

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 09:13:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124950.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_SRR3124950 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124950_1.fastq.gz SRR3124950_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 09:13:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124950.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,491,108
Mapped reads	4,438,428 / 98.83%
Unmapped reads	52,680 / 1.17%
Mapped paired reads	4,438,428 / 98.83%
Mapped reads, first in pair	2,221,089 / 49.46%
Mapped reads, second in pair	2,217,339 / 49.37%
Mapped reads, both in pair	4,421,430 / 98.45%
Mapped reads, singletons	16,998 / 0.38%
Secondary alignments	0
Supplementary alignments	22,304 / 0.5%
Read min/max/mean length	30 / 101 / 101.2
Duplicated reads (estimated)	227,181 / 5.06%
Duplication rate	2.76%
Clipped reads	2,628,969 / 58.54%

2.2. ACGT Content

Number/percentage of A's	117,244,849 / 28.92%
Number/percentage of C's	79,136,321 / 19.52%
Number/percentage of T's	119,881,477 / 29.57%
Number/percentage of G's	88,822,538 / 21.91%
Number/percentage of N's	266,869 / 0.07%

GC Percentage	41.44%
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2.3. Coverage

Mean	0.131
Standard Deviation	1.357

2.4. Mapping Quality

Mean Mapping Quality	52.79
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2.5. Insert size

Mean	89,730.86
Standard Deviation	2,827,336.96
P25/Median/P75	137 / 170 / 216

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	3,503,987
Insertions	61,367
Mapped reads with at least one insertion	1.35%
Deletions	133,888
Mapped reads with at least one deletion	2.95%
Homopolymer indels	45.98%

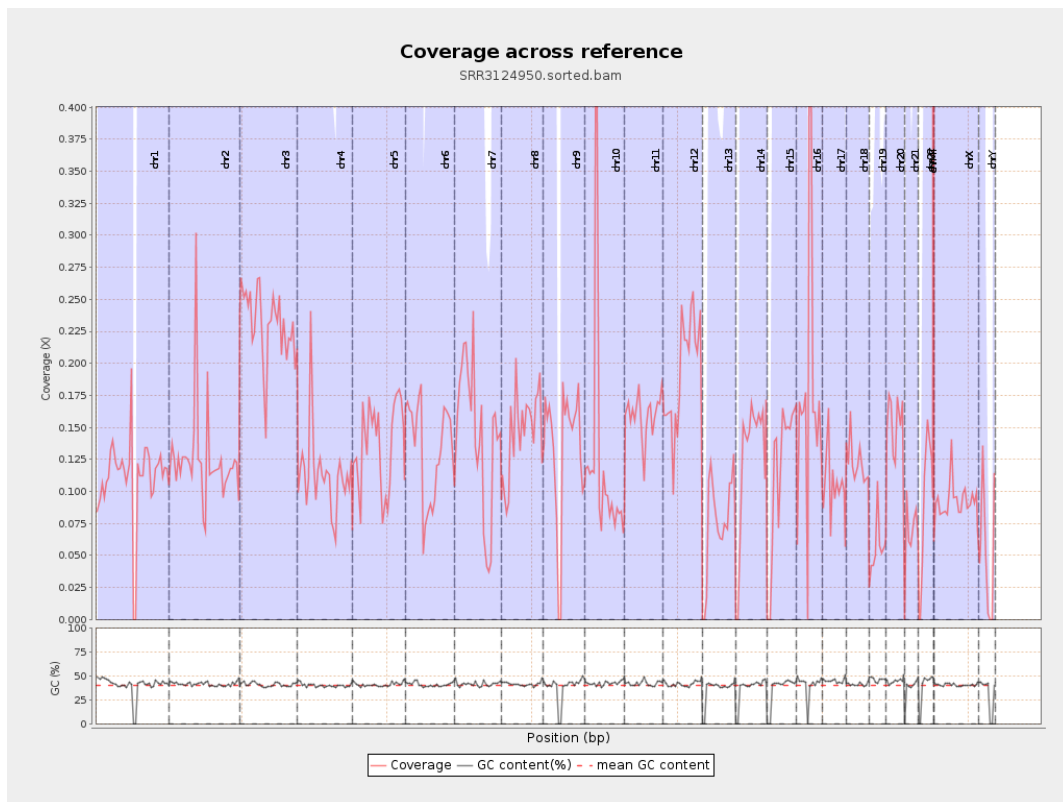
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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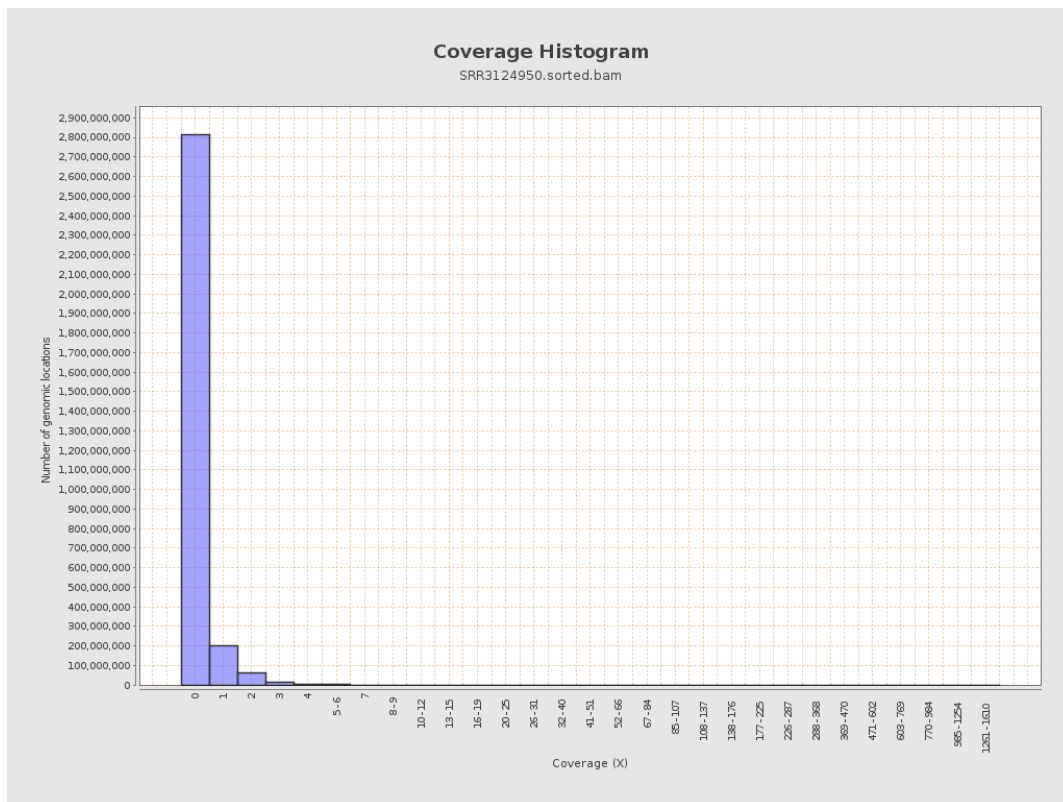
		bases	coverage	deviation
chr1	249250621	27606921	0.1108	1.256
chr2	243199373	30286547	0.1245	1.4069
chr3	198022430	45600595	0.2303	0.6554
chr4	191154276	21429495	0.1121	0.86
chr5	180915260	24595814	0.136	0.4808
chr6	171115067	22737657	0.1329	0.9261
chr7	159138663	23184882	0.1457	2.0276
chr8	146364022	21304327	0.1456	0.6543
chr9	141213431	18954159	0.1342	1.6901
chr10	135534747	16382567	0.1209	3.4126
chr11	135006516	21321940	0.1579	1.2044
chr12	133851895	25700468	0.192	0.5688
chr13	115169878	8736894	0.0759	0.3406
chr14	107349540	13395065	0.1248	0.4917
chr15	102531392	11814090	0.1152	0.4369
chr16	90354753	16266279	0.18	3.0854
chr17	81195210	8394746	0.1034	1.1005
chr18	78077248	9586973	0.1228	1.6656
chr19	59128983	3379430	0.0572	0.8392
chr20	63025520	9533063	0.1513	0.5297
chr21	48129895	3269836	0.0679	0.5221
chr22	51304566	4668370	0.091	0.4088
chrMT	16571	41908	2.529	2.4479
chrX	155270560	14353377	0.0924	0.5945

chrY	59373566	3032199	0.0511	1.2879
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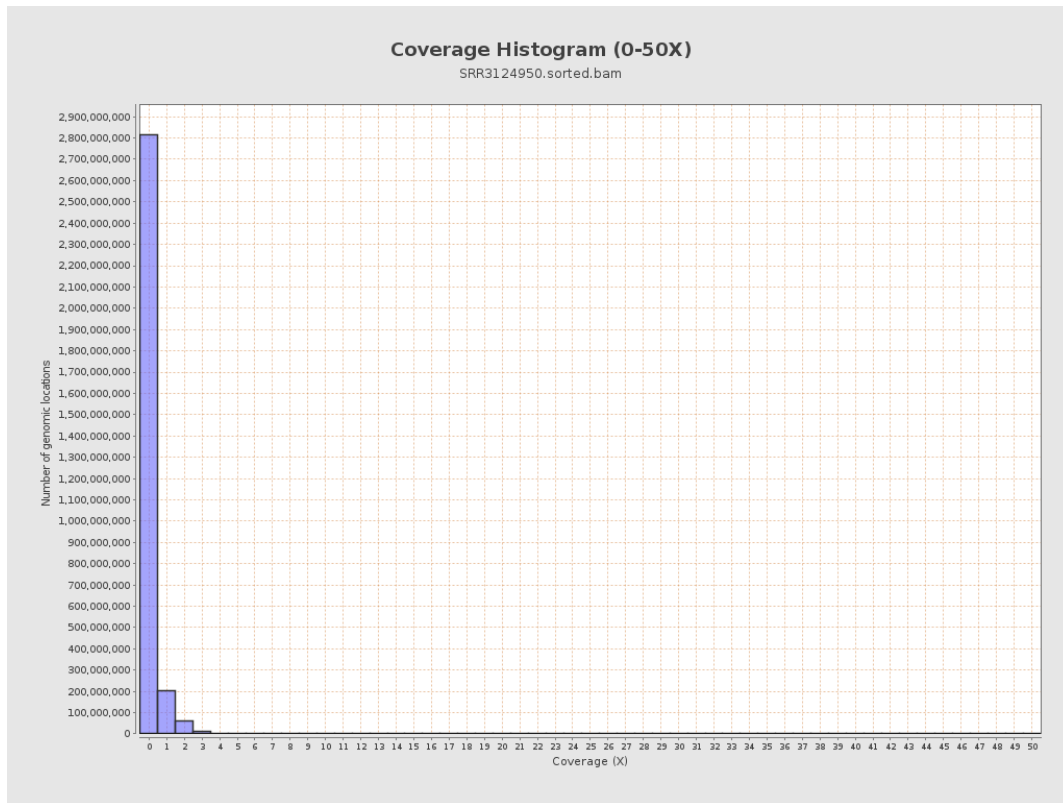
3. Results : Coverage across reference



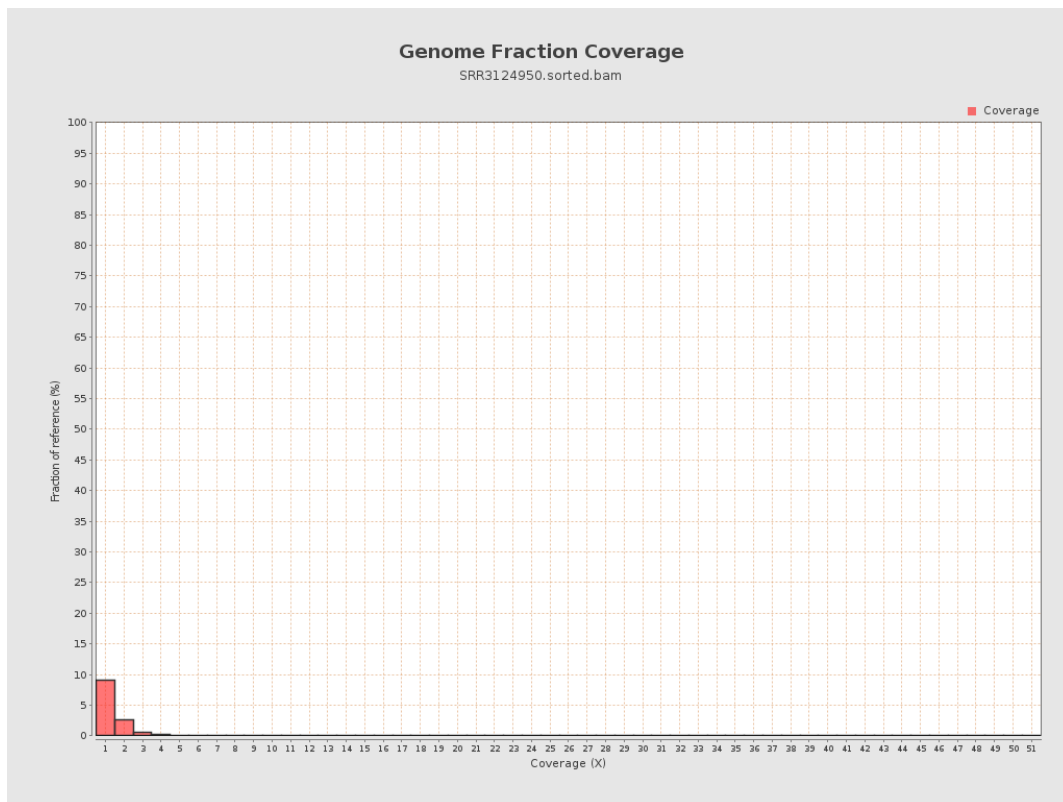
4. Results : Coverage Histogram



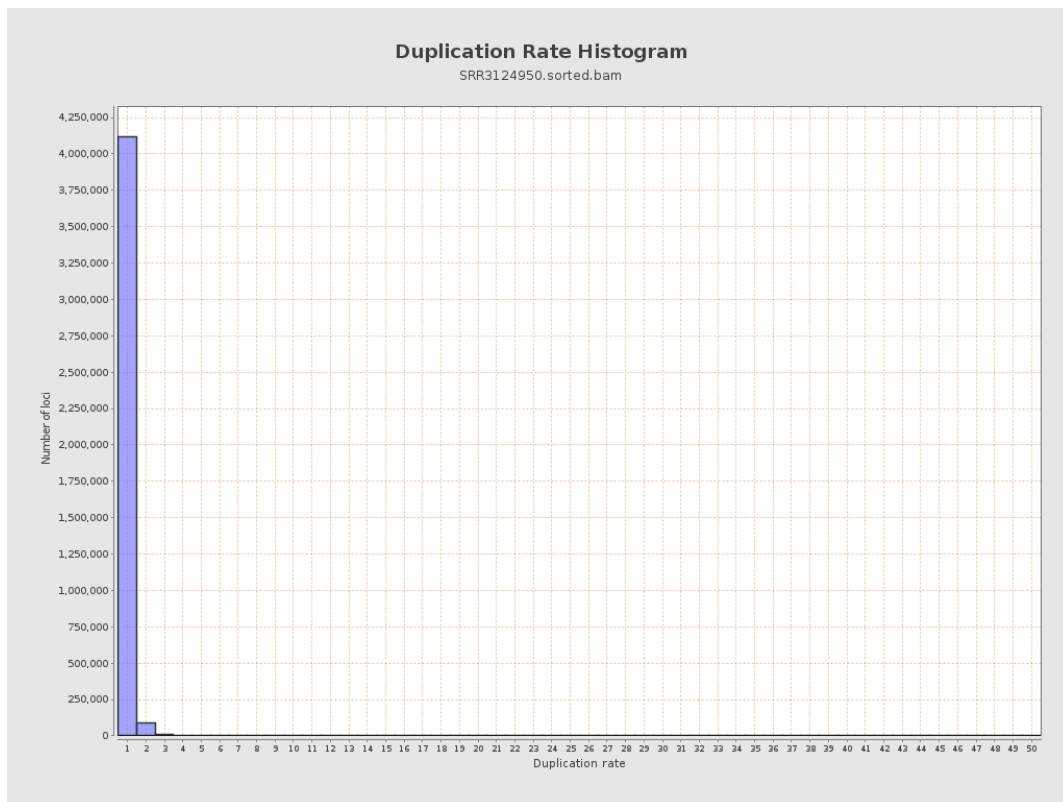
5. Results : Coverage Histogram (0-50X)



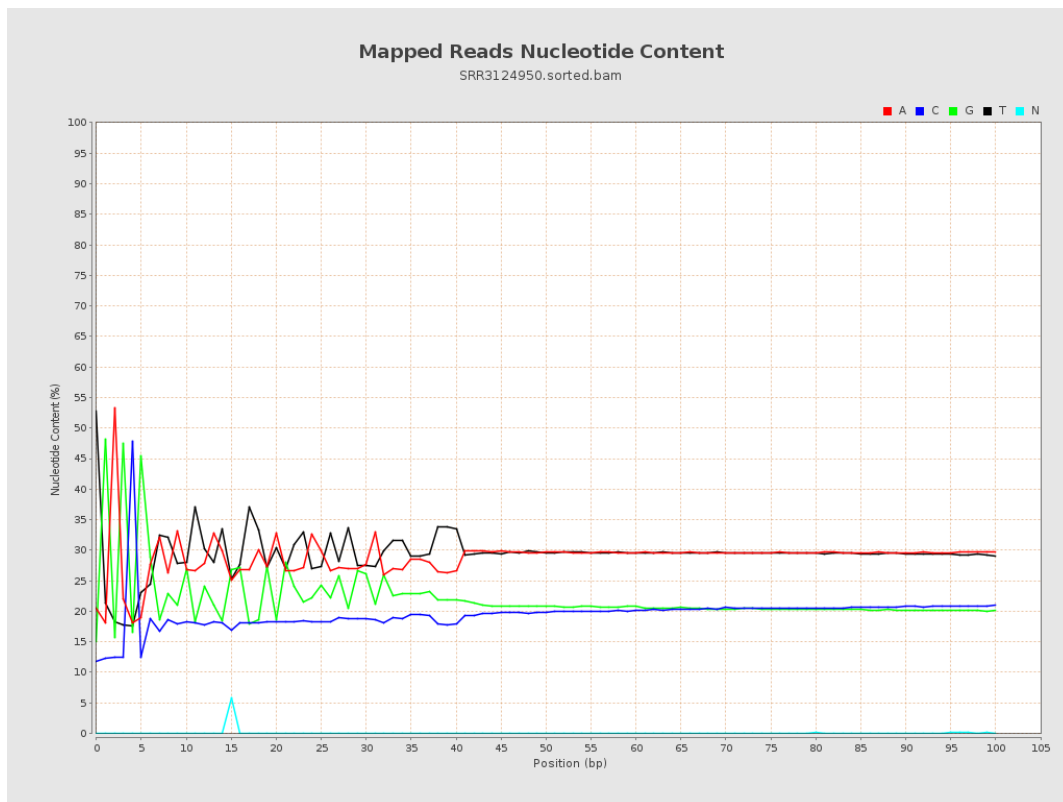
6. Results : Genome Fraction Coverage



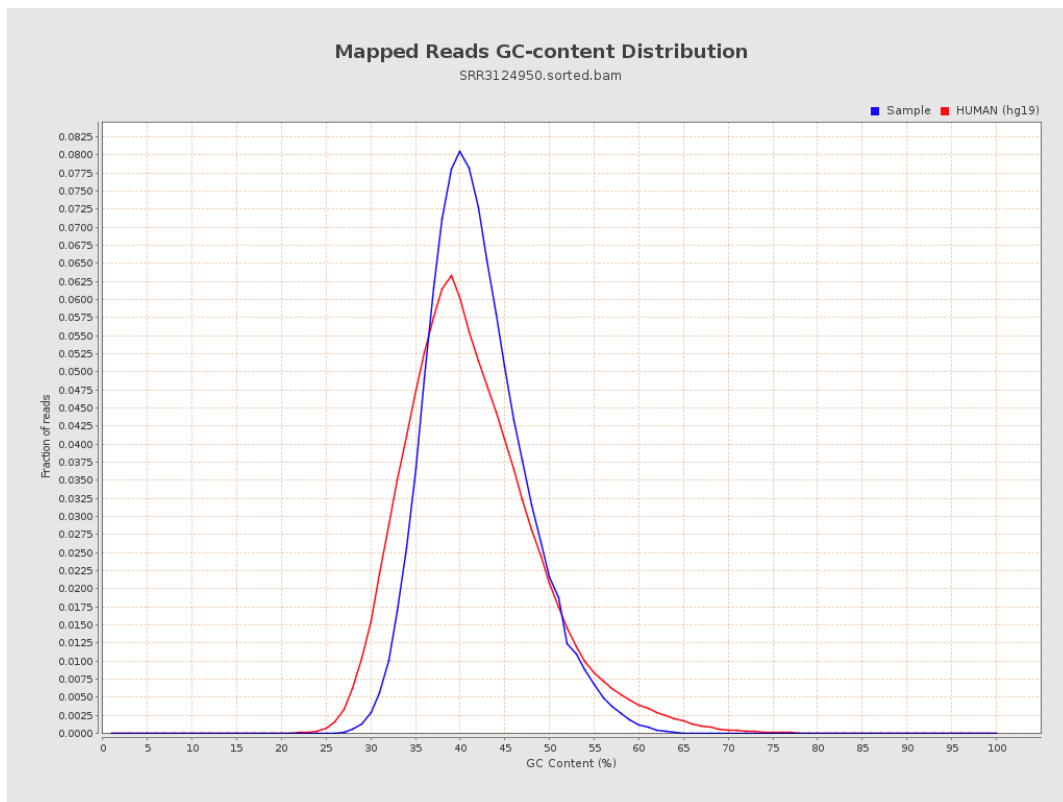
7. Results : Duplication Rate Histogram



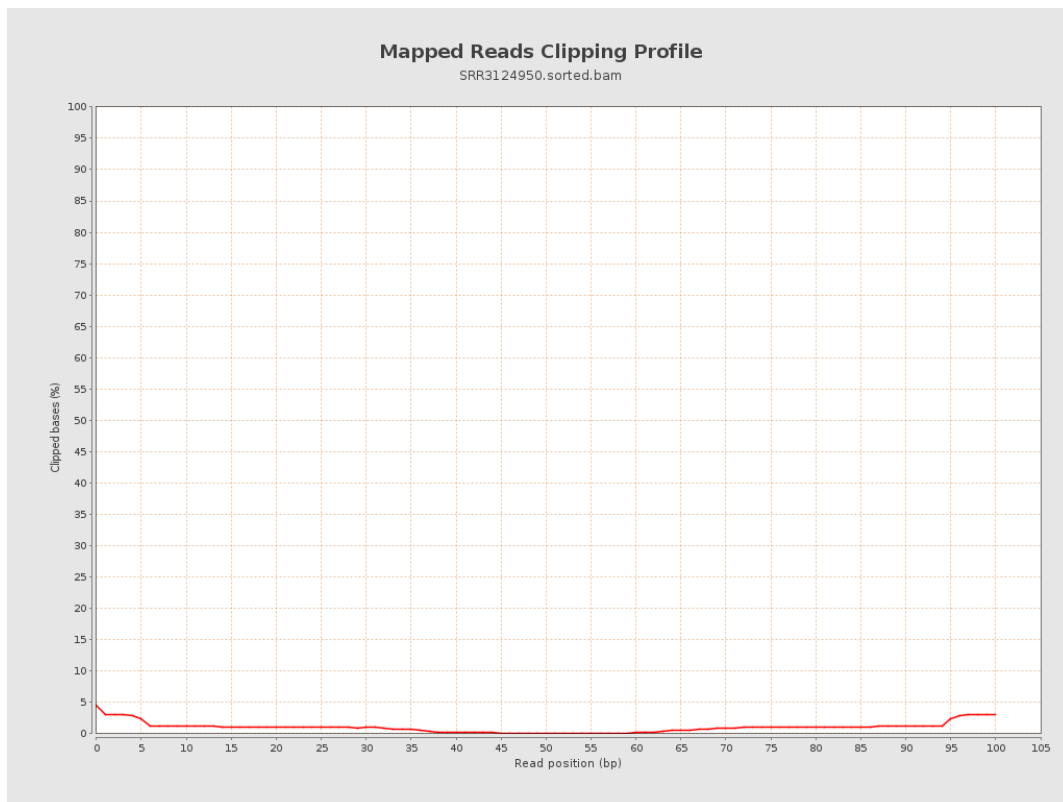
8. Results : Mapped Reads Nucleotide Content



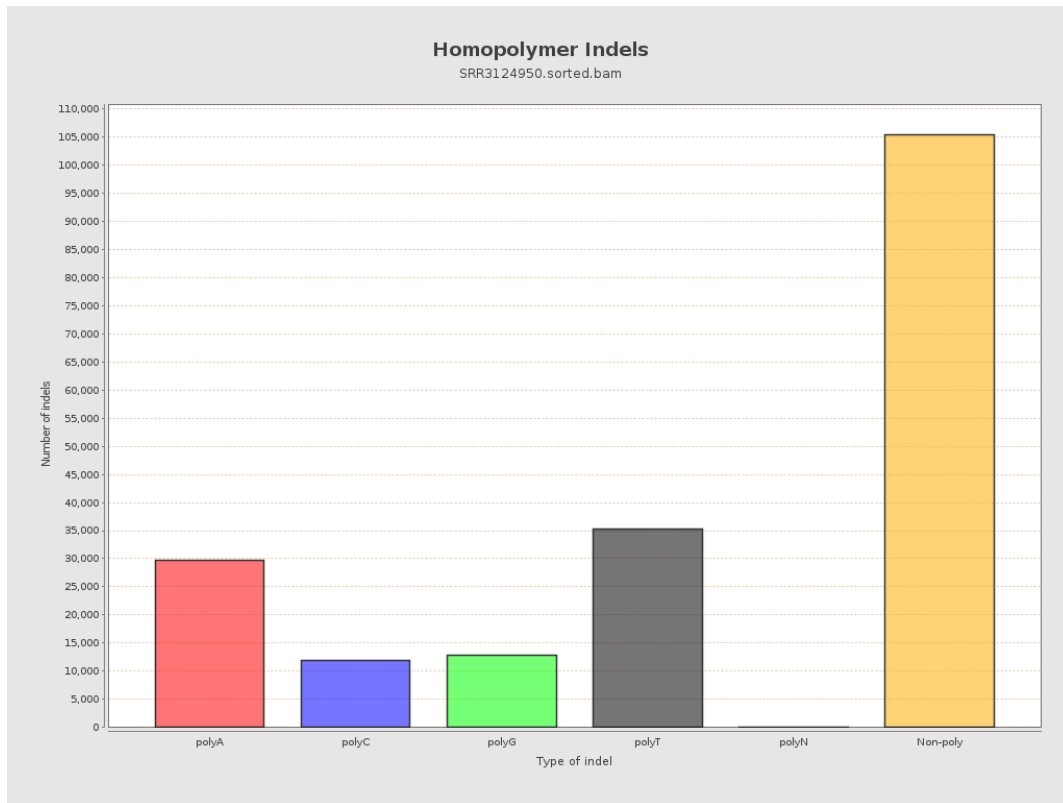
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



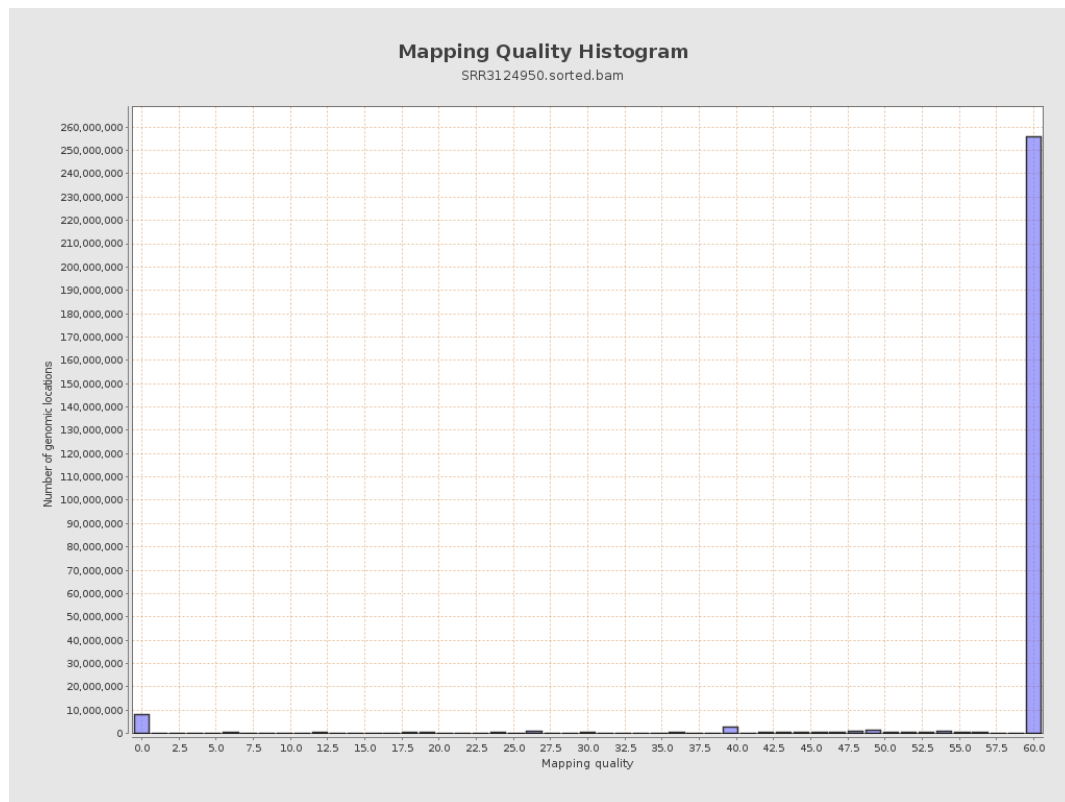
11. Results : Homopolymer Indels



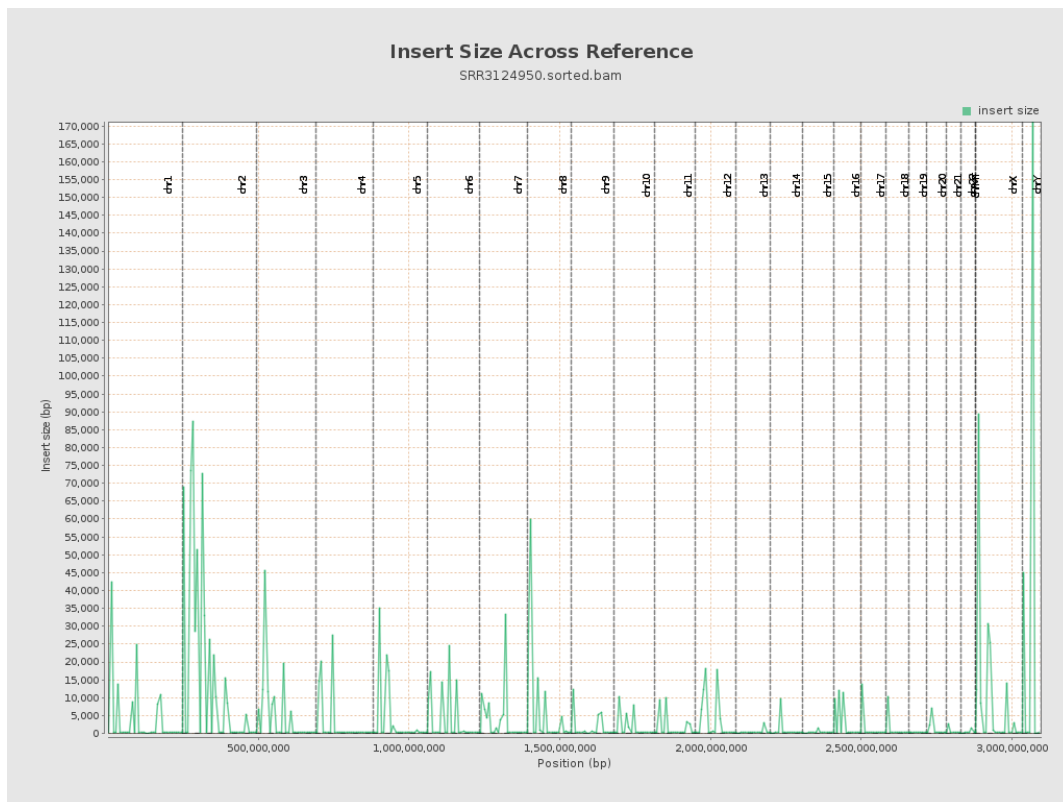
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

