Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 03:13:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR975258.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_SRR975258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975258_1.fastq.gz SRR975258_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 03:13:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR975258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	70,102,960
Mapped reads	70,022,072 / 99.88%
Unmapped reads	80,888 / 0.12%
Mapped paired reads	70,022,072 / 99.88%
Mapped reads, first in pair	35,011,442 / 49.94%
Mapped reads, second in pair	35,010,630 / 49.94%
Mapped reads, both in pair	69,995,000 / 99.85%
Mapped reads, singletons	27,072 / 0.04%
Secondary alignments	0
Supplementary alignments	154,094 / 0.22%
Read min/max/mean length	30 / 101 / 101.09
Duplicated reads (estimated)	32,028,964 / 45.69%
Duplication rate	42.2%
Clipped reads	34,994,433 / 49.92%

2.2. ACGT Content

Number/percentage of A's	1,773,263,849 / 25.87%
Number/percentage of C's	1,660,732,914 / 24.23%
Number/percentage of T's	1,770,481,420 / 25.83%
Number/percentage of G's	1,650,604,207 / 24.08%
Number/percentage of N's	125,373 / 0%

GC Percentage	48.3%

2.3. Coverage

Mean	2.2147
Standard Deviation	17.7927

2.4. Mapping Quality

Mean Mapping Quality	56.24

2.5. Insert size

Mean	79,592.96
Standard Deviation	2,786,696.66
P25/Median/P75	155 / 193 / 246

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	19,248,097
Insertions	570,484
Mapped reads with at least one insertion	0.81%
Deletions	344,835
Mapped reads with at least one deletion	0.48%
Homopolymer indels	32.04%

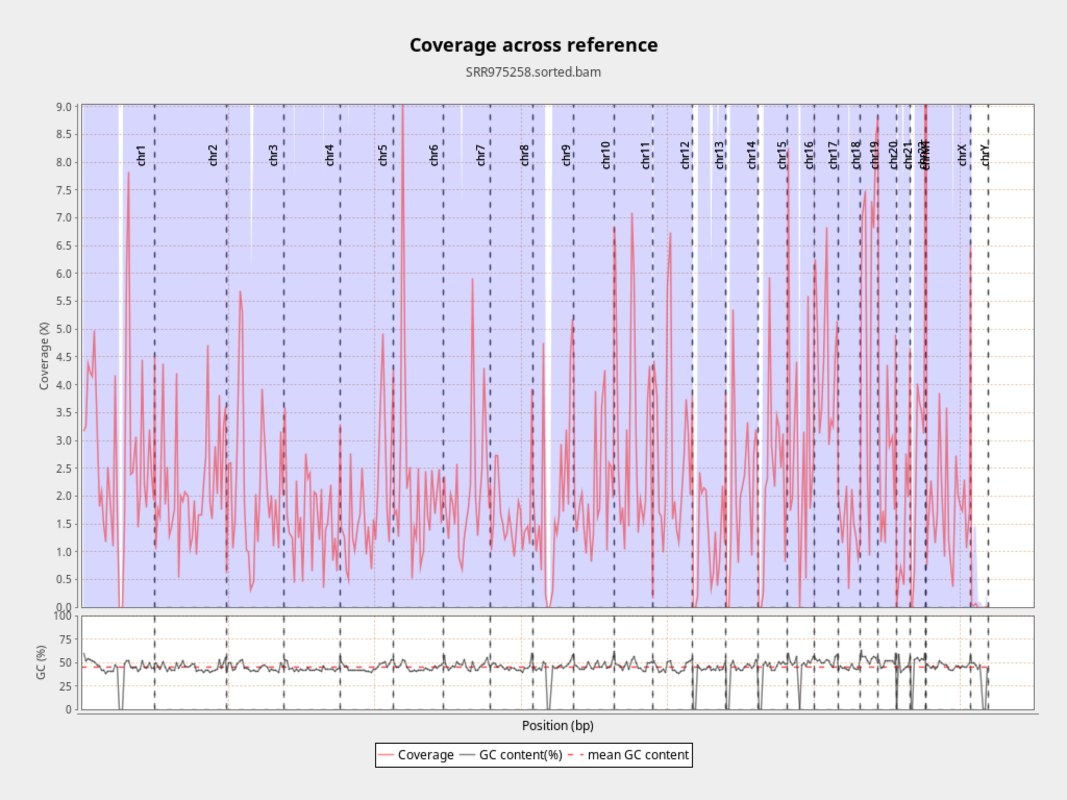
2.7. Chromosome stats

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

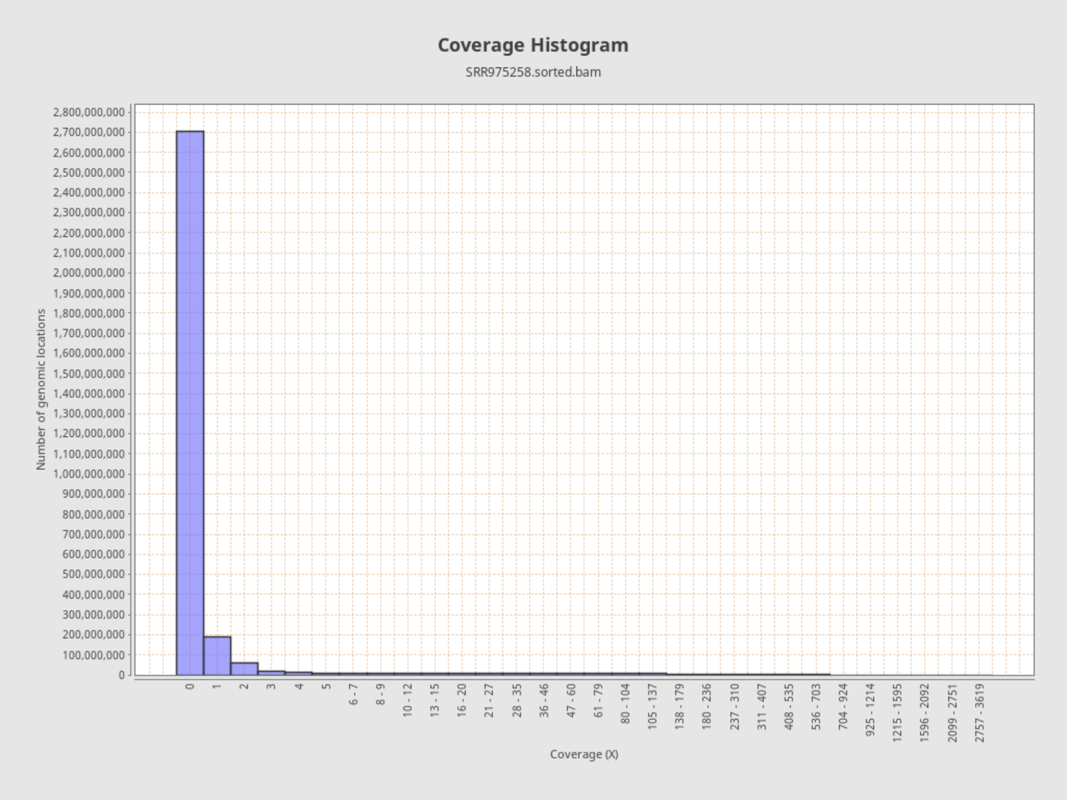
		bases	coverage	deviation
chr1	249250621	686528948	2.7544	20.2641
chr2	243199373	525353355	2.1602	17.3699
chr3	198022430	422824910	2.1352	17.2133
chr4	191154276	299982315	1.5693	15.0775
chr5	180915260	333291801	1.8423	16.0995
chr6	171115067	385571021	2.2533	18.7423
chr7	159138663	332033667	2.0864	17.5804
chr8	146364022	241877196	1.6526	14.6962
chr9	141213431	270615643	1.9164	16.1661
chr10	135534747	277722391	2.0491	16.8872
chr11	135006516	409031921	3.0297	21.6576
chr12	133851895	368248735	2.7512	19.8152
chr13	115169878	138489704	1.2025	12.811
chr14	107349540	221161087	2.0602	17.1853
chr15	102531392	231658224	2.2594	17.463
chr16	90354753	248792228	2.7535	19.1202
chr17	81195210	353893872	4.3586	24.6027
chr18	78077248	111557703	1.4288	13.8227
chr19	59128983	346989589	5.8684	27.6055
chr20	63025520	161884549	2.5686	18.8771
chr21	48129895	72041016	1.4968	15.799
chr22	51304566	126635841	2.4683	17.2794
chrMT	16571	472820	28.533	61.7913
chrX	155270560	288102332	1.8555	17.3871

chrY	59373566	1199645	0.0202	0.7413

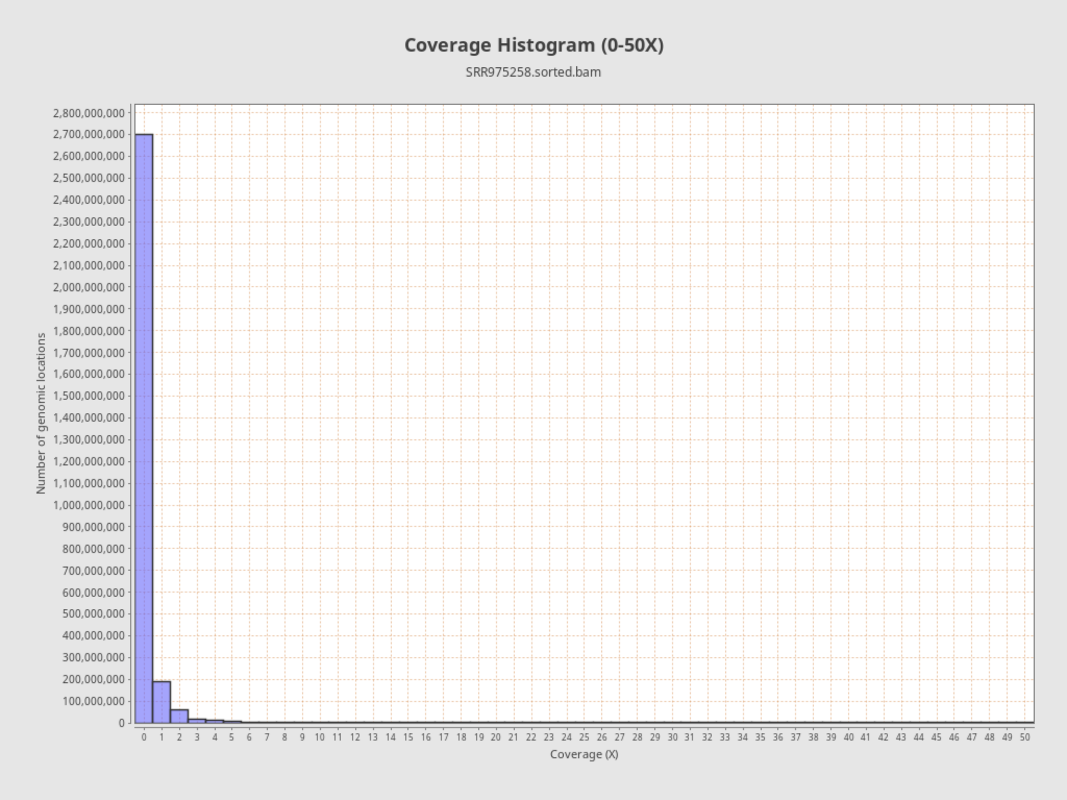
3. Results : Coverage across reference



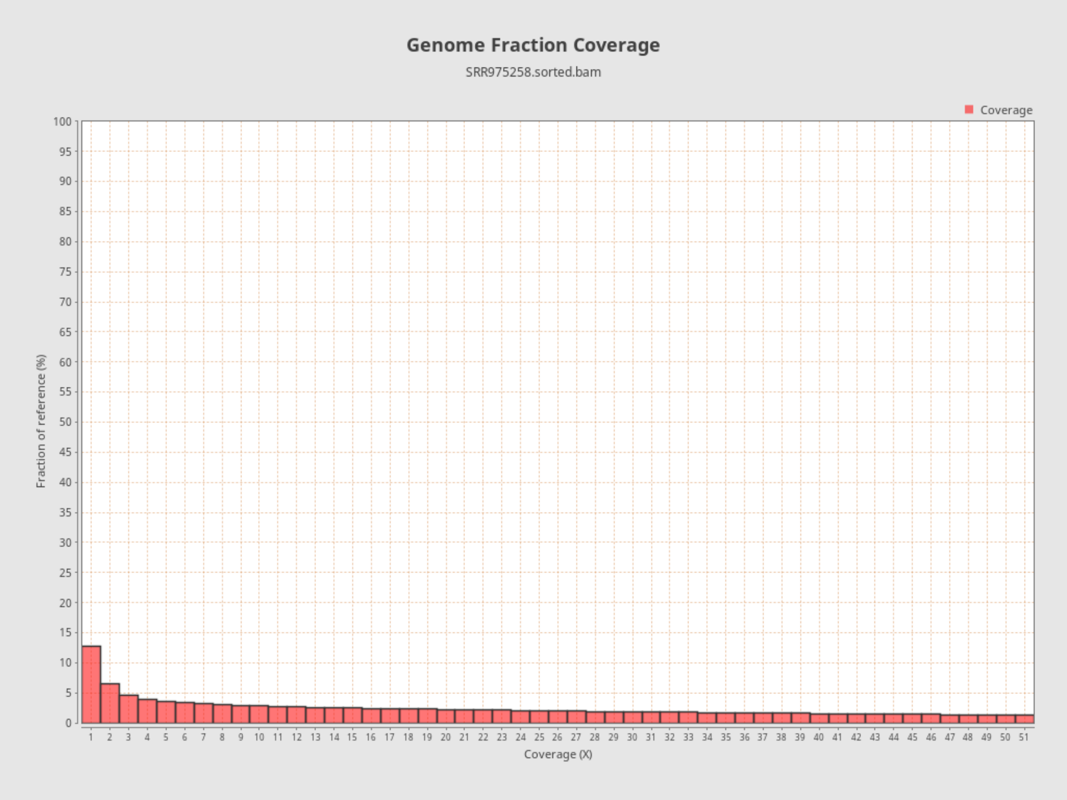
4. Results : Coverage Histogram



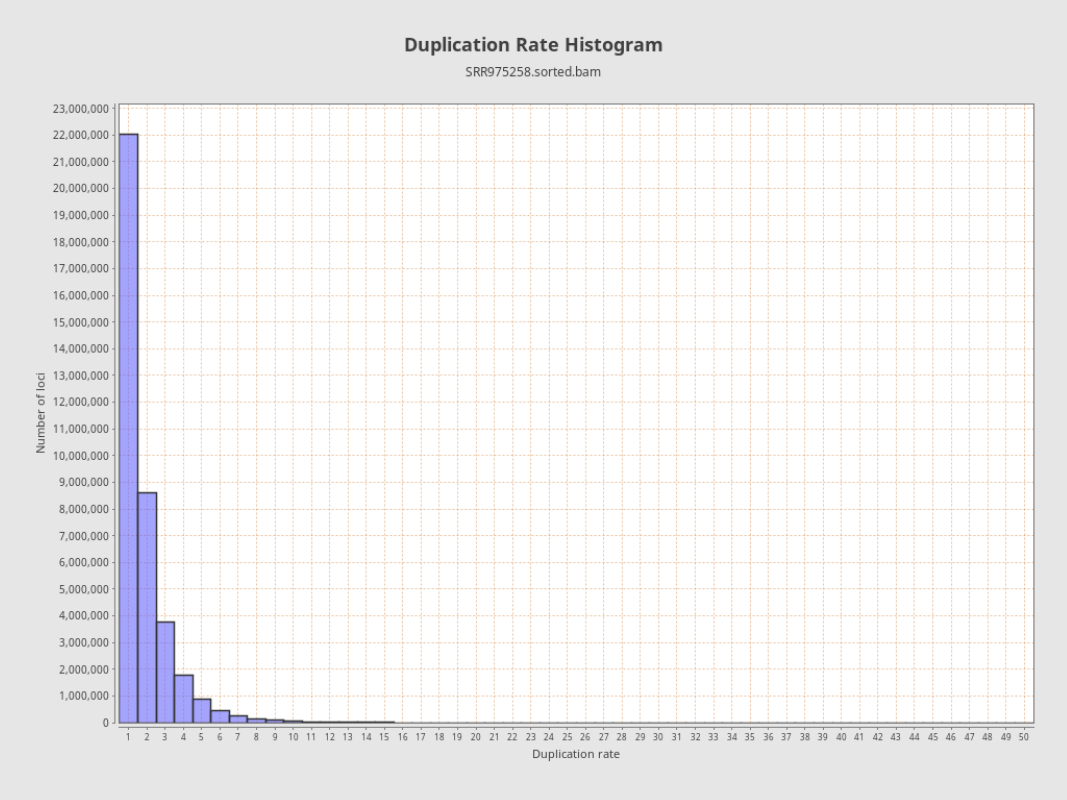
5. Results : Coverage Histogram (0-50X)



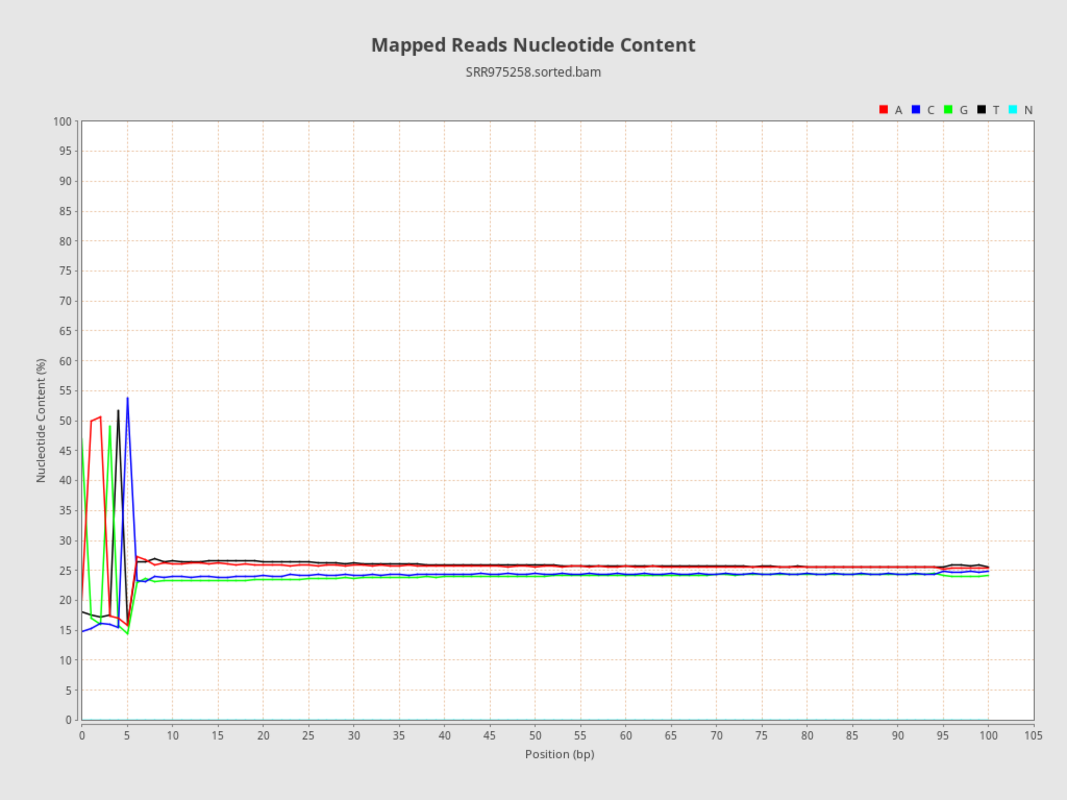
6. Results : Genome Fraction Coverage



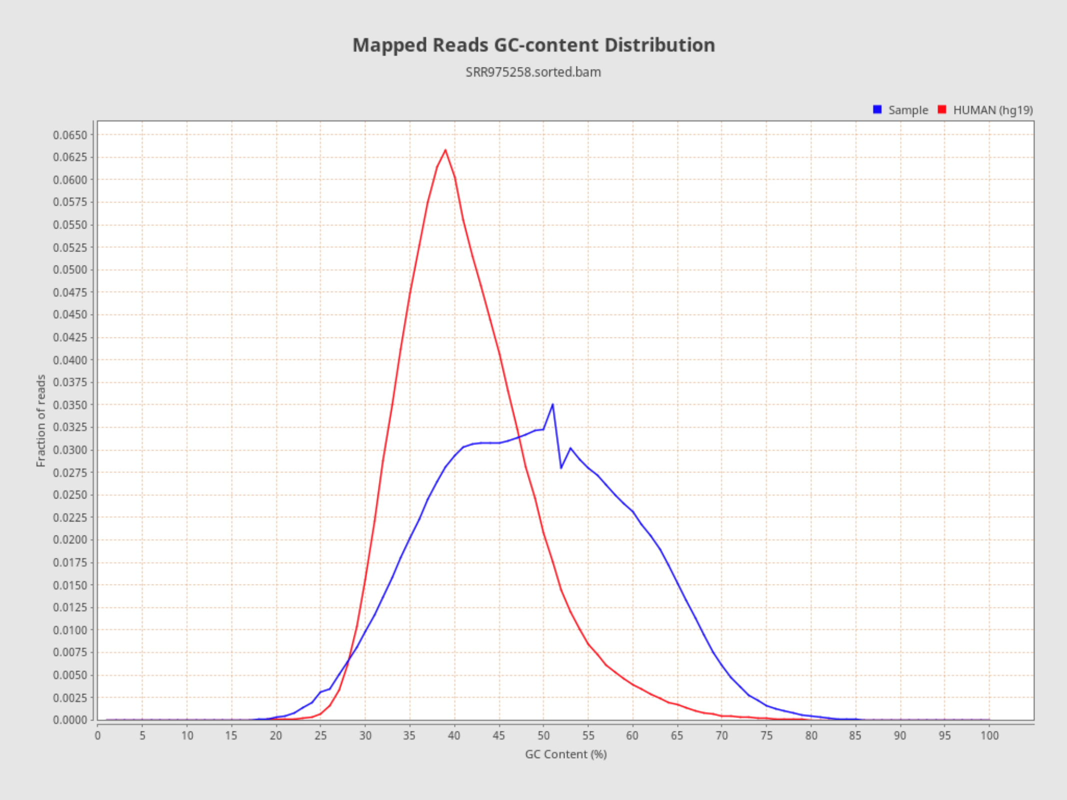
7. Results : Duplication Rate Histogram



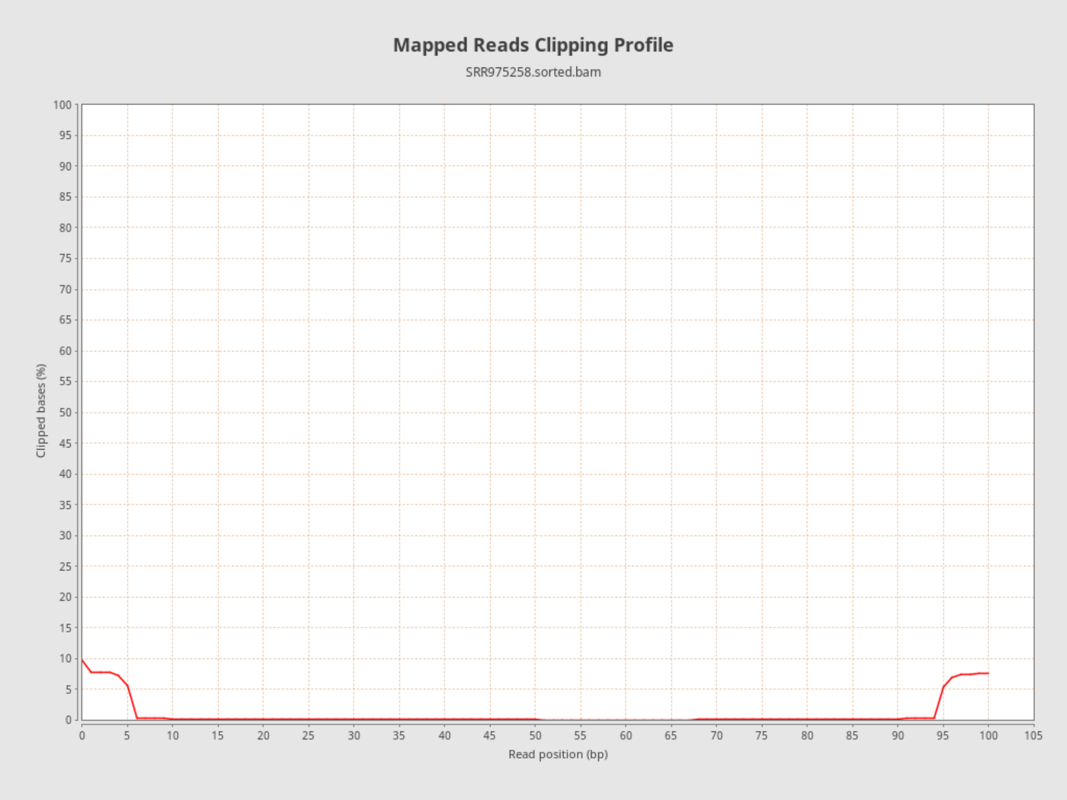
8. Results : Mapped Reads Nucleotide Content



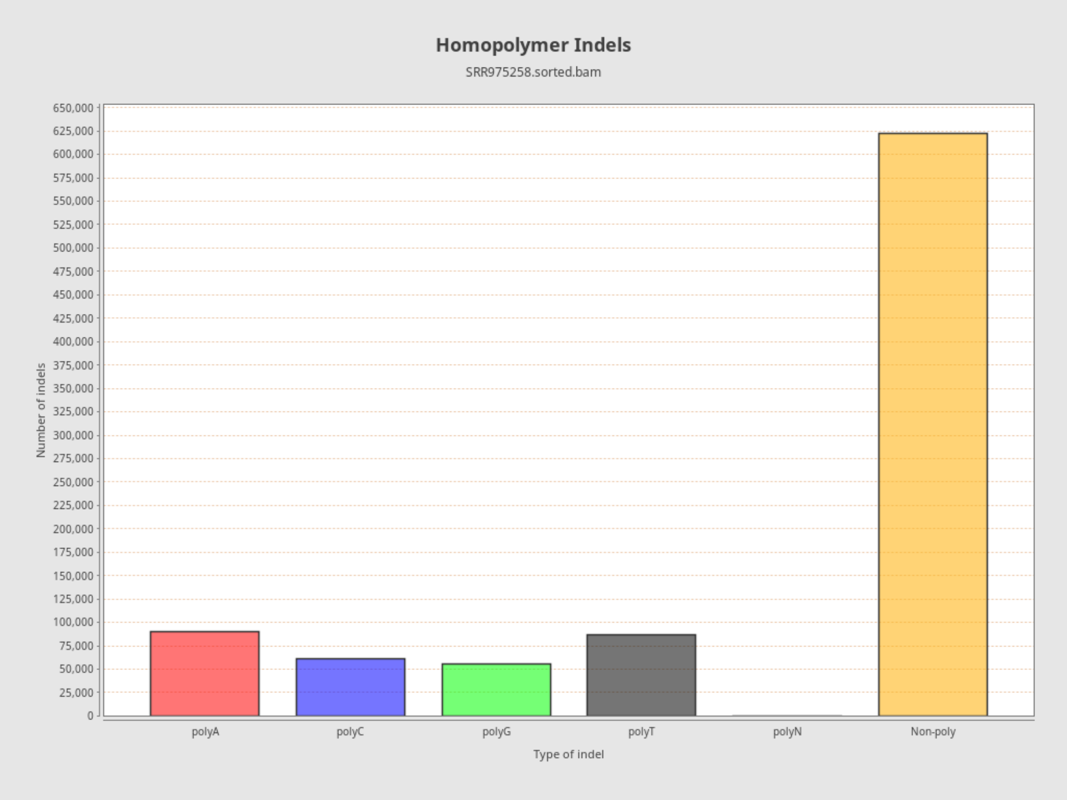
9. Results : Mapped Reads GC-content Distribution



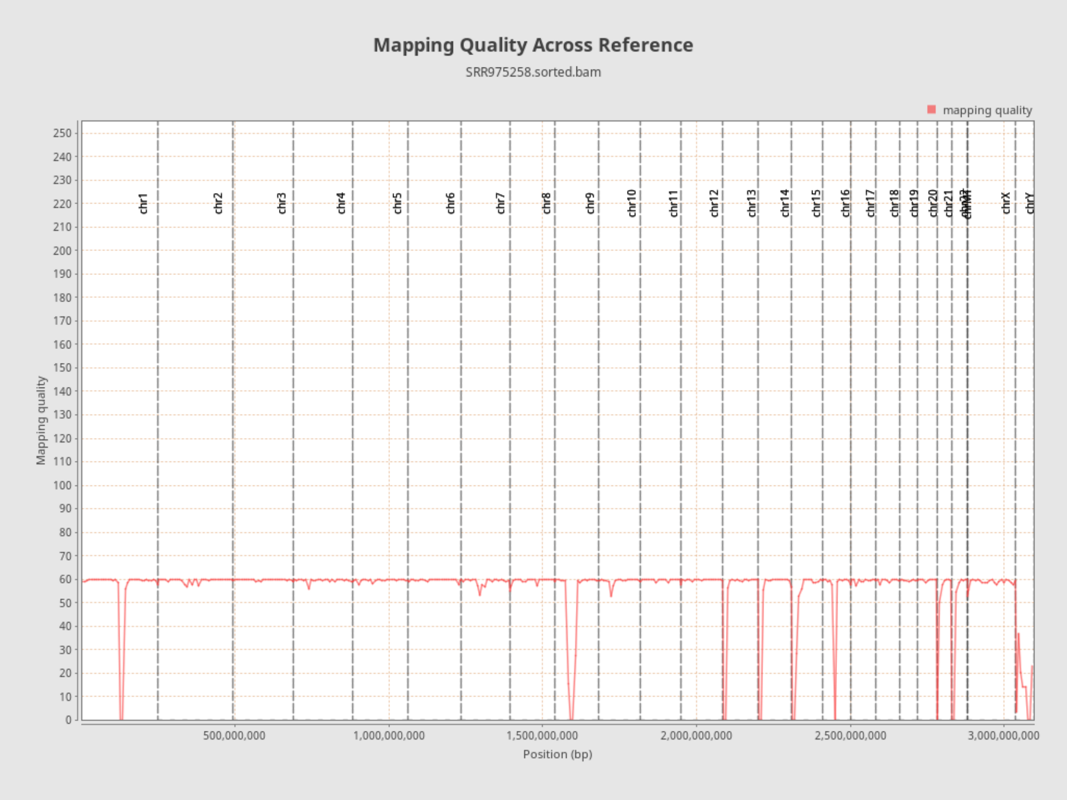
10. Results : Mapped Reads Clipping Profile



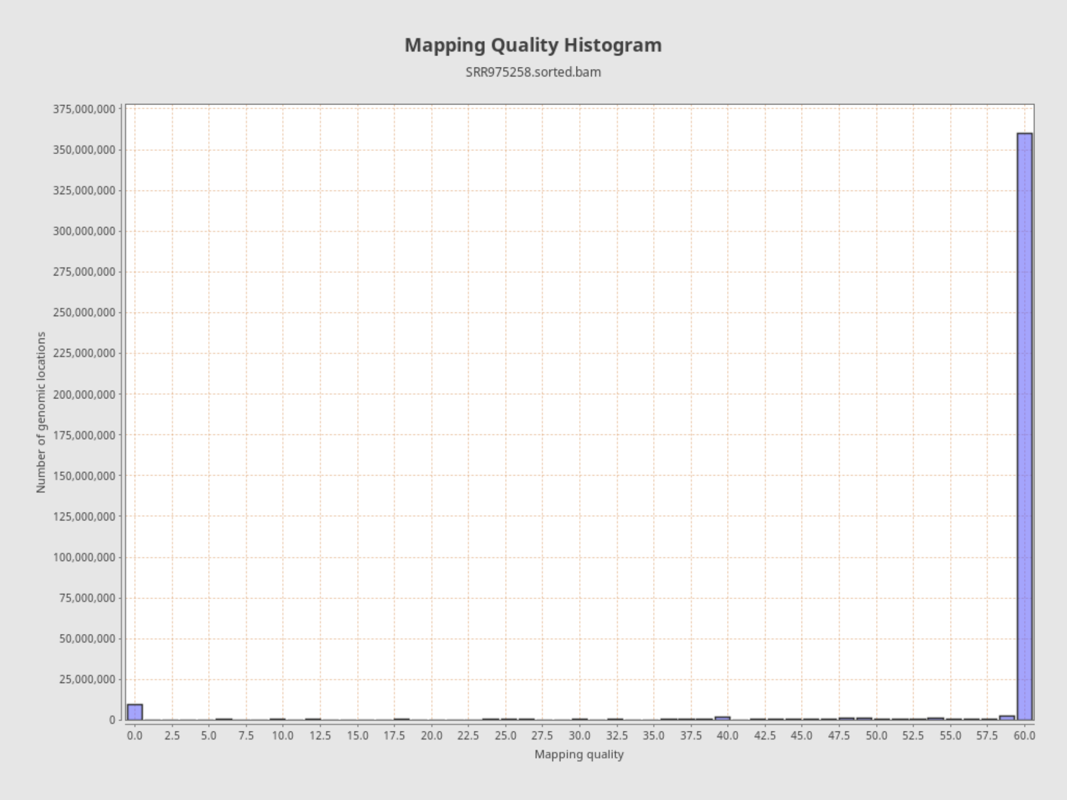
11. Results : Homopolymer Indels



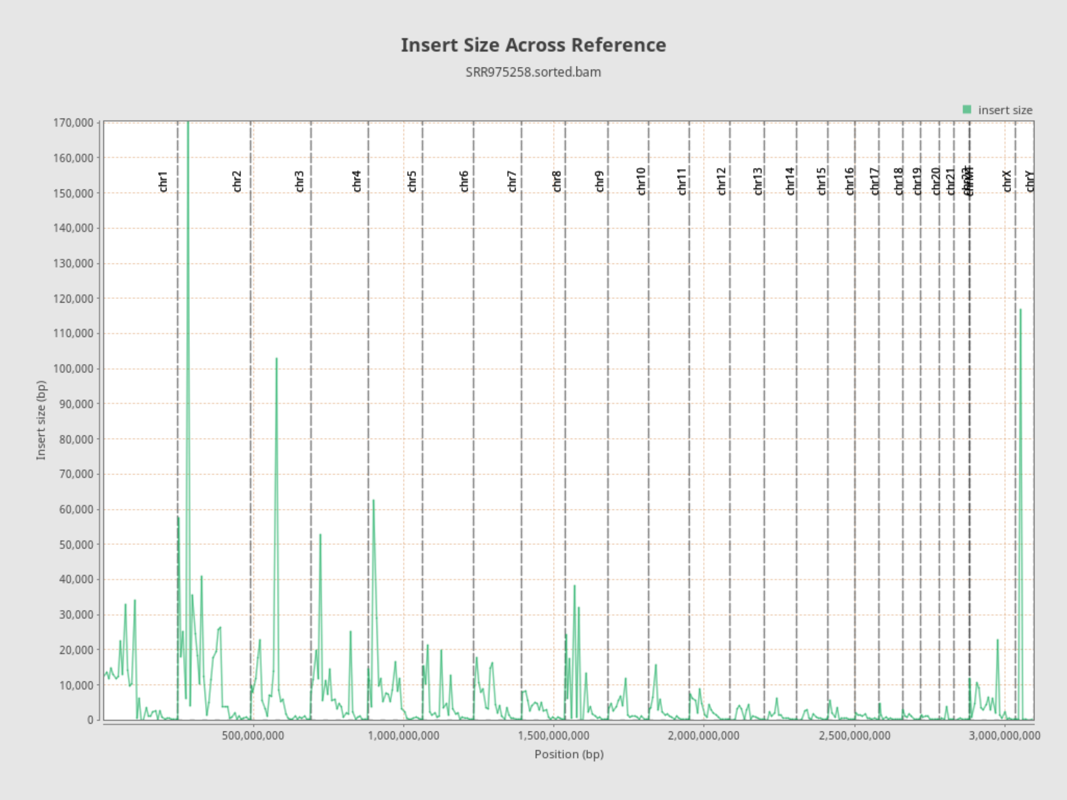
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram