

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 02:07:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124894.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_SRR3124894 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124894_1.fastq.gz SRR3124894_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 02:07:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124894.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,308,442
Mapped reads	4,254,865 / 98.76%
Unmapped reads	53,577 / 1.24%
Mapped paired reads	4,254,865 / 98.76%
Mapped reads, first in pair	2,128,785 / 49.41%
Mapped reads, second in pair	2,126,080 / 49.35%
Mapped reads, both in pair	4,240,516 / 98.42%
Mapped reads, singletons	14,349 / 0.33%
Secondary alignments	0
Supplementary alignments	17,926 / 0.42%
Read min/max/mean length	30 / 101 / 101.17
Duplicated reads (estimated)	213,493 / 4.96%
Duplication rate	2.75%
Clipped reads	2,536,901 / 58.88%

2.2. ACGT Content

Number/percentage of A's	114,386,951 / 29.38%
Number/percentage of C's	77,568,282 / 19.92%
Number/percentage of T's	114,507,173 / 29.41%
Number/percentage of G's	82,619,772 / 21.22%
Number/percentage of N's	254,459 / 0.07%

GC Percentage	41.14%
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2.3. Coverage

Mean	0.1258
Standard Deviation	1.3076

2.4. Mapping Quality

Mean Mapping Quality	52.51
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2.5. Insert size

Mean	55,085.59
Standard Deviation	2,199,903.37
P25/Median/P75	135 / 168 / 213

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	3,289,828
Insertions	64,830
Mapped reads with at least one insertion	1.49%
Deletions	120,757
Mapped reads with at least one deletion	2.78%
Homopolymer indels	46.54%

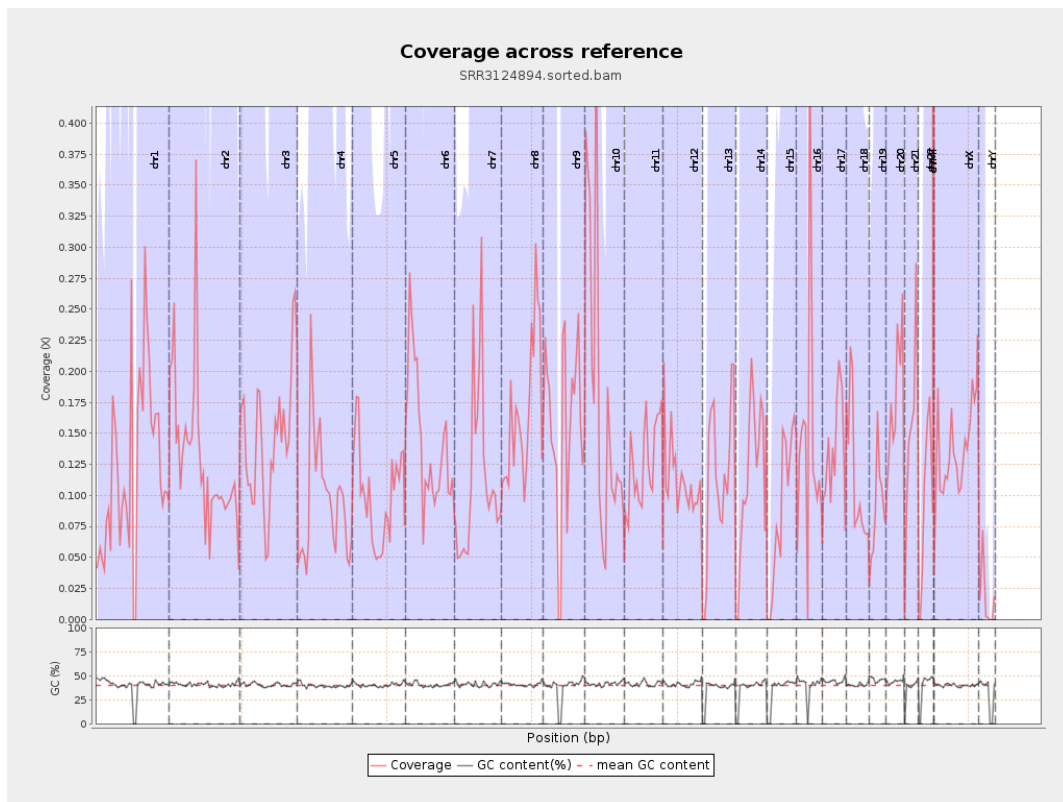
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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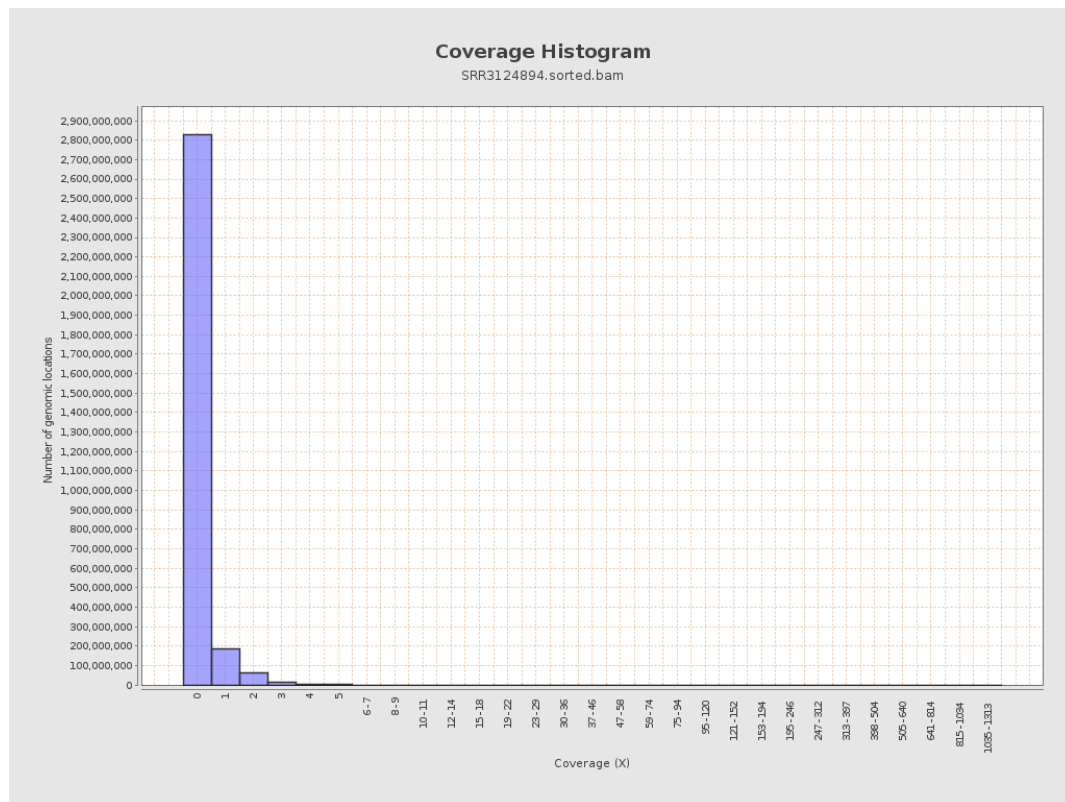
		bases	coverage	deviation
chr1	249250621	30165893	0.121	1.3198
chr2	243199373	31808441	0.1308	1.5093
chr3	198022430	28792988	0.1454	0.5089
chr4	191154276	17881333	0.0935	1.2146
chr5	180915260	17910967	0.099	0.4112
chr6	171115067	24314657	0.1421	0.7656
chr7	159138663	18107564	0.1138	2.2693
chr8	146364022	24483230	0.1673	0.7175
chr9	141213431	22031648	0.156	1.8674
chr10	135534747	24129440	0.178	3.0079
chr11	135006516	16950758	0.1256	0.6273
chr12	133851895	15039467	0.1124	0.429
chr13	115169878	13052283	0.1133	0.4298
chr14	107349540	12347877	0.115	0.4813
chr15	102531392	8968659	0.0875	0.3807
chr16	90354753	12734229	0.1409	2.2517
chr17	81195210	11064552	0.1363	1.0615
chr18	78077248	8945096	0.1146	1.9783
chr19	59128983	5382375	0.091	0.8309
chr20	63025520	11175591	0.1773	0.6197
chr21	48129895	7213213	0.1499	0.6831
chr22	51304566	4938534	0.0963	0.4092
chrMT	16571	90237	5.4455	4.2984
chrX	155270560	20998156	0.1352	0.5908

chrY	59373566	1016045	0.0171	1.1571
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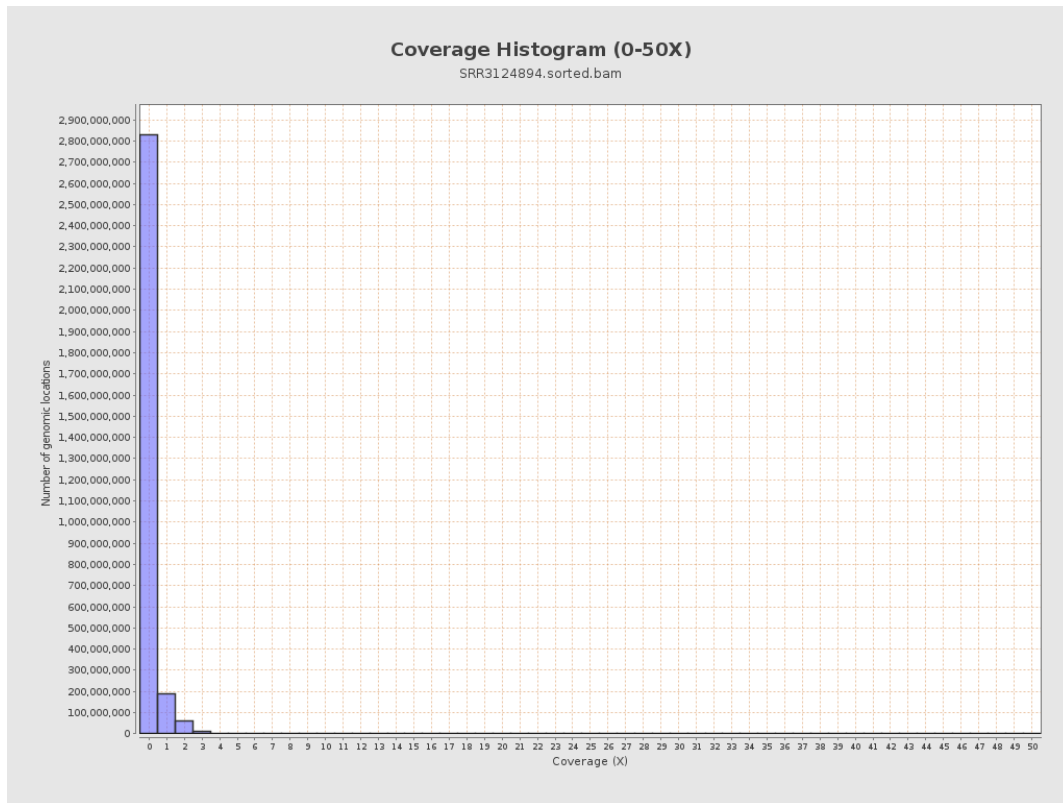
3. Results : Coverage across reference



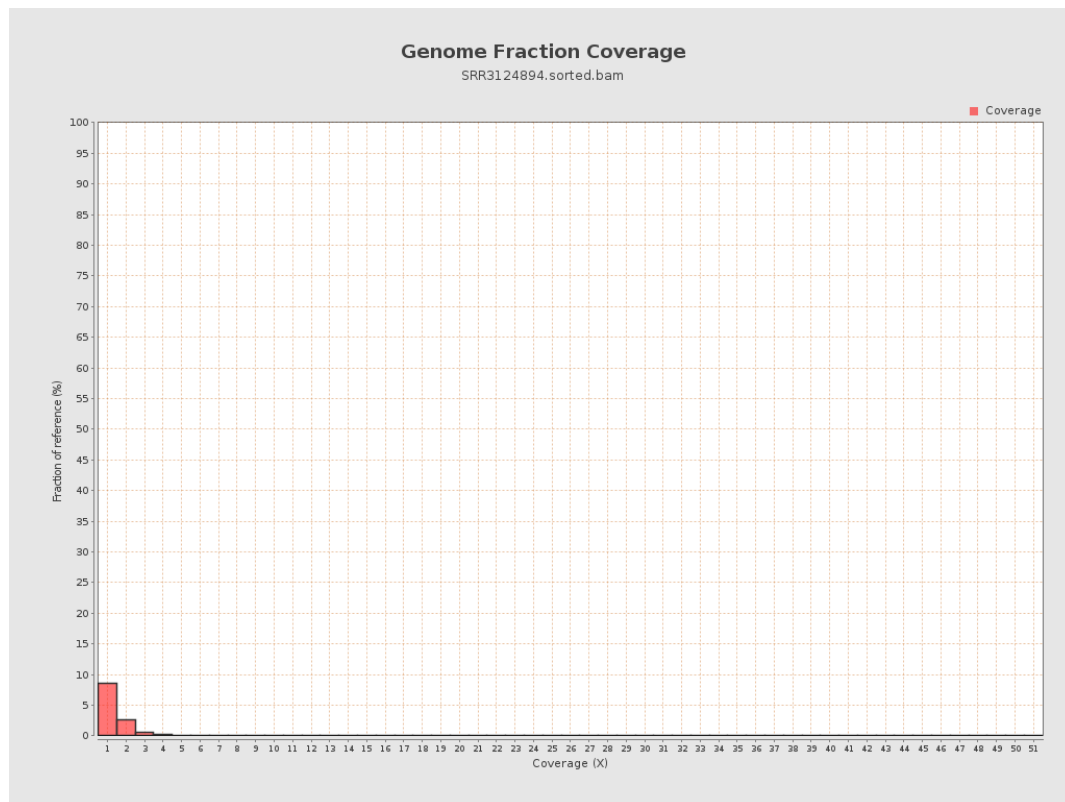
4. Results : Coverage Histogram



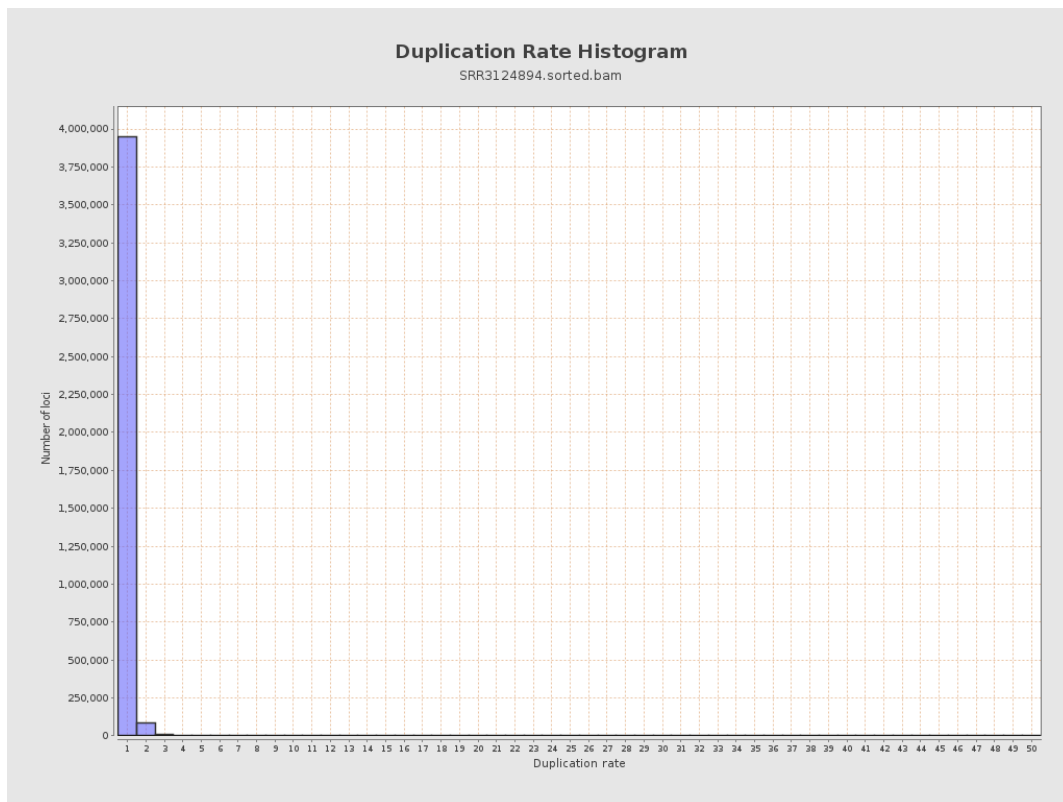
5. Results : Coverage Histogram (0-50X)



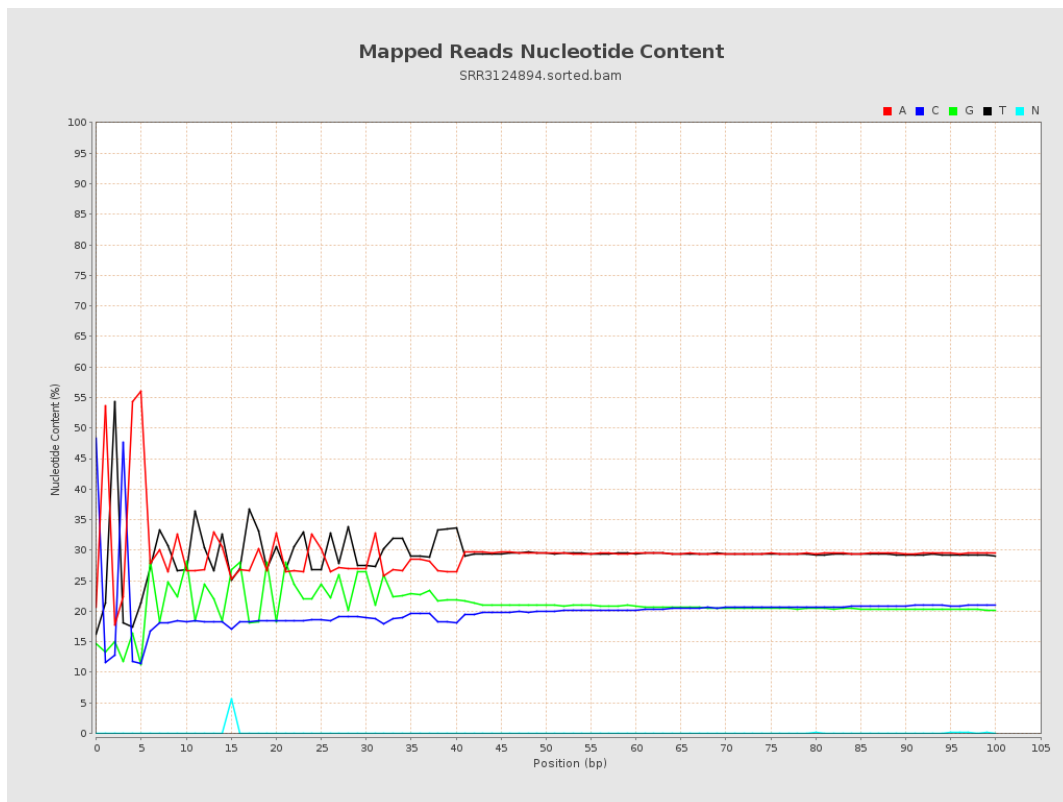
6. Results : Genome Fraction Coverage



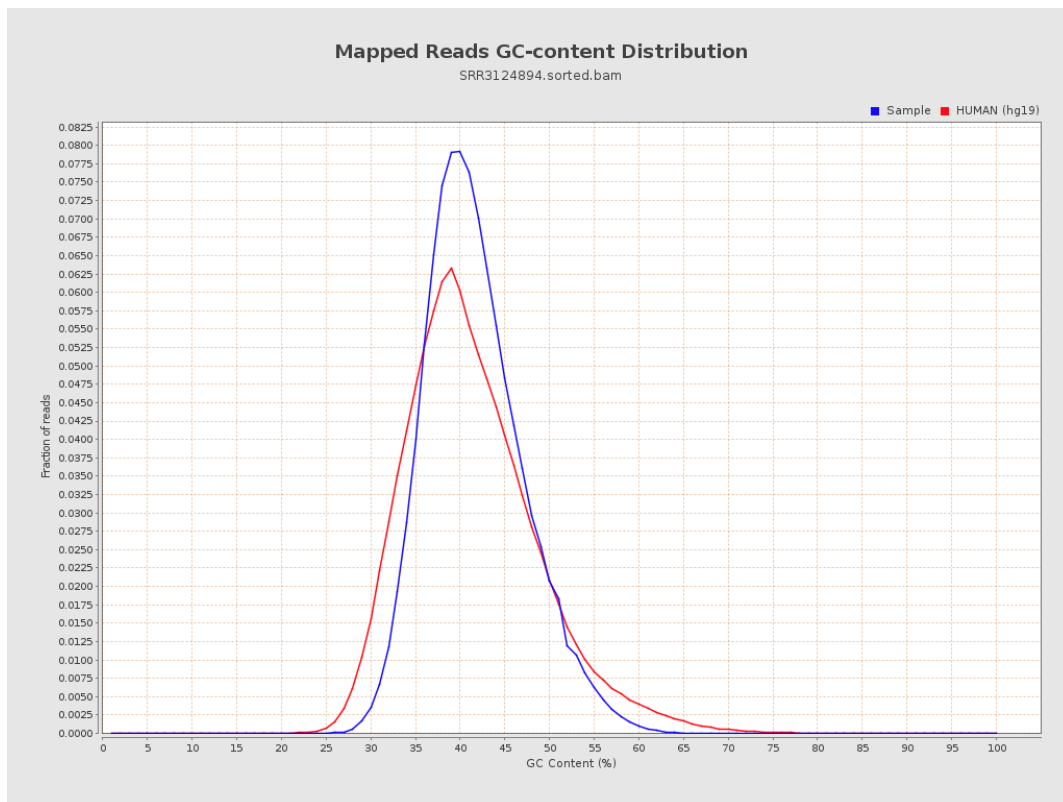
7. Results : Duplication Rate Histogram



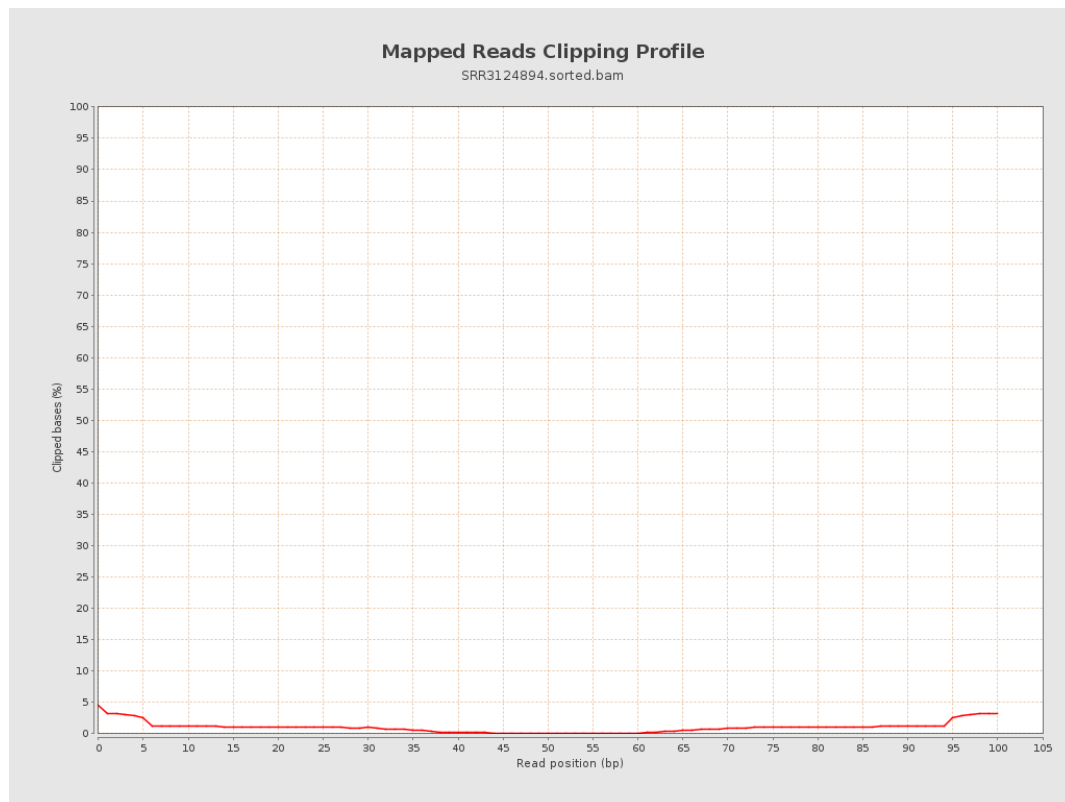
8. Results : Mapped Reads Nucleotide Content



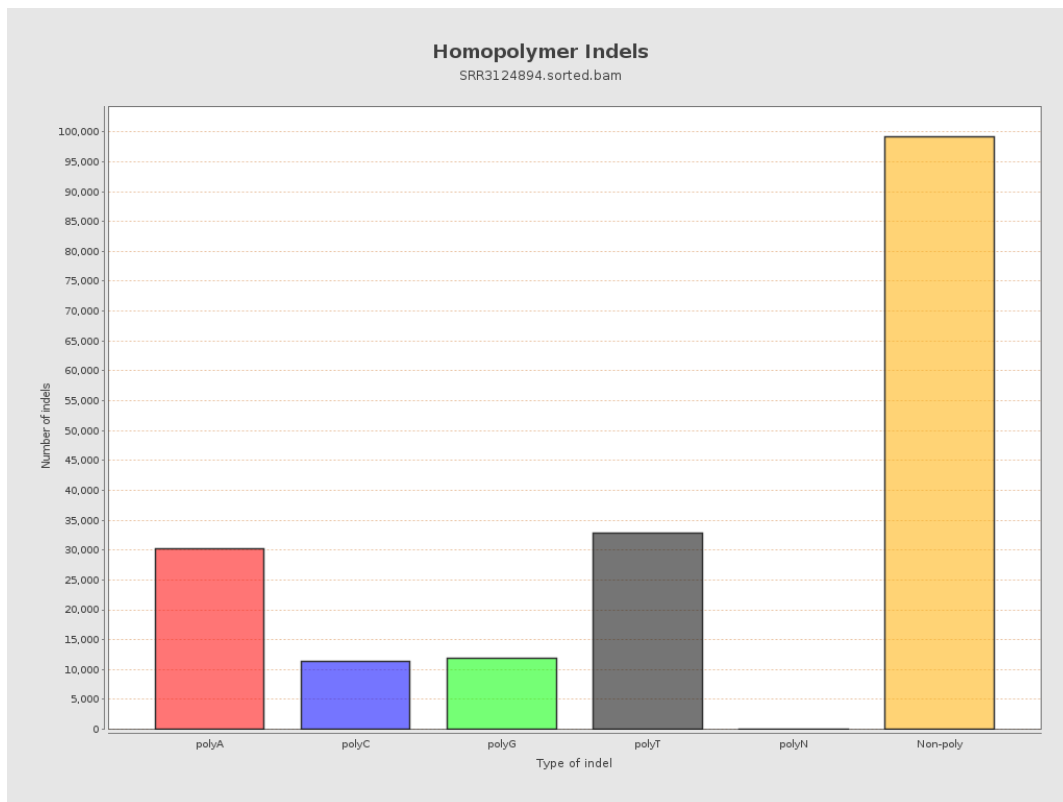
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



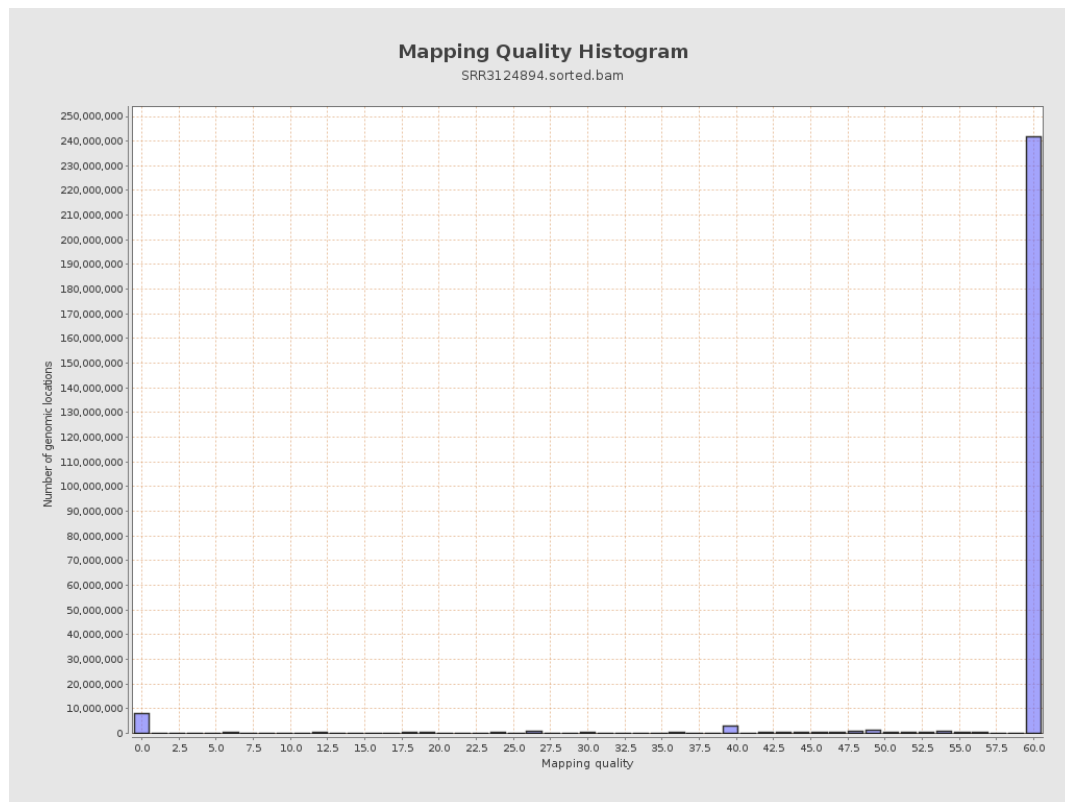
11. Results : Homopolymer Indels



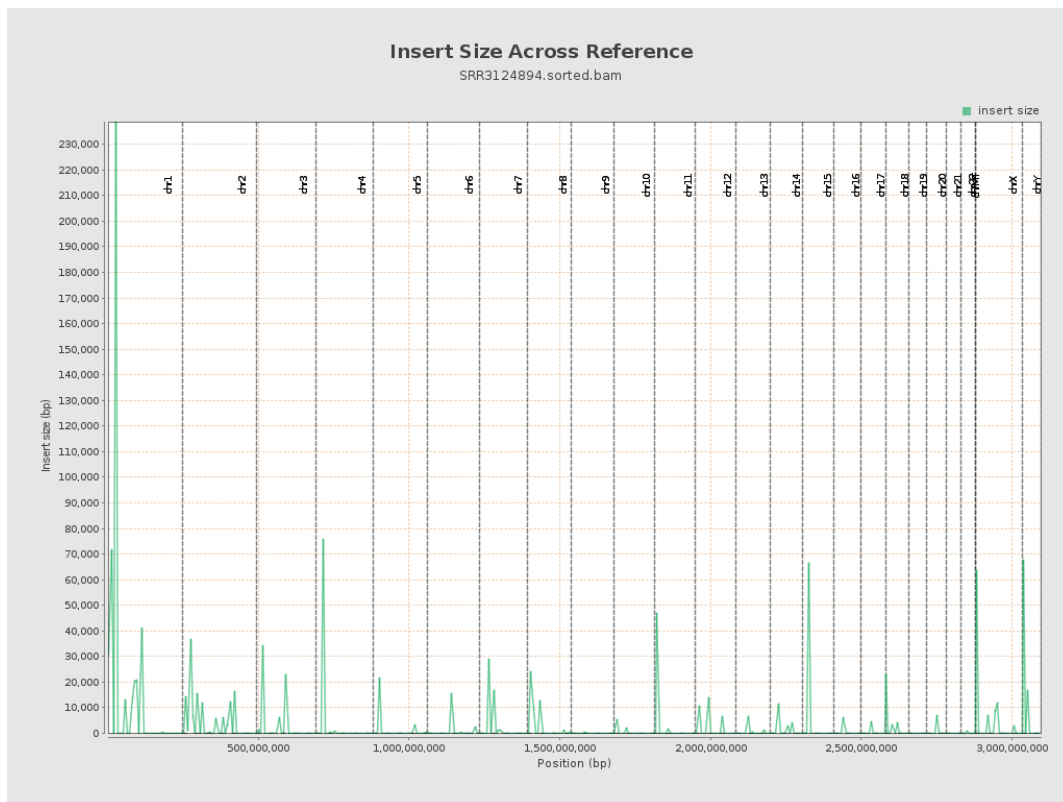
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

