

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 02:27:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472581.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_SRR3472581 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472581_1.fastq.gz SRR3472581_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 02:27:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472581.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,080,520
Mapped reads	9,240,683 / 91.67%
Unmapped reads	839,837 / 8.33%
Mapped paired reads	9,240,683 / 91.67%
Mapped reads, first in pair	4,664,511 / 46.27%
Mapped reads, second in pair	4,576,172 / 45.4%
Mapped reads, both in pair	9,016,940 / 89.45%
Mapped reads, singletons	223,743 / 2.22%
Secondary alignments	0
Supplementary alignments	282,769 / 2.81%
Read min/max/mean length	30 / 100 / 101.09
Duplicated reads (estimated)	1,469,508 / 14.58%
Duplication rate	13.42%
Clipped reads	7,048,147 / 69.92%

2.2. ACGT Content

Number/percentage of A's	195,572,790 / 26.03%
Number/percentage of C's	147,609,011 / 19.64%
Number/percentage of T's	226,493,201 / 30.14%
Number/percentage of G's	181,285,813 / 24.12%
Number/percentage of N's	509,371 / 0.07%

GC Percentage	43.77%
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2.3. Coverage

Mean	0.2428
Standard Deviation	2.3937

2.4. Mapping Quality

Mean Mapping Quality	50.71
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2.5. Insert size

Mean	232,585.42
Standard Deviation	4,621,951.01
P25/Median/P75	93 / 133 / 185

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	8,996,765
Insertions	69,948
Mapped reads with at least one insertion	0.74%
Deletions	168,490
Mapped reads with at least one deletion	1.79%
Homopolymer indels	43.17%

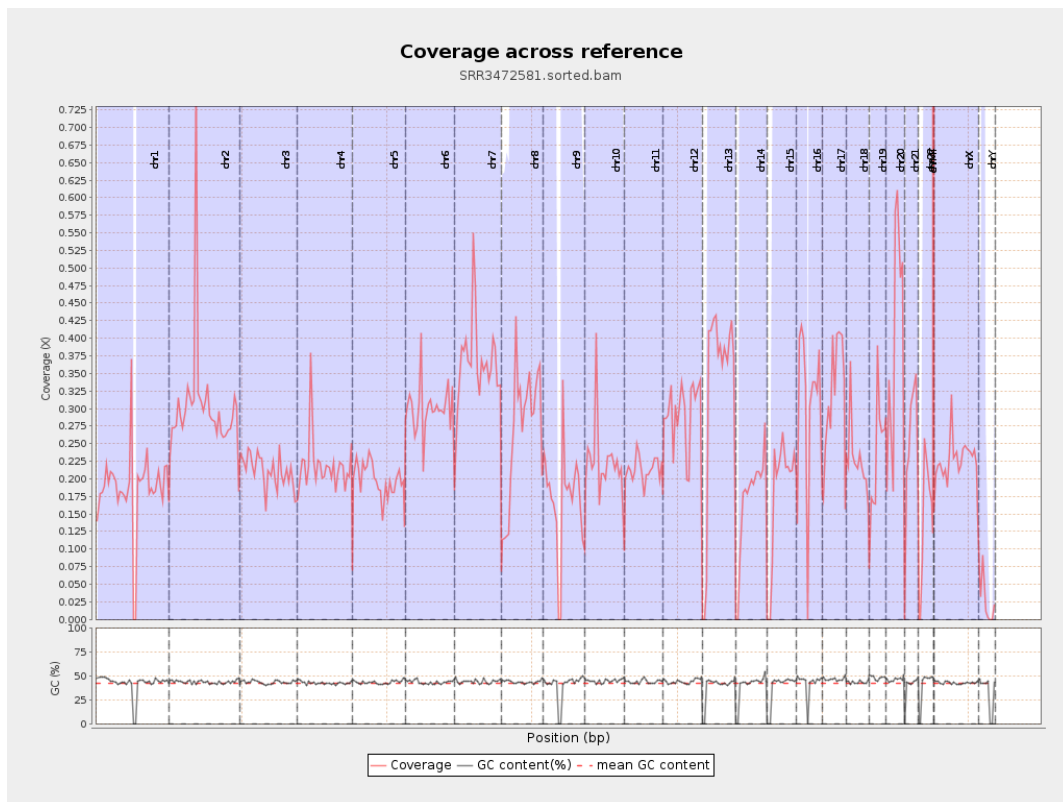
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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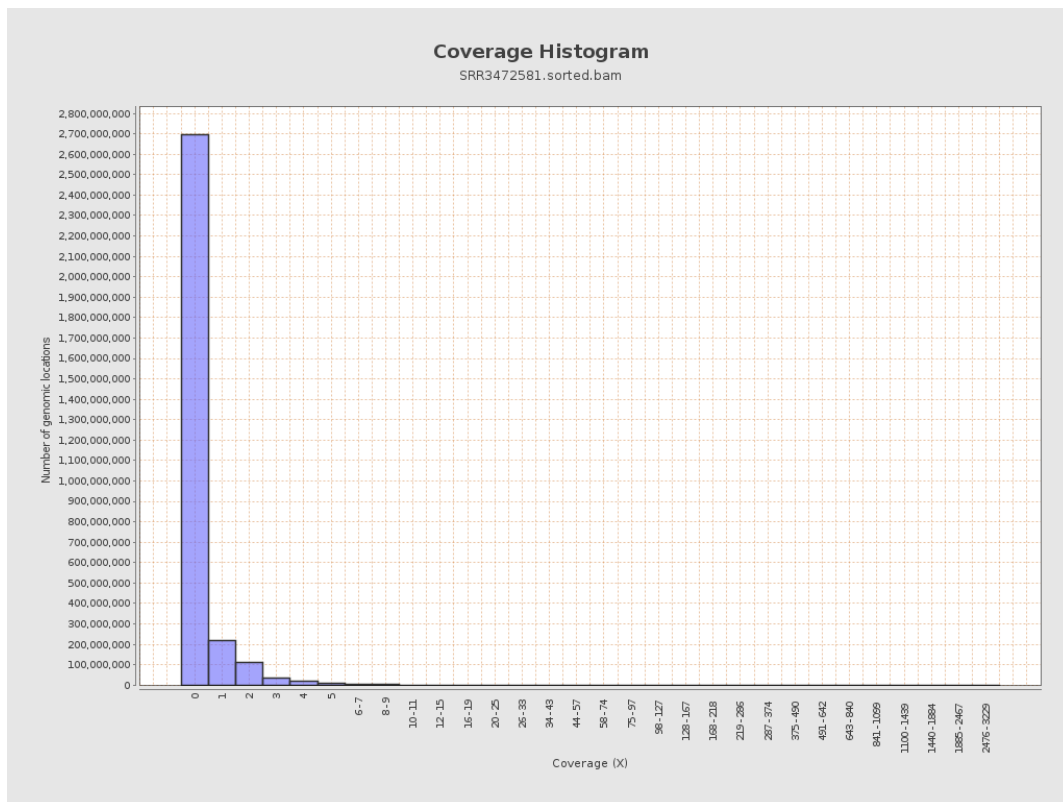
		bases	coverage	deviation
chr1	249250621	46331903	0.1859	3.0295
chr2	243199373	74030208	0.3044	3.8569
chr3	198022430	41847127	0.2113	0.713
chr4	191154276	41599756	0.2176	1.2095
chr5	180915260	35809354	0.1979	0.779
chr6	171115067	51176993	0.2991	1.5295
chr7	159138663	58766908	0.3693	3.8399
chr8	146364022	39296888	0.2685	2.1377
chr9	141213431	24011985	0.17	2.8228
chr10	135534747	30369602	0.2241	2.1002
chr11	135006516	28487058	0.211	1.9686
chr12	133851895	38870576	0.2904	0.8792
chr13	115169878	37723912	0.3276	0.9504
chr14	107349540	18245178	0.17	4.7946
chr15	102531392	18689434	0.1823	0.6801
chr16	90354753	27641727	0.3059	1.2838
chr17	81195210	25978269	0.3199	2.1903
chr18	78077248	17958558	0.23	4.6529
chr19	59128983	14090101	0.2383	2.1616
chr20	63025520	24875840	0.3947	1.3253
chr21	48129895	11863030	0.2465	1.0466
chr22	51304566	7282779	0.142	0.6029
chrMT	16571	190152	11.475	7.549
chrX	155270560	35099148	0.2261	1.1384

chrY	59373566	1546432	0.026	0.9354
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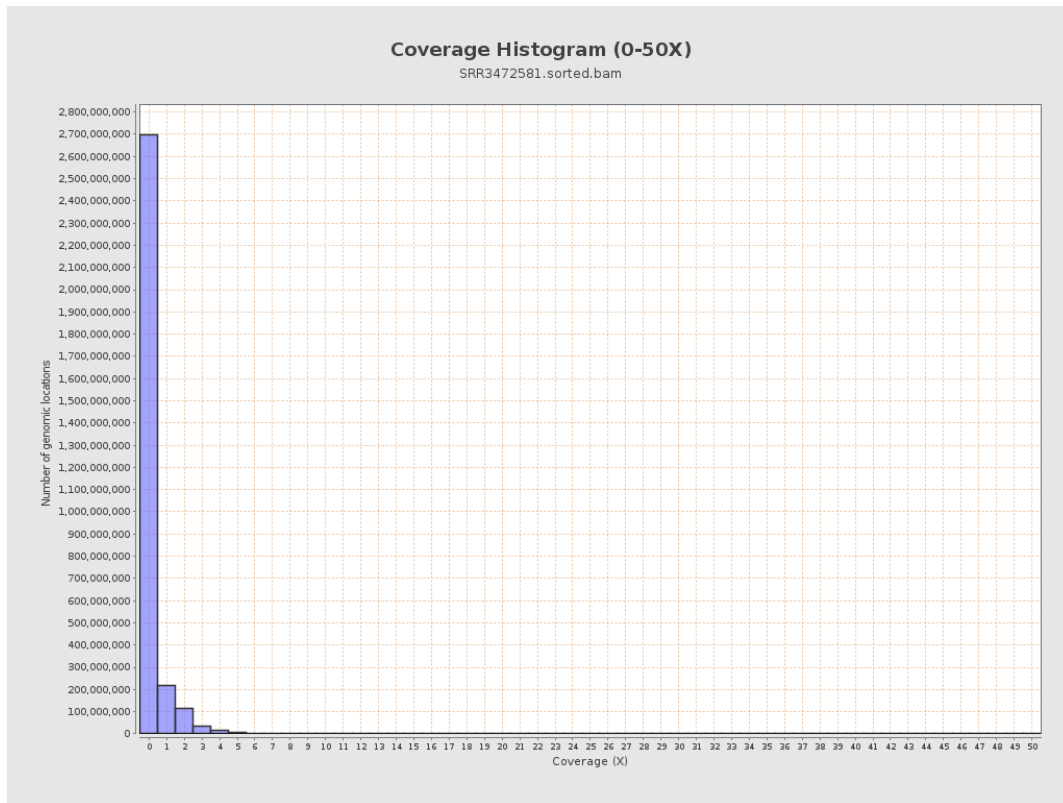
3. Results : Coverage across reference



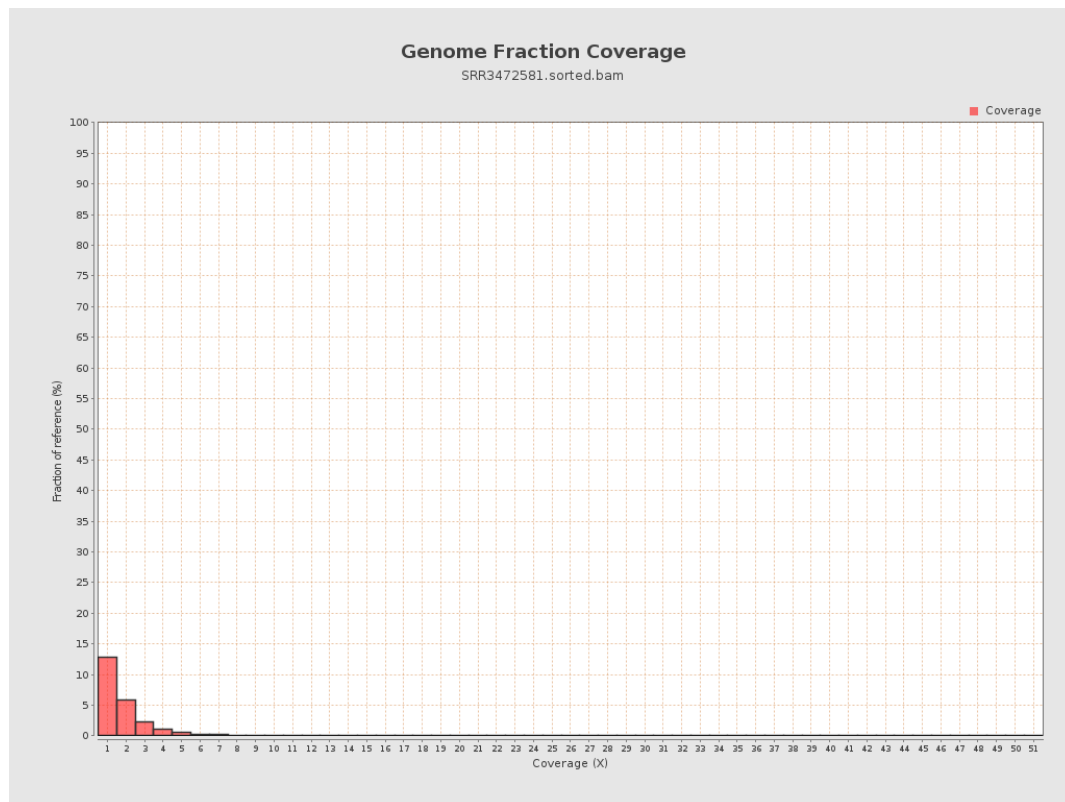
4. Results : Coverage Histogram



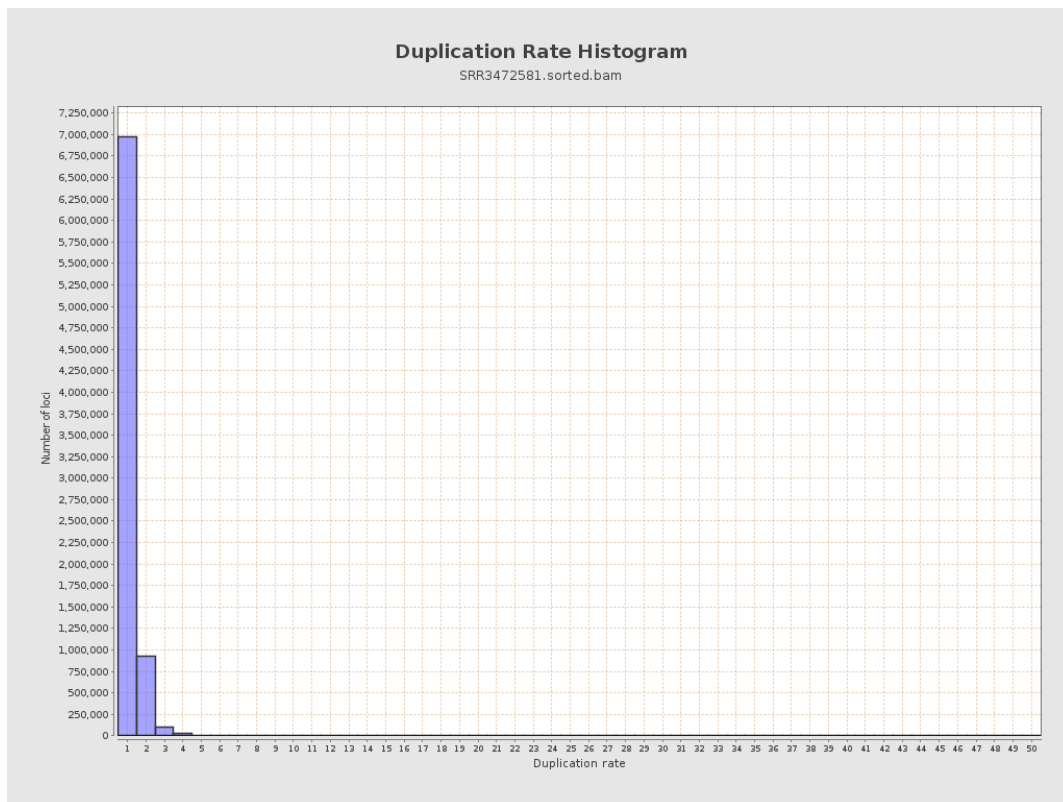
5. Results : Coverage Histogram (0-50X)



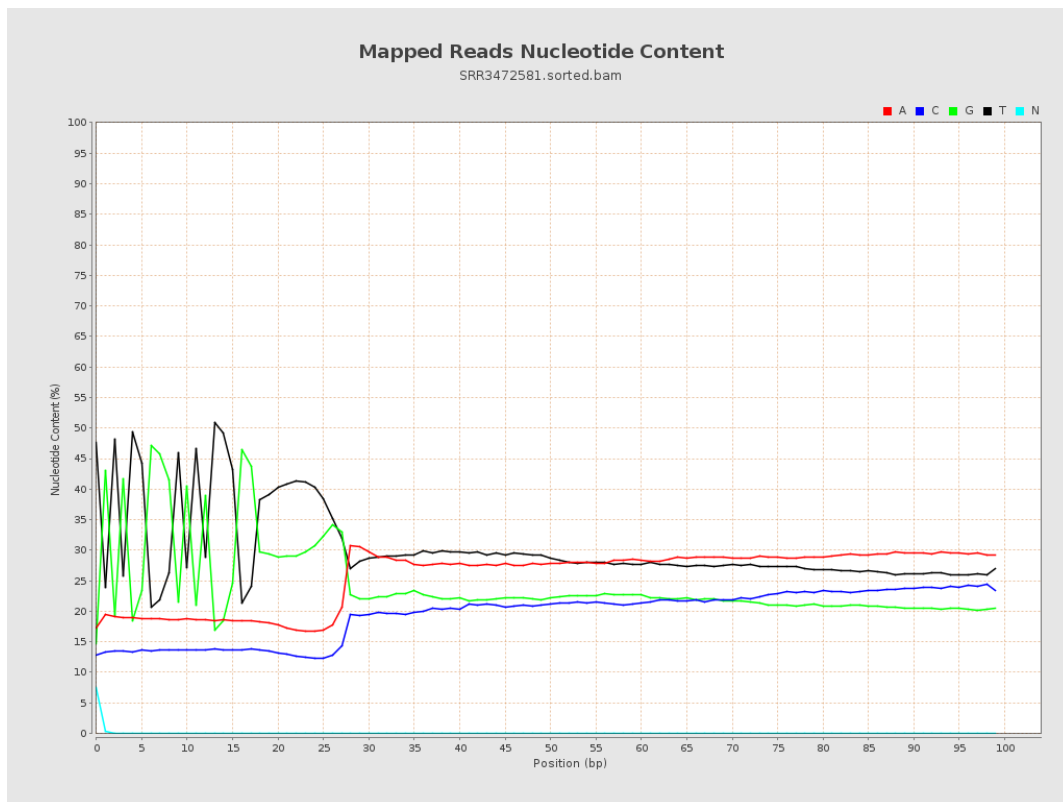
6. Results : Genome Fraction Coverage



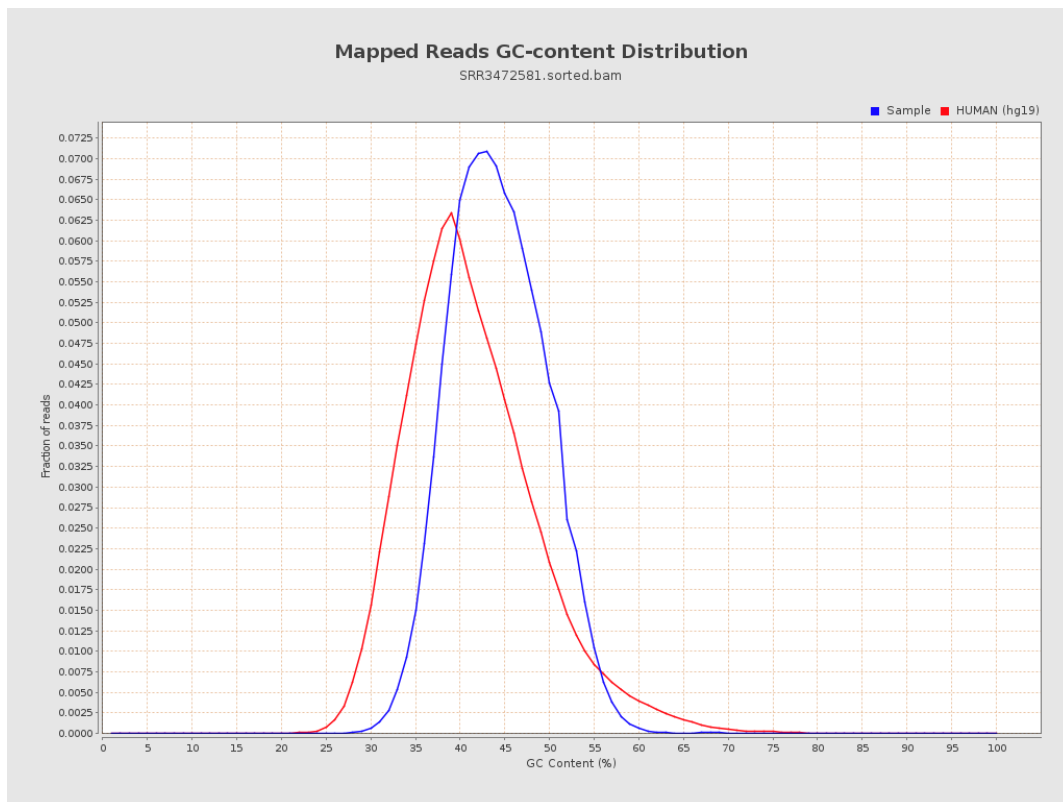
7. Results : Duplication Rate Histogram



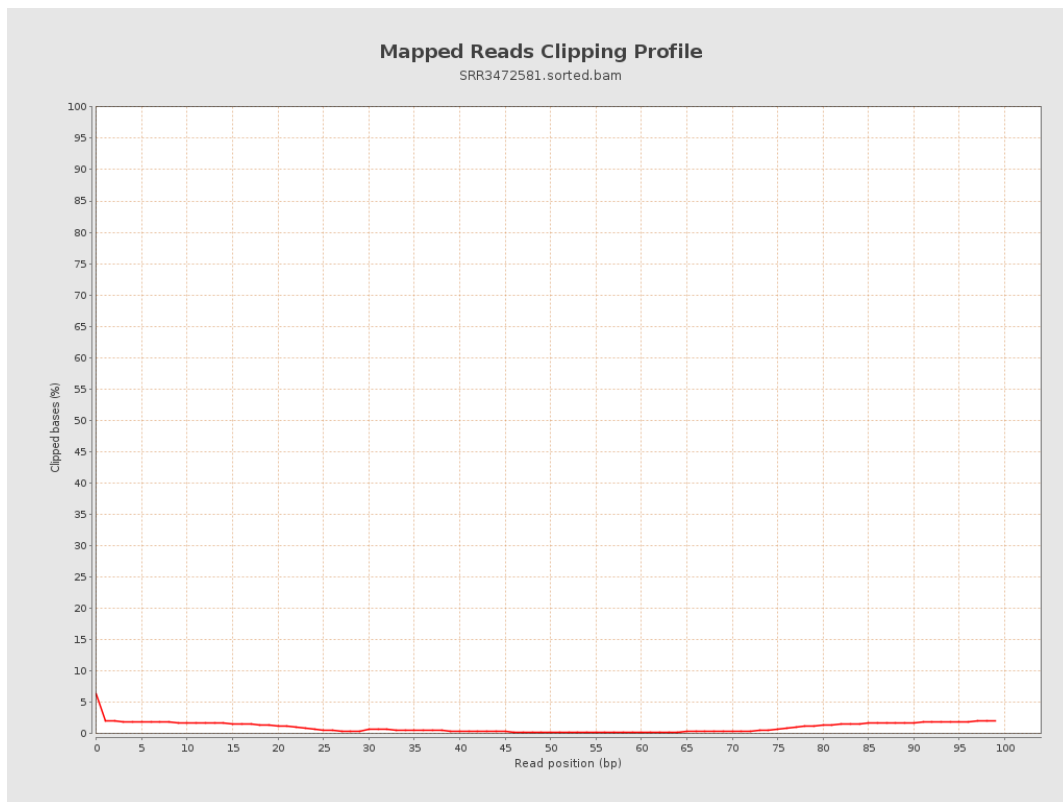
8. Results : Mapped Reads Nucleotide Content



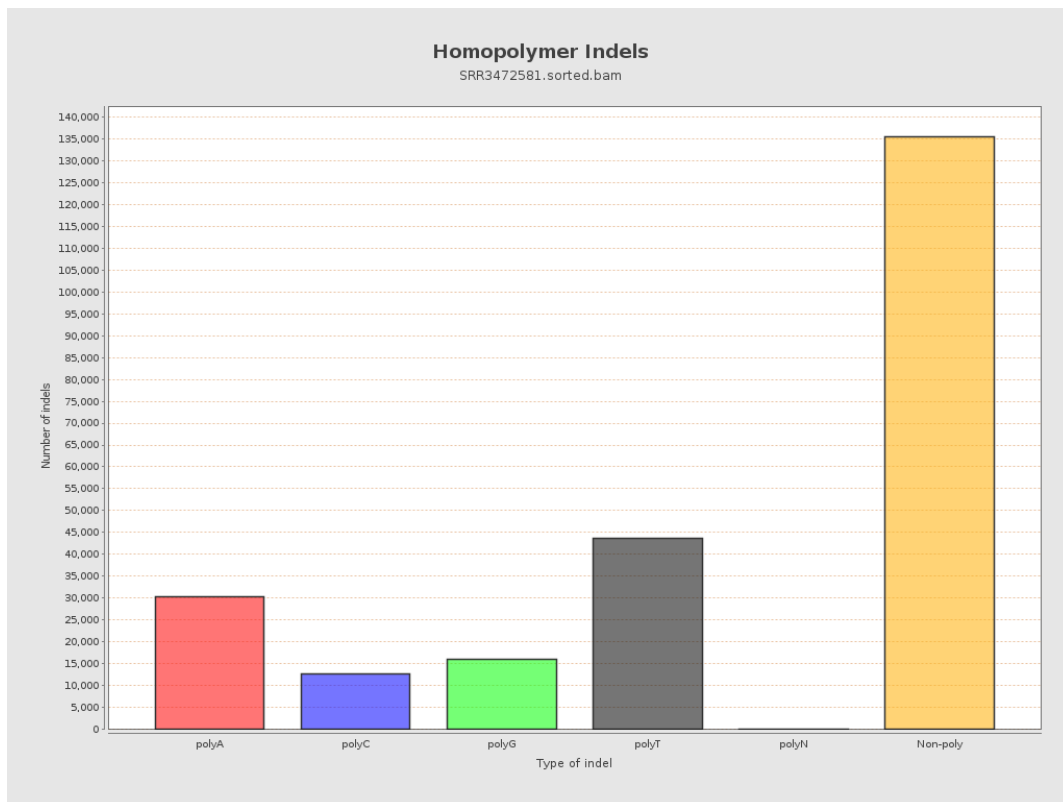
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



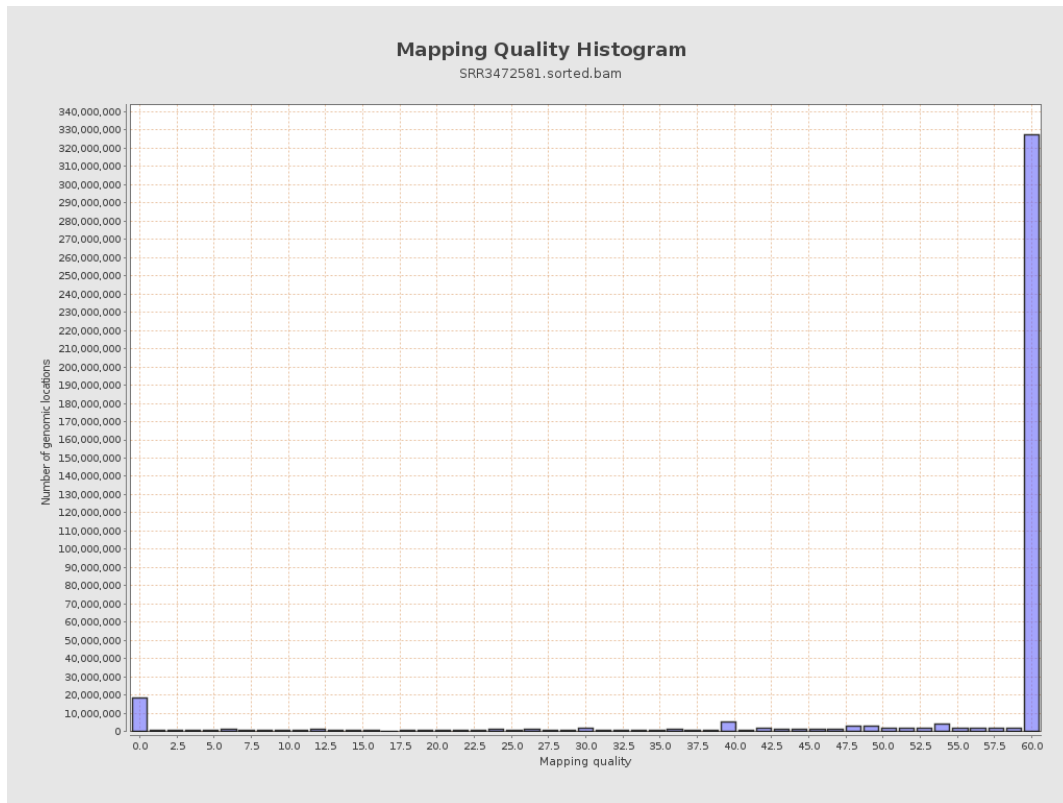
11. Results : Homopolymer Indels



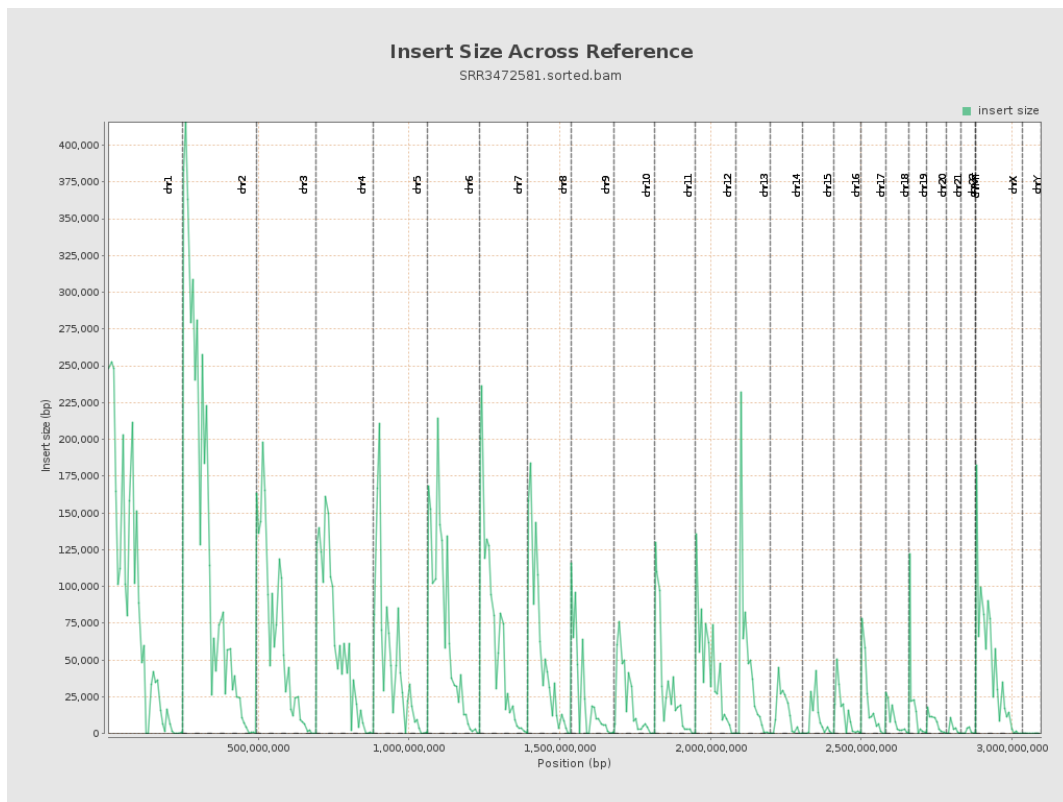
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

