

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:42:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472439.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_SRR3472439 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472439_1.fastq.gz SRR3472439_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:42:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472439.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,724,004
Mapped reads	17,565,732 / 99.11%
Unmapped reads	158,272 / 0.89%
Mapped paired reads	17,565,732 / 99.11%
Mapped reads, first in pair	8,808,439 / 49.7%
Mapped reads, second in pair	8,757,293 / 49.41%
Mapped reads, both in pair	17,480,782 / 98.63%
Mapped reads, singletons	84,950 / 0.48%
Secondary alignments	0
Supplementary alignments	64,913 / 0.37%
Read min/max/mean length	30 / 100 / 99.26
Duplicated reads (estimated)	11,287,809 / 63.69%
Duplication rate	47.37%
Clipped reads	1,238,294 / 6.99%

2.2. ACGT Content

Number/percentage of A's	458,685,958 / 26.65%
Number/percentage of C's	402,859,965 / 23.41%
Number/percentage of T's	460,204,730 / 26.74%
Number/percentage of G's	399,199,093 / 23.19%
Number/percentage of N's	213,407 / 0.01%

GC Percentage	46.6%
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2.3. Coverage

Mean	0.5561
Standard Deviation	18.4623

2.4. Mapping Quality

Mean Mapping Quality	54.78
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2.5. Insert size

Mean	18,596.72
Standard Deviation	1,383,962.73
P25/Median/P75	149 / 205 / 276

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	8,908,996
Insertions	101,715
Mapped reads with at least one insertion	0.57%
Deletions	79,719
Mapped reads with at least one deletion	0.45%
Homopolymer indels	45.26%

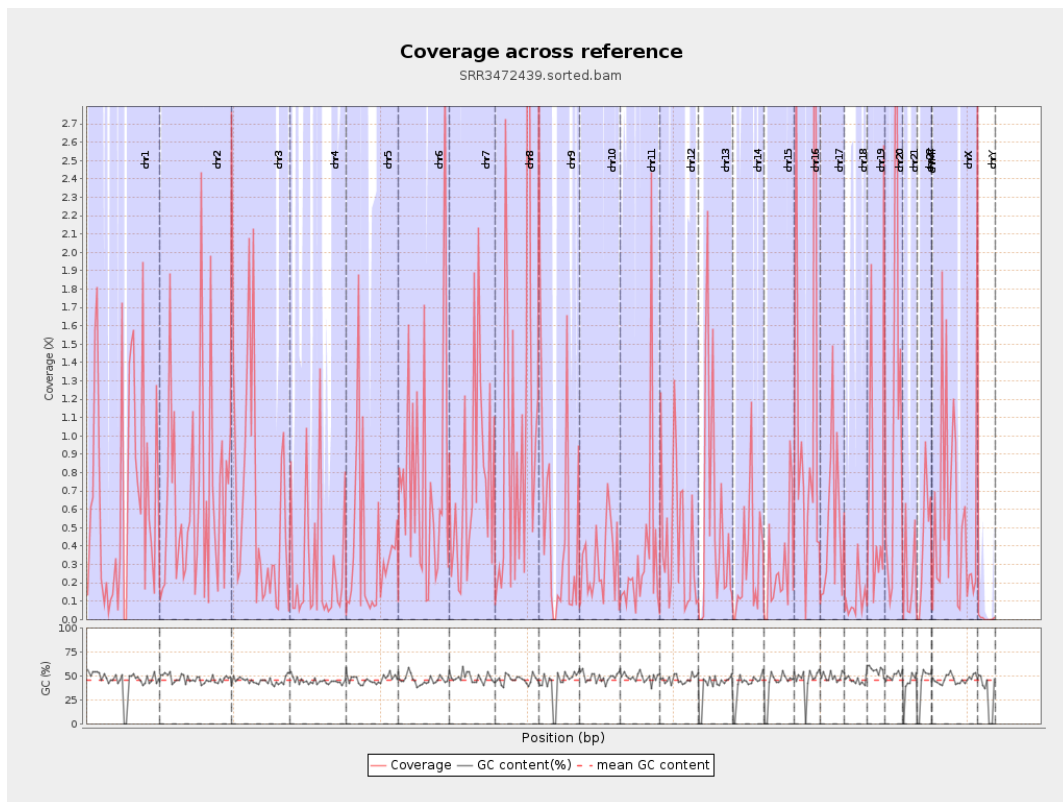
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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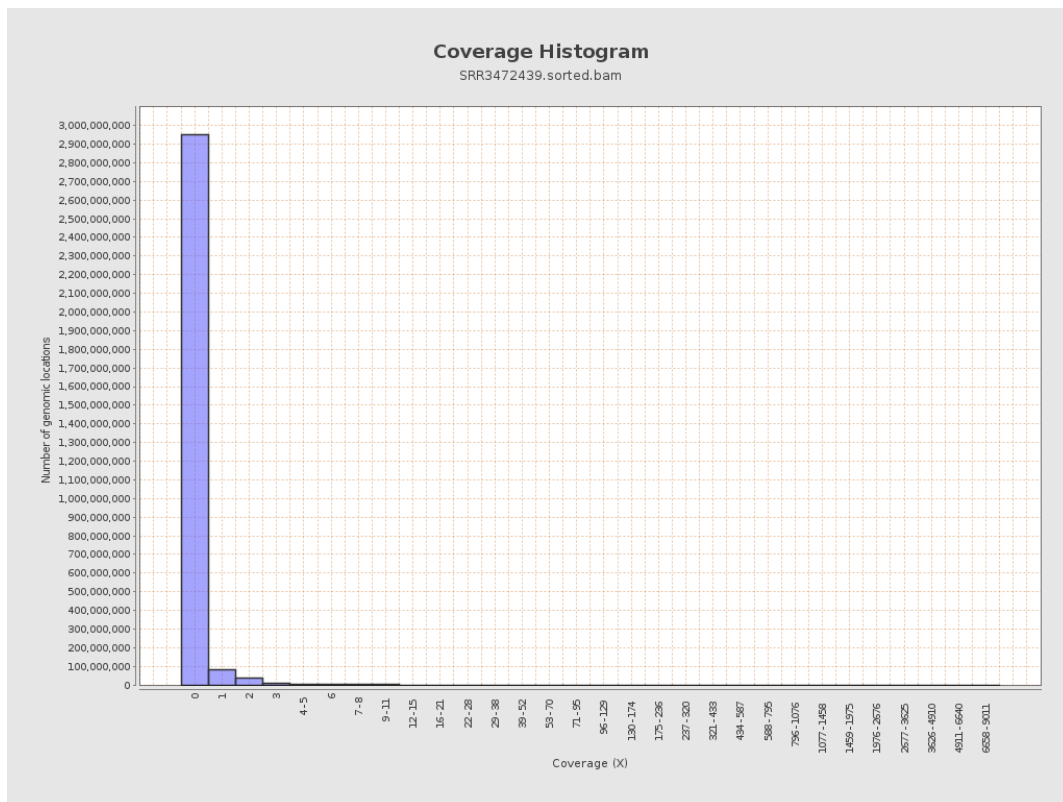
		bases	coverage	deviation
chr1	249250621	167606626	0.6724	21.2121
chr2	243199373	161432971	0.6638	21.2929
chr3	198022430	128565759	0.6492	15.342
chr4	191154276	52201155	0.2731	12.5128
chr5	180915260	66294128	0.3664	11.9099
chr6	171115067	127731160	0.7465	18.8434
chr7	159138663	122609530	0.7705	22.4767
chr8	146364022	155623161	1.0633	30.1615
chr9	141213431	74182464	0.5253	21.1681
chr10	135534747	41626275	0.3071	12.1142
chr11	135006516	47195990	0.3496	15.3451
chr12	133851895	59207379	0.4423	12.2642
chr13	115169878	65085776	0.5651	19.3184
chr14	107349540	31474063	0.2932	8.0872
chr15	102531392	29787867	0.2905	9.0382
chr16	90354753	105597269	1.1687	31.5468
chr17	81195210	43685174	0.538	12.0431
chr18	78077248	9136756	0.117	5.181
chr19	59128983	37889469	0.6408	17.9473
chr20	63025520	72828568	1.1555	33.96
chr21	48129895	11235324	0.2334	11.179
chr22	51304566	21979037	0.4284	14.8252
chrMT	16571	5489	0.3312	0.7394
chrX	155270560	88045119	0.567	17.9026

chrY	59373566	337834	0.0057	0.3597
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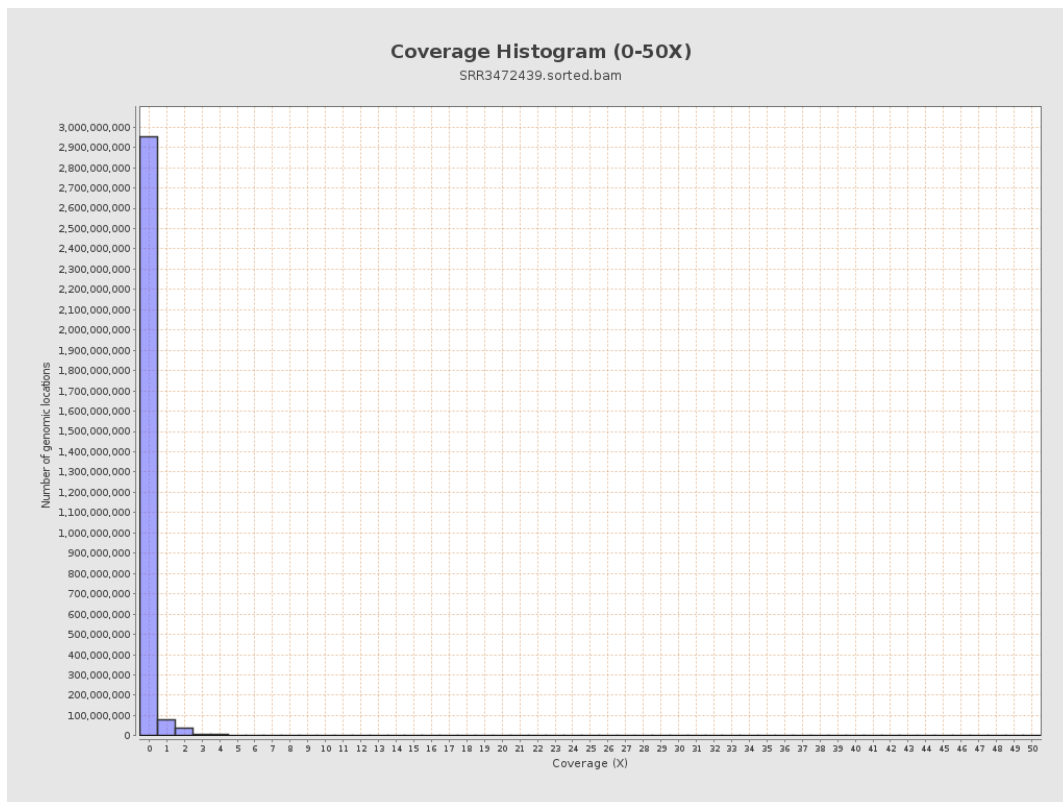
3. Results : Coverage across reference



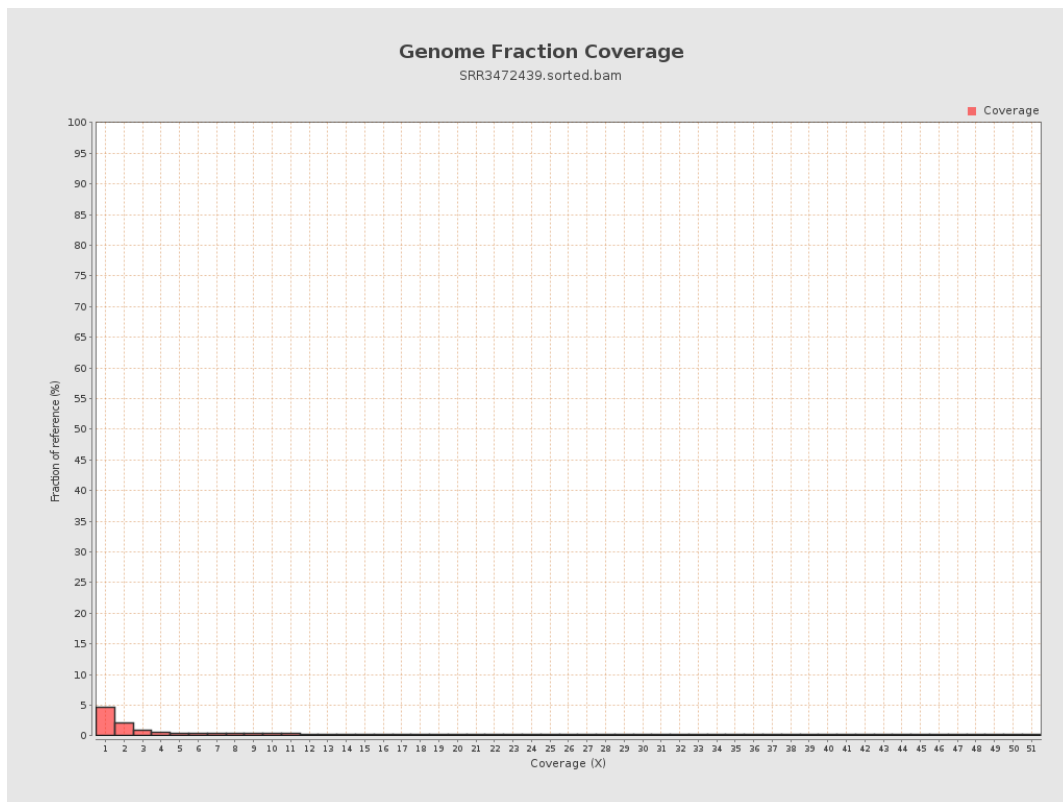
4. Results : Coverage Histogram



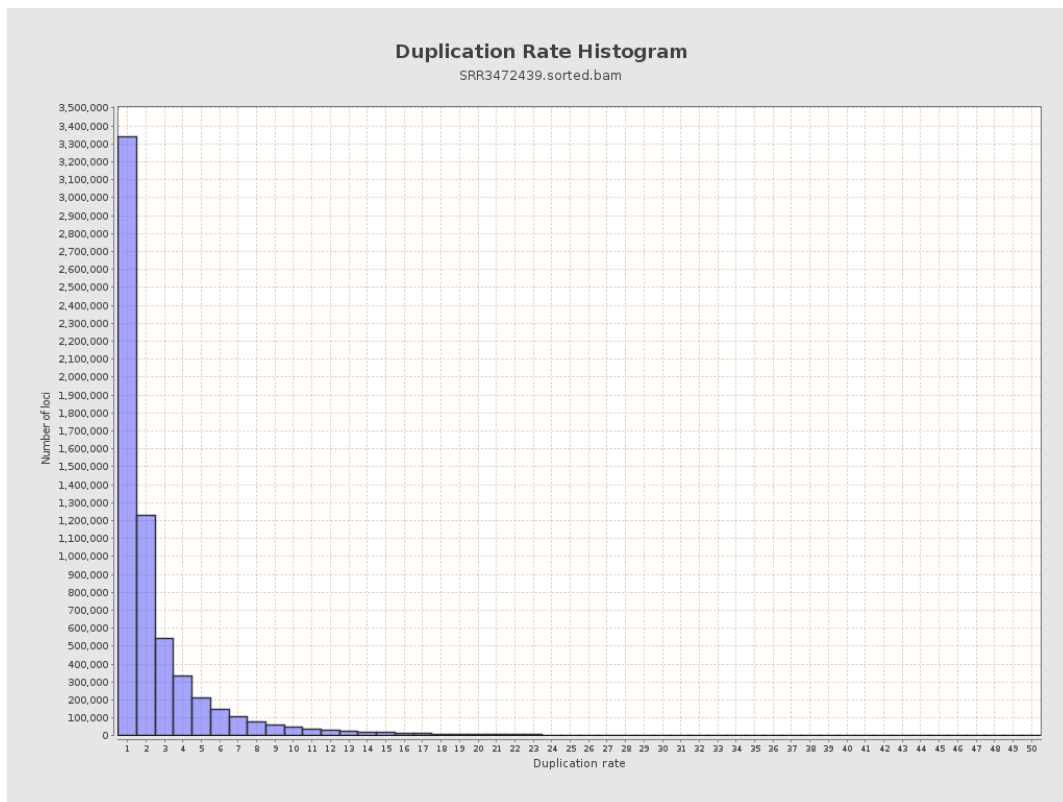
5. Results : Coverage Histogram (0-50X)



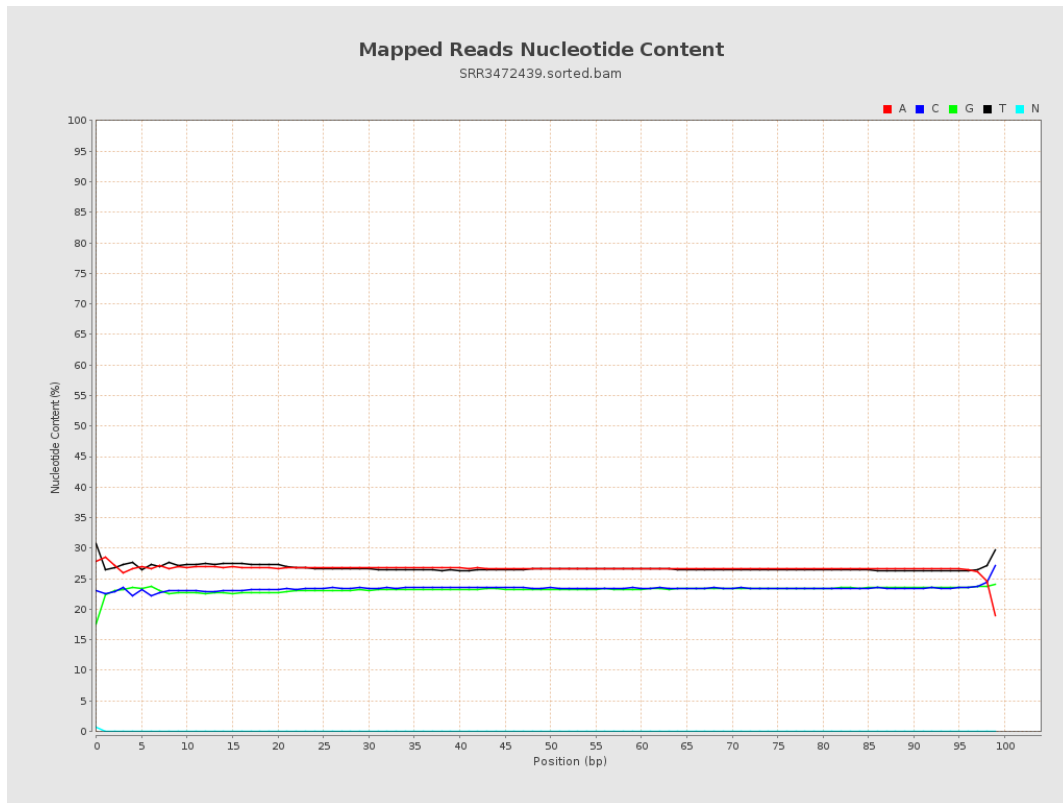
6. Results : Genome Fraction Coverage



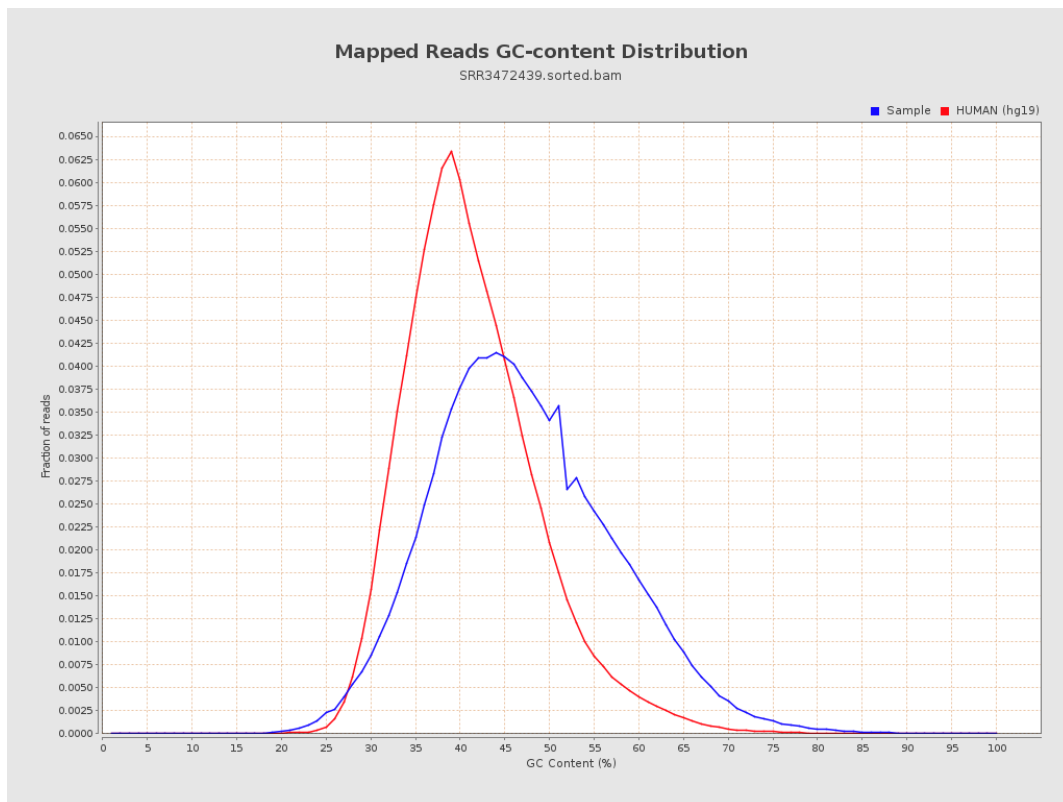
7. Results : Duplication Rate Histogram



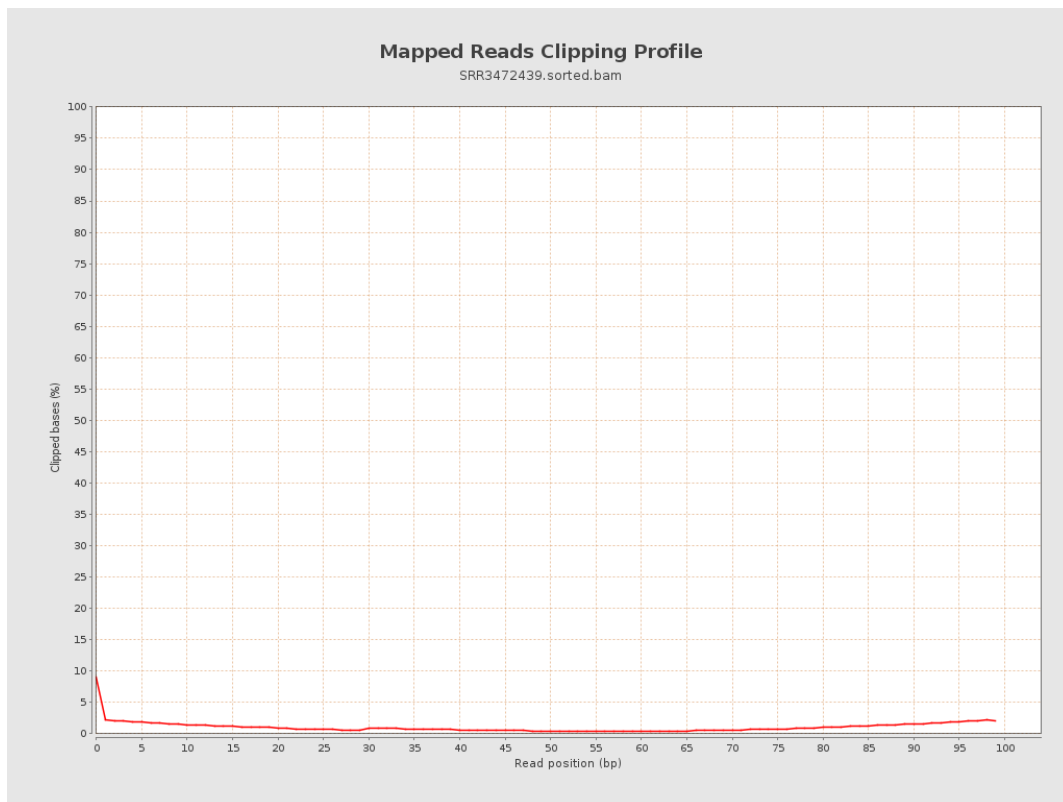
8. Results : Mapped Reads Nucleotide Content



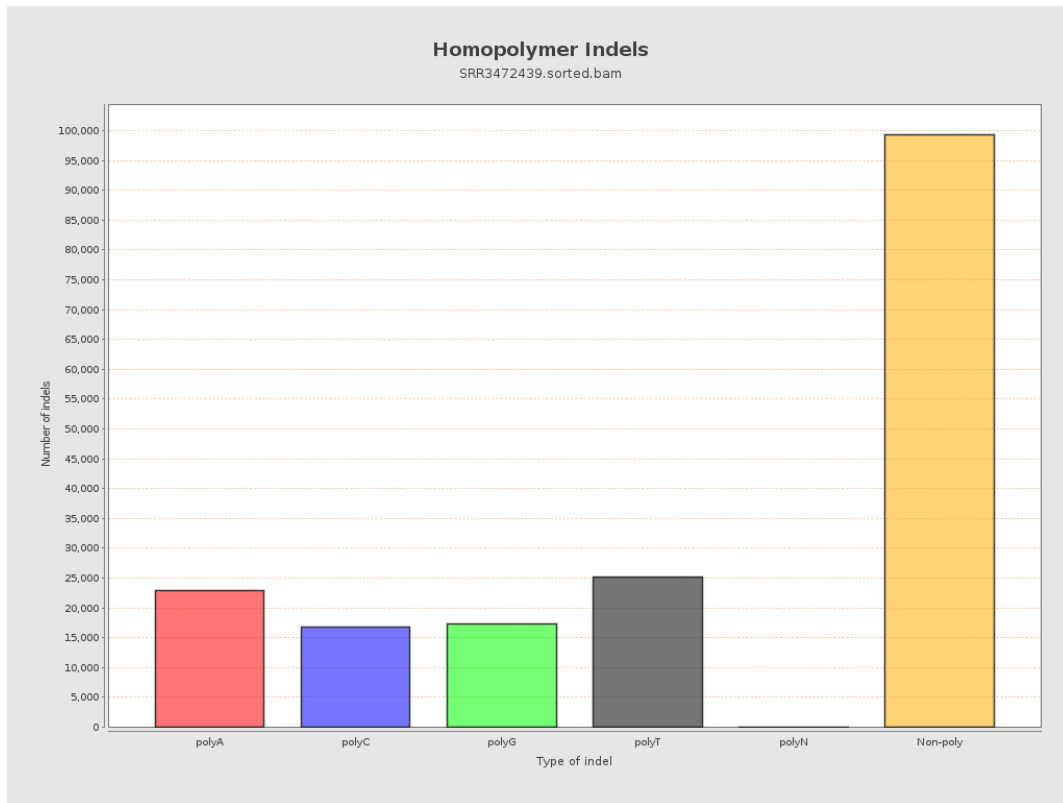
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



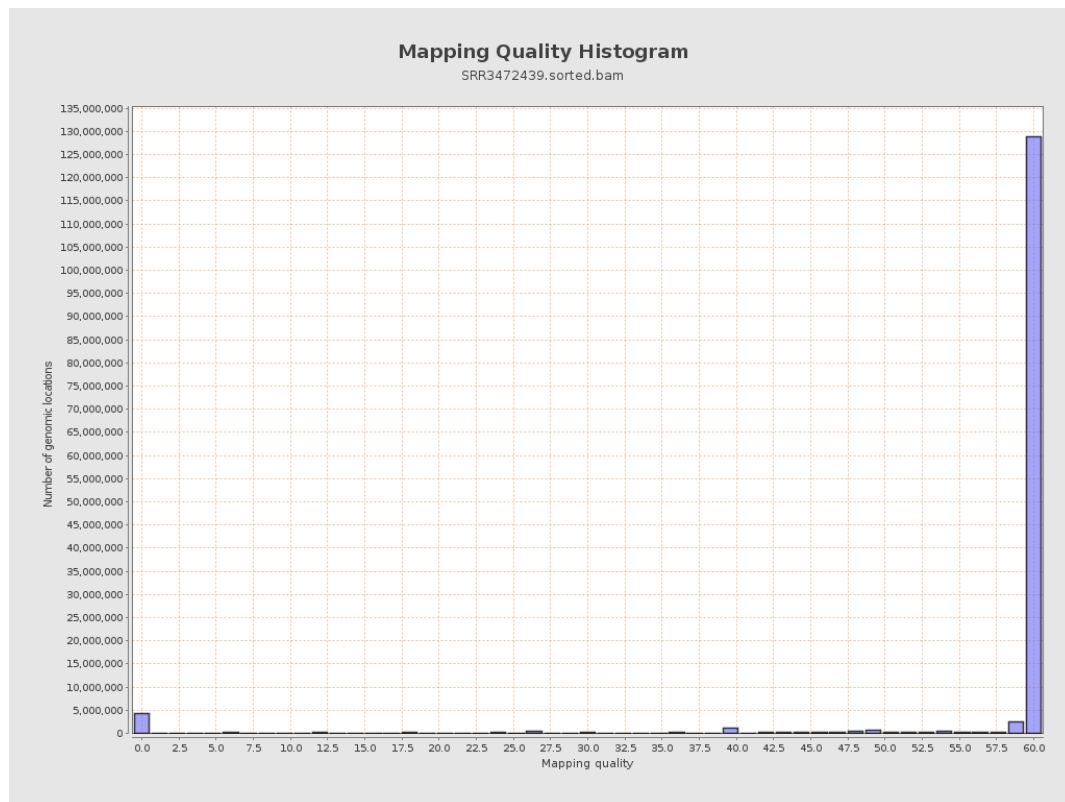
11. Results : Homopolymer Indels



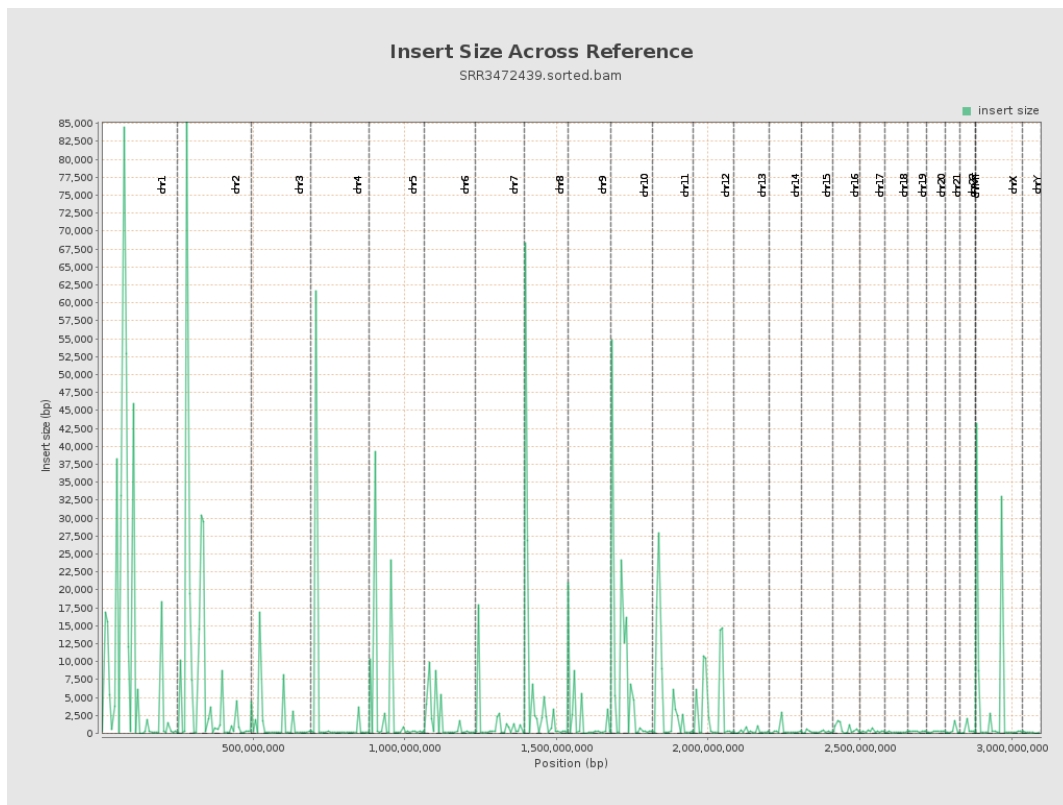
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

