

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 12:30:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124978.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_SRR3124978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124978_1.fastq.gz SRR3124978_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 12:30:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,824,732
Mapped reads	5,703,252 / 97.91%
Unmapped reads	121,480 / 2.09%
Mapped paired reads	5,703,252 / 97.91%
Mapped reads, first in pair	2,858,139 / 49.07%
Mapped reads, second in pair	2,845,113 / 48.85%
Mapped reads, both in pair	5,674,300 / 97.42%
Mapped reads, singletons	28,952 / 0.5%
Secondary alignments	0
Supplementary alignments	53,212 / 0.91%
Read min/max/mean length	30 / 101 / 101.37
Duplicated reads (estimated)	694,595 / 11.92%
Duplication rate	8.42%
Clipped reads	3,061,079 / 52.55%

2.2. ACGT Content

Number/percentage of A's	139,175,802 / 28.55%
Number/percentage of C's	89,966,625 / 18.45%
Number/percentage of T's	146,889,236 / 30.13%
Number/percentage of G's	111,485,057 / 22.87%
Number/percentage of N's	5,109 / 0%

GC Percentage	41.32%
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2.3. Coverage

Mean	0.1576
Standard Deviation	1.9025

2.4. Mapping Quality

Mean Mapping Quality	52.41
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2.5. Insert size

Mean	88,094.41
Standard Deviation	2,779,352.01
P25/Median/P75	133 / 178 / 242

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	3,708,265
Insertions	78,872
Mapped reads with at least one insertion	1.34%
Deletions	159,555
Mapped reads with at least one deletion	2.73%
Homopolymer indels	46.32%

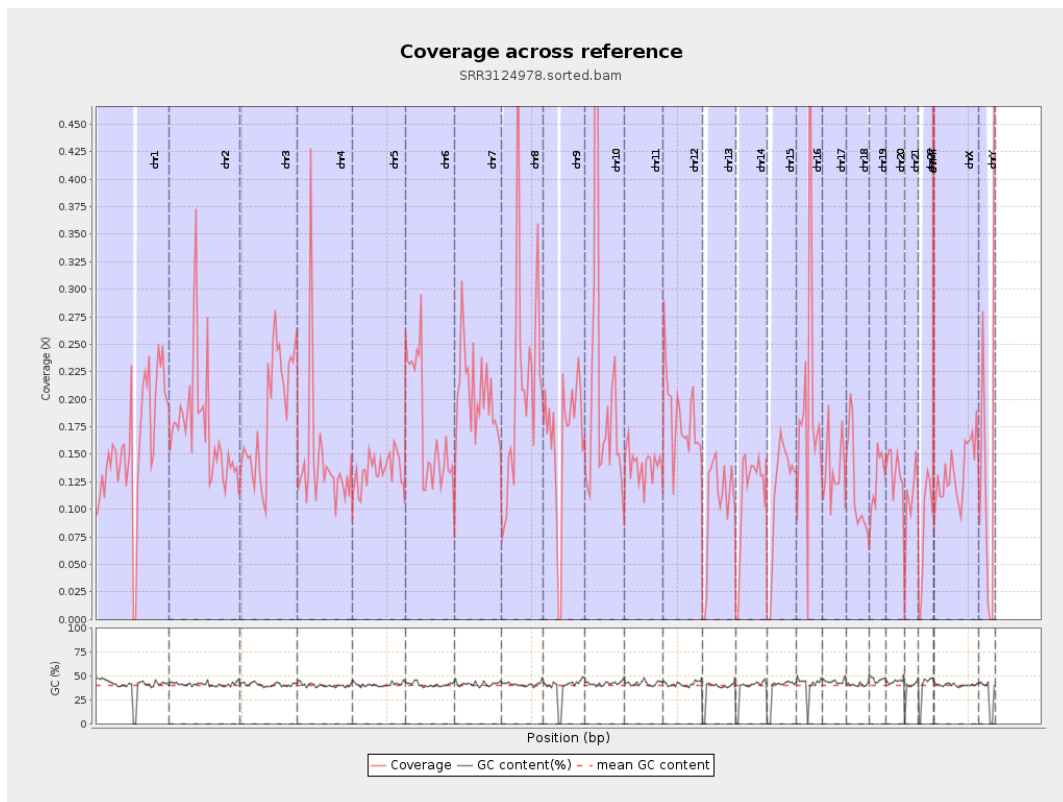
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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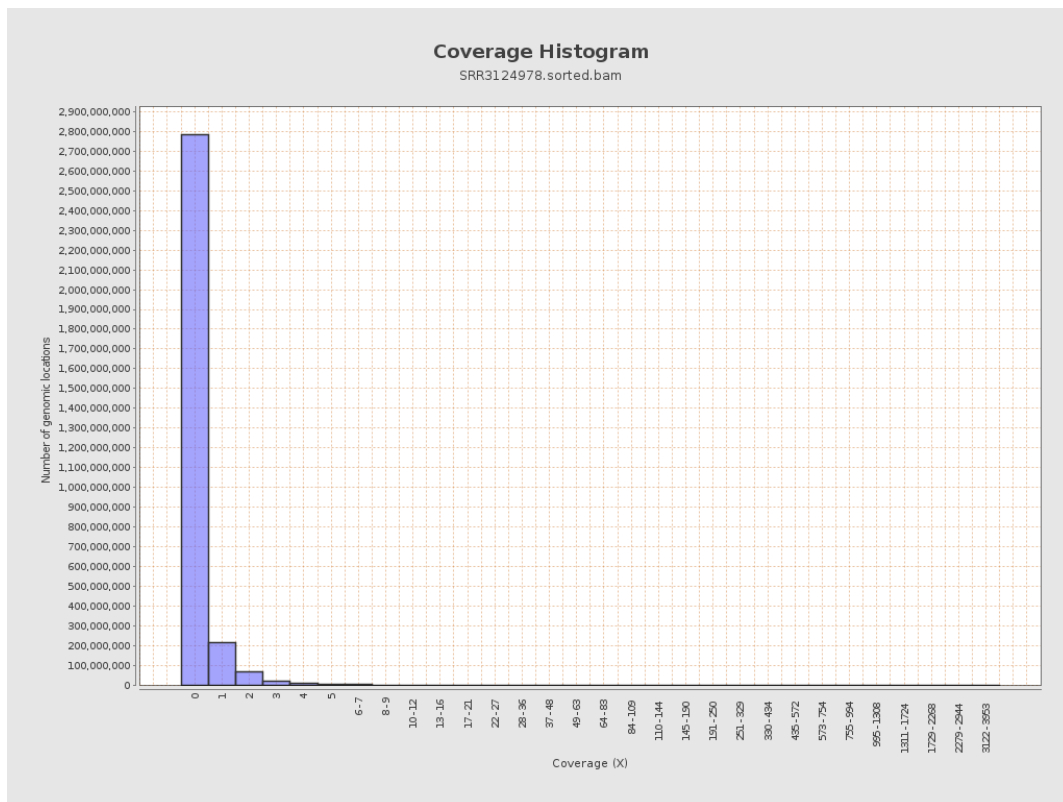
		bases	coverage	deviation
chr1	249250621	39583649	0.1588	1.4264
chr2	243199373	42460967	0.1746	2.1634
chr3	198022430	36782819	0.1858	0.6485
chr4	191154276	27099668	0.1418	1.845
chr5	180915260	24440963	0.1351	0.5352
chr6	171115067	29762960	0.1739	0.9943
chr7	159138663	32841182	0.2064	1.6732
chr8	146364022	31345734	0.2142	0.8197
chr9	141213431	23386916	0.1656	1.8659
chr10	135534747	28624340	0.2112	6.1609
chr11	135006516	18872169	0.1398	0.8435
chr12	133851895	24581458	0.1836	0.613
chr13	115169878	11920626	0.1035	0.4348
chr14	107349540	11964322	0.1115	0.5599
chr15	102531392	11828435	0.1154	0.4825
chr16	90354753	17480387	0.1935	3.2394
chr17	81195210	10872809	0.1339	1.4073
chr18	78077248	9488727	0.1215	1.8956
chr19	59128983	7522587	0.1272	0.8508
chr20	63025520	8429860	0.1338	0.7204
chr21	48129895	5171733	0.1075	0.9616
chr22	51304566	4208850	0.082	0.4553
chrMT	16571	241396	14.5674	9.3854
chrX	155270560	20694643	0.1333	0.6946

chrY	59373566	8210032	0.1383	3.1686
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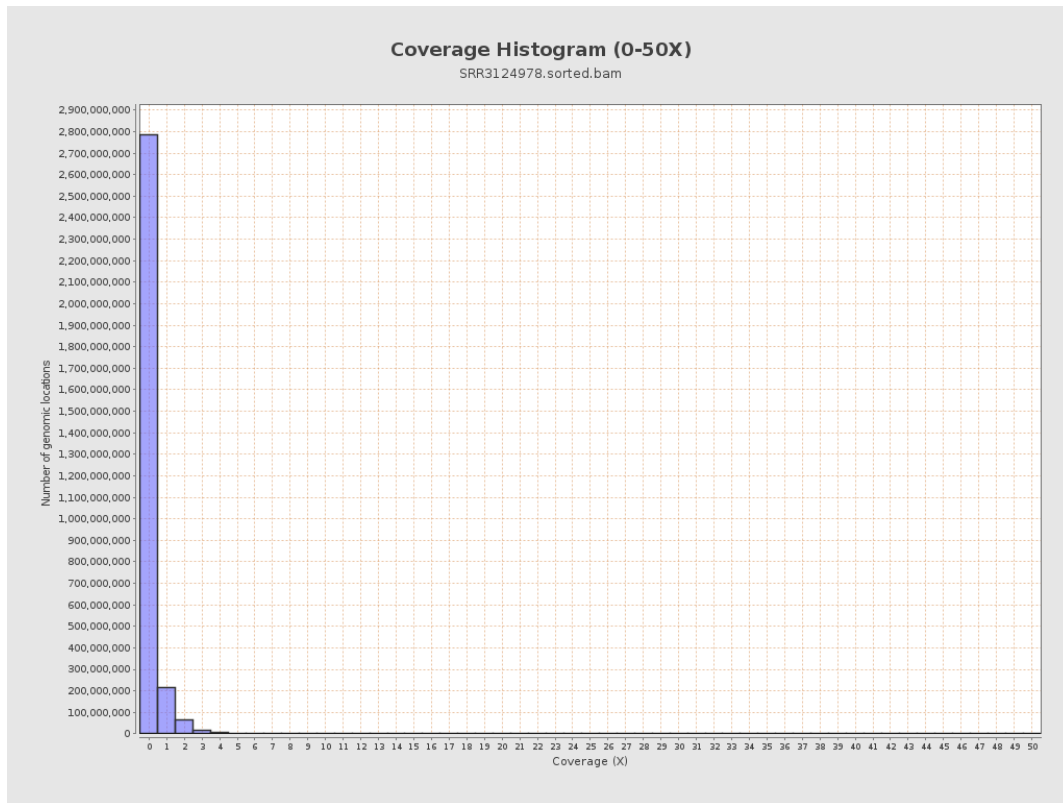
3. Results : Coverage across reference



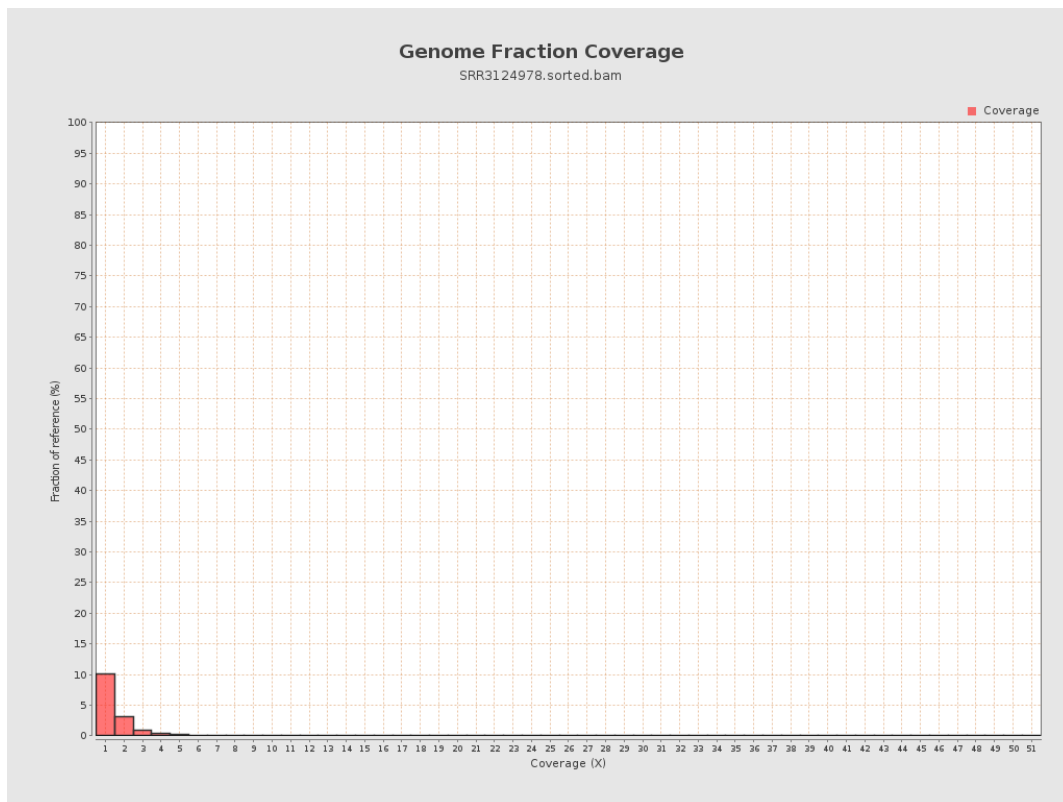
4. Results : Coverage Histogram



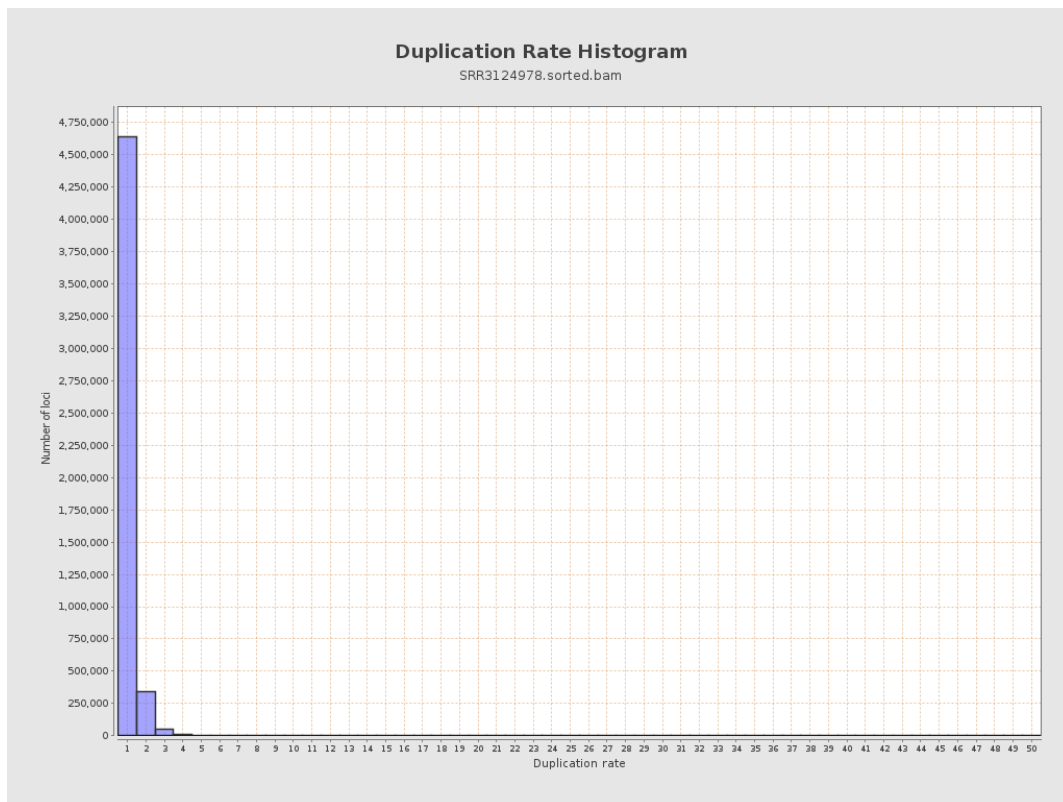
5. Results : Coverage Histogram (0-50X)



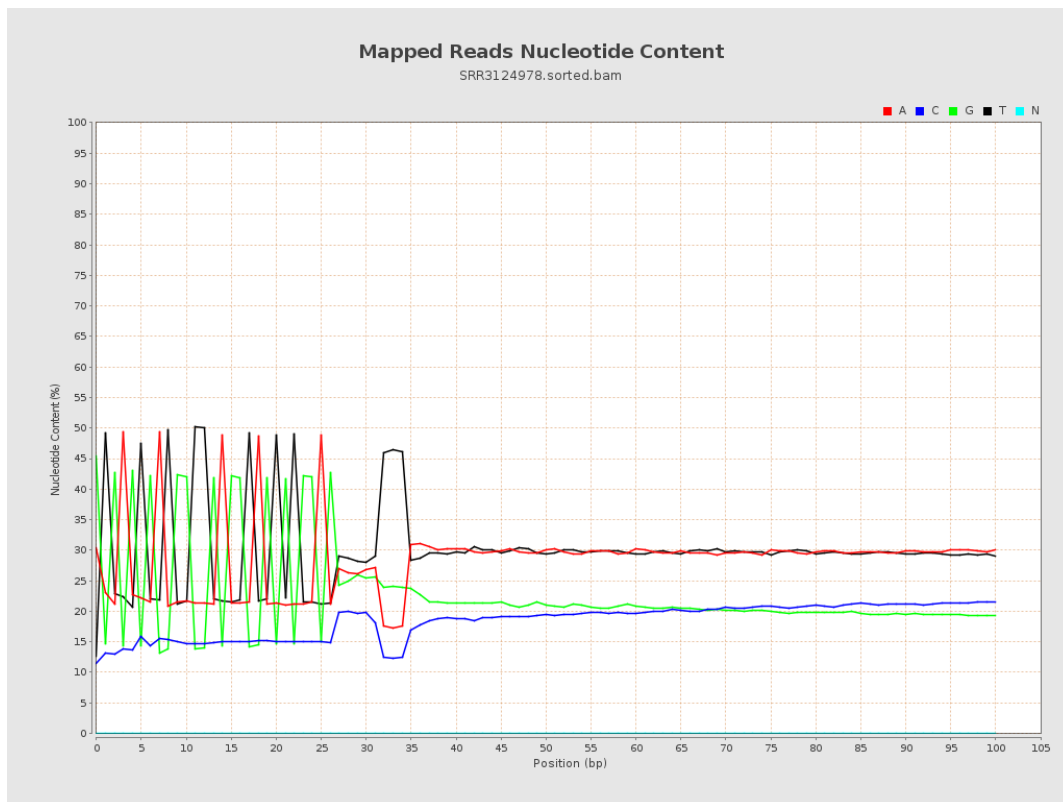
6. Results : Genome Fraction Coverage



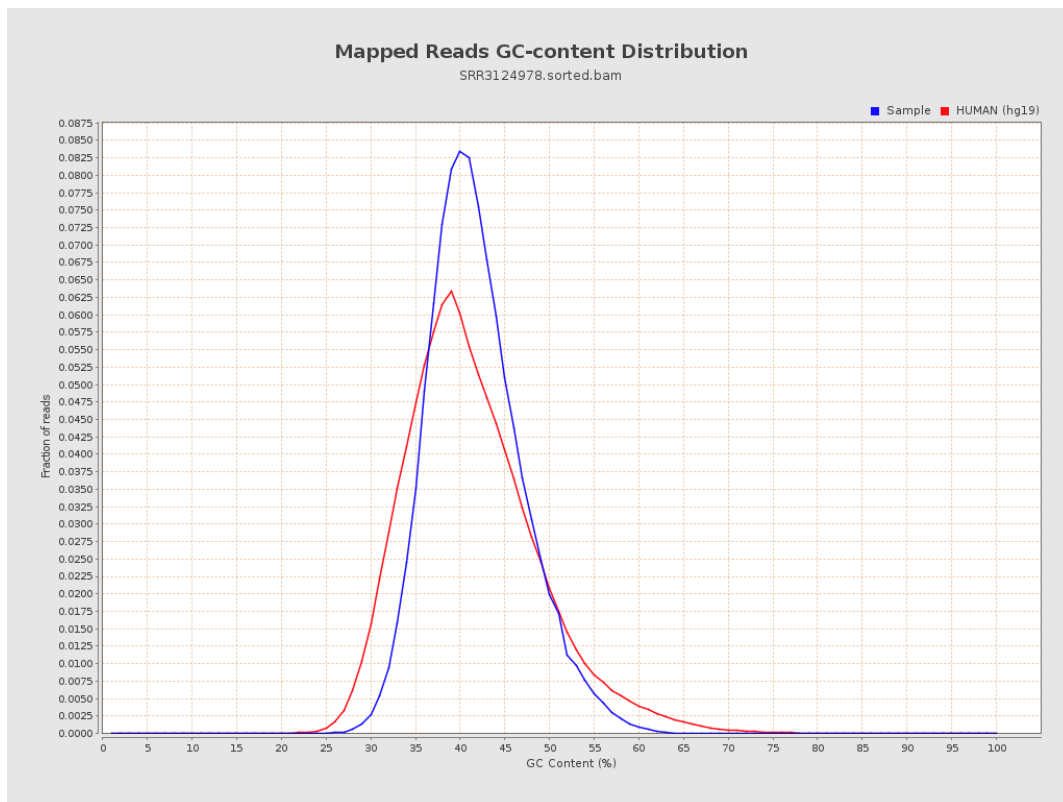
7. Results : Duplication Rate Histogram



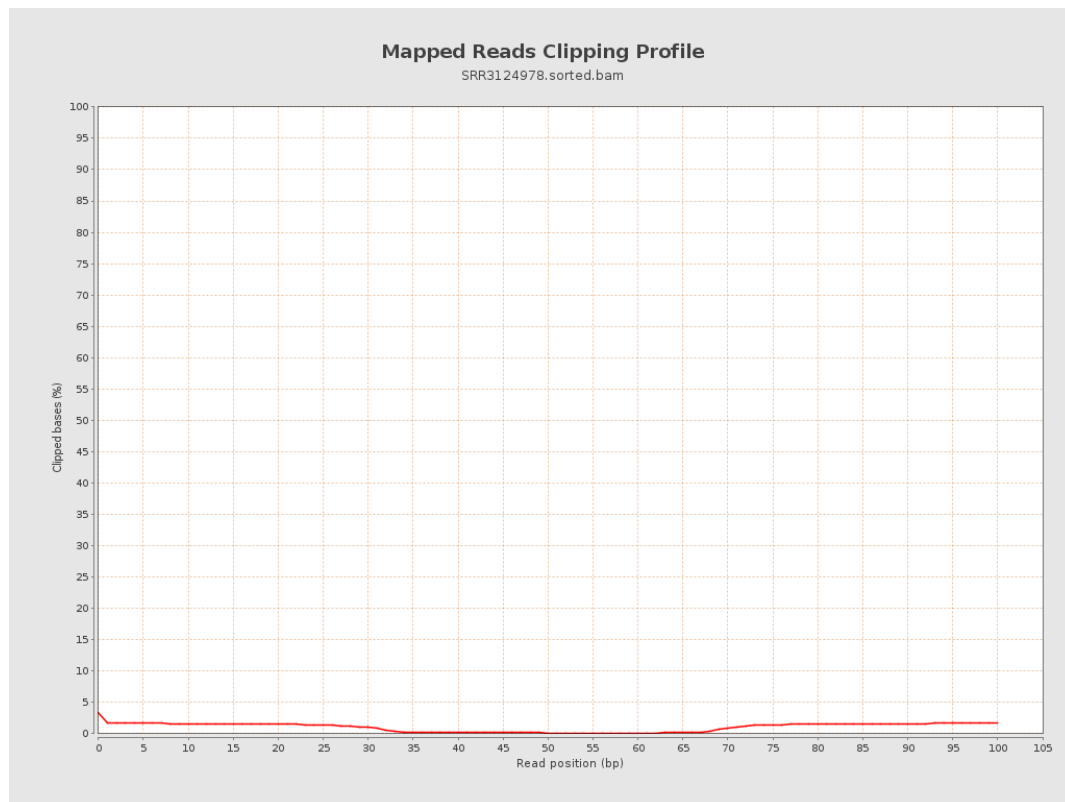
8. Results : Mapped Reads Nucleotide Content



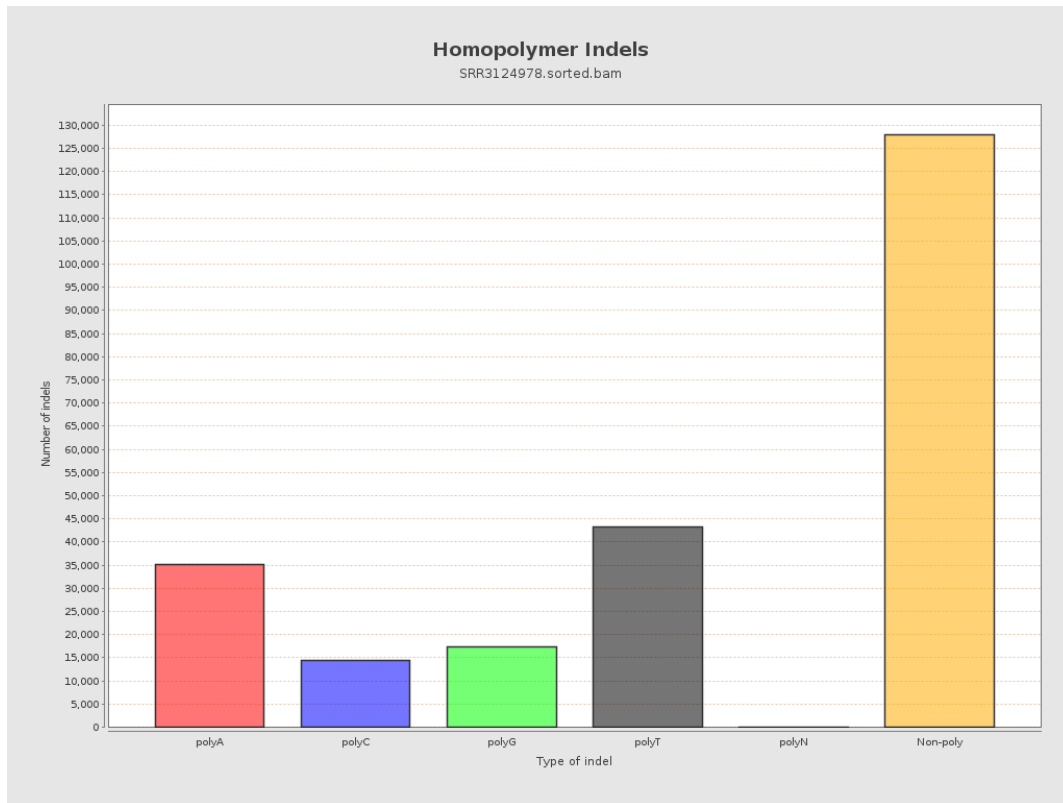
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



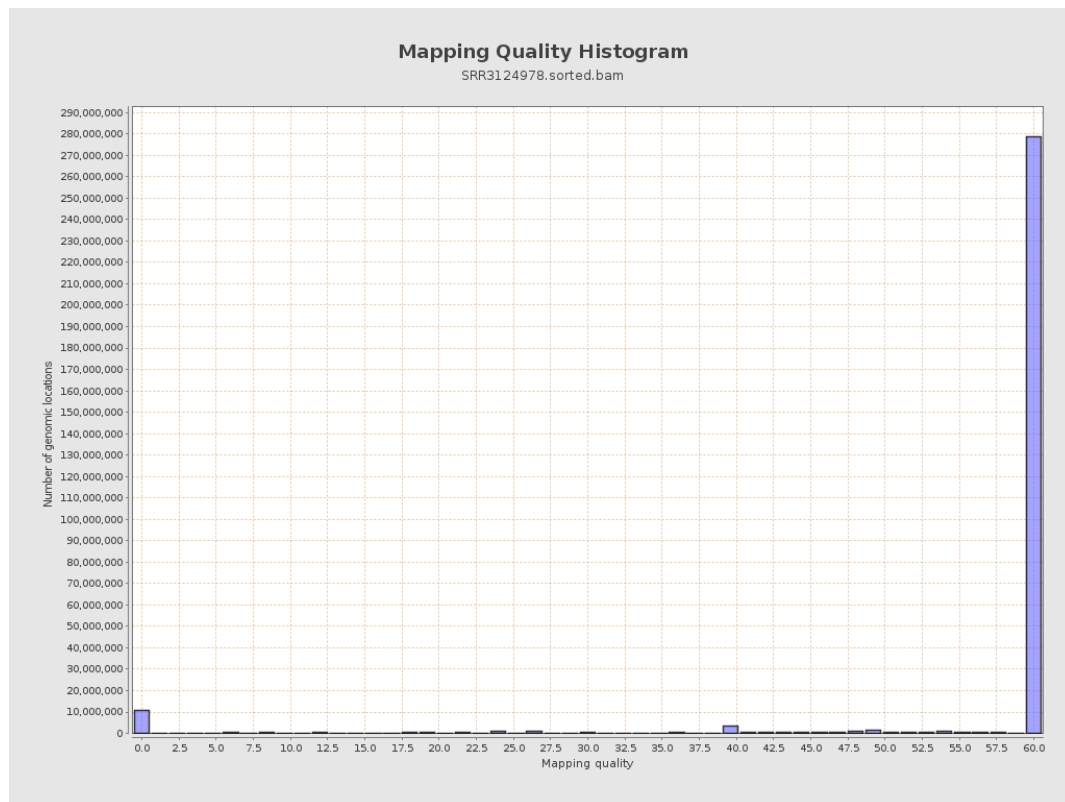
11. Results : Homopolymer Indels



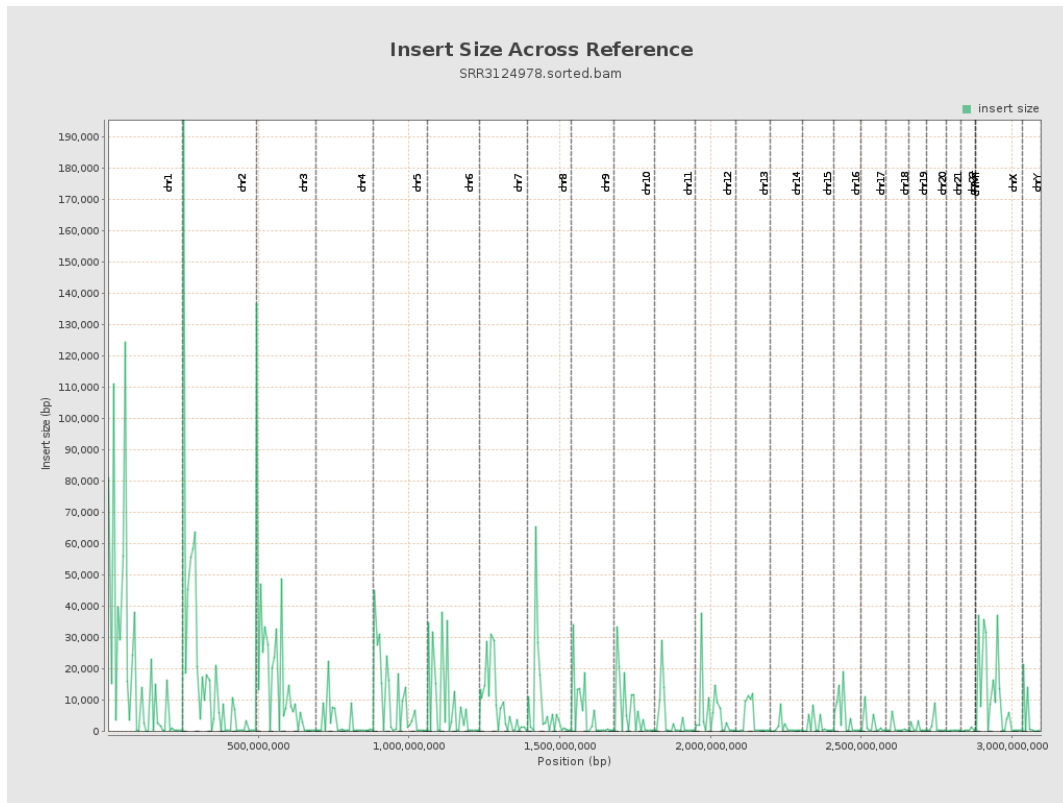
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

