

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 22:12:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472451.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_SRR3472451 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472451_1.fastq.gz SRR3472451_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 22:12:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472451.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,545,878
Mapped reads	15,424,376 / 99.22%
Unmapped reads	121,502 / 0.78%
Mapped paired reads	15,424,376 / 99.22%
Mapped reads, first in pair	7,734,317 / 49.75%
Mapped reads, second in pair	7,690,059 / 49.47%
Mapped reads, both in pair	15,356,682 / 98.78%
Mapped reads, singletons	67,694 / 0.44%
Secondary alignments	0
Supplementary alignments	55,122 / 0.35%
Read min/max/mean length	30 / 100 / 99.2
Duplicated reads (estimated)	9,397,981 / 60.45%
Duplication rate	46.61%
Clipped reads	1,123,390 / 7.23%

2.2. ACGT Content

Number/percentage of A's	406,070,057 / 26.91%
Number/percentage of C's	349,243,296 / 23.15%
Number/percentage of T's	407,702,076 / 27.02%
Number/percentage of G's	345,523,041 / 22.9%
Number/percentage of N's	184,273 / 0.01%

GC Percentage	46.05%
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2.3. Coverage

Mean	0.4874
Standard Deviation	15.1609

2.4. Mapping Quality

Mean Mapping Quality	54.86
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2.5. Insert size

Mean	15,652.77
Standard Deviation	1,224,127.78
P25/Median/P75	146 / 202 / 271

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	7,450,946
Insertions	93,101
Mapped reads with at least one insertion	0.6%
Deletions	70,681
Mapped reads with at least one deletion	0.45%
Homopolymer indels	45.58%

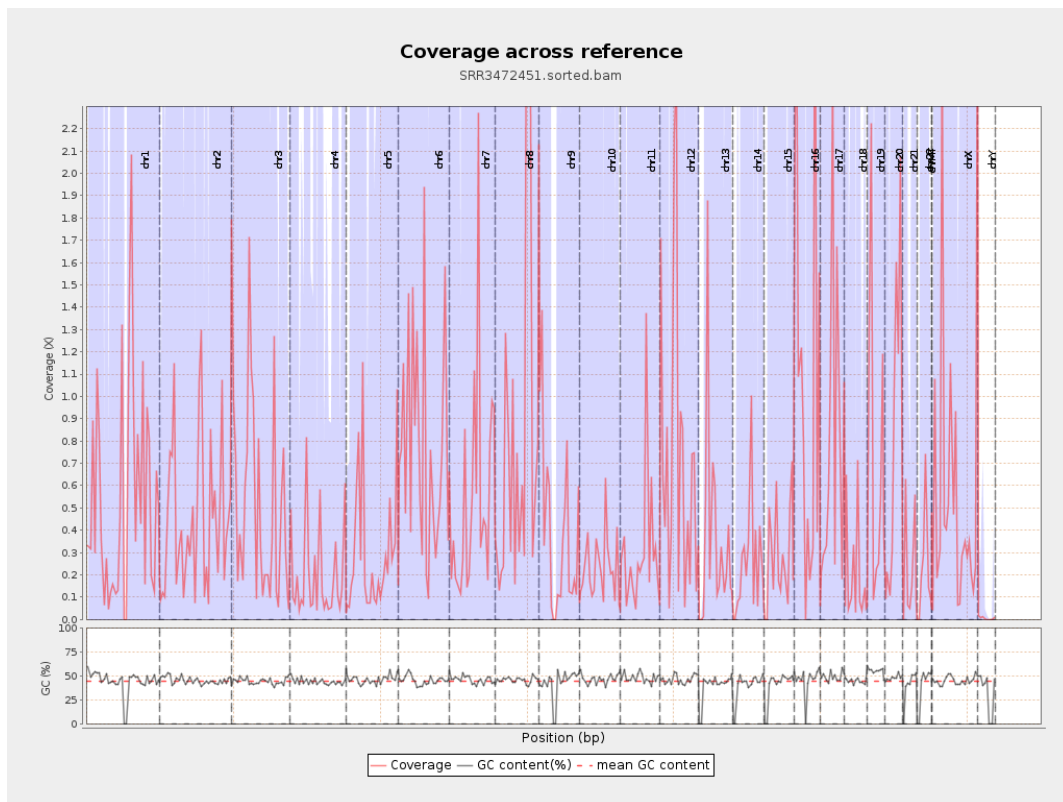
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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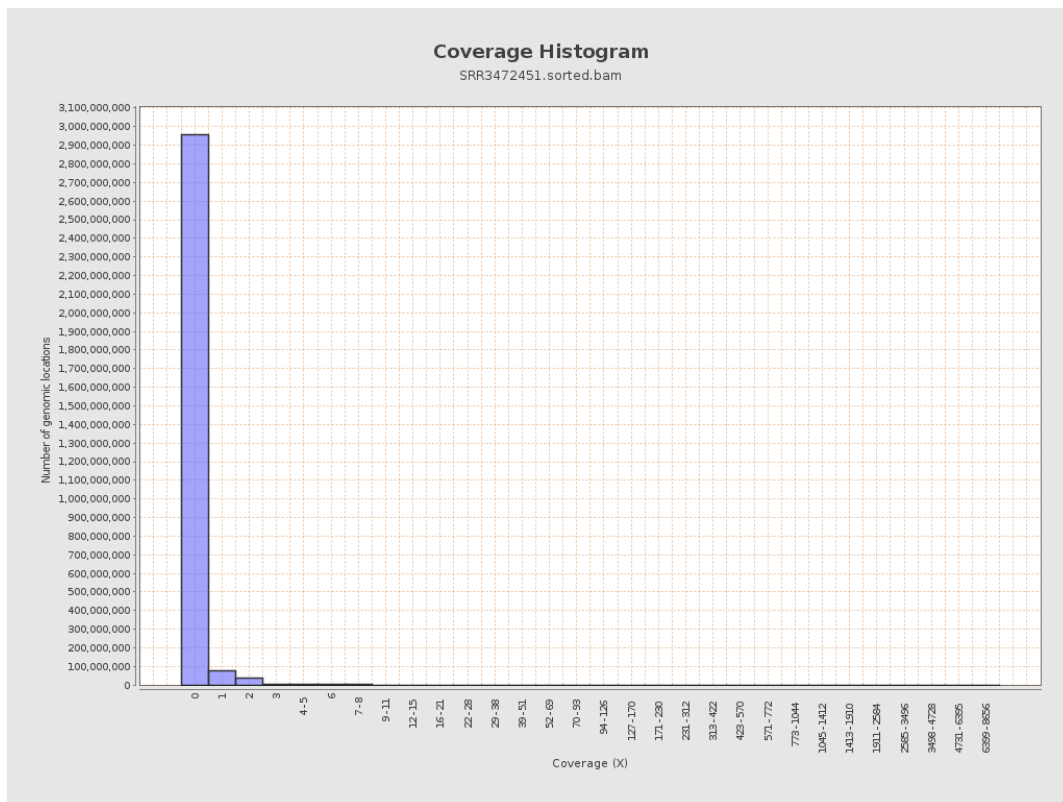
		bases	coverage	deviation
chr1	249250621	135962827	0.5455	15.5218
chr2	243199373	109710514	0.4511	13.5351
chr3	198022430	105613188	0.5333	14.642
chr4	191154276	37053595	0.1938	7.4052
chr5	180915260	55524476	0.3069	9.9756
chr6	171115067	131374857	0.7678	16.8042
chr7	159138663	88175948	0.5541	18.0035
chr8	146364022	125683639	0.8587	25.9167
chr9	141213431	56924907	0.4031	10.8293
chr10	135534747	32286650	0.2382	9.8375
chr11	135006516	40508293	0.3	10.7732
chr12	133851895	99662516	0.7446	20.0404
chr13	115169878	41822895	0.3631	11.4438
chr14	107349540	26922153	0.2508	7.567
chr15	102531392	29446083	0.2872	9.5743
chr16	90354753	102818684	1.1379	28.5544
chr17	81195210	65755592	0.8098	17.2359
chr18	78077248	16995209	0.2177	9.6302
chr19	59128983	46072863	0.7792	18.0931
chr20	63025520	51918428	0.8238	23.0561
chr21	48129895	11637679	0.2418	12.6133
chr22	51304566	11400740	0.2222	8.5016
chrMT	16571	7965	0.4807	0.8618
chrX	155270560	85280627	0.5492	15.7726

chrY	59373566	327504	0.0055	0.3348
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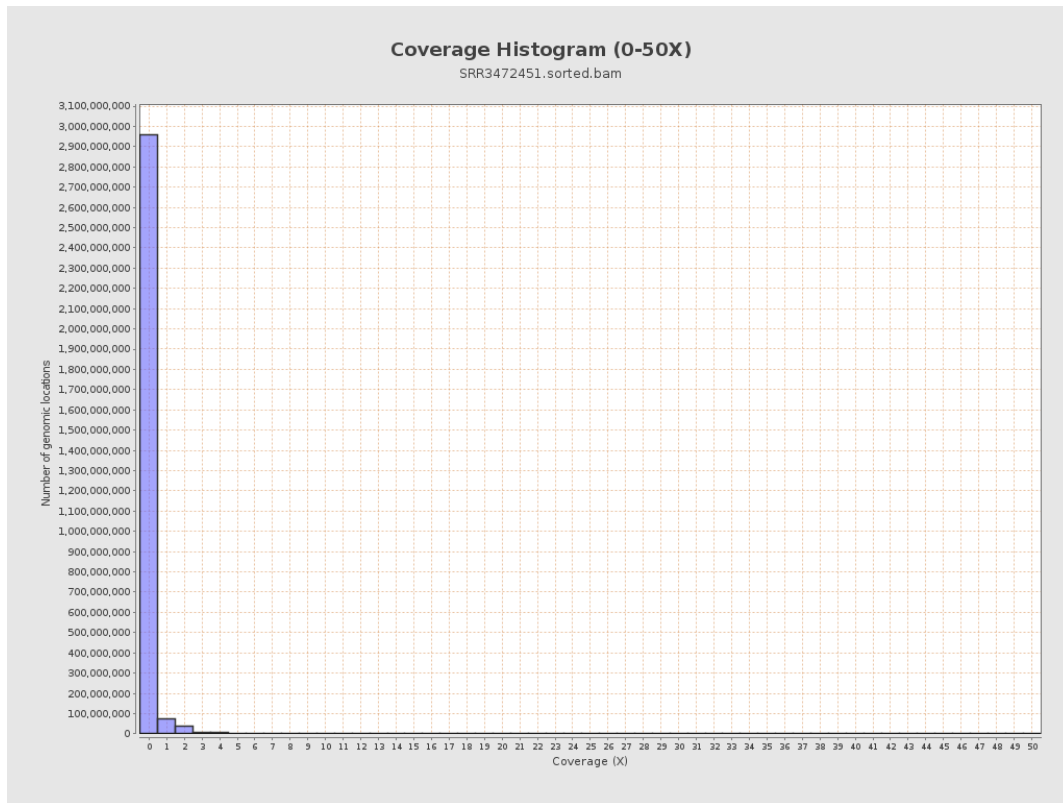
3. Results : Coverage across reference



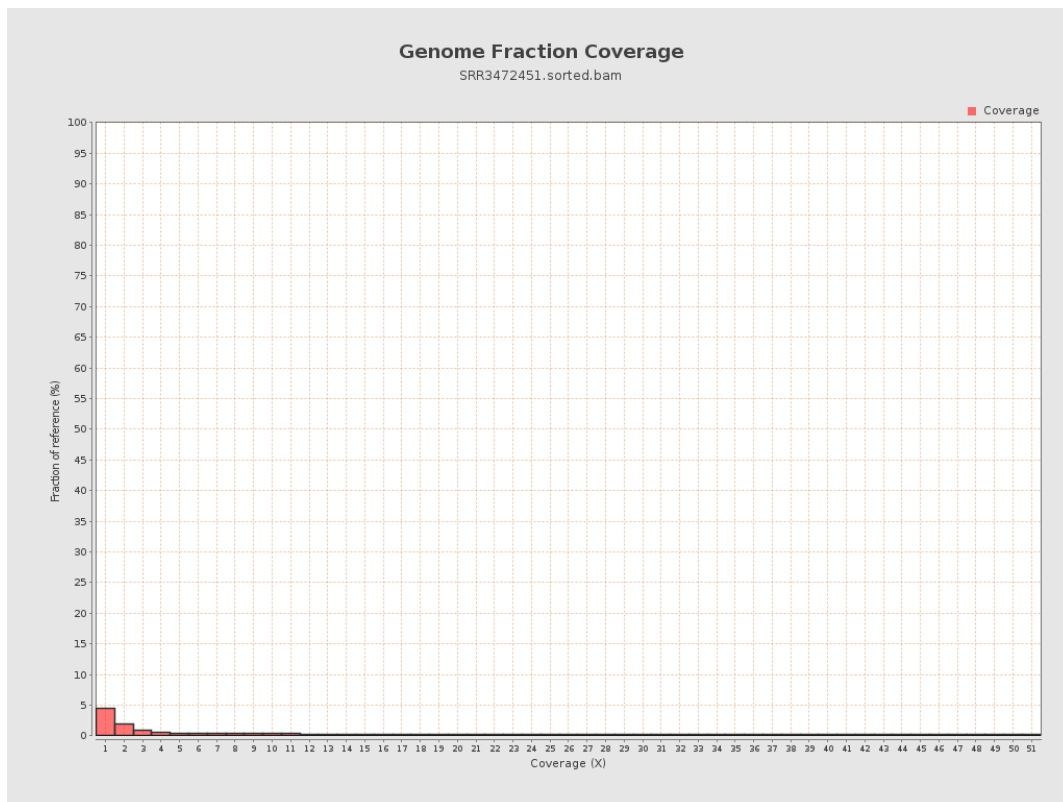
4. Results : Coverage Histogram



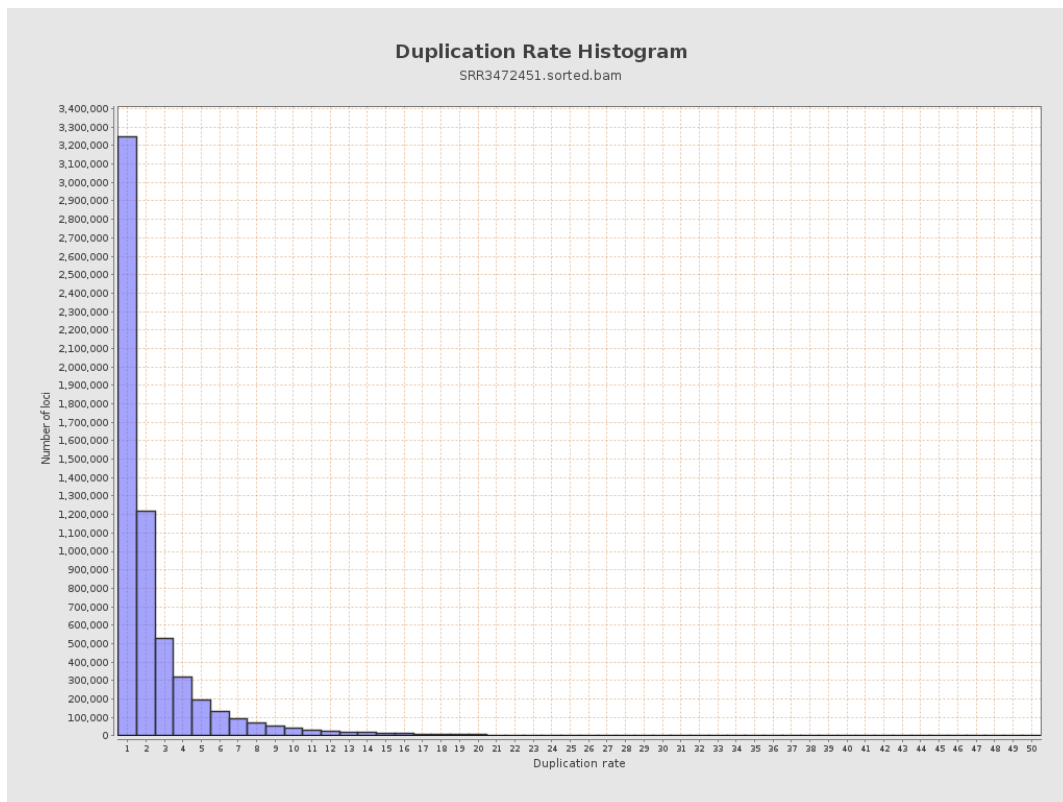
5. Results : Coverage Histogram (0-50X)



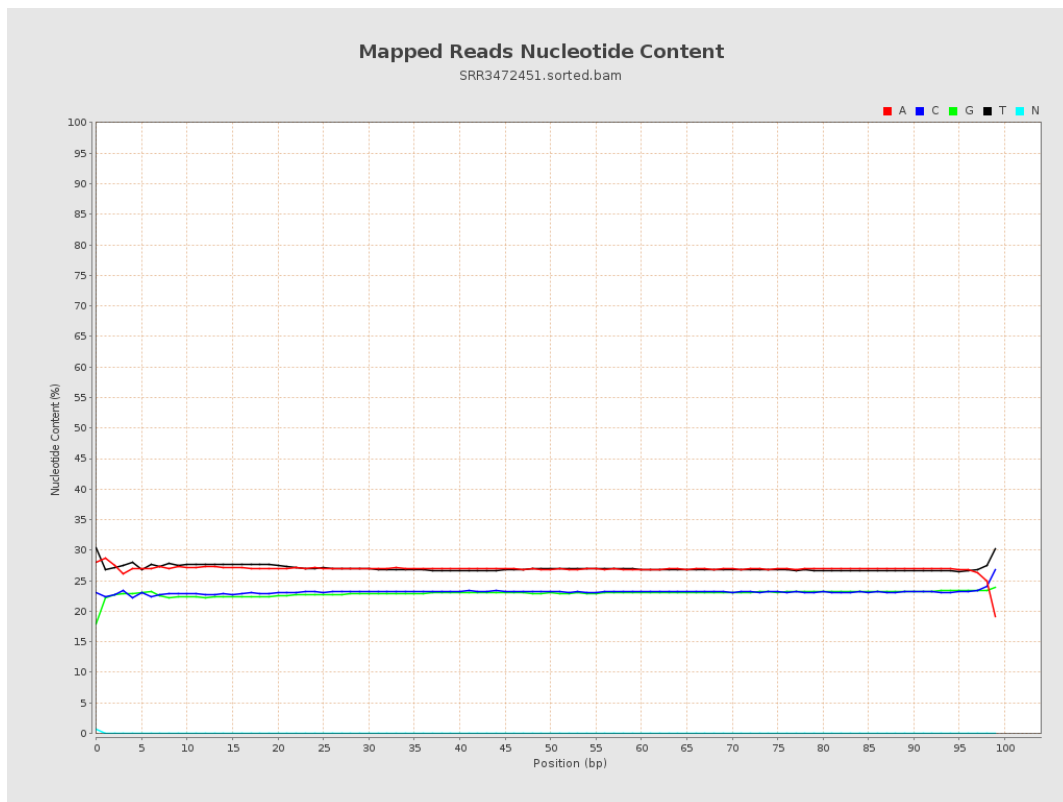
6. Results : Genome Fraction Coverage



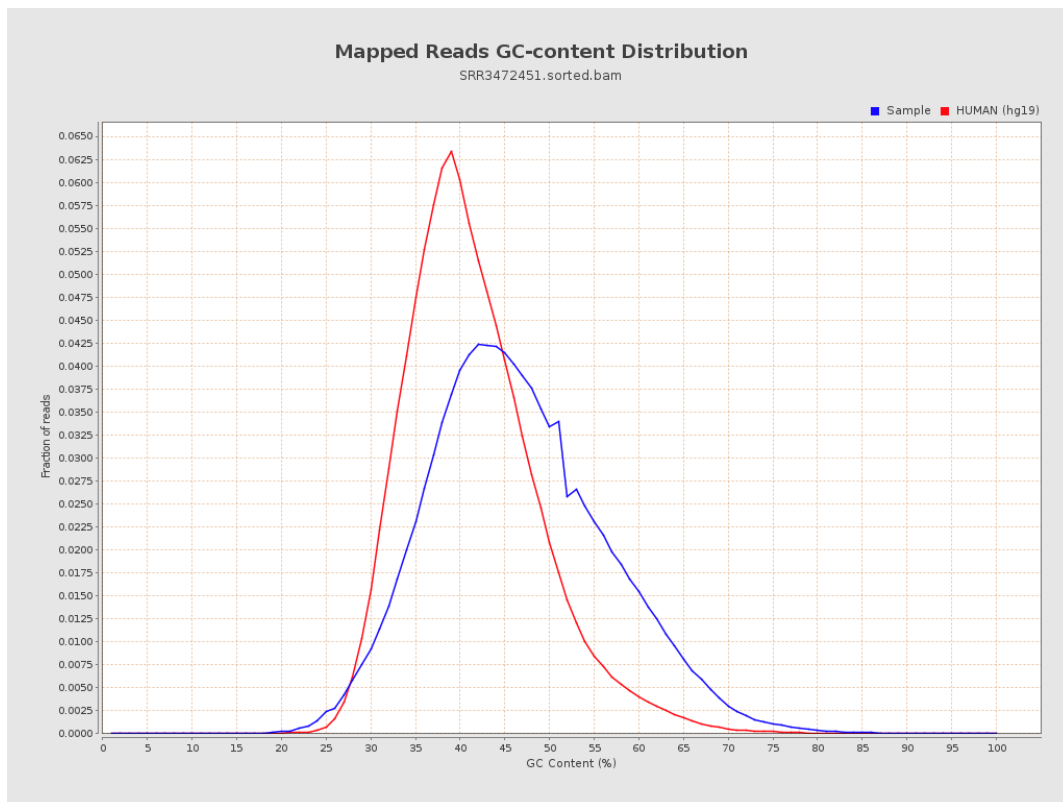
7. Results : Duplication Rate Histogram



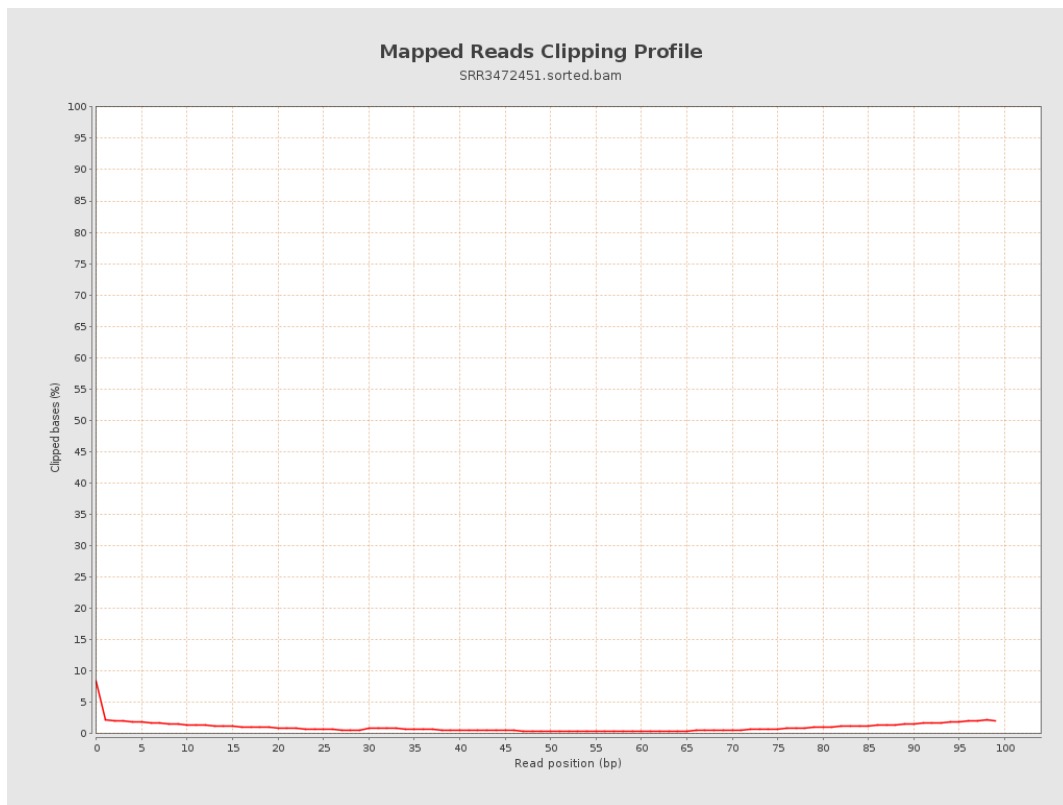
8. Results : Mapped Reads Nucleotide Content



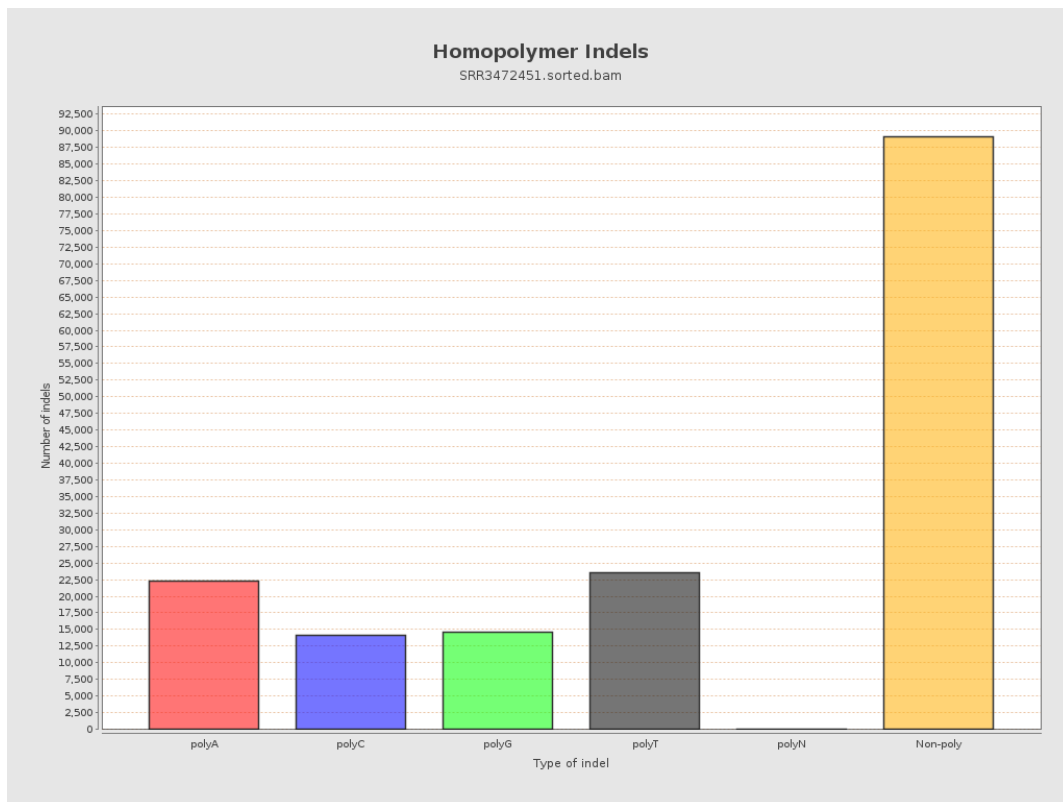
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



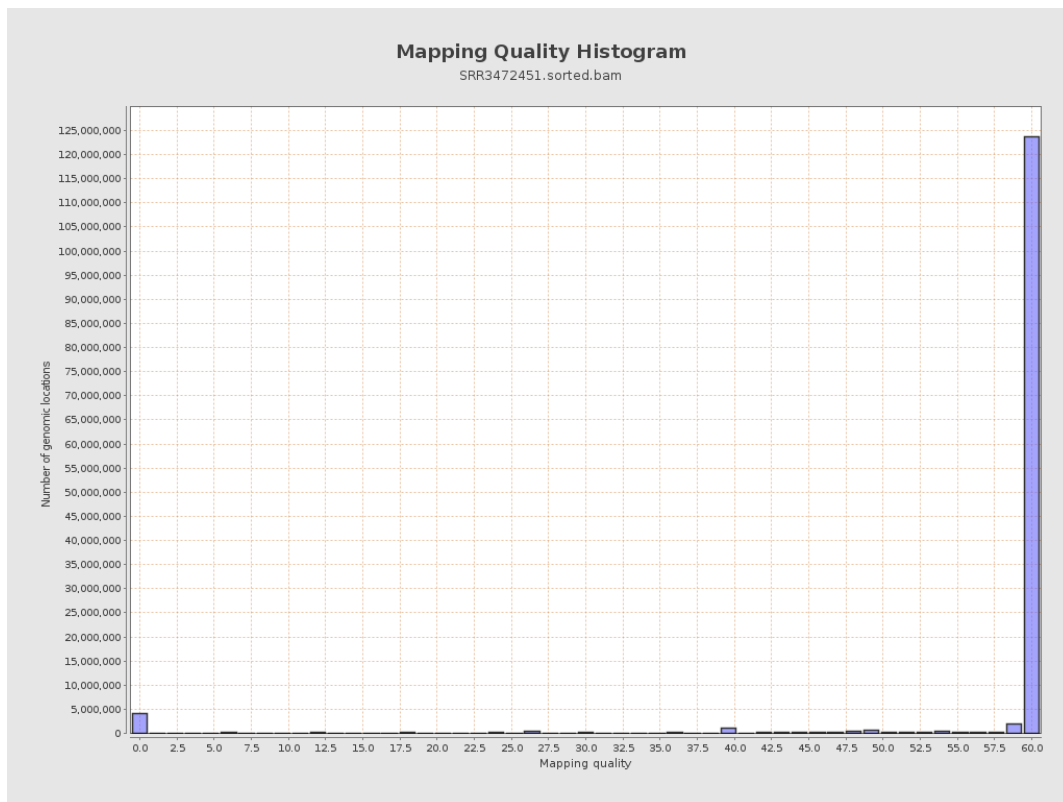
11. Results : Homopolymer Indels



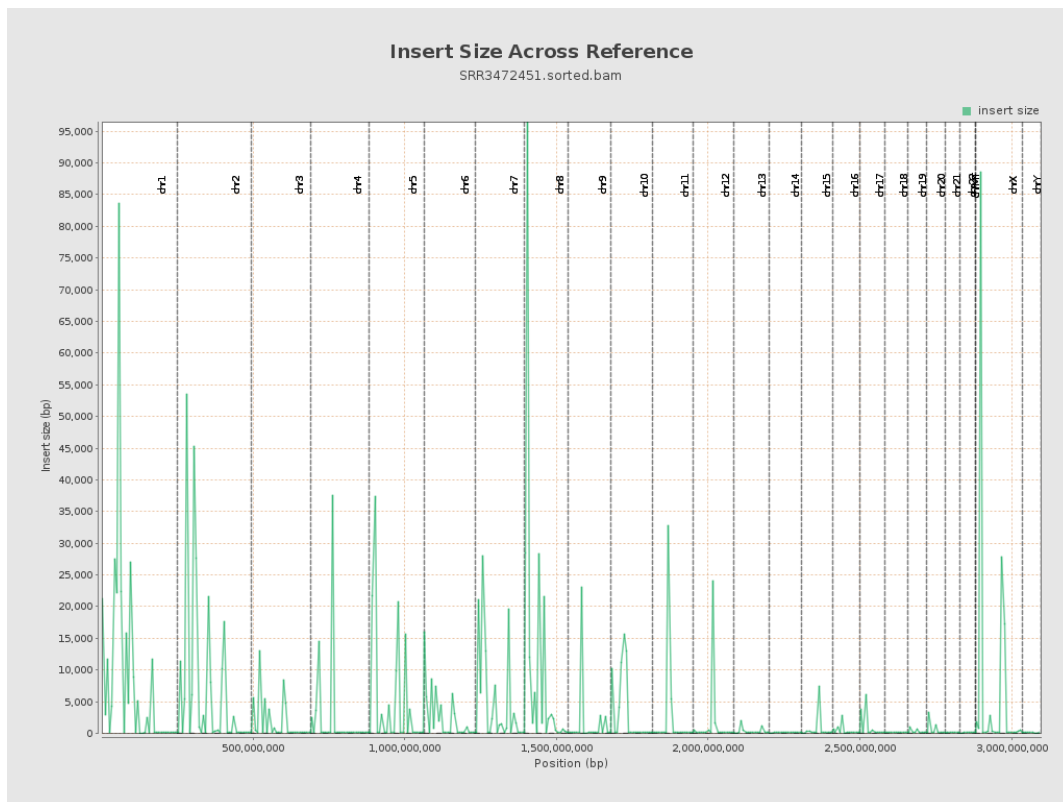
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

