

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:03:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472531.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_SRR3472531 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472531_1.fastq.gz SRR3472531_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:03:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472531.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,502,702
Mapped reads	16,314,280 / 98.86%
Unmapped reads	188,422 / 1.14%
Mapped paired reads	16,314,280 / 98.86%
Mapped reads, first in pair	8,183,951 / 49.59%
Mapped reads, second in pair	8,130,329 / 49.27%
Mapped reads, both in pair	16,213,328 / 98.25%
Mapped reads, singletons	100,952 / 0.61%
Secondary alignments	0
Supplementary alignments	63,476 / 0.38%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	10,148,920 / 61.5%
Duplication rate	45.51%
Clipped reads	1,284,173 / 7.78%

2.2. ACGT Content

Number/percentage of A's	439,519,657 / 27.35%
Number/percentage of C's	366,546,551 / 22.81%
Number/percentage of T's	436,719,168 / 27.17%
Number/percentage of G's	364,079,191 / 22.65%
Number/percentage of N's	250,147 / 0.02%

GC Percentage	45.46%
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2.3. Coverage

Mean	0.5192
Standard Deviation	17.9491

2.4. Mapping Quality

Mean Mapping Quality	55
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2.5. Insert size

Mean	30,913.74
Standard Deviation	1,788,262.7
P25/Median/P75	172 / 238 / 318

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	9,934,128
Insertions	97,572
Mapped reads with at least one insertion	0.59%
Deletions	79,679
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.21%

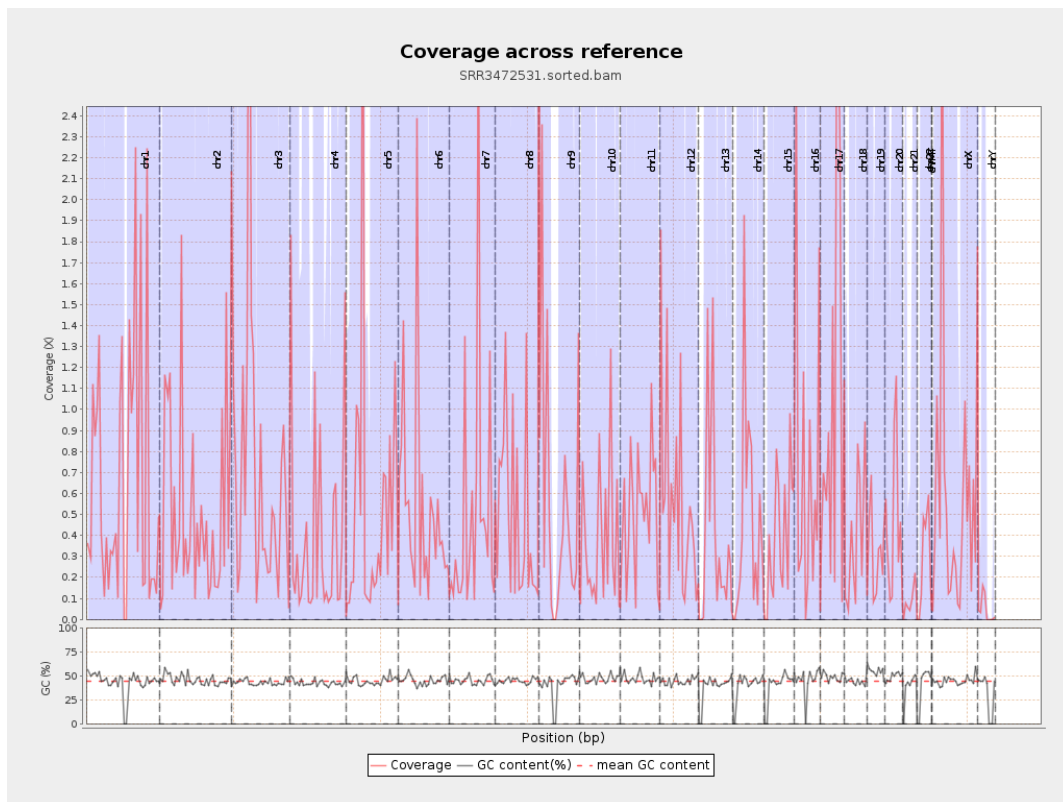
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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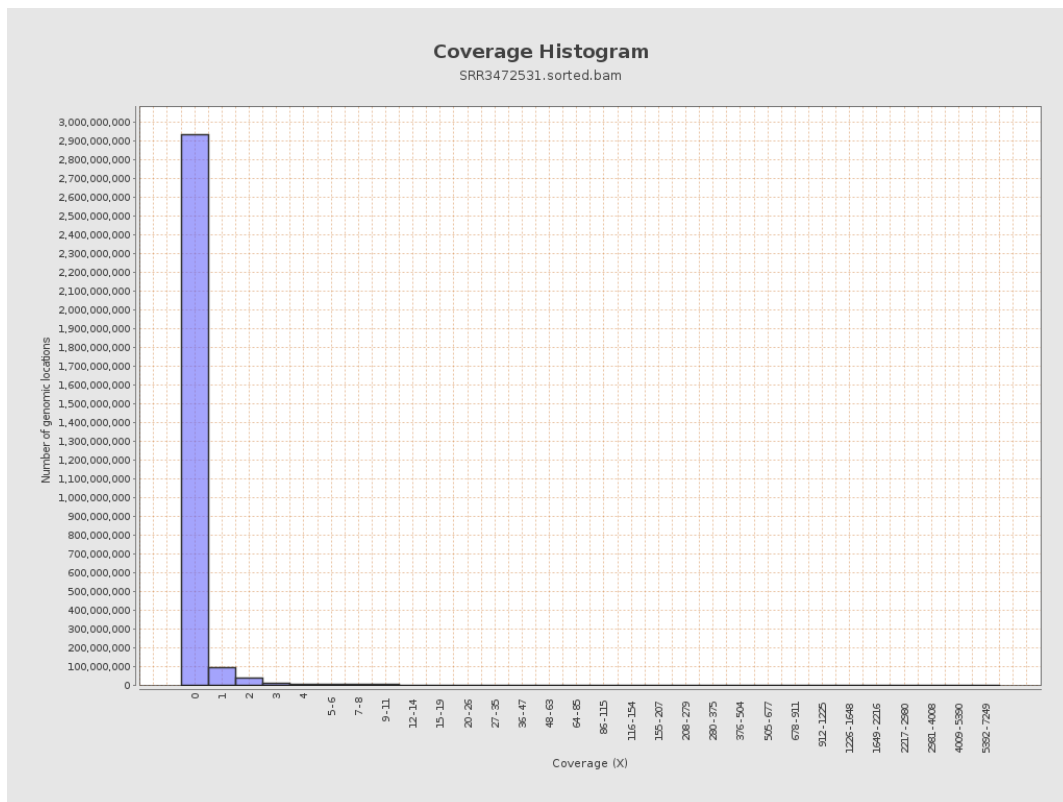
		bases	coverage	deviation
chr1	249250621	165964140	0.6659	24.8814
chr2	243199373	123286667	0.5069	20.5958
chr3	198022430	149753692	0.7562	19.0979
chr4	191154276	72131102	0.3773	13.7547
chr5	180915260	98318942	0.5435	19.3722
chr6	171115067	89982537	0.5259	15.2212
chr7	159138663	80982191	0.5089	18.3567
chr8	146364022	72622895	0.4962	16.3892
chr9	141213431	80640399	0.5711	14.4308
chr10	135534747	50251181	0.3708	14.1823
chr11	135006516	70331929	0.521	16.7161
chr12	133851895	76830102	0.574	15.6918
chr13	115169878	45528415	0.3953	16.6955
chr14	107349540	48567114	0.4524	19.3969
chr15	102531392	39892005	0.3891	11.0937
chr16	90354753	68471693	0.7578	26.5326
chr17	81195210	82038244	1.0104	26.3959
chr18	78077248	31096512	0.3983	13.7084
chr19	59128983	18867912	0.3191	7.1312
chr20	63025520	29912217	0.4746	12.8136
chr21	48129895	4542680	0.0944	3.0481
chr22	51304566	13906234	0.2711	7.5847
chrMT	16571	2037	0.1229	0.4823
chrX	155270560	90520040	0.583	20.7208

chrY	59373566	2876082	0.0484	1.7792
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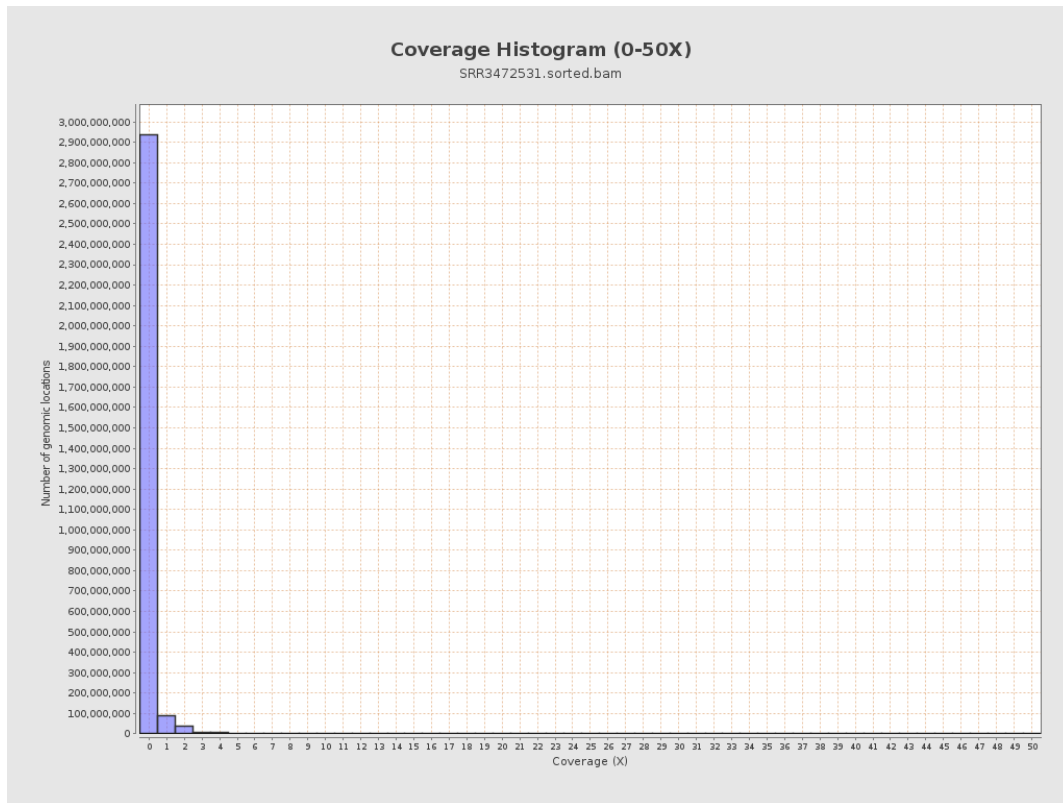
3. Results : Coverage across reference



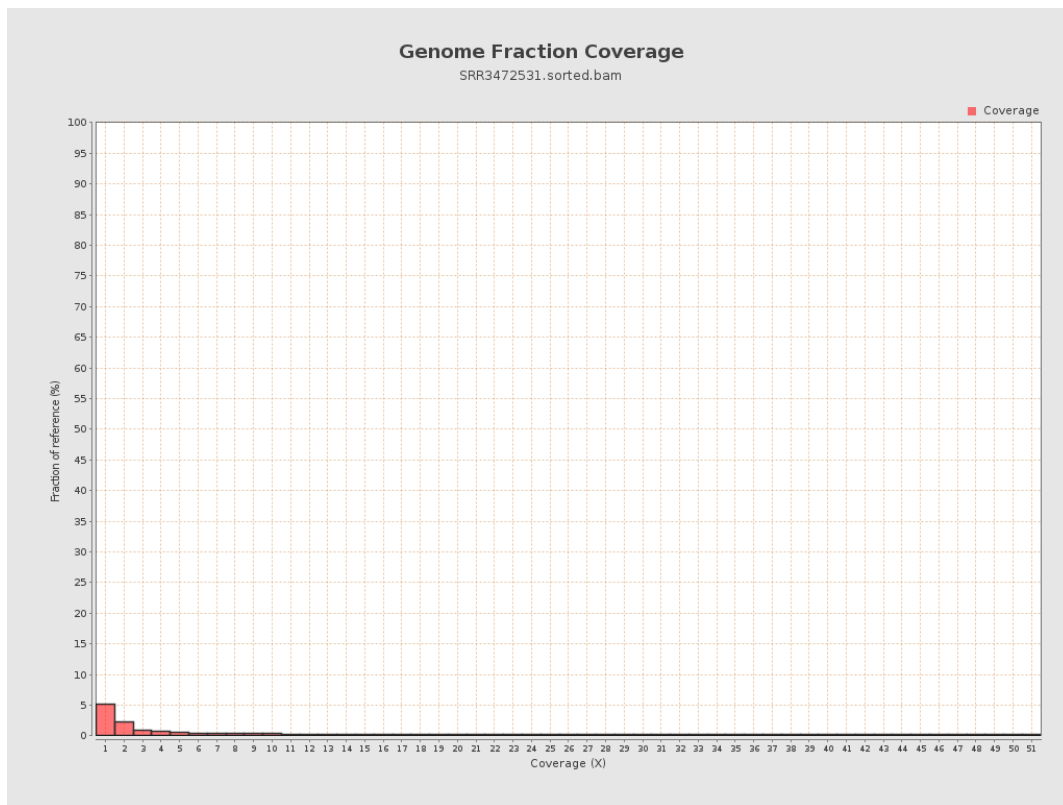
4. Results : Coverage Histogram



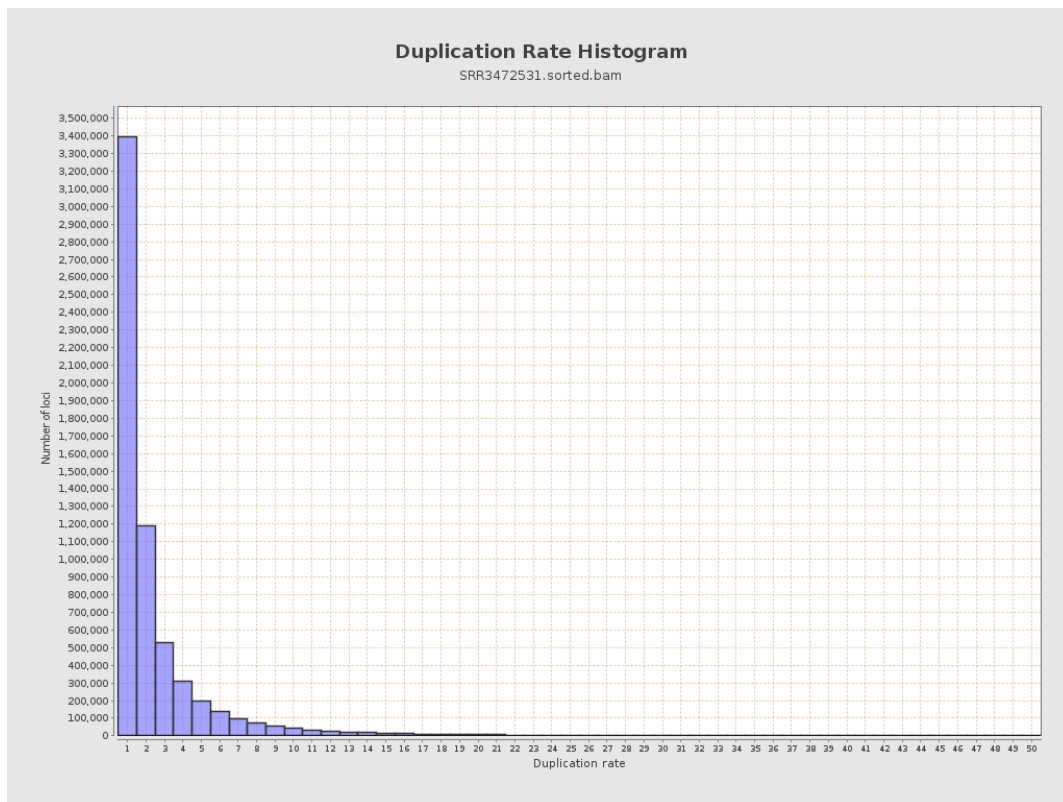
5. Results : Coverage Histogram (0-50X)



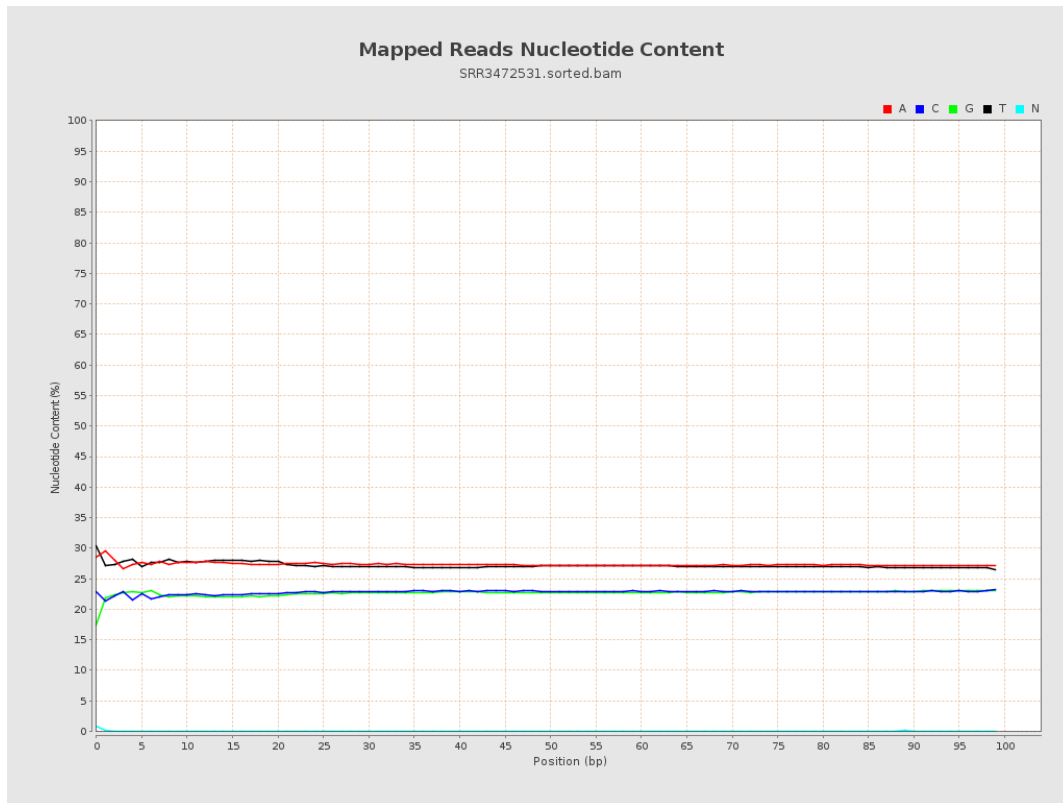
6. Results : Genome Fraction Coverage



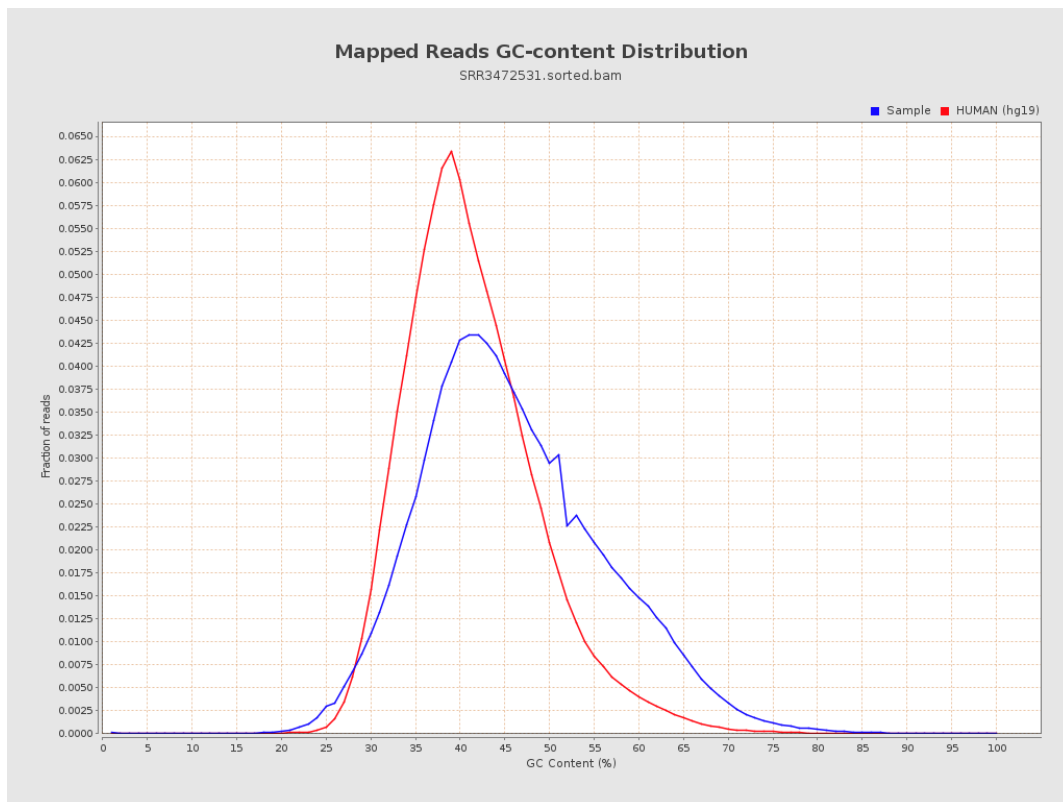
7. Results : Duplication Rate Histogram



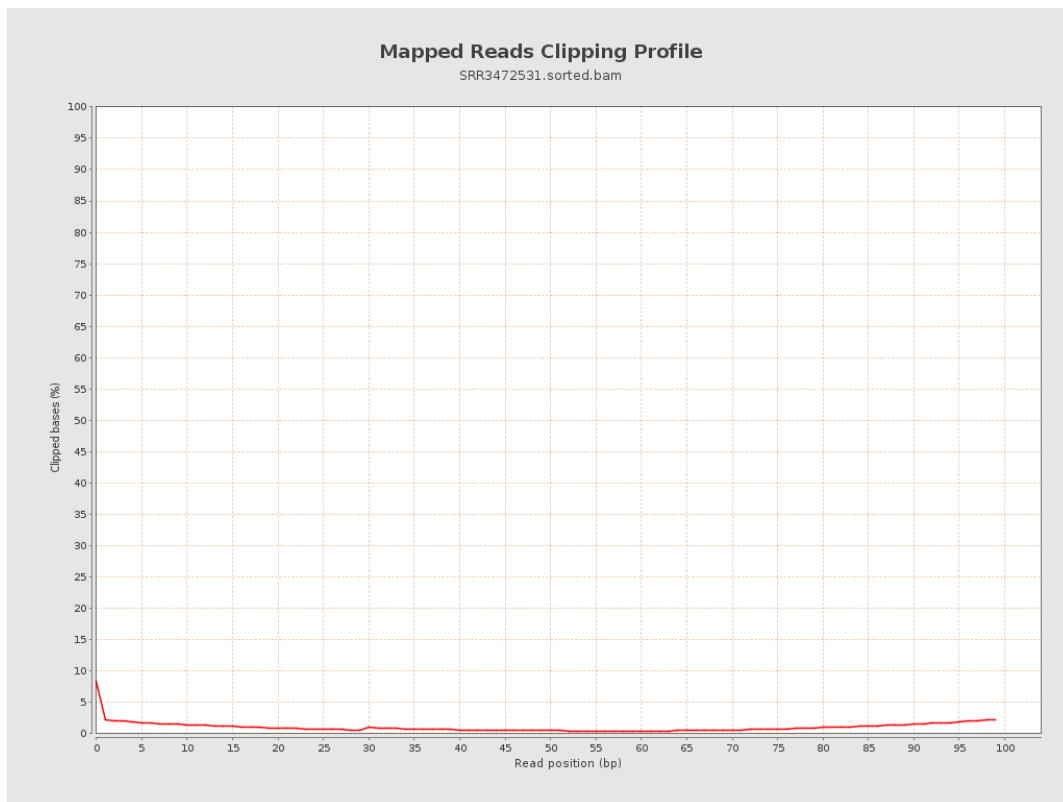
8. Results : Mapped Reads Nucleotide Content



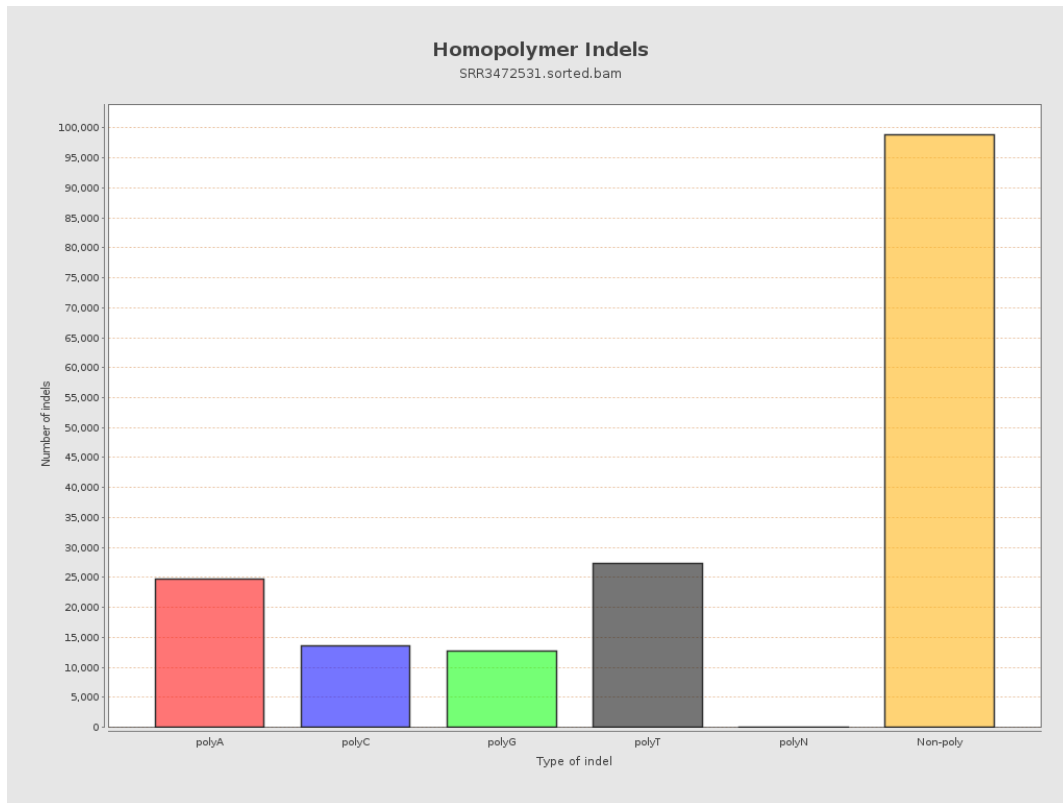
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



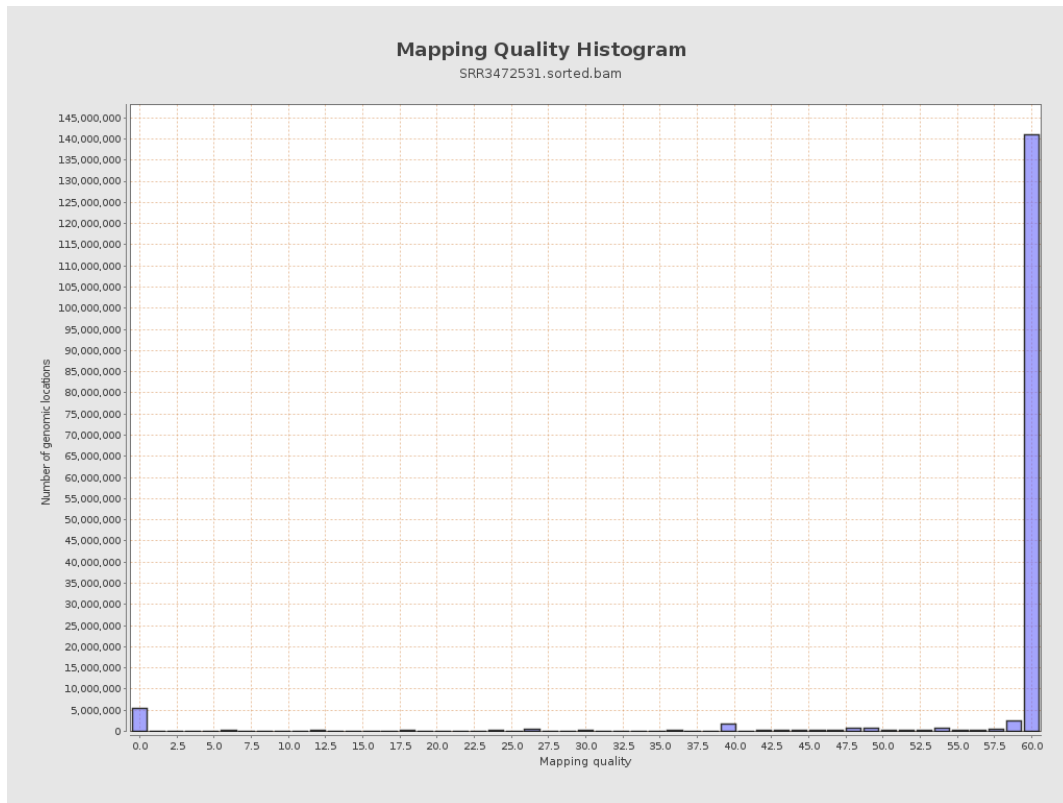
11. Results : Homopolymer Indels



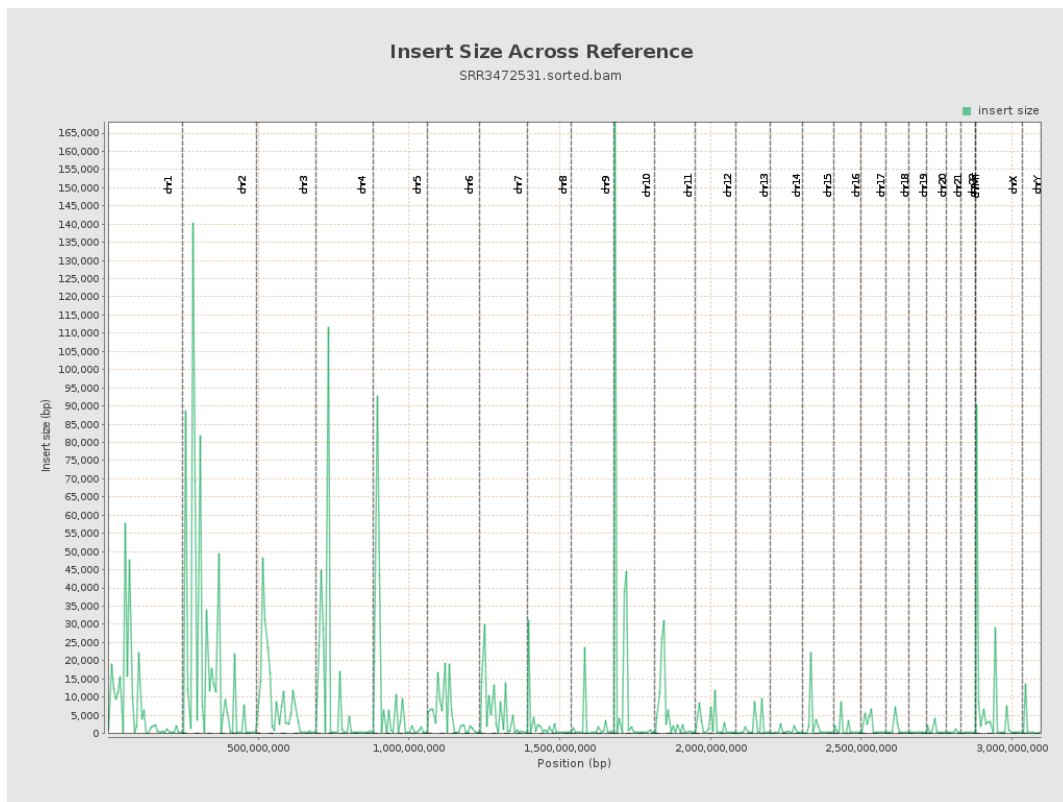
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

