

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/02 20:13:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672010.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_SRR21672010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672010_1.fastq.gz SRR21672010_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 02 20:13:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	471,619,134
Mapped reads	431,627,279 / 91.52%
Unmapped reads	39,991,855 / 8.48%
Mapped paired reads	431,627,279 / 91.52%
Mapped reads, first in pair	215,877,097 / 45.77%
Mapped reads, second in pair	215,750,182 / 45.75%
Mapped reads, both in pair	430,689,798 / 91.32%
Mapped reads, singletons	937,481 / 0.2%
Secondary alignments	0
Supplementary alignments	2,045,399 / 0.43%
Read min/max/mean length	15 / 150 / 149.58
Duplicated reads (estimated)	92,193,964 / 19.55%
Duplication rate	17.07%
Clipped reads	20,454,454 / 4.34%

2.2. ACGT Content

Number/percentage of A's	19,024,286,344 / 29.76%
Number/percentage of C's	12,984,647,665 / 20.31%
Number/percentage of T's	18,863,770,359 / 29.51%
Number/percentage of G's	13,059,139,329 / 20.43%
Number/percentage of N's	295,452 / 0%

GC Percentage	40.74%
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2.3. Coverage

Mean	20.6607
Standard Deviation	208.8137

2.4. Mapping Quality

Mean Mapping Quality	54.6
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2.5. Insert size

Mean	32,967.74
Standard Deviation	1,692,289.19
P25/Median/P75	322 / 371 / 420

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	415,424,601
Insertions	9,239,724
Mapped reads with at least one insertion	2.02%
Deletions	9,710,589
Mapped reads with at least one deletion	2.15%
Homopolymer indels	45.47%

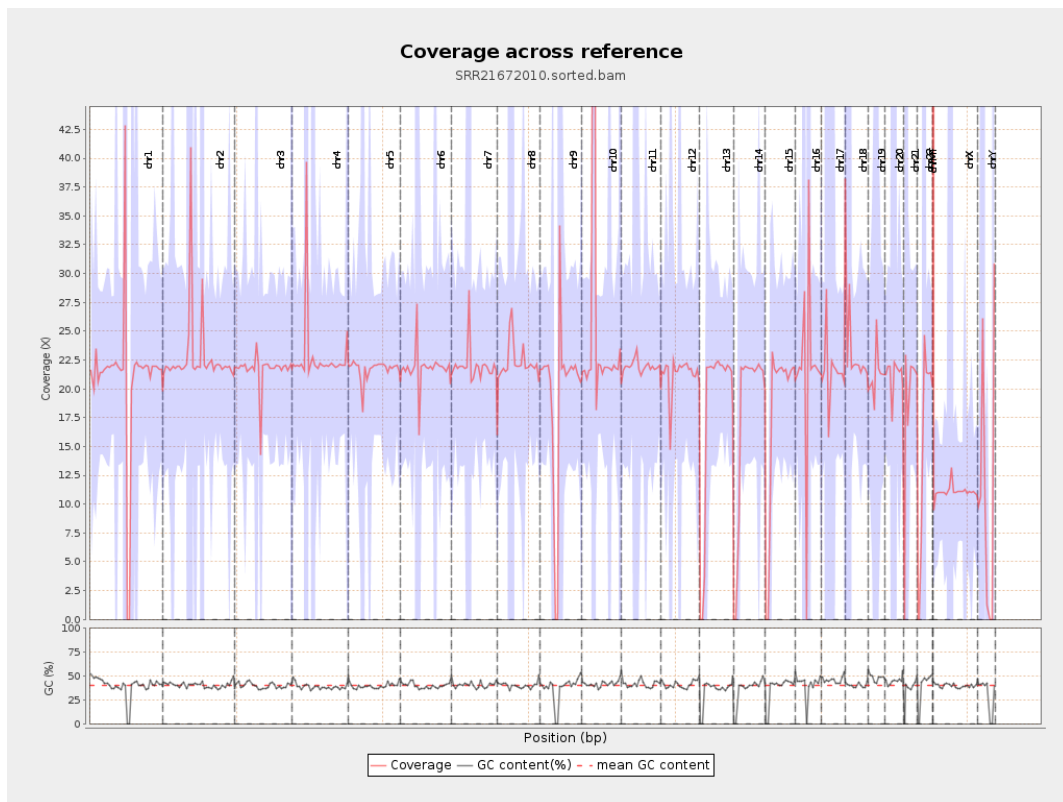
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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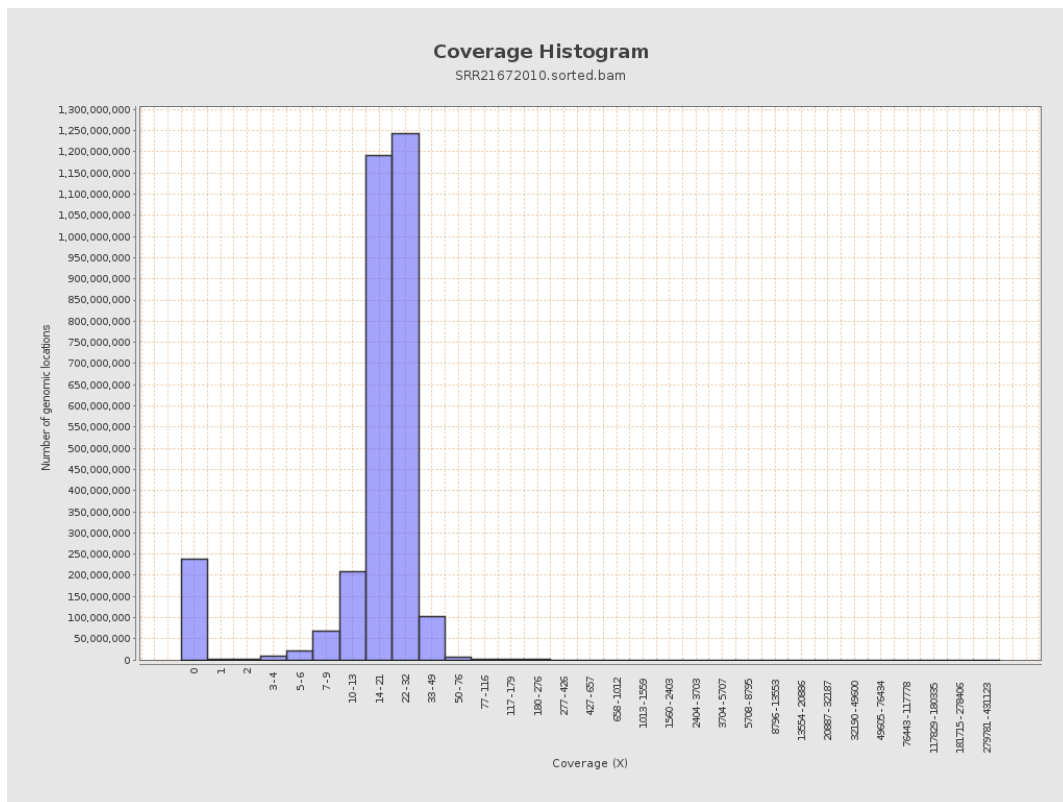
		bases	coverage	deviation
chr1	249250621	5236849867	21.0104	455.4868
chr2	243199373	5547596528	22.8109	117.9899
chr3	198022430	4294017540	21.6845	13.9368
chr4	191154276	4368486542	22.8532	171.1991
chr5	180915260	3919109383	21.6627	15.598
chr6	171115067	3732590413	21.8133	68.625
chr7	159138663	3503388546	22.0147	166.9187
chr8	146364022	3269755861	22.3399	272.8571
chr9	141213431	2776132711	19.6591	277.3148
chr10	135534747	3378556556	24.9276	473.2423
chr11	135006516	2962230631	21.9414	115.3969
chr12	133851895	2852048707	21.3075	16.0861
chr13	115169878	2102068687	18.2519	11.8546
chr14	107349540	1938392308	18.0568	14.3237
chr15	102531392	1824053952	17.7902	12.1825
chr16	90354753	1964891209	21.7464	139.6
chr17	81195210	1755686676	21.623	99.9645
chr18	78077248	1819452712	23.3032	272.1674
chr19	59128983	1257265708	21.2631	209.4408
chr20	63025520	1334115791	21.1679	62.9652
chr21	48129895	918135910	19.0762	95.9665
chr22	51304566	783692973	15.2753	78.2397
chrMT	16571	30841679	1,861.1839	181.6063
chrX	155270560	1719835427	11.0764	32.504

chrY	59373566	670046450	11.2853	215.4253
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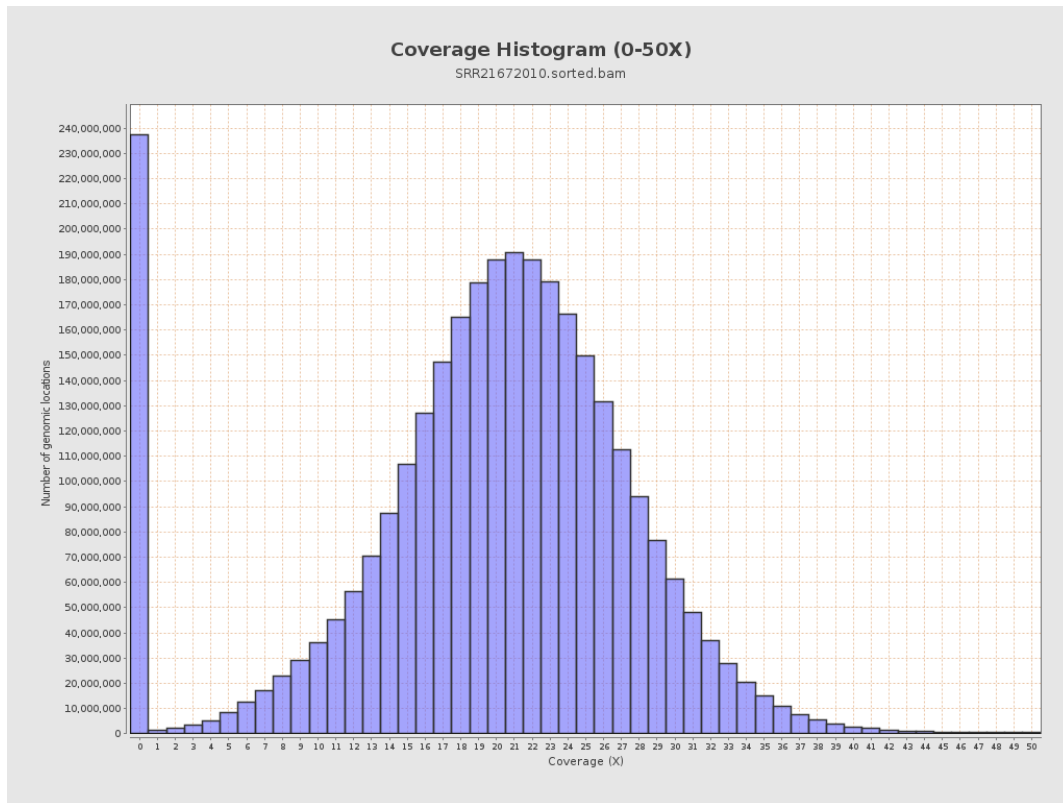
3. Results : Coverage across reference



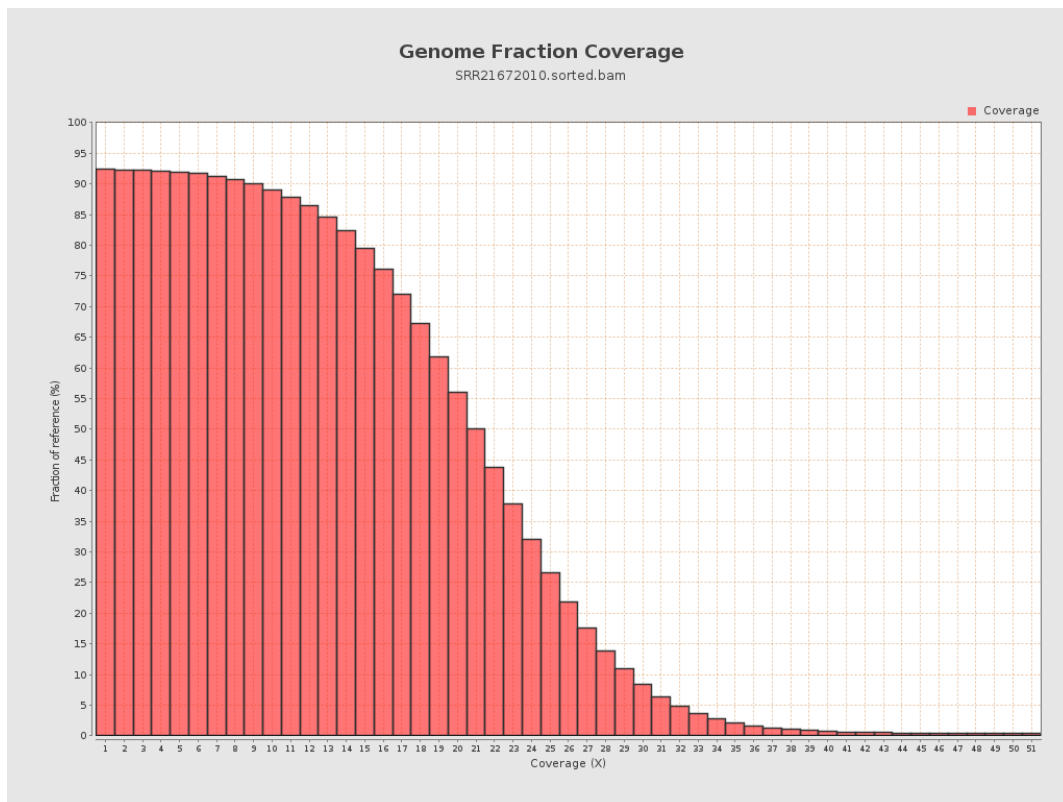
4. Results : Coverage Histogram



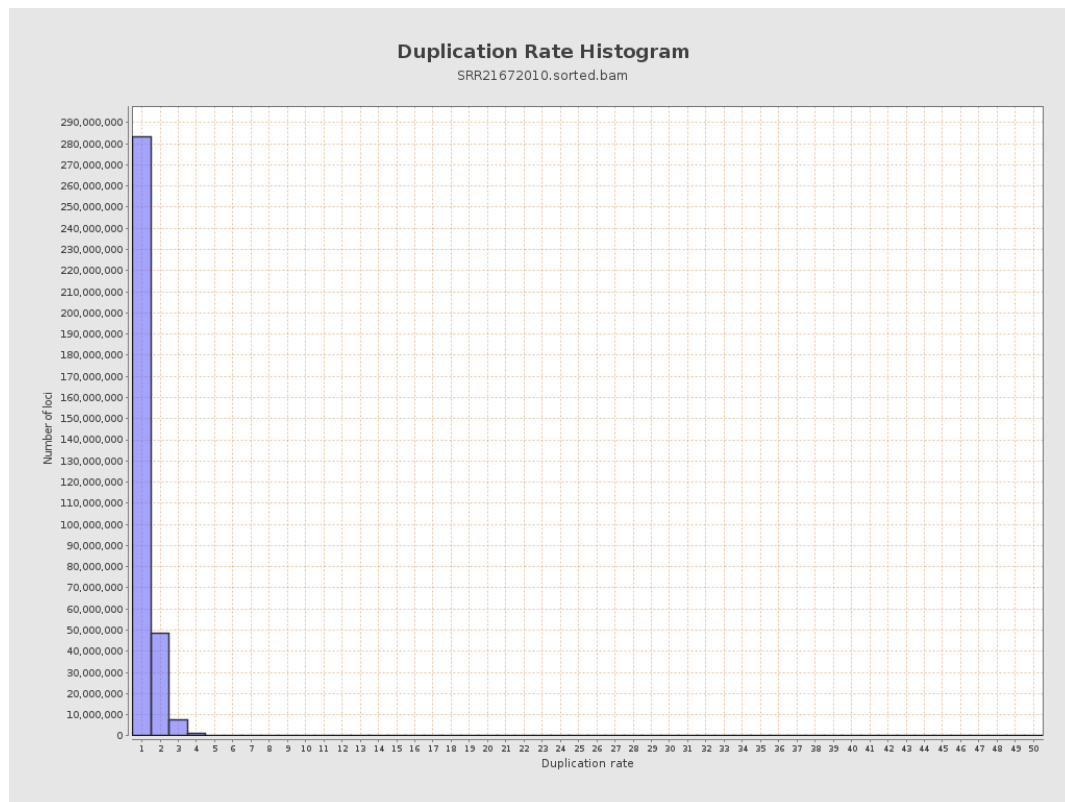
5. Results : Coverage Histogram (0-50X)



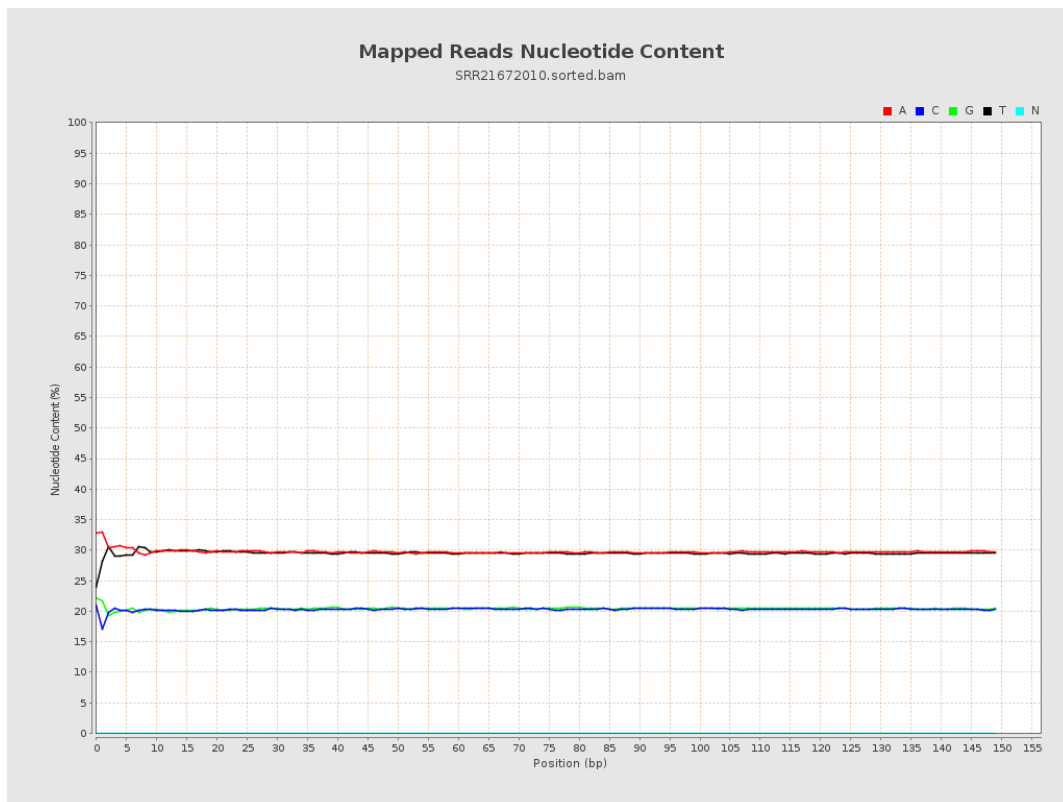
6. Results : Genome Fraction Coverage



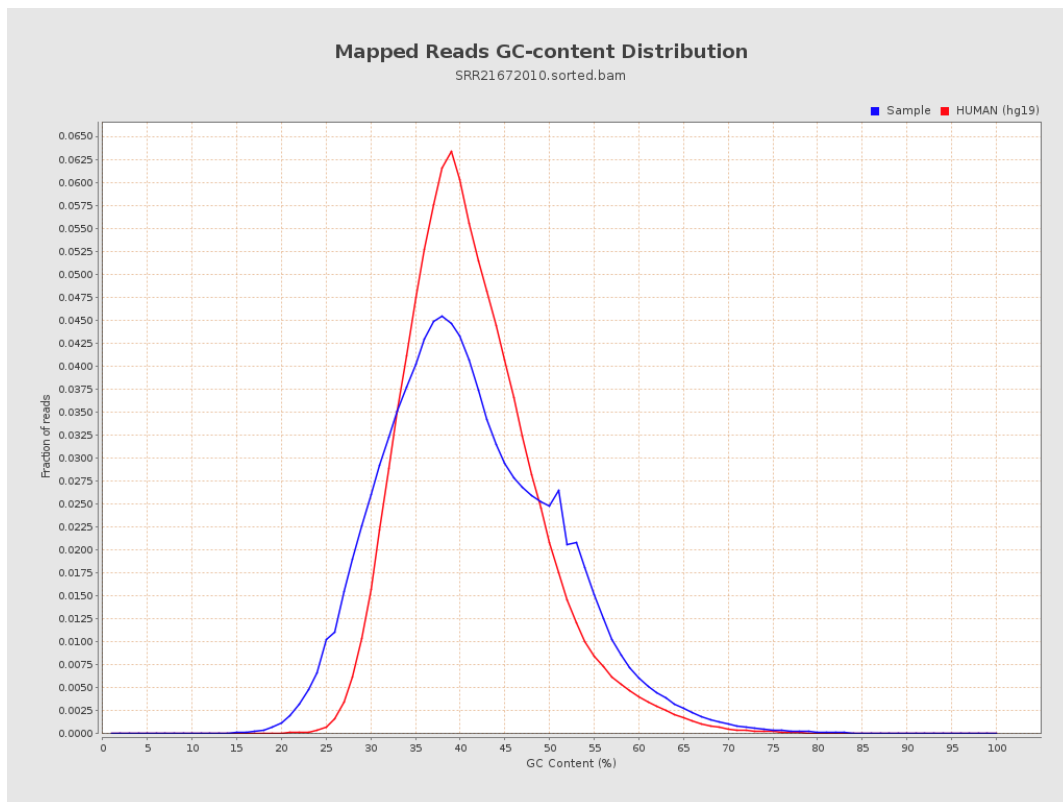
7. Results : Duplication Rate Histogram



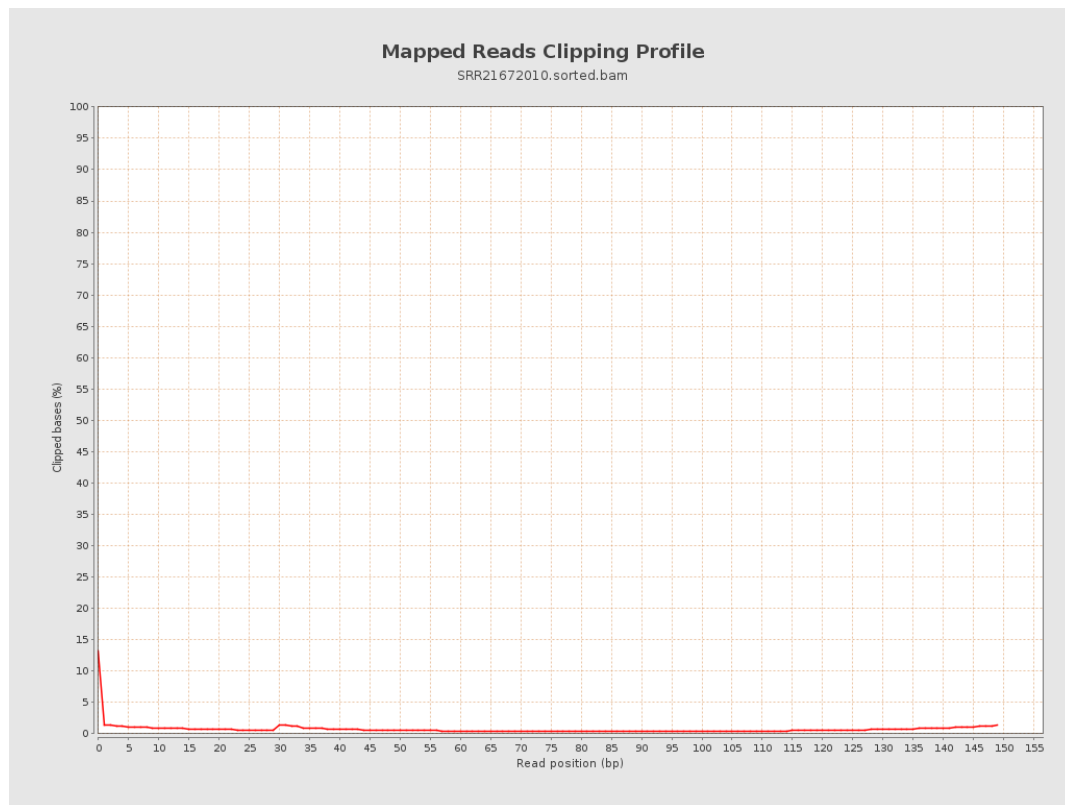
8. Results : Mapped Reads Nucleotide Content



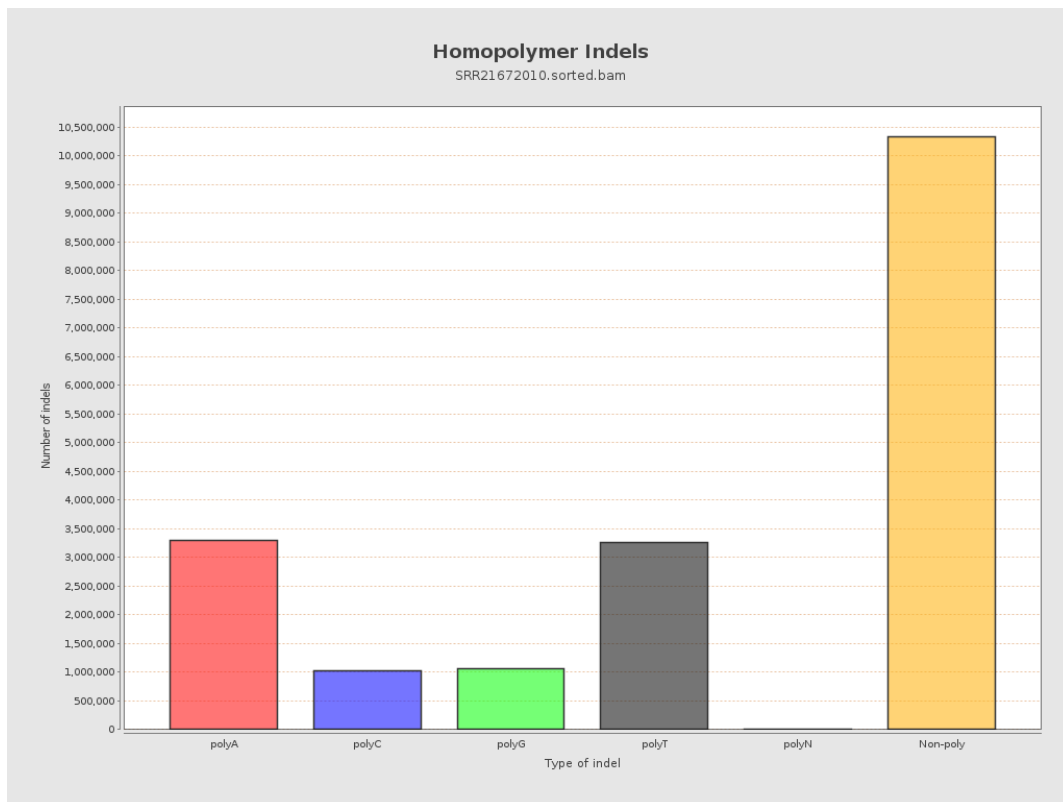
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



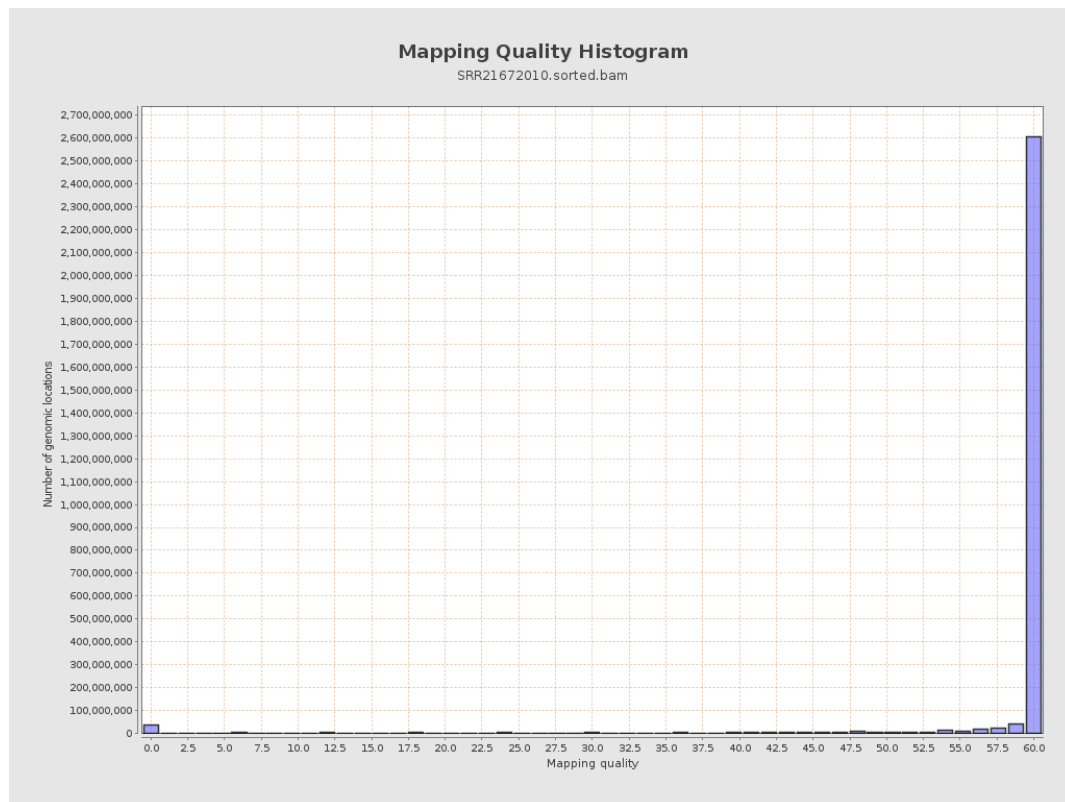
11. Results : Homopolymer Indels



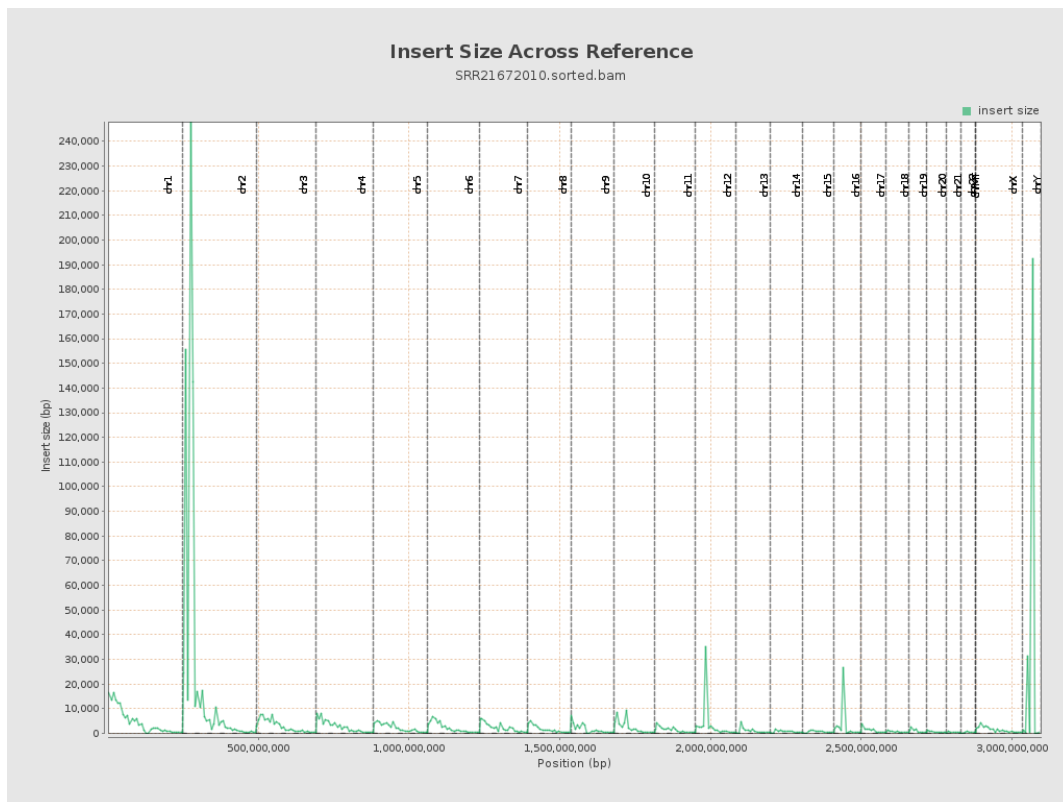
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

