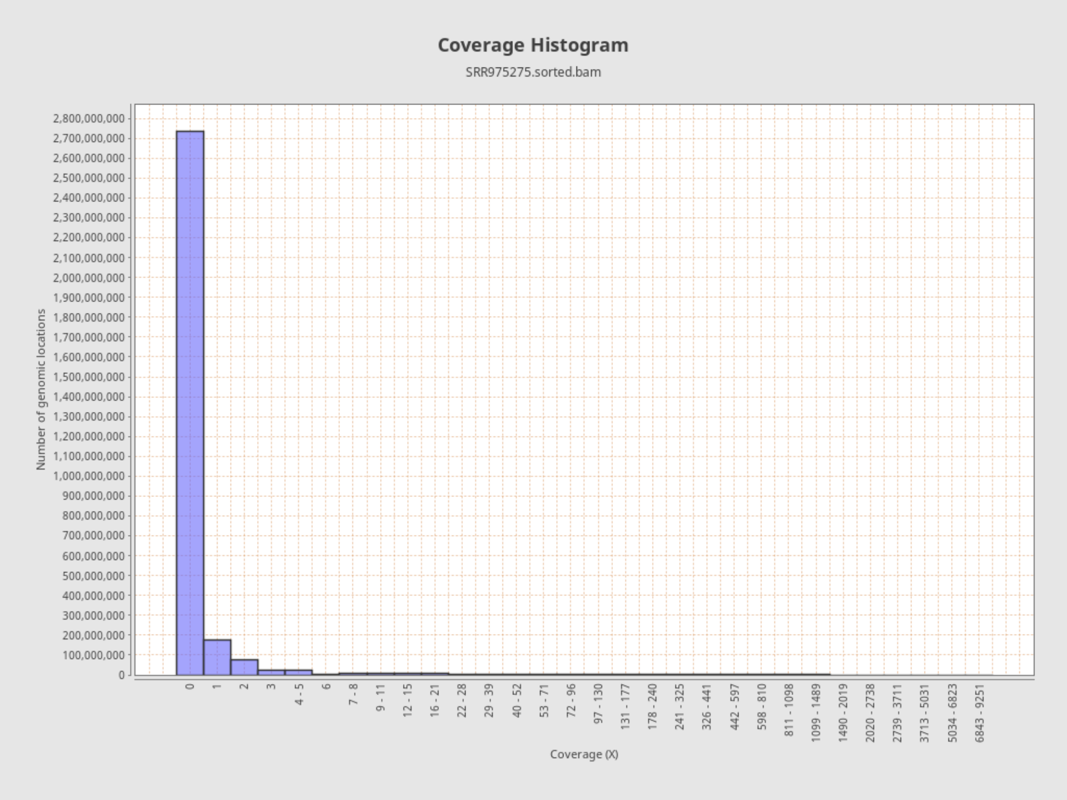
		bases	coverage	deviation
chr1	249250621	598067729	2.3995	30.6233
chr2	243199373	345542329	1.4208	18.6536
chr3	198022430	250177304	1.2634	18.0297
chr4	191154276	210375357	1.1006	16.7119
chr5	180915260	237606473	1.3134	18.3677
chr6	171115067	460776551	2.6928	40.4585
chr7	159138663	254781013	1.601	23.5838
chr8	146364022	169017932	1.1548	16.7112
chr9	141213431	202977708	1.4374	20.0618
chr10	135534747	209710374	1.5473	20.303
chr11	135006516	227259106	1.6833	21.5759
chr12	133851895	276999394	2.0694	25.6921
chr13	115169878	97362643	0.8454	15.5077
chr14	107349540	162701838	1.5156	21.1326
chr15	102531392	175482478	1.7115	22.2609
chr16	90354753	157941986	1.748	21.5885
chr17	81195210	206039931	2.5376	26.2809
chr18	78077248	86525324	1.1082	17.8525
chr19	59128983	223938689	3.7873	38.6839
chr20	63025520	131912243	2.093	27.2531
chr21	48129895	49882882	1.0364	17.7329
chr22	51304566	88144420	1.7181	21.7055
chrMT	16571	134899	8.1407	15.1617
chrX	155270560	118042826	0.7602	12.9881

chrY	59373566	1174490	0.0198	0.9267

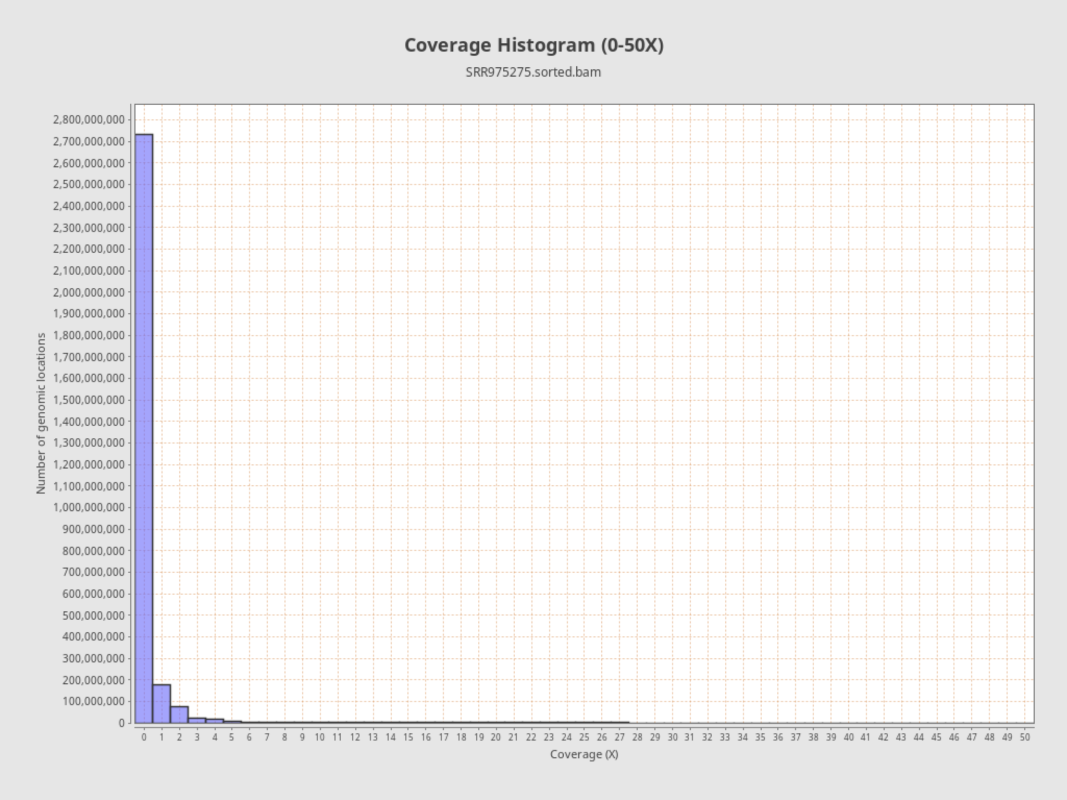
3. Results : Coverage across reference



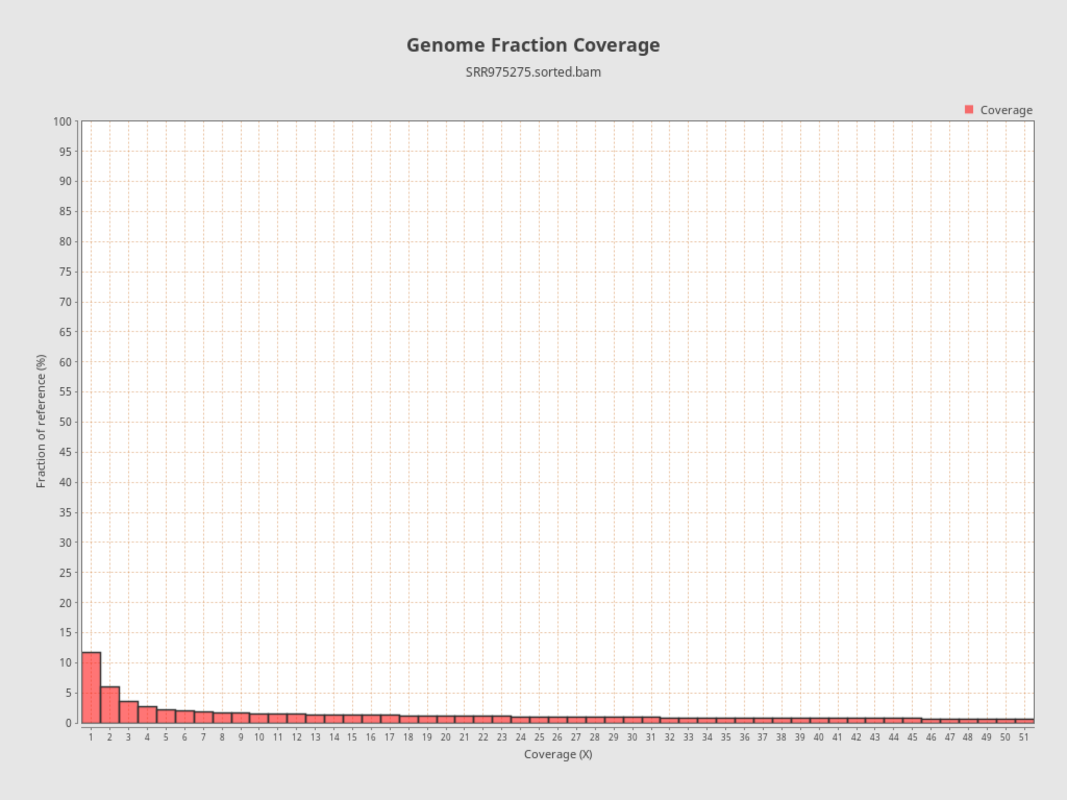
4. Results : Coverage Histogram



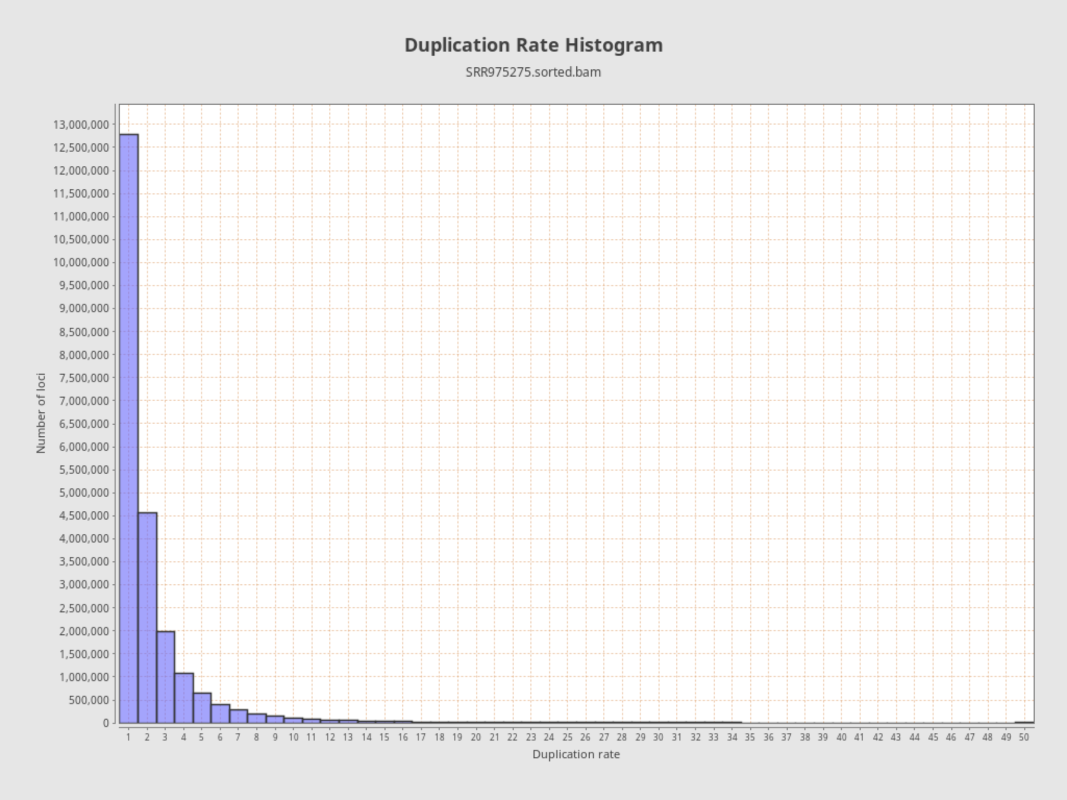
5. Results : Coverage Histogram (0-50X)



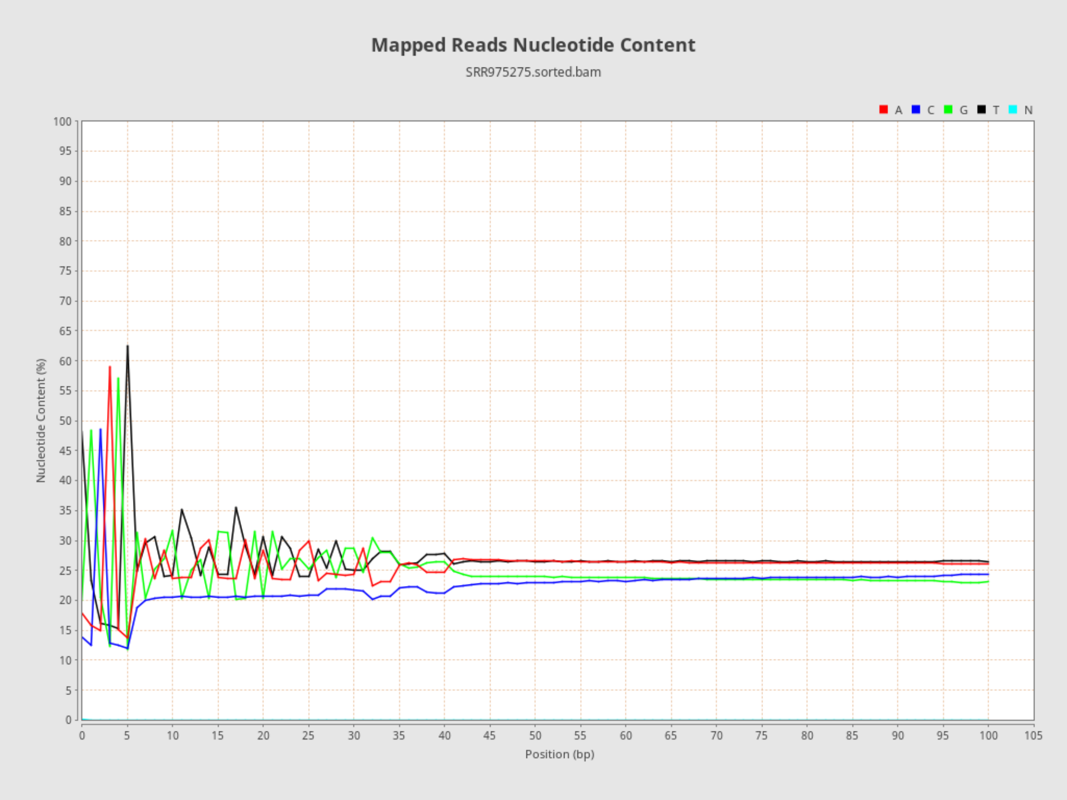
6. Results : Genome Fraction Coverage



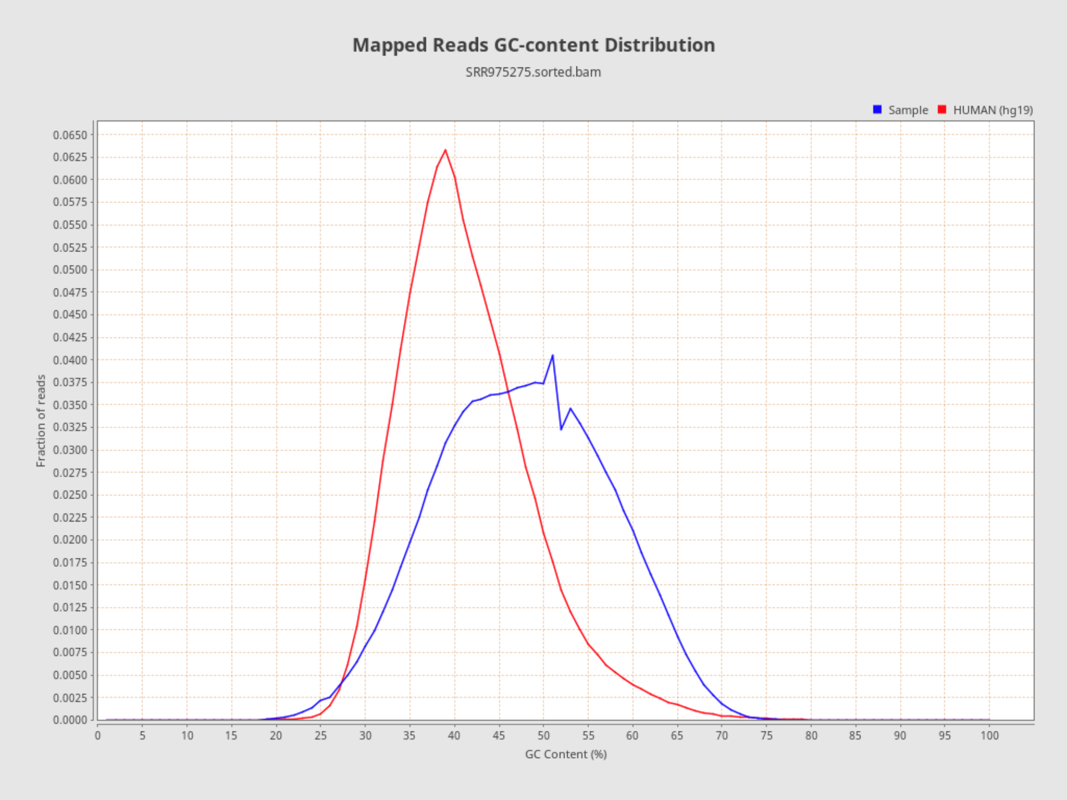
7. Results : Duplication Rate Histogram



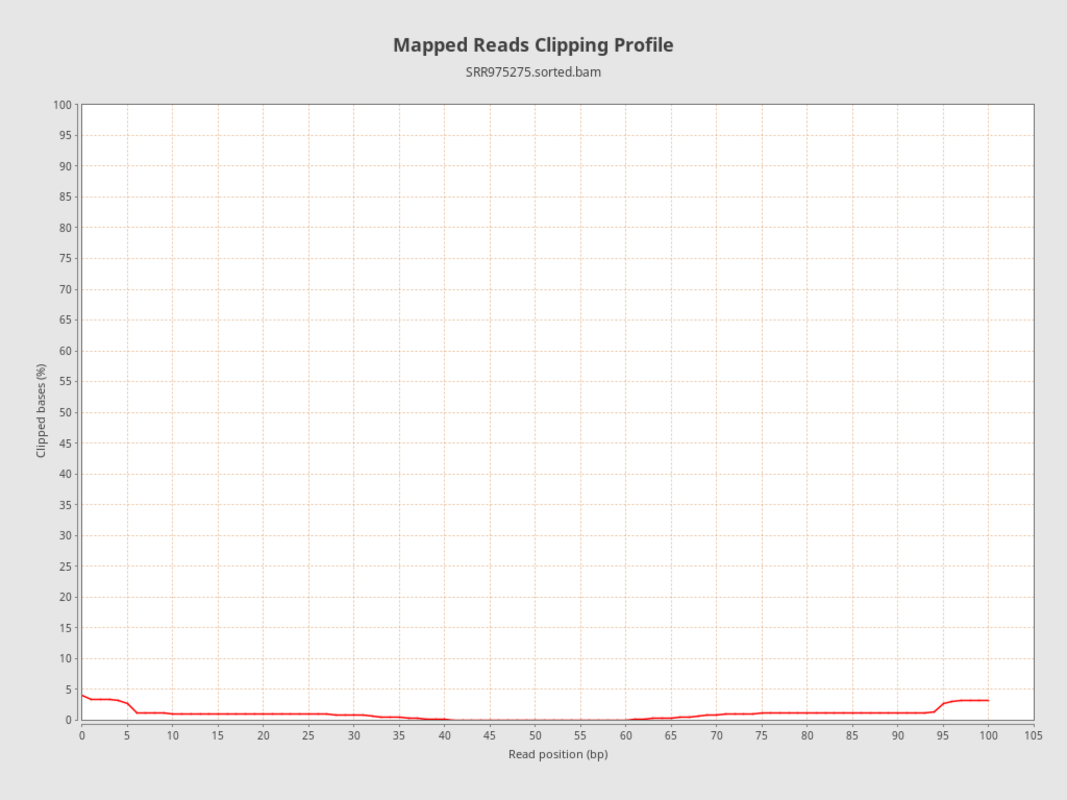
8. Results : Mapped Reads Nucleotide Content



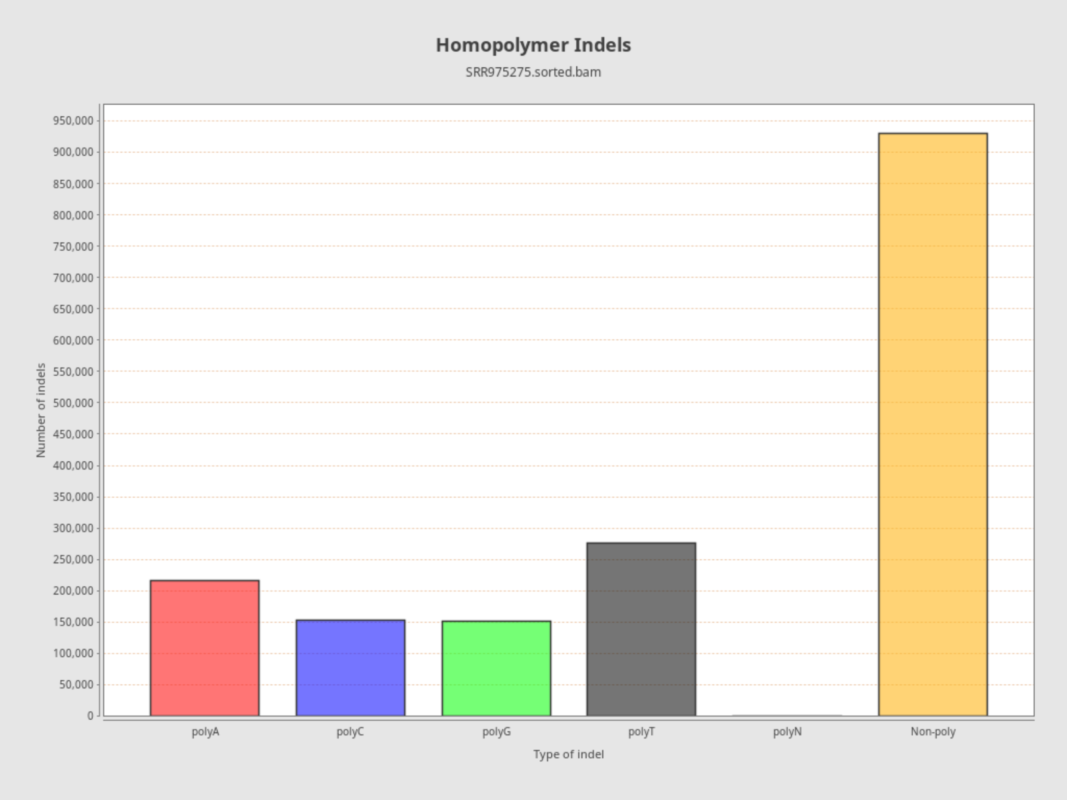
9. Results : Mapped Reads GC-content Distribution



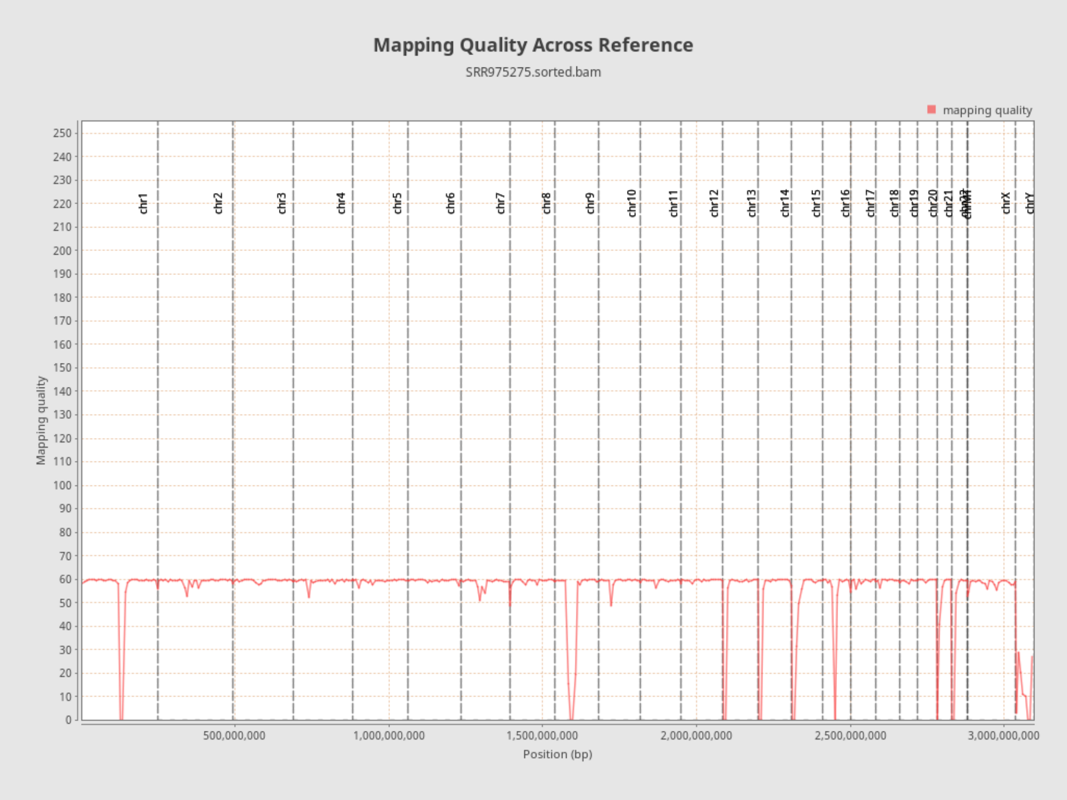
10. Results : Mapped Reads Clipping Profile



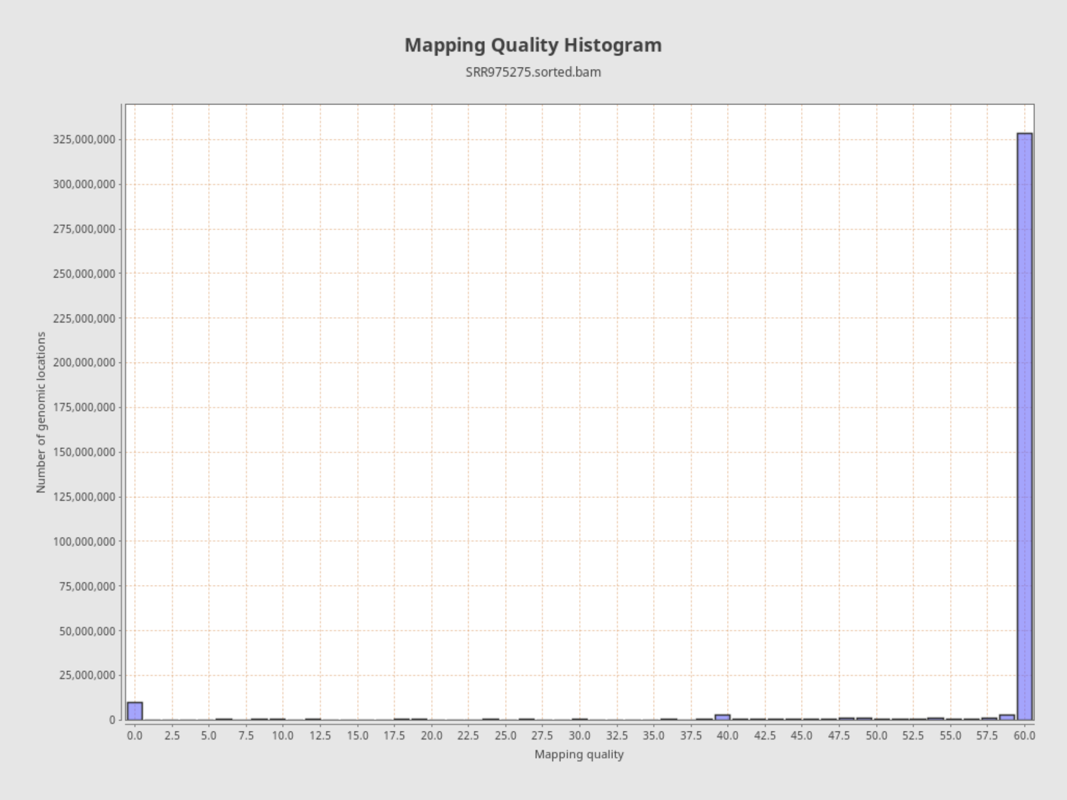
11. Results : Homopolymer Indels



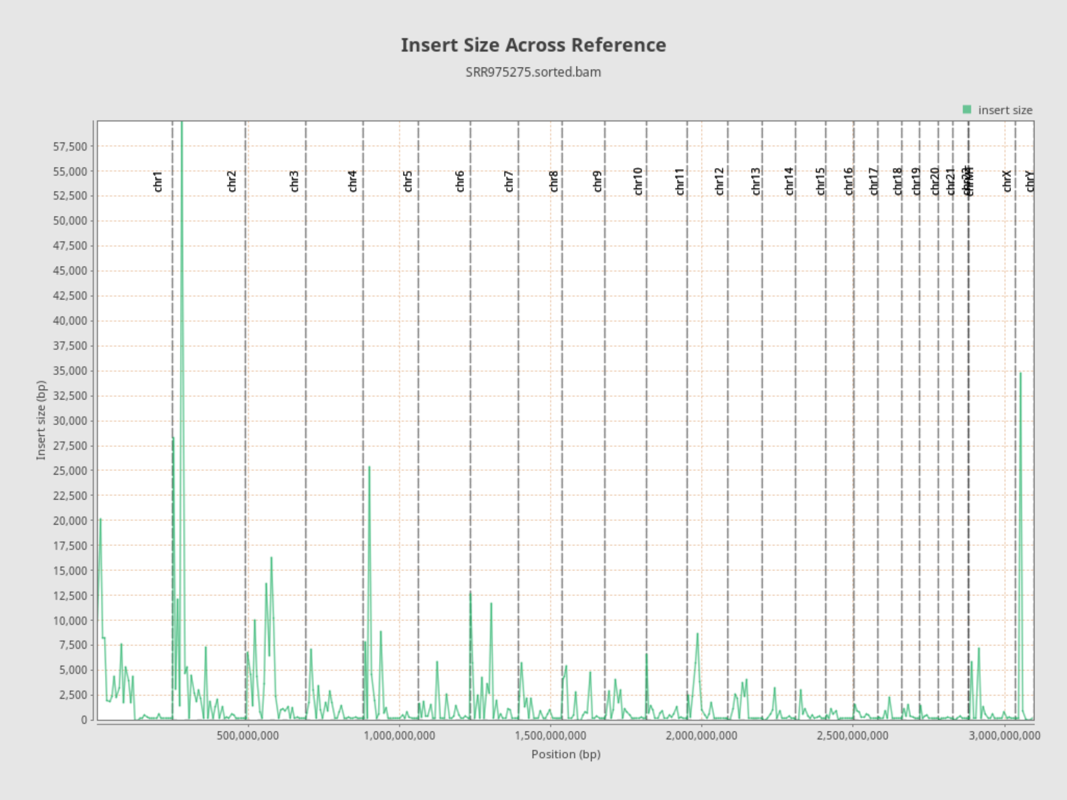
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram