

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 09:04:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671991.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_SRR21671991 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671991_1.fastq.gz SRR21671991_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 09:04:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671991.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,220,828
Mapped reads	22,110,996 / 99.51%
Unmapped reads	109,832 / 0.49%
Mapped paired reads	22,110,996 / 99.51%
Mapped reads, first in pair	11,058,222 / 49.77%
Mapped reads, second in pair	11,052,774 / 49.74%
Mapped reads, both in pair	22,090,252 / 99.41%
Mapped reads, singletons	20,744 / 0.09%
Secondary alignments	0
Supplementary alignments	92,295 / 0.42%
Read min/max/mean length	15 / 150 / 147.11
Duplicated reads (estimated)	19,136,693 / 86.12%
Duplication rate	56.65%
Clipped reads	9,862,917 / 44.39%

2.2. ACGT Content

Number/percentage of A's	762,505,620 / 25.2%
Number/percentage of C's	698,225,102 / 23.08%
Number/percentage of T's	795,911,931 / 26.31%
Number/percentage of G's	768,972,123 / 25.42%
Number/percentage of N's	8,424 / 0%

GC Percentage	48.49%
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2.3. Coverage

Mean	0.9777
Standard Deviation	69.0349

2.4. Mapping Quality

Mean Mapping Quality	53
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2.5. Insert size

Mean	34,565.71
Standard Deviation	1,777,619.53
P25/Median/P75	176 / 240 / 318

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	22,647,816
Insertions	201,305
Mapped reads with at least one insertion	0.89%
Deletions	588,477
Mapped reads with at least one deletion	2.61%
Homopolymer indels	46.49%

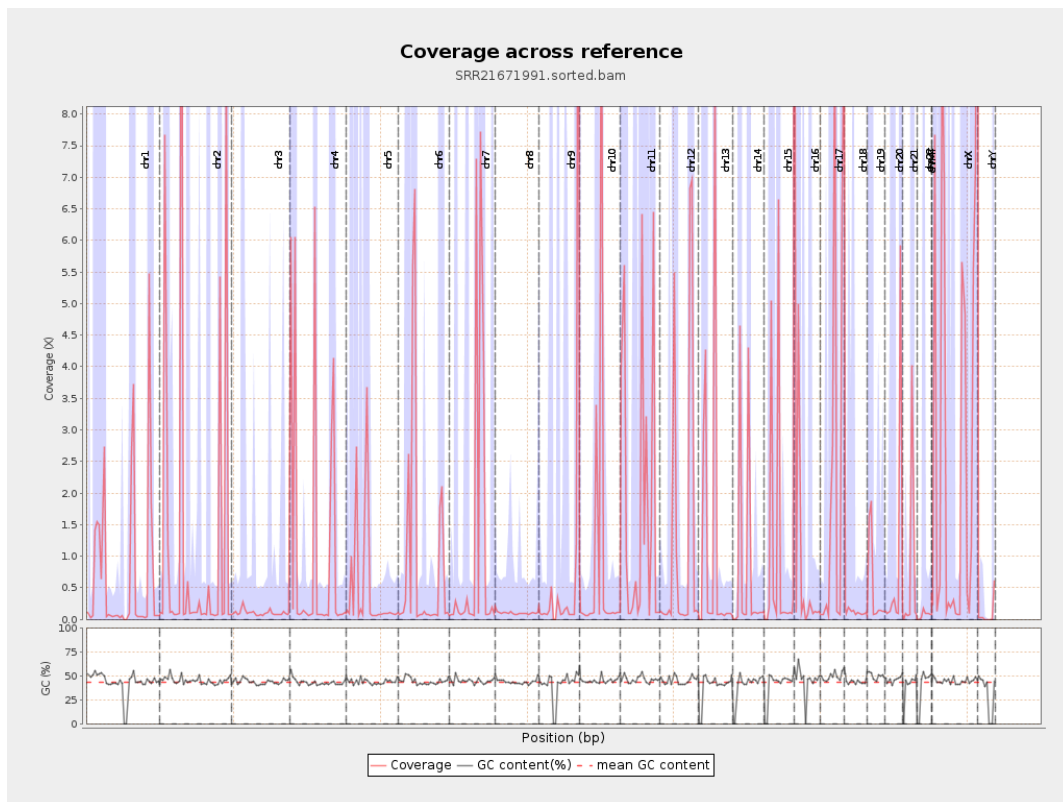
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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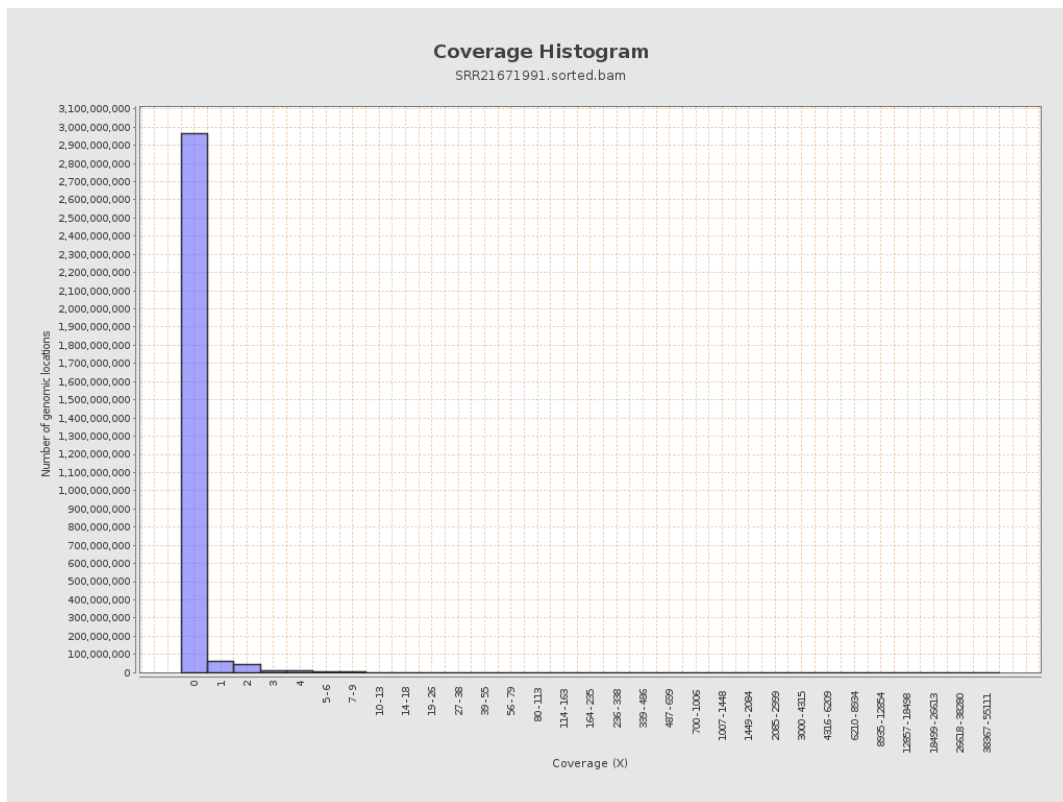
		bases	coverage	deviation
chr1	249250621	175504134	0.7041	50.9217
chr2	243199373	306114623	1.2587	81.2328
chr3	198022430	20576032	0.1039	5.5543
chr4	191154276	202429464	1.059	72.3738
chr5	180915260	85203894	0.471	44.0813
chr6	171115067	159281521	0.9308	69.4894
chr7	159138663	163718826	1.0288	79.1675
chr8	146364022	14386882	0.0983	1.0571
chr9	141213431	144774082	1.0252	73.6733
chr10	135534747	127892011	0.9436	55.6018
chr11	135006516	239488452	1.7739	88.4142
chr12	133851895	167237296	1.2494	91.4209
chr13	115169878	133110708	1.1558	89.6121
chr14	107349540	76605529	0.7136	55.1437
chr15	102531392	100770648	0.9828	61.8527
chr16	90354753	125725462	1.3915	61.0896
chr17	81195210	206914786	2.5484	107.2497
chr18	78077248	9315564	0.1193	4.8848
chr19	59128983	32116675	0.5432	45.1125
chr20	63025520	54729344	0.8684	67.0498
chr21	48129895	34442821	0.7156	57.973
chr22	51304566	3938136	0.0768	6.0505
chrMT	16571	7115	0.4294	1.3095
chrX	155270560	437109854	2.8151	126.0352

chrY	59373566	5304261	0.0893	11.9082
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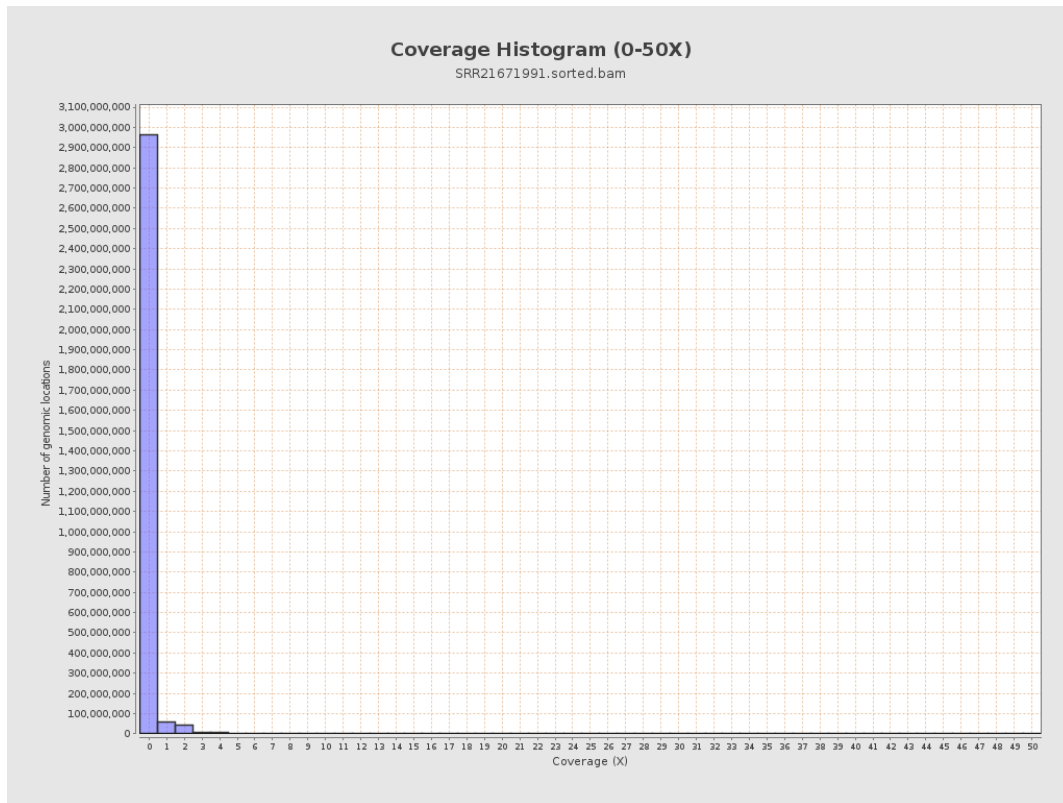
3. Results : Coverage across reference



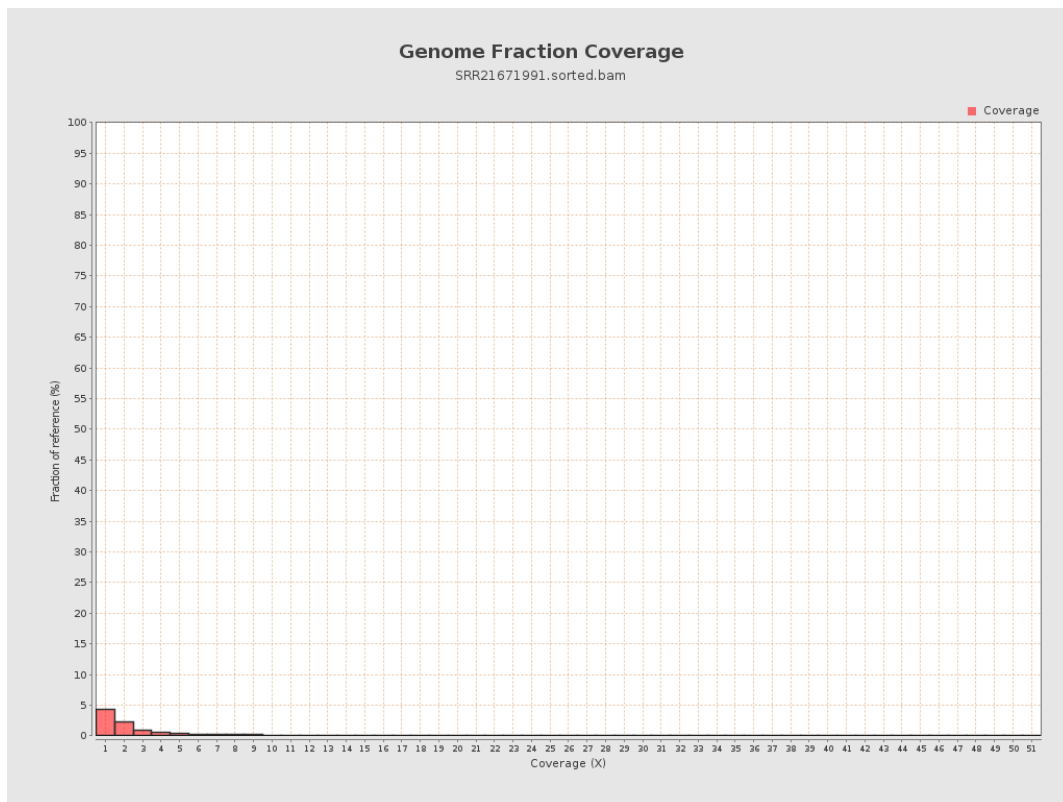
4. Results : Coverage Histogram



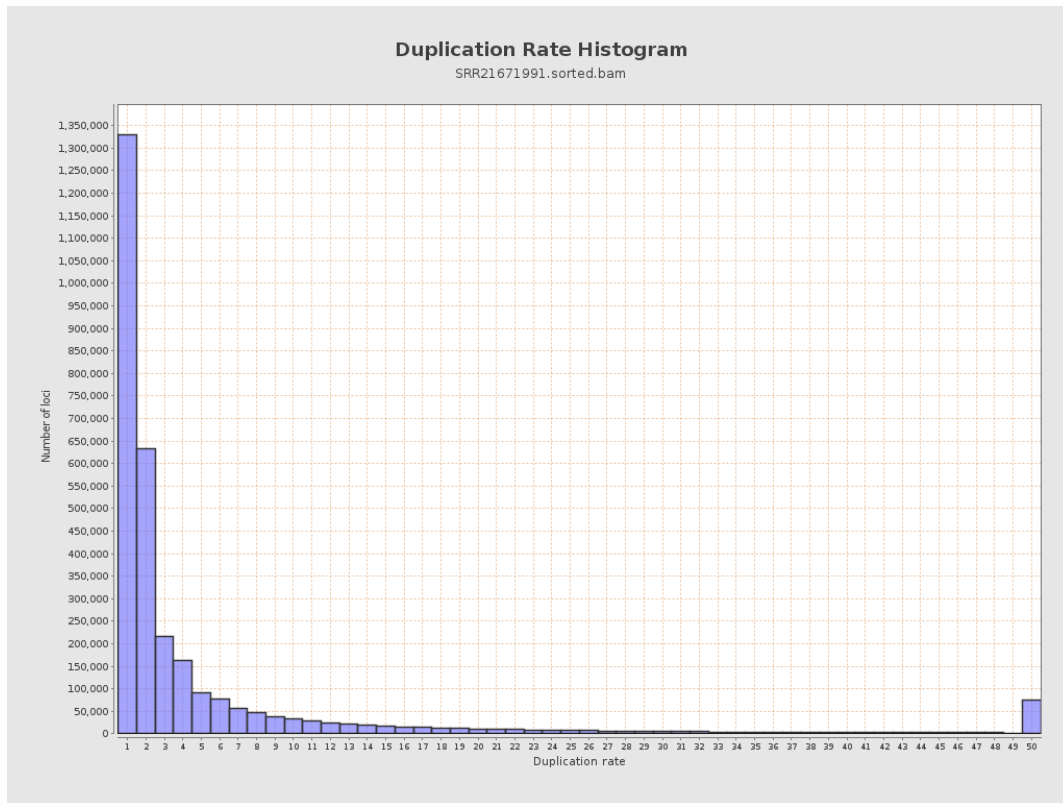
5. Results : Coverage Histogram (0-50X)



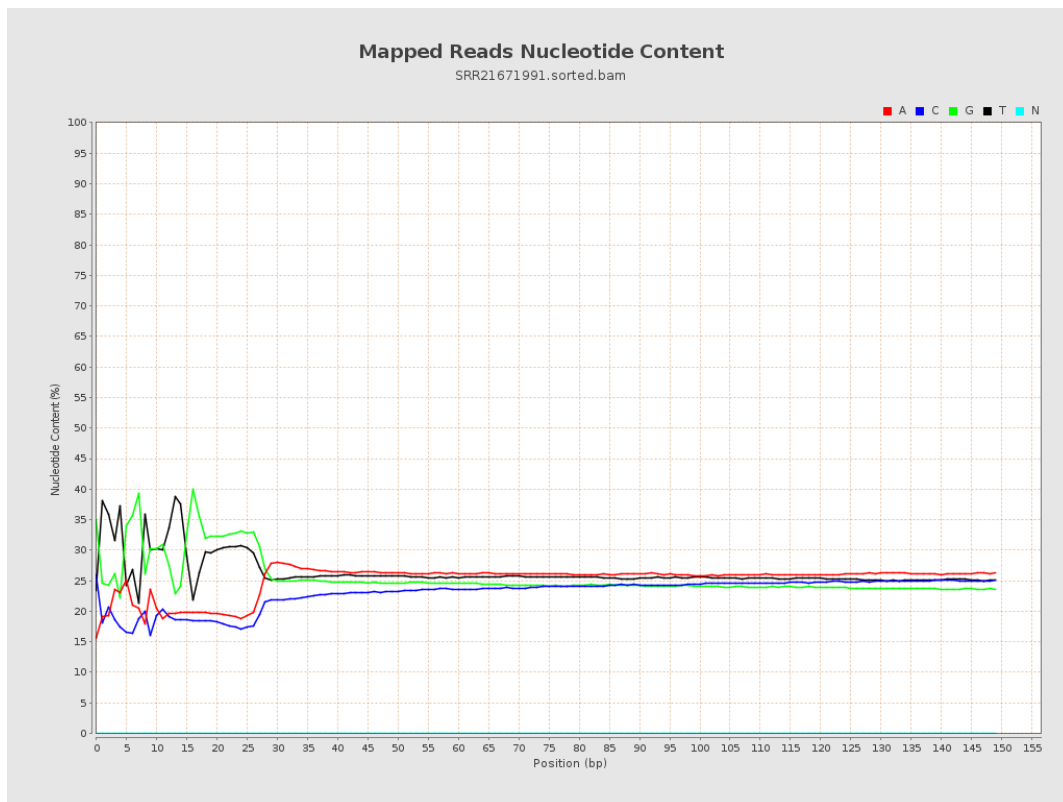
6. Results : Genome Fraction Coverage



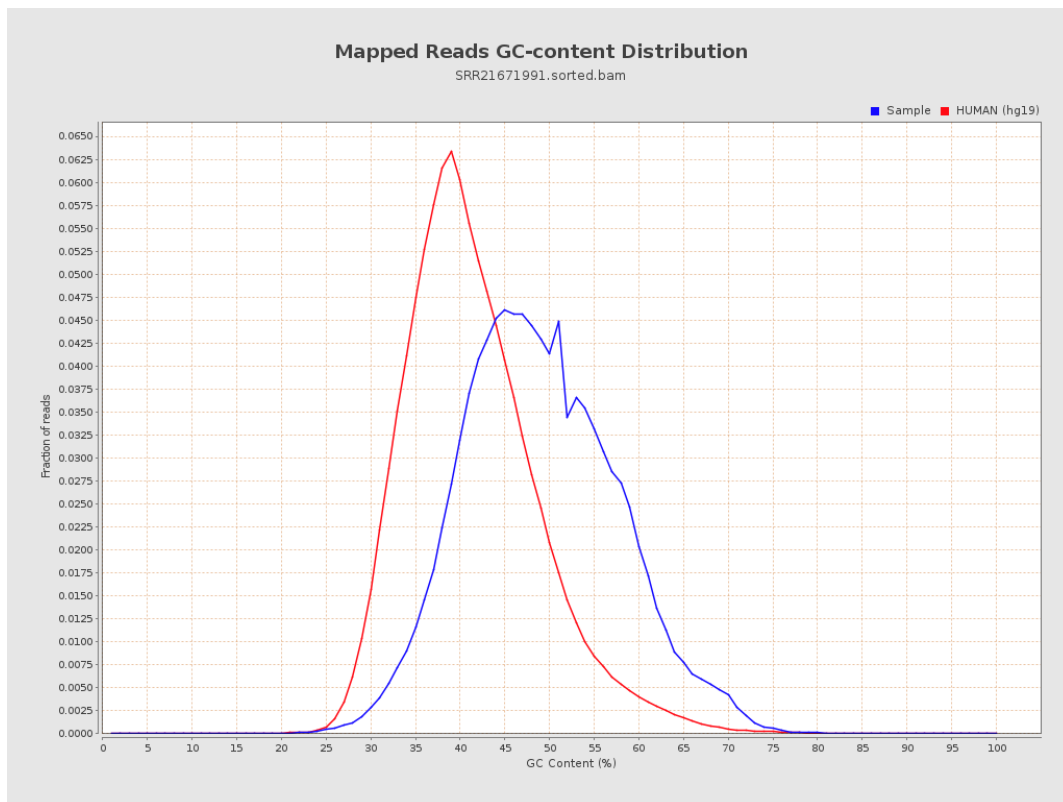
7. Results : Duplication Rate Histogram



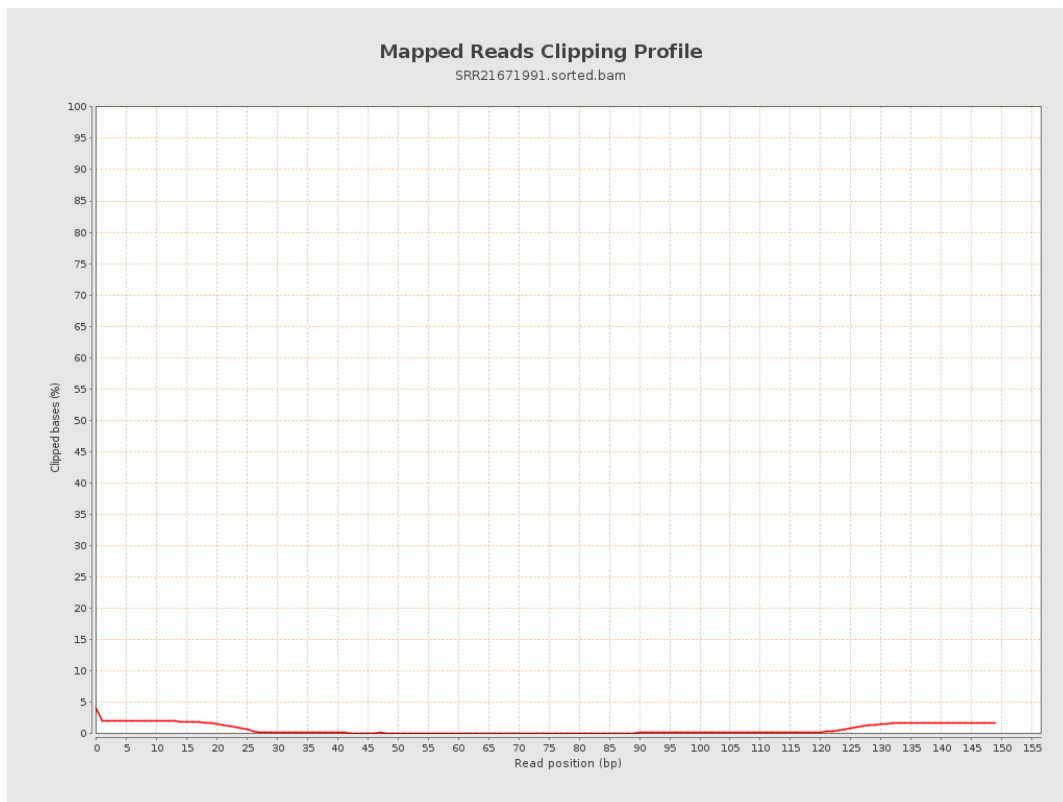
8. Results : Mapped Reads Nucleotide Content



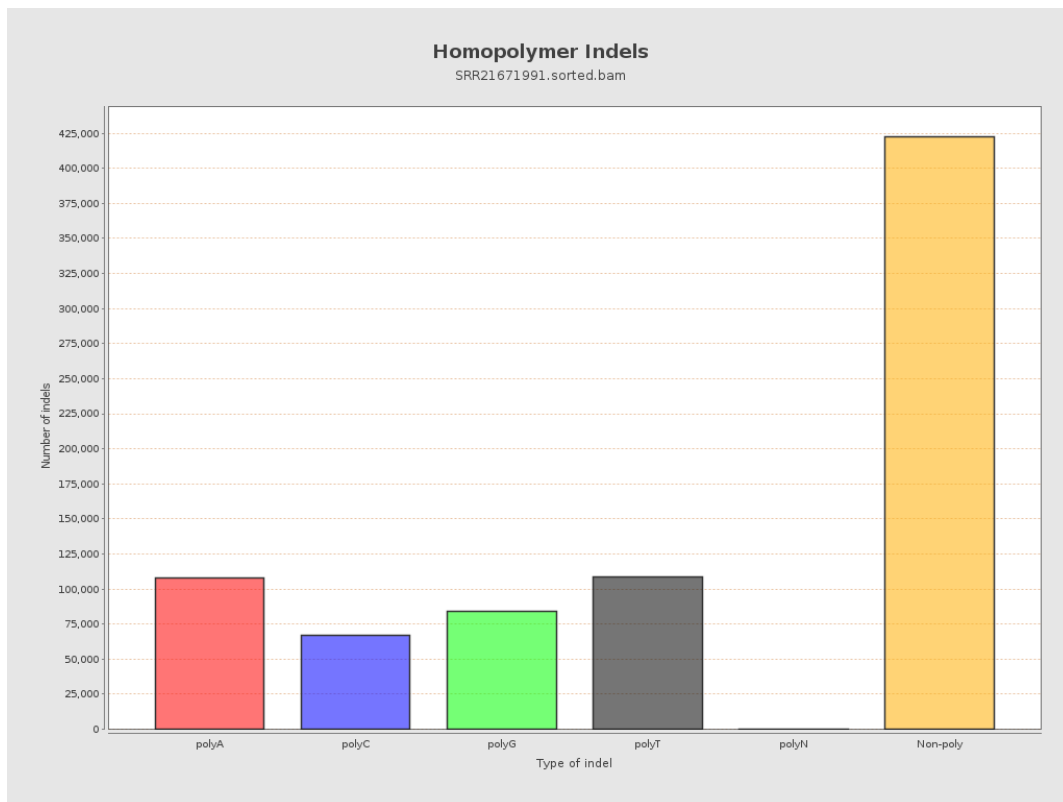
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



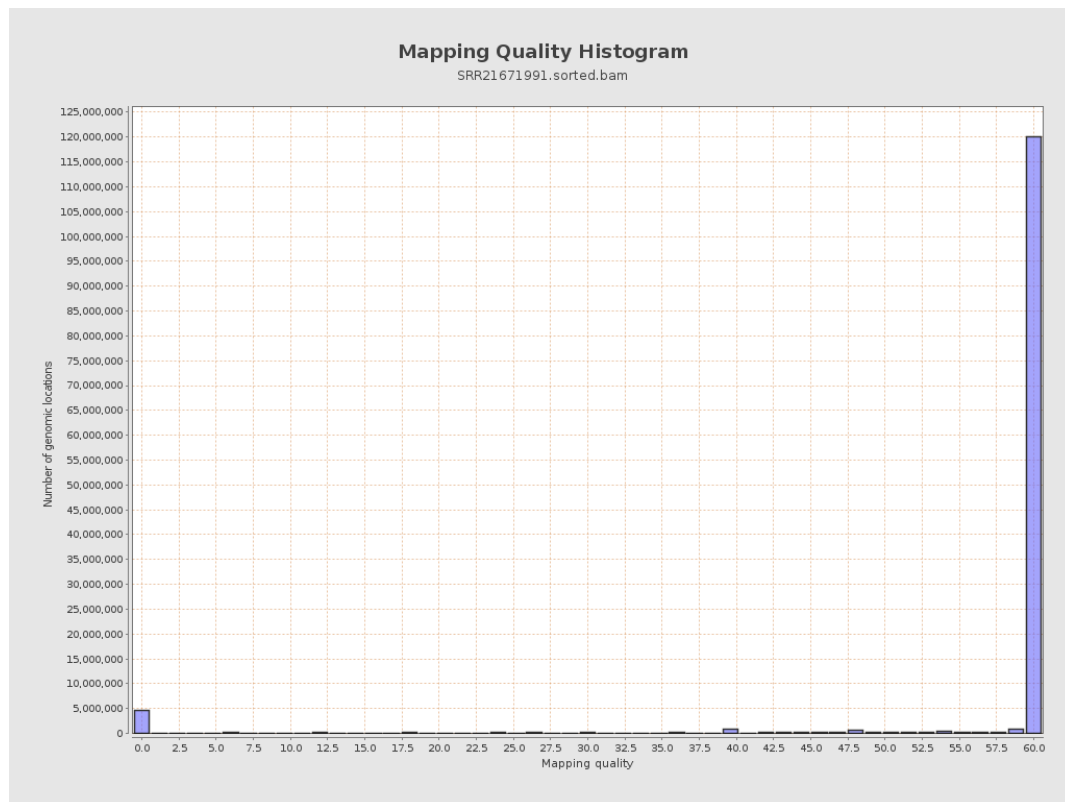
11. Results : Homopolymer Indels



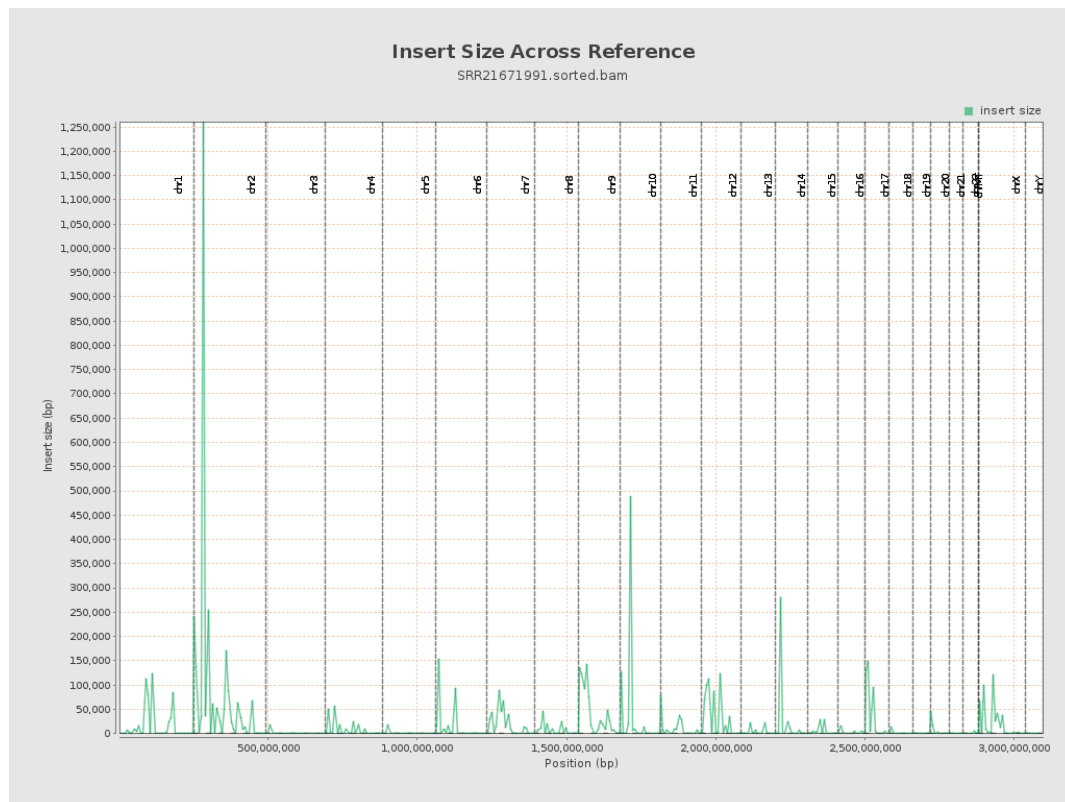
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

