

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 03:06:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472743.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_SRR3472743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472743_1.fastq.gz SRR3472743_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 03:06:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,252,480
Mapped reads	21,086,866 / 99.22%
Unmapped reads	165,614 / 0.78%
Mapped paired reads	21,086,866 / 99.22%
Mapped reads, first in pair	10,575,107 / 49.76%
Mapped reads, second in pair	10,511,759 / 49.46%
Mapped reads, both in pair	20,982,158 / 98.73%
Mapped reads, singletons	104,708 / 0.49%
Secondary alignments	0
Supplementary alignments	75,932 / 0.36%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	13,695,904 / 64.44%
Duplication rate	47%
Clipped reads	1,605,863 / 7.56%

2.2. ACGT Content

Number/percentage of A's	574,230,359 / 27.62%
Number/percentage of C's	468,318,529 / 22.52%
Number/percentage of T's	571,765,214 / 27.5%
Number/percentage of G's	464,692,241 / 22.35%
Number/percentage of N's	401,069 / 0.02%

GC Percentage	44.87%
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2.3. Coverage

Mean	0.6718
Standard Deviation	21.9326

2.4. Mapping Quality

Mean Mapping Quality	55.11
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2.5. Insert size

Mean	24,135.92
Standard Deviation	1,548,407.8
P25/Median/P75	174 / 241 / 322

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	12,540,716
Insertions	119,109
Mapped reads with at least one insertion	0.56%
Deletions	117,198
Mapped reads with at least one deletion	0.55%
Homopolymer indels	45.29%

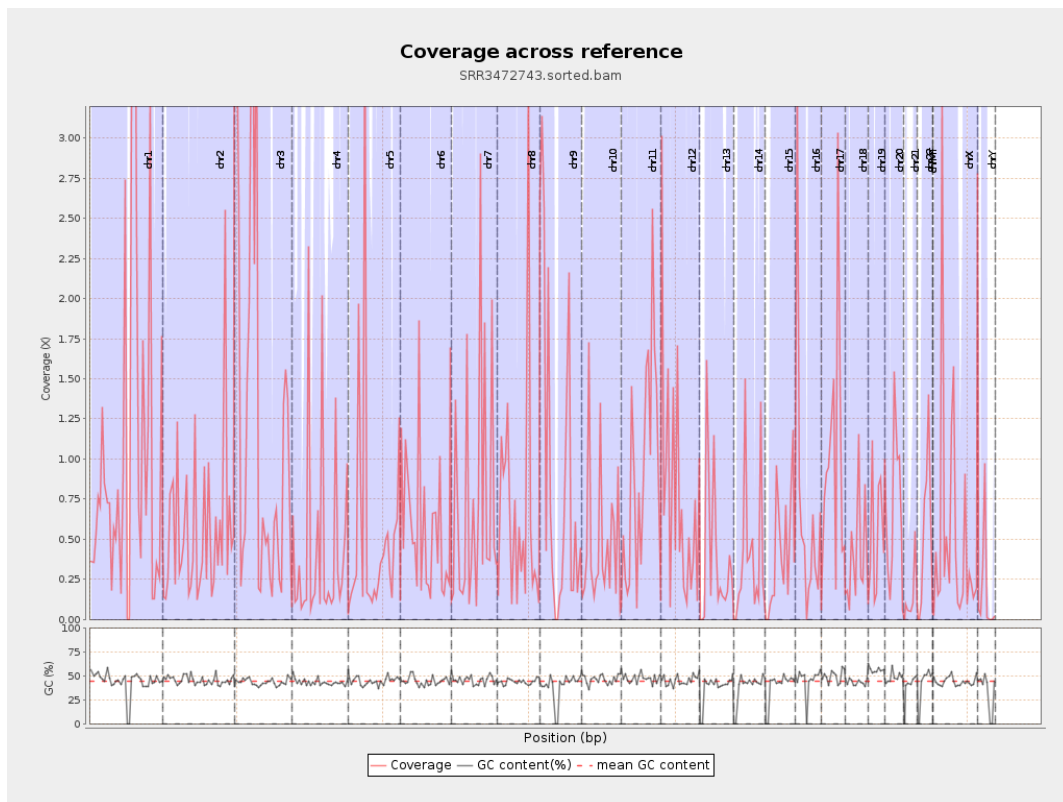
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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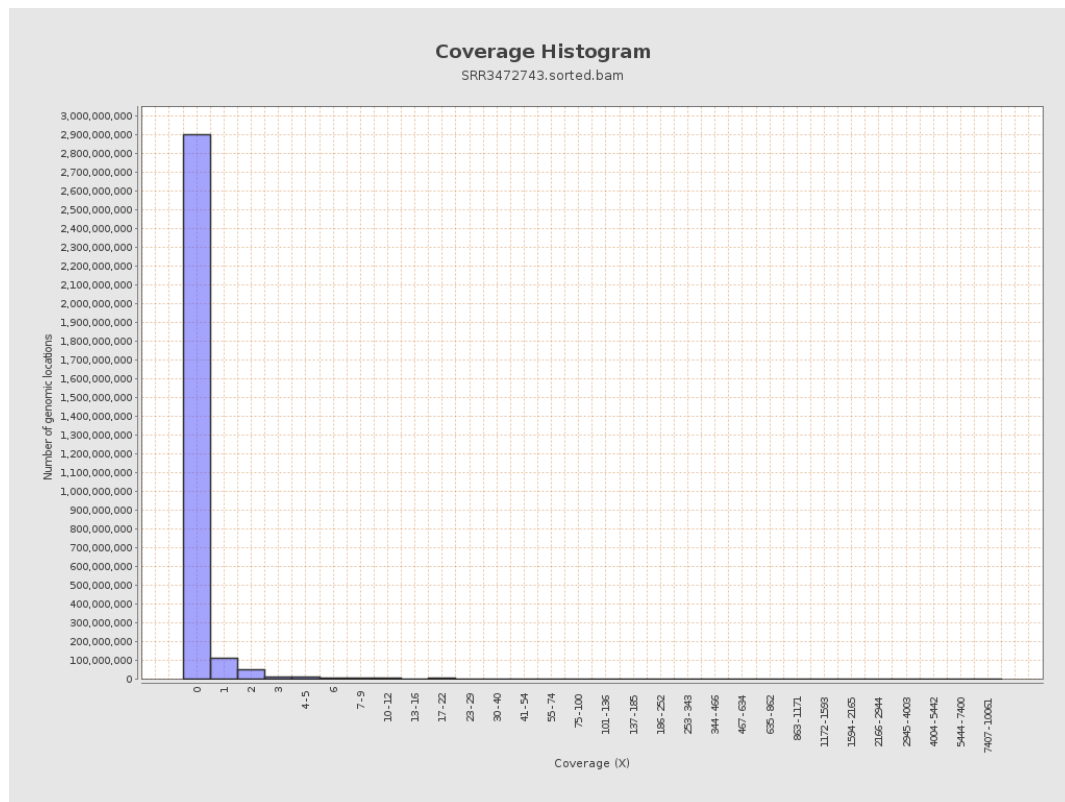
		bases	coverage	deviation
chr1	249250621	258180368	1.0358	32.9692
chr2	243199373	133210608	0.5477	19.0423
chr3	198022430	257357579	1.2996	27.7242
chr4	191154276	84759383	0.4434	17.615
chr5	180915260	101874689	0.5631	16.9404
chr6	171115067	99307425	0.5804	14.8877
chr7	159138663	118286023	0.7433	26.8084
chr8	146364022	97082554	0.6633	22.5013
chr9	141213431	119667903	0.8474	22.1515
chr10	135534747	65737090	0.485	24.2357
chr11	135006516	122934995	0.9106	30.0633
chr12	133851895	102963007	0.7692	21.396
chr13	115169878	45477438	0.3949	14.5213
chr14	107349540	42912248	0.3997	12.7581
chr15	102531392	42537799	0.4149	11.6344
chr16	90354753	60482381	0.6694	18.2851
chr17	81195210	85963741	1.0587	27.0227
chr18	78077248	31478937	0.4032	17.0968
chr19	59128983	32085833	0.5426	14.2267
chr20	63025520	42095234	0.6679	17.8956
chr21	48129895	7118643	0.1479	5.1776
chr22	51304566	29135097	0.5679	16.1671
chrMT	16571	2381	0.1437	0.4594
chrX	155270560	88300673	0.5687	22.8189

chrY	59373566	10758809	0.1812	14.2894
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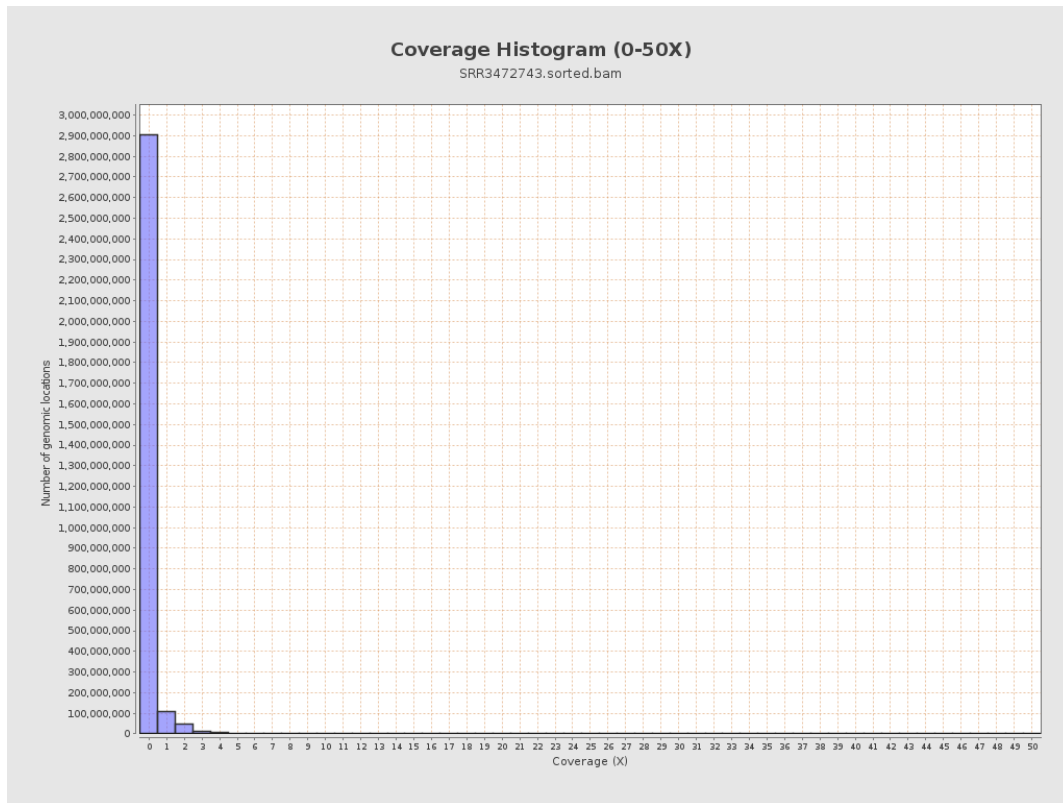
3. Results : Coverage across reference



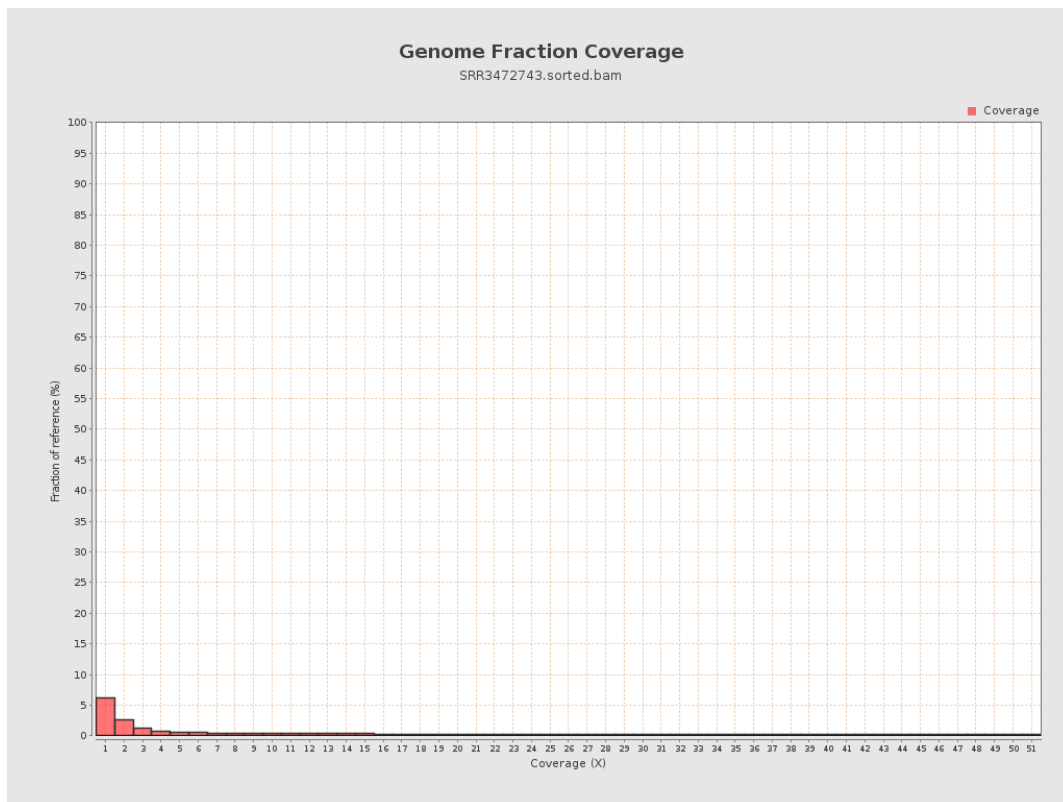
4. Results : Coverage Histogram



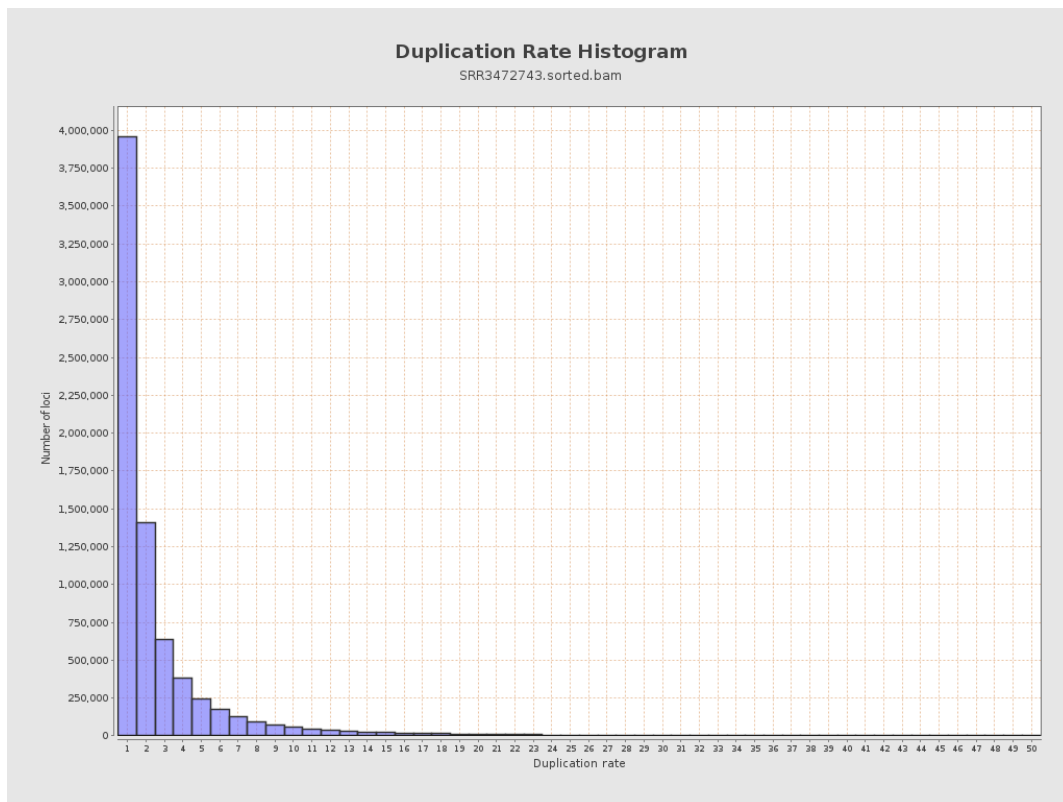
5. Results : Coverage Histogram (0-50X)



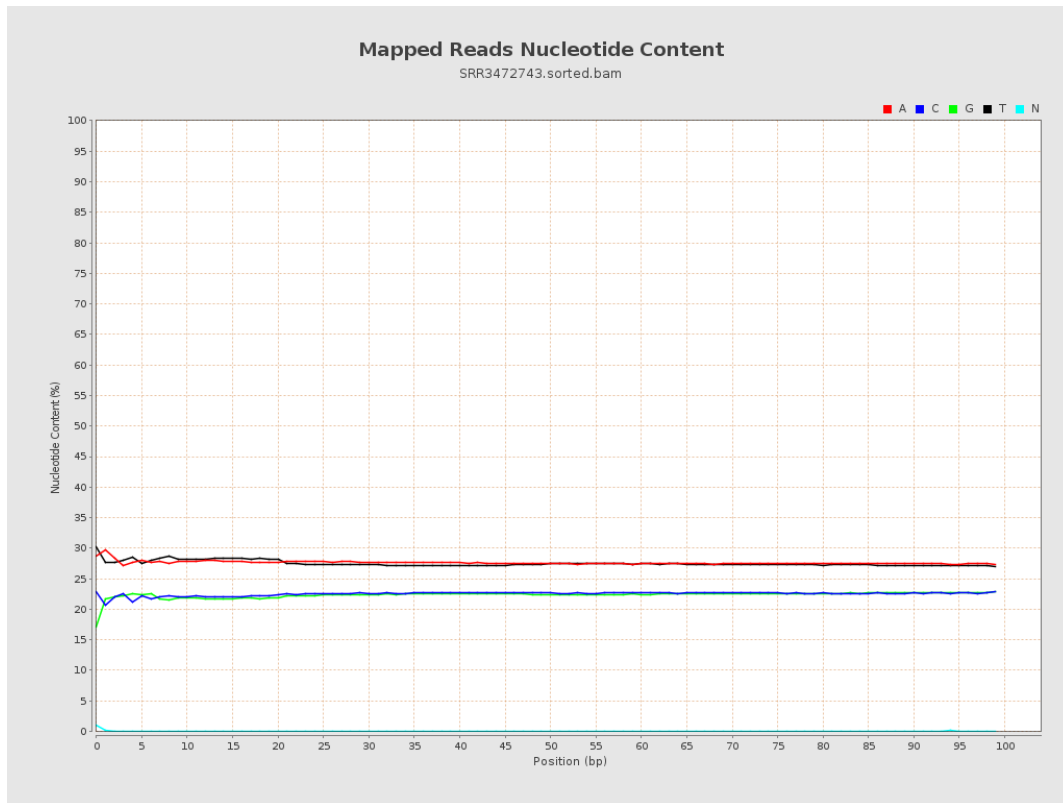
6. Results : Genome Fraction Coverage



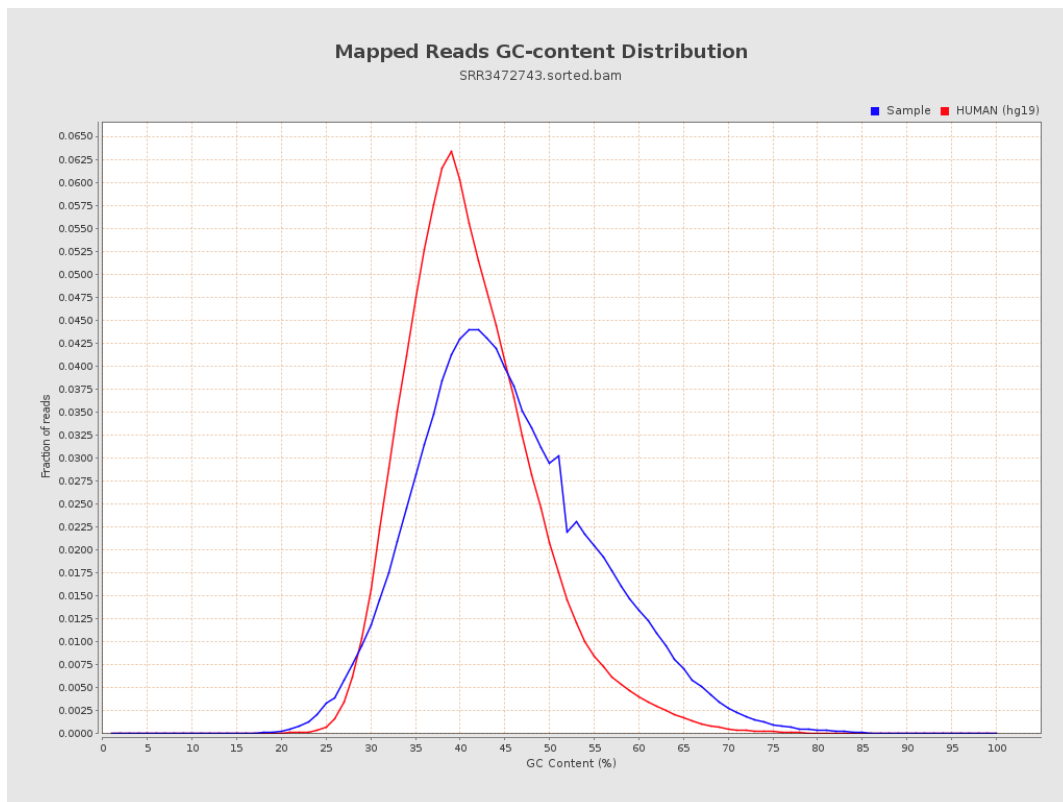
7. Results : Duplication Rate Histogram



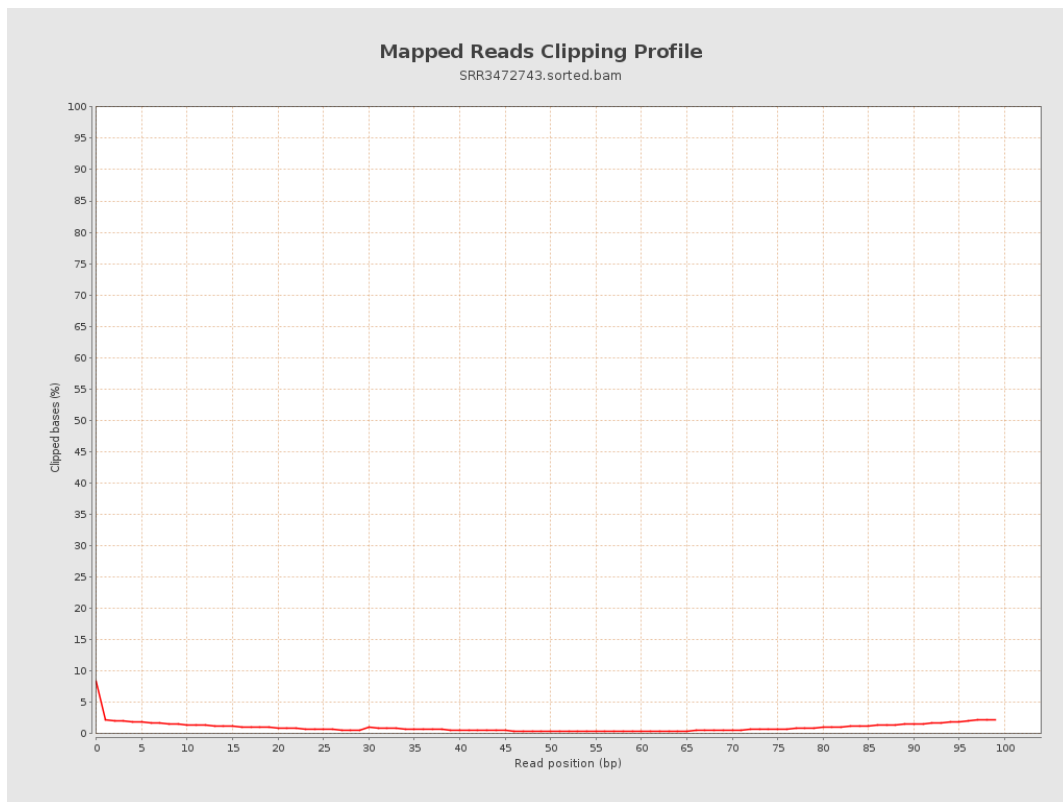
8. Results : Mapped Reads Nucleotide Content



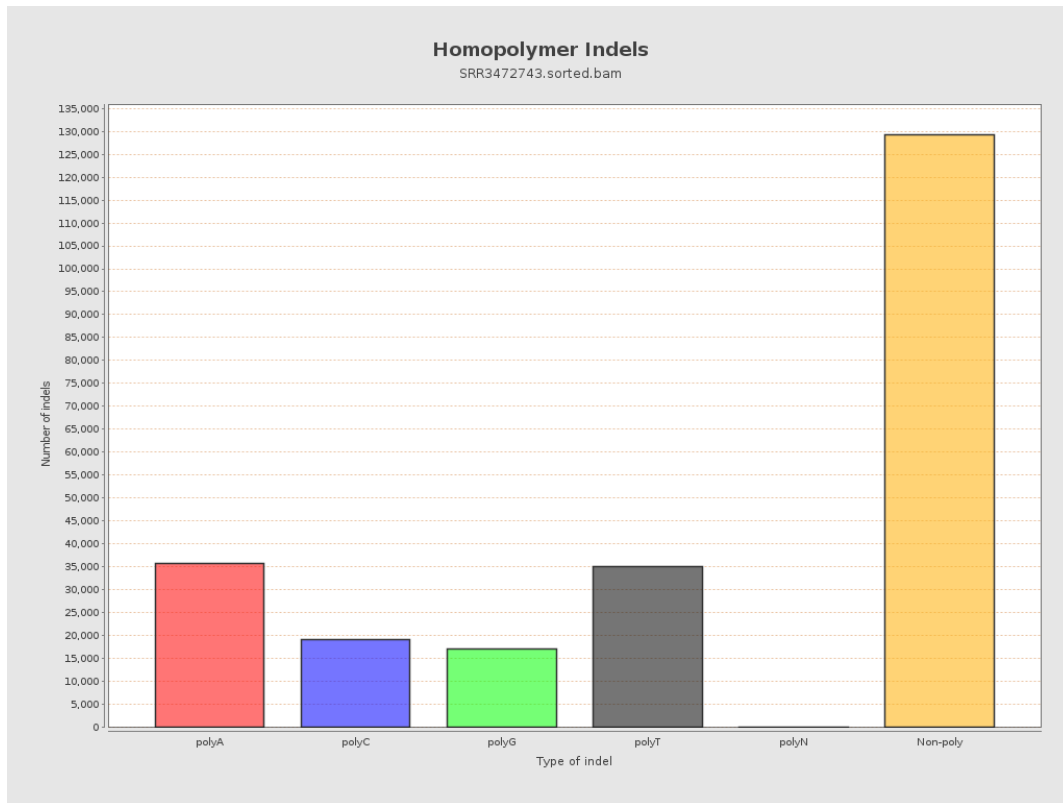
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



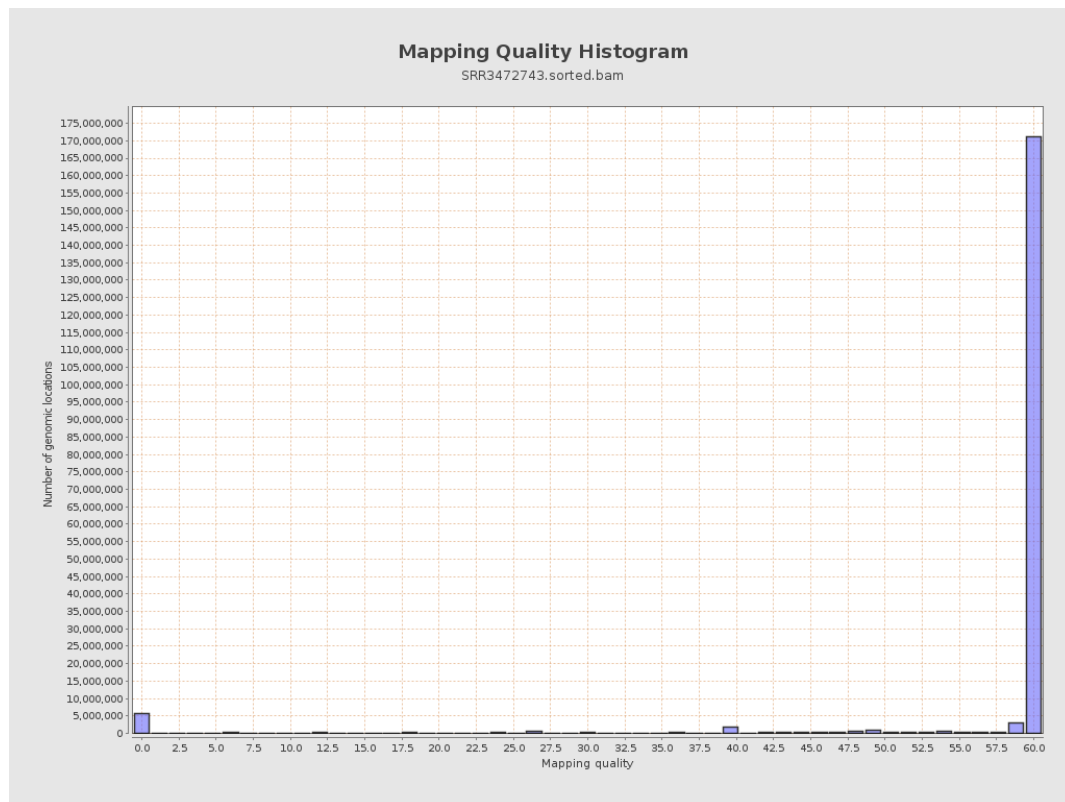
11. Results : Homopolymer Indels



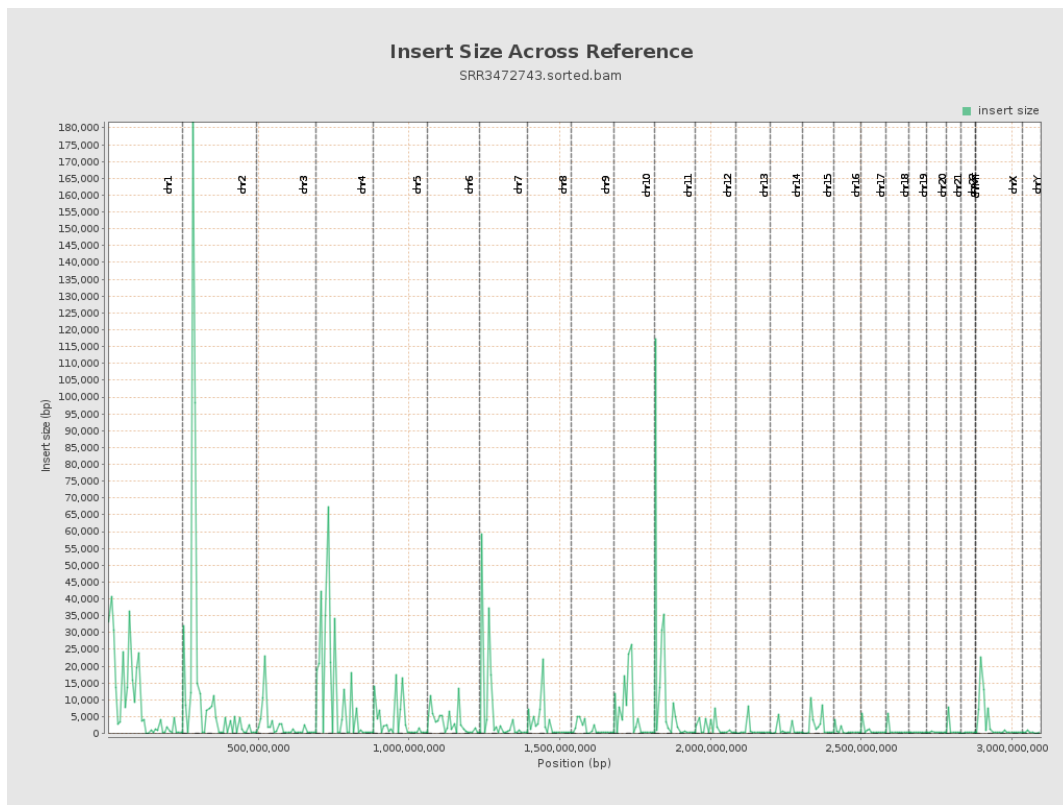
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

