

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 10:56:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124964.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_SRR3124964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124964_1.fastq.gz SRR3124964_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 10:56:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,232,644
Mapped reads	3,937,556 / 93.03%
Unmapped reads	295,088 / 6.97%
Mapped paired reads	3,937,556 / 93.03%
Mapped reads, first in pair	2,006,021 / 47.39%
Mapped reads, second in pair	1,931,535 / 45.63%
Mapped reads, both in pair	3,833,984 / 90.58%
Mapped reads, singletons	103,572 / 2.45%
Secondary alignments	0
Supplementary alignments	13,924 / 0.33%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	380,533 / 8.99%
Duplication rate	5.96%
Clipped reads	2,036,430 / 48.11%

2.2. ACGT Content

Number/percentage of A's	66,876,417 / 27.81%
Number/percentage of C's	42,677,063 / 17.75%
Number/percentage of T's	72,890,328 / 30.31%
Number/percentage of G's	58,003,761 / 24.12%
Number/percentage of N's	0 / 0%

GC Percentage	41.87%
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2.3. Coverage

Mean	0.0777
Standard Deviation	1.1522

2.4. Mapping Quality

Mean Mapping Quality	51.45
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2.5. Insert size

Mean	75,739.34
Standard Deviation	2,599,067.63
P25/Median/P75	121 / 165 / 230

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	2,005,923
Insertions	33,669
Mapped reads with at least one insertion	0.84%
Deletions	79,353
Mapped reads with at least one deletion	1.99%
Homopolymer indels	45.75%

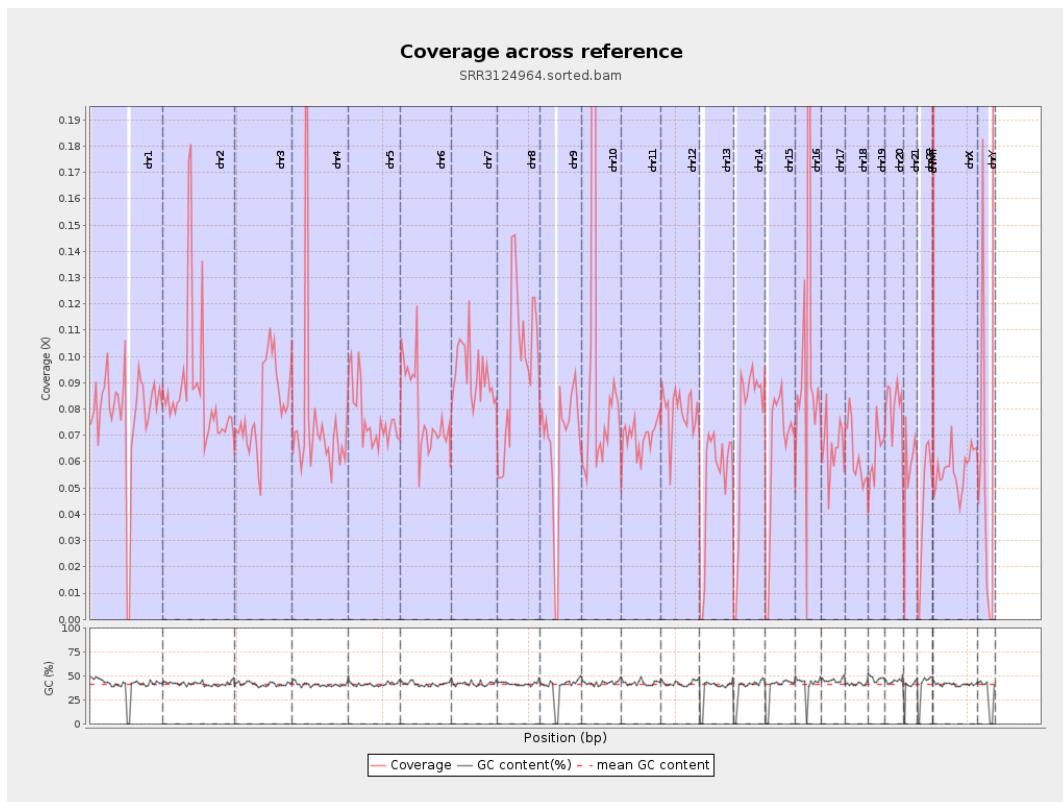
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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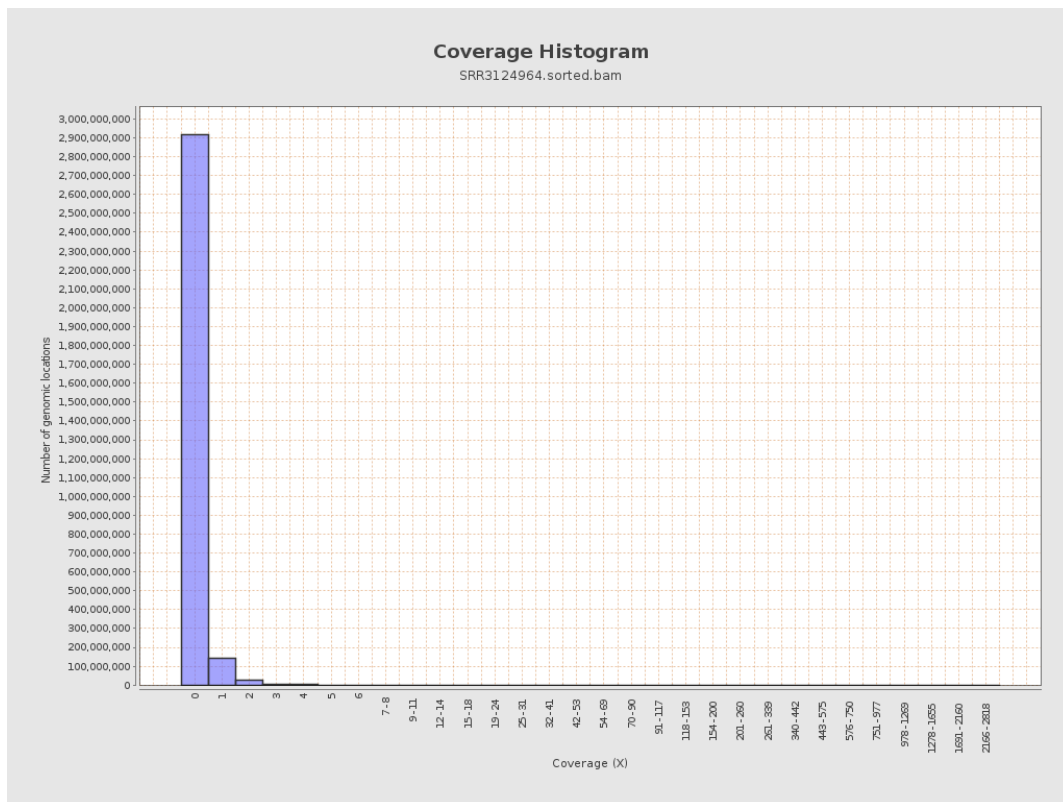
		bases	coverage	deviation
chr1	249250621	19493153	0.0782	0.5929
chr2	243199373	21267070	0.0874	1.2114
chr3	198022430	16010670	0.0809	0.4207
chr4	191154276	14713736	0.077	1.0205
chr5	180915260	13817642	0.0764	0.3553
chr6	171115067	13508786	0.0789	0.4486
chr7	159138663	14868903	0.0934	0.6491
chr8	146364022	14266954	0.0975	0.4507
chr9	141213431	9570858	0.0678	0.6822
chr10	135534747	14081399	0.1039	4.0225
chr11	135006516	9376511	0.0695	0.4214
chr12	133851895	10652263	0.0796	0.352
chr13	115169878	6061048	0.0526	0.278
chr14	107349540	7877601	0.0734	0.3859
chr15	102531392	6461310	0.063	0.3197
chr16	90354753	9540585	0.1056	2.1661
chr17	81195210	5326275	0.0656	0.5665
chr18	78077248	4918264	0.063	0.8931
chr19	59128983	3753032	0.0635	0.5105
chr20	63025520	5148163	0.0817	0.5184
chr21	48129895	2771436	0.0576	0.5834
chr22	51304566	2229932	0.0435	0.3032
chrMT	16571	96696	5.8353	4.3602
chrX	155270560	8881360	0.0572	0.3795

chrY	59373566	5884447	0.0991	2.4382
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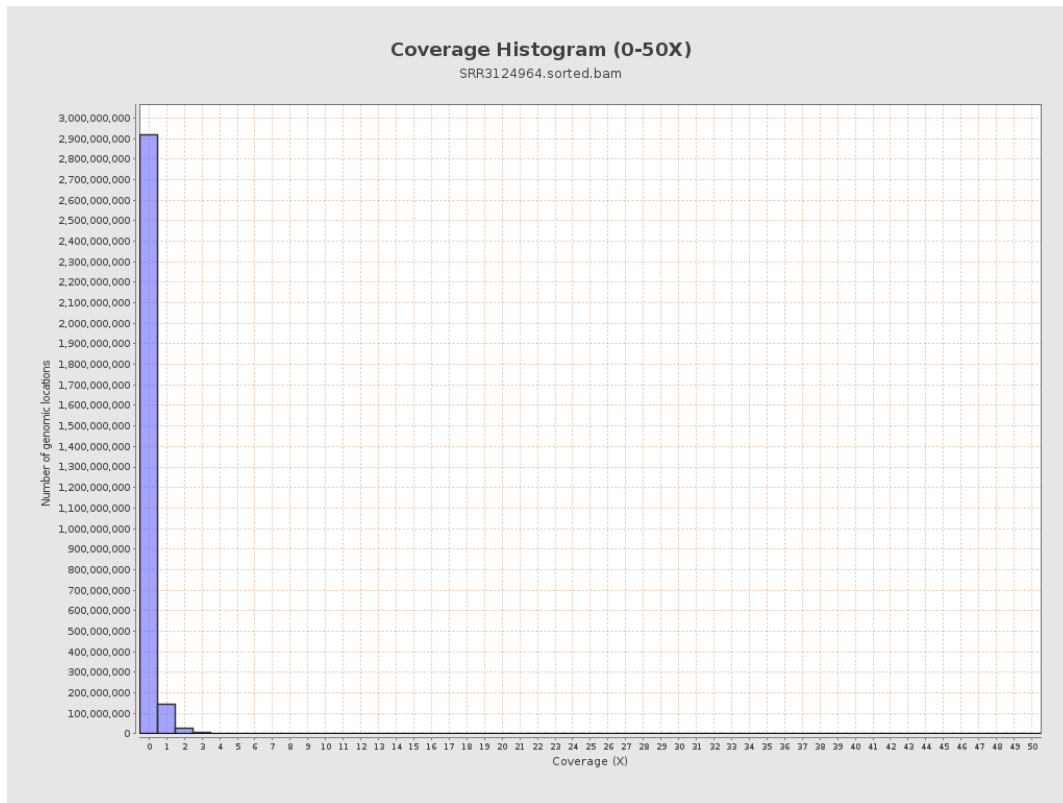
3. Results : Coverage across reference



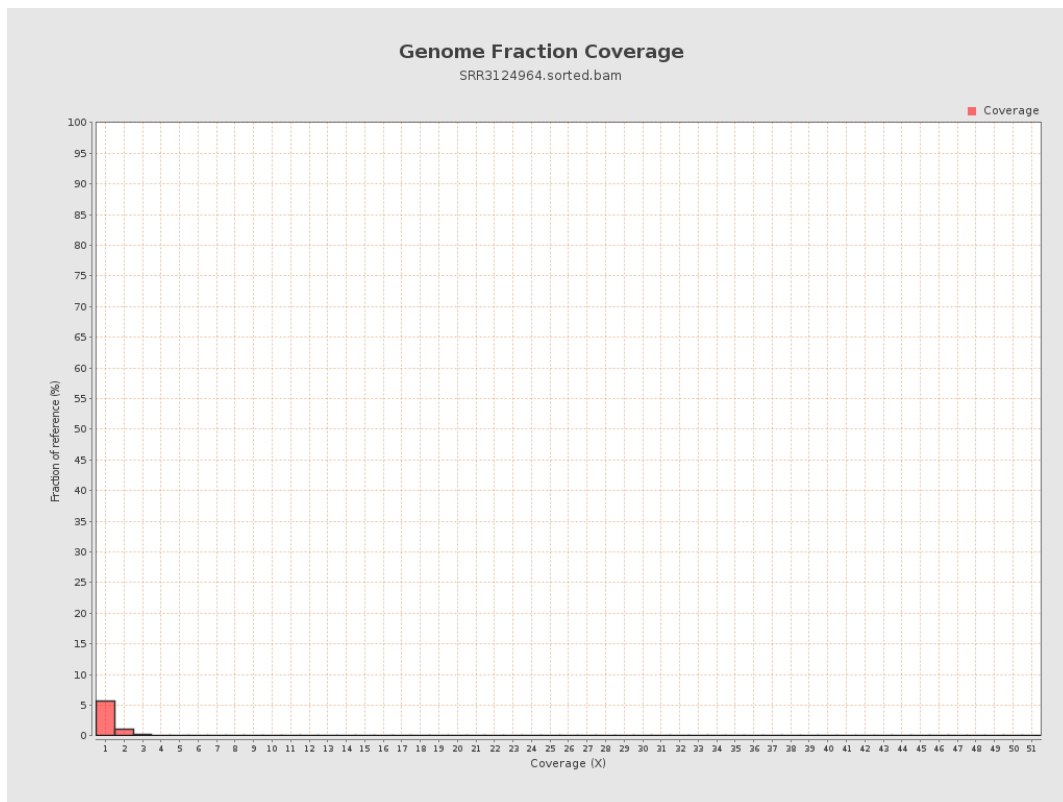
4. Results : Coverage Histogram



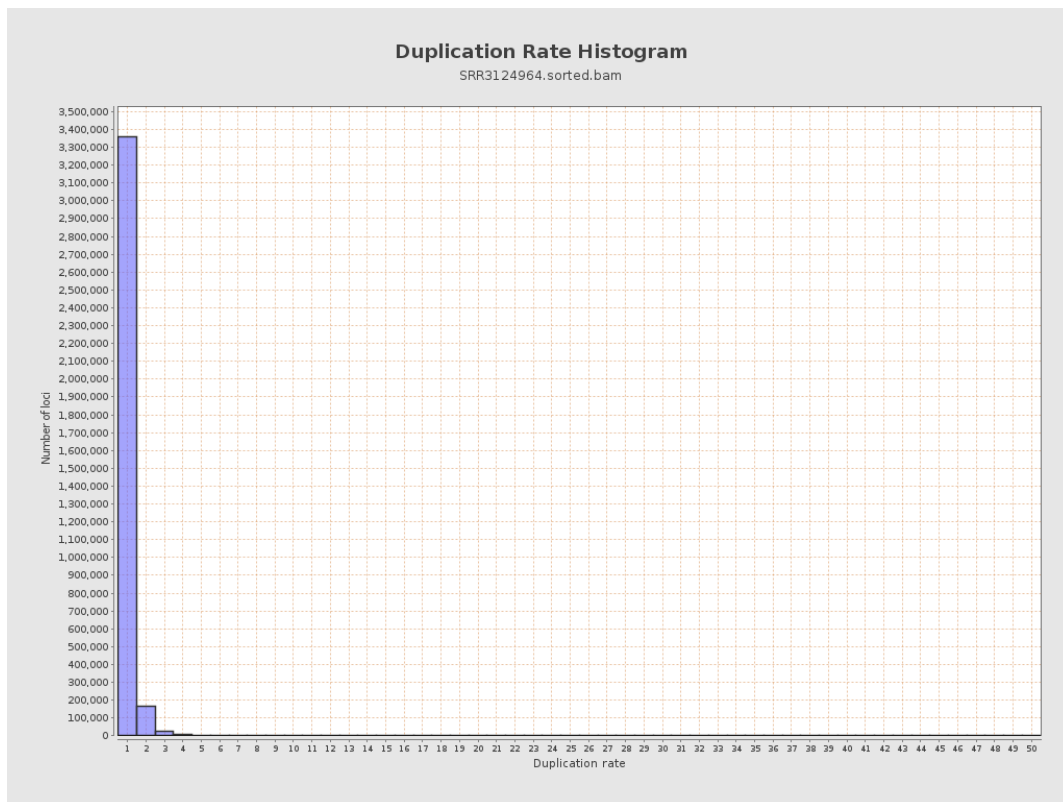
5. Results : Coverage Histogram (0-50X)



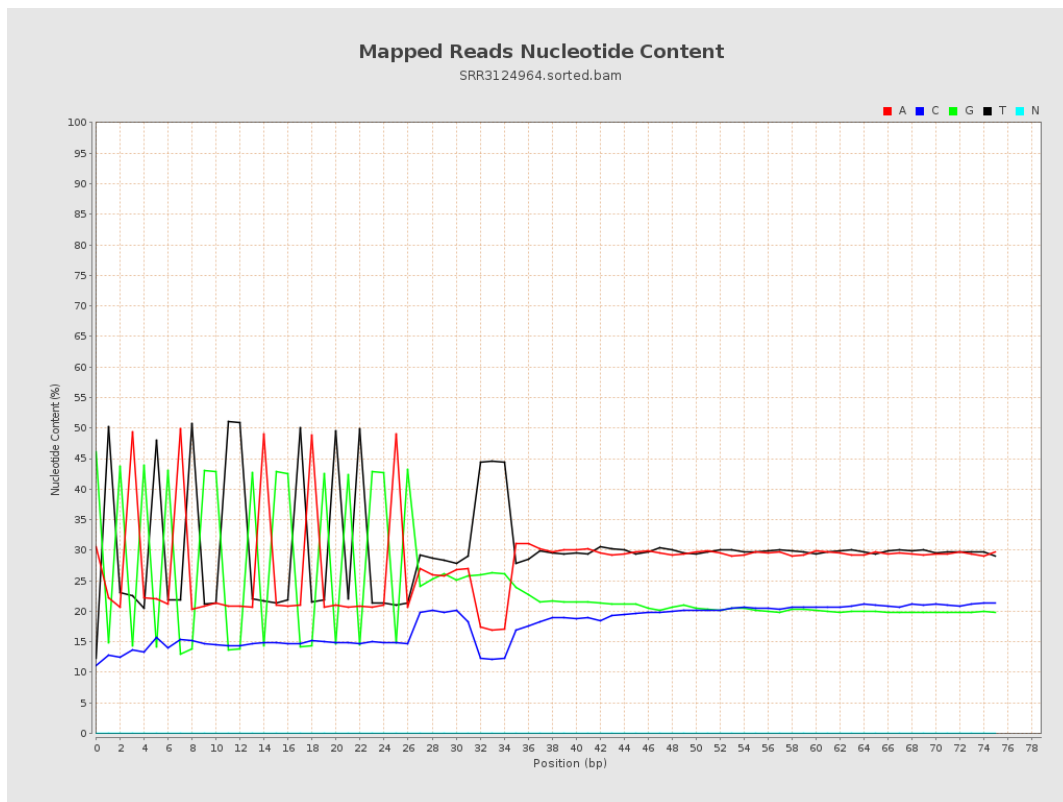
6. Results : Genome Fraction Coverage



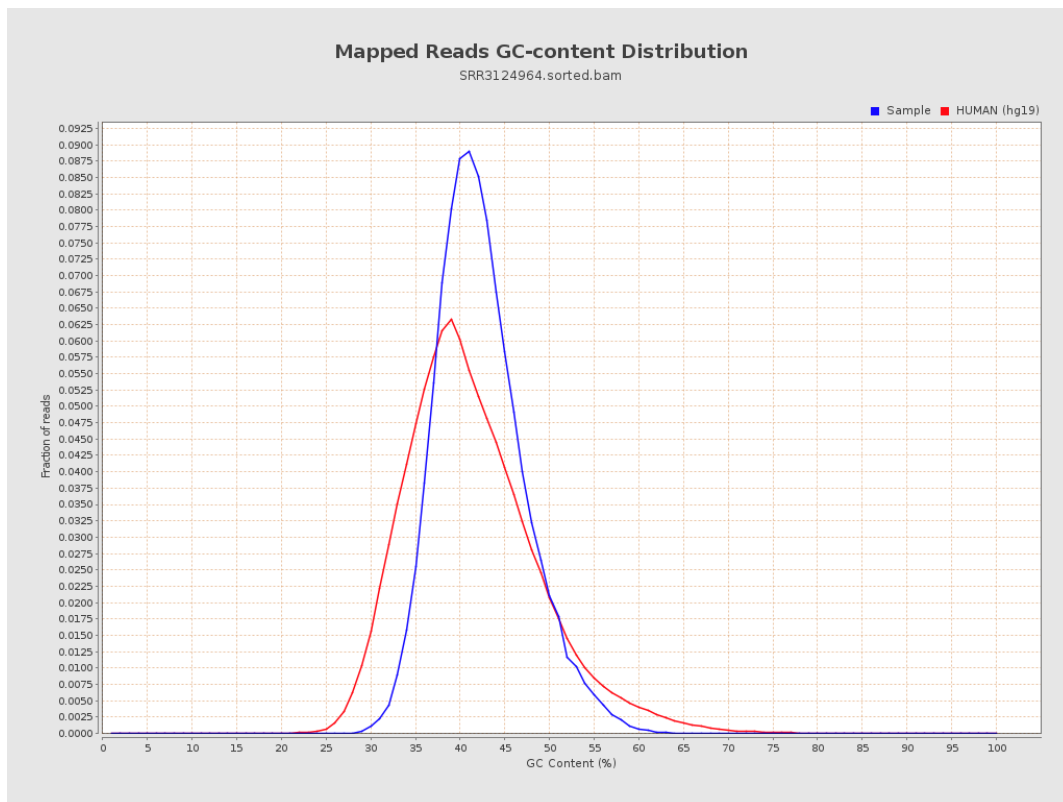
7. Results : Duplication Rate Histogram



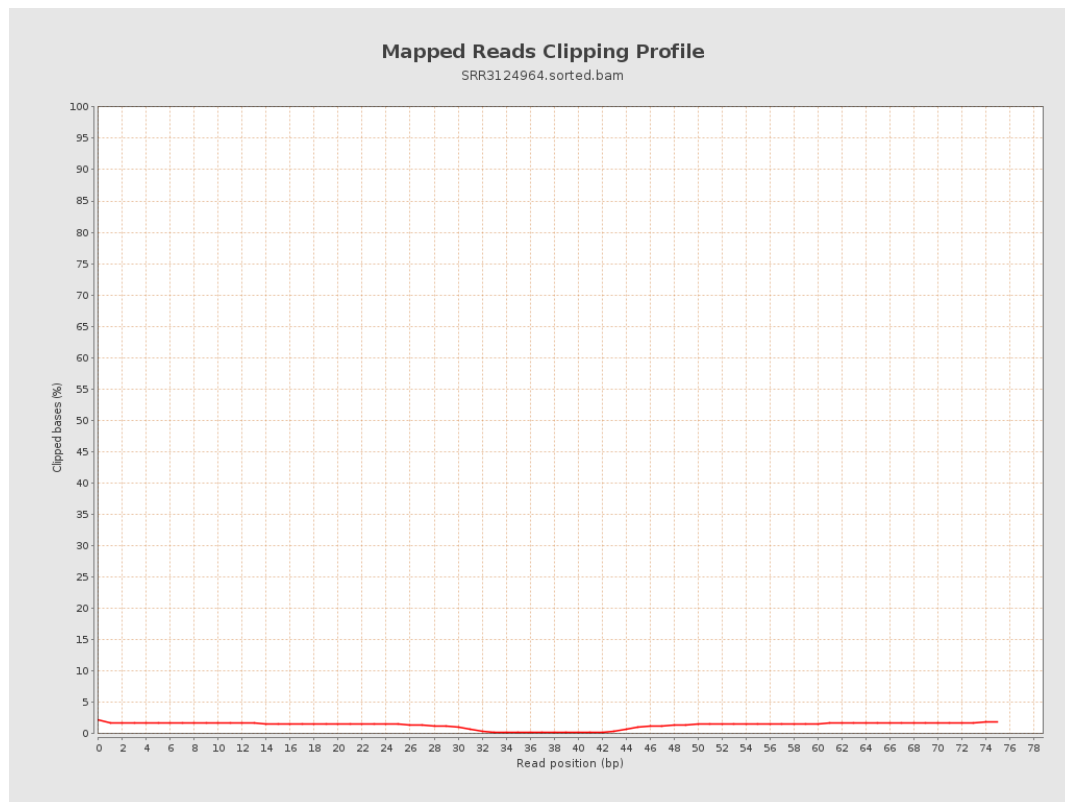
8. Results : Mapped Reads Nucleotide Content



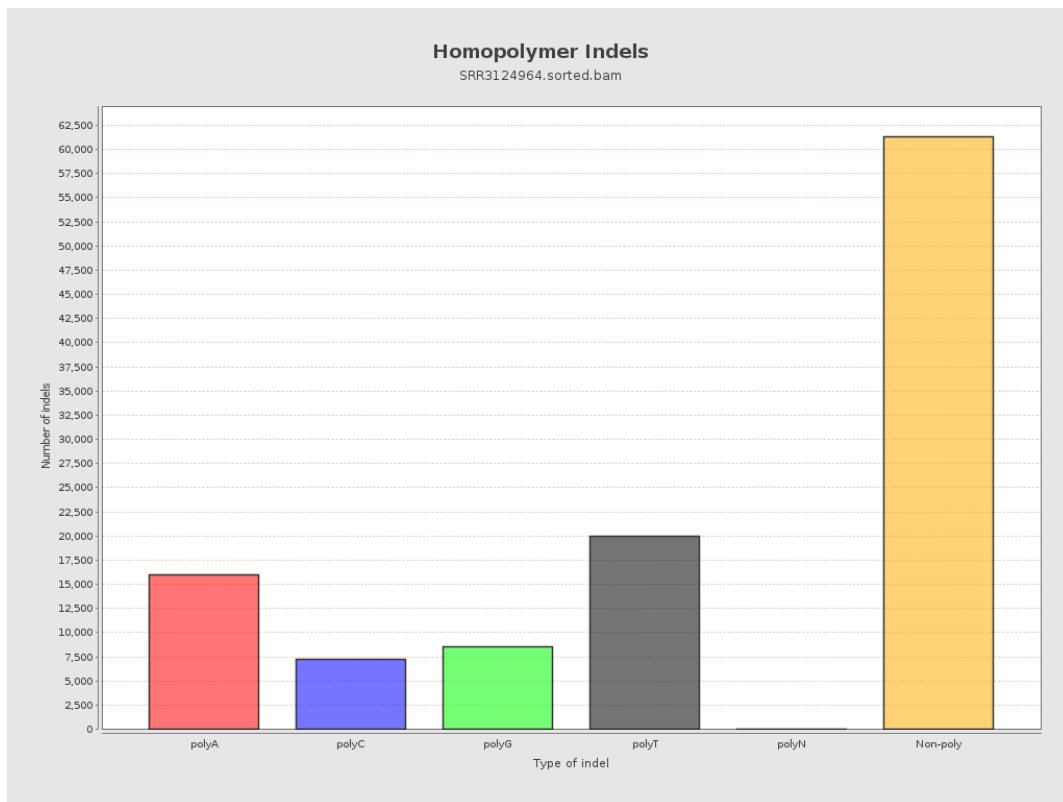
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



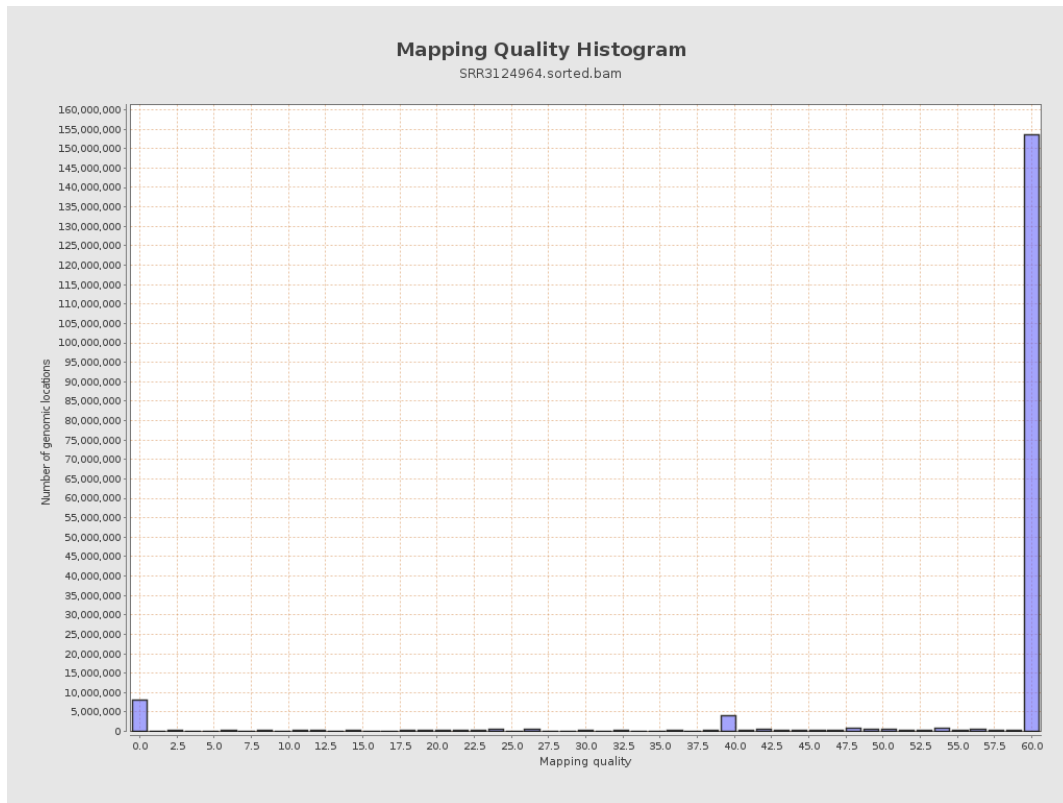
11. Results : Homopolymer Indels



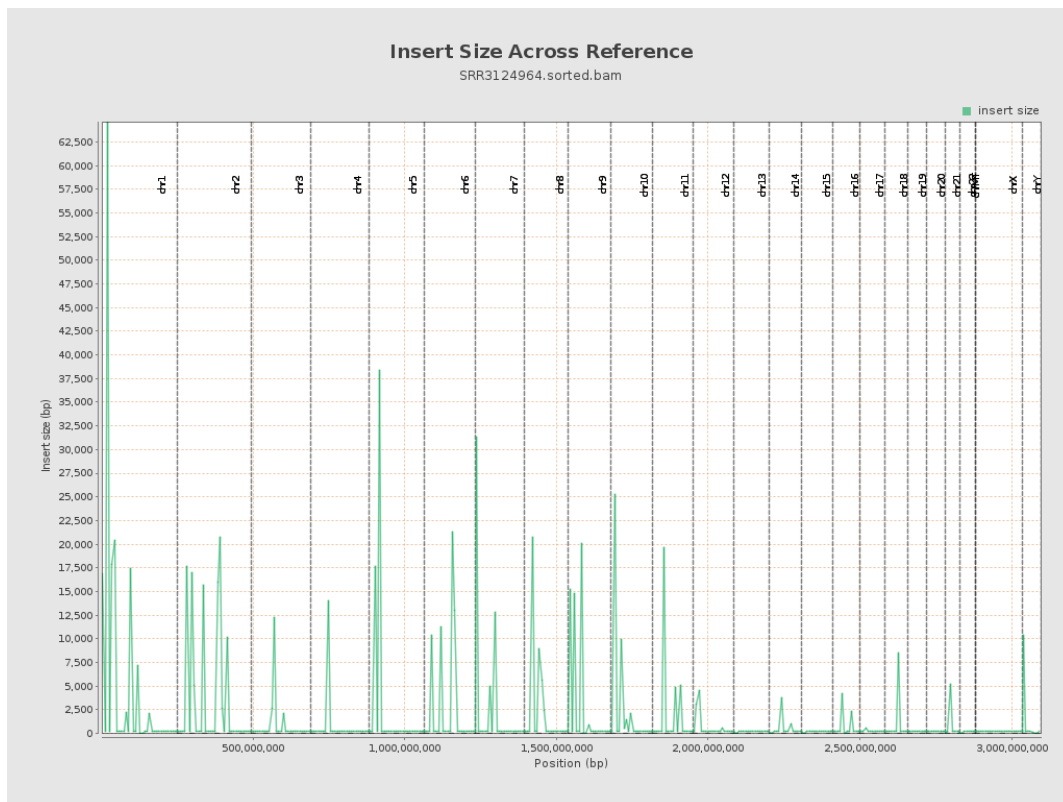
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

