

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 06:18:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124926.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_SRR3124926 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124926_1.fastq.gz SRR3124926_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 06:18:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,213,594
Mapped reads	6,137,419 / 98.77%
Unmapped reads	76,175 / 1.23%
Mapped paired reads	6,137,419 / 98.77%
Mapped reads, first in pair	3,070,932 / 49.42%
Mapped reads, second in pair	3,066,487 / 49.35%
Mapped reads, both in pair	6,113,650 / 98.39%
Mapped reads, singletons	23,769 / 0.38%
Secondary alignments	0
Supplementary alignments	35,196 / 0.57%
Read min/max/mean length	30 / 101 / 101.23
Duplicated reads (estimated)	404,264 / 6.51%
Duplication rate	3.28%
Clipped reads	3,640,112 / 58.58%

2.2. ACGT Content

Number/percentage of A's	163,278,304 / 29.05%
Number/percentage of C's	109,852,185 / 19.54%
Number/percentage of T's	169,226,418 / 30.1%
Number/percentage of G's	119,780,529 / 21.31%
Number/percentage of N's	9,797 / 0%

GC Percentage	40.85%
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2.3. Coverage

Mean	0.1817
Standard Deviation	2.2441

2.4. Mapping Quality

Mean Mapping Quality	52.54
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2.5. Insert size

Mean	80,438.04
Standard Deviation	2,736,882.99
P25/Median/P75	134 / 165 / 208

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	4,439,204
Insertions	97,527
Mapped reads with at least one insertion	1.56%
Deletions	187,974
Mapped reads with at least one deletion	3%
Homopolymer indels	45.57%

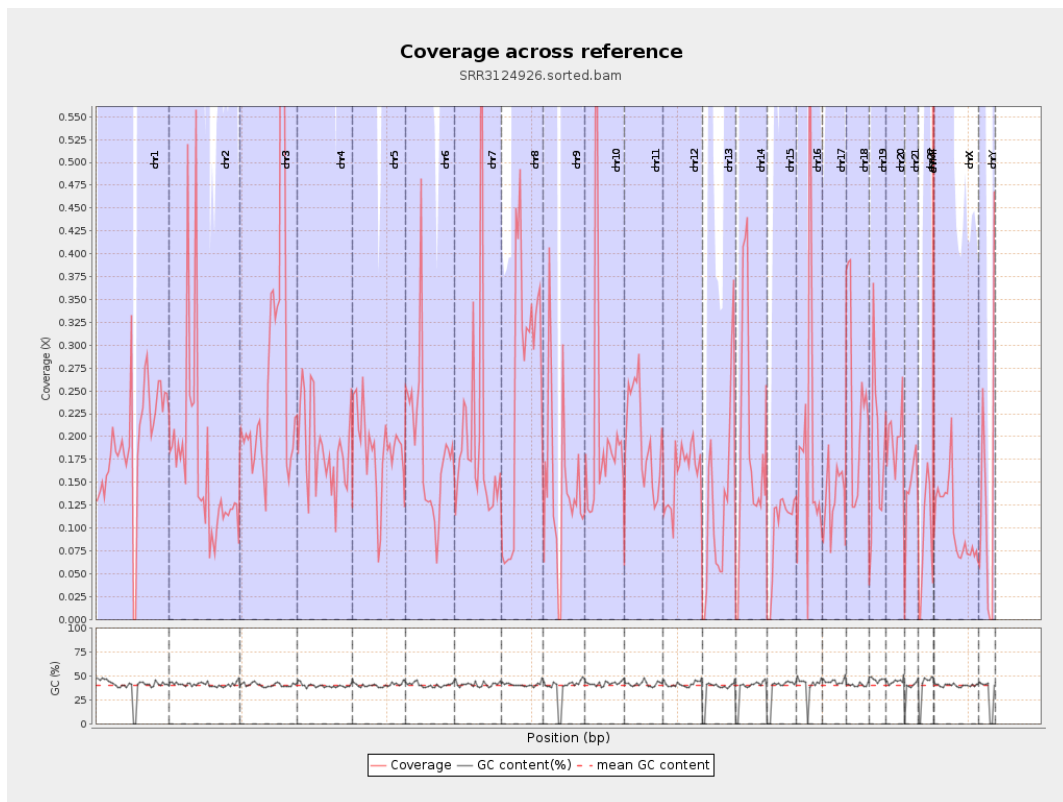
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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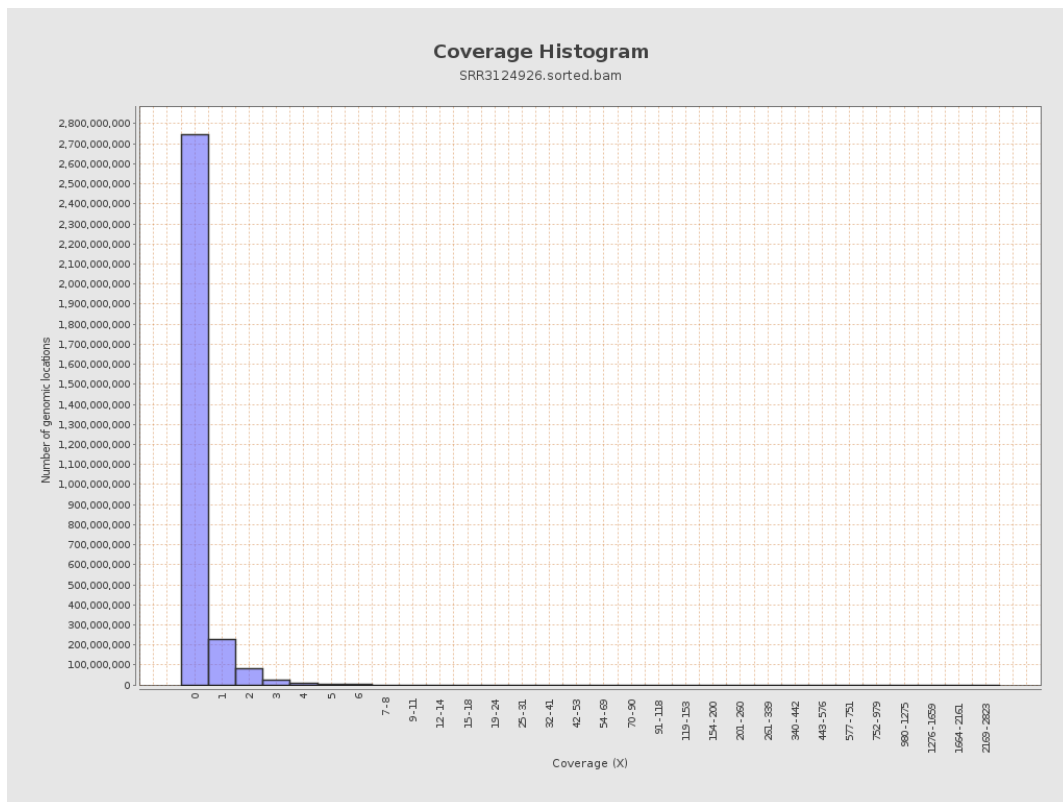
		bases	coverage	deviation
chr1	249250621	48318599	0.1939	2.6209
chr2	243199373	41801726	0.1719	2.3677
chr3	198022430	54715478	0.2763	0.872
chr4	191154276	35707616	0.1868	1.0966
chr5	180915260	33483354	0.1851	0.5963
chr6	171115067	32122716	0.1877	2.6435
chr7	159138663	32303067	0.203	2.8657
chr8	146364022	37718454	0.2577	0.9703
chr9	141213431	21075325	0.1492	3.2808
chr10	135534747	27327861	0.2016	5.4469
chr11	135006516	26467885	0.196	1.858
chr12	133851895	21294635	0.1591	0.5389
chr13	115169878	14738147	0.128	0.4877
chr14	107349540	20029452	0.1866	0.7109
chr15	102531392	10089877	0.0984	0.4148
chr16	90354753	16821155	0.1862	3.6718
chr17	81195210	10730580	0.1322	1.4948
chr18	78077248	18727295	0.2399	3.6602
chr19	59128983	11098051	0.1877	1.5462
chr20	63025520	12425159	0.1971	0.6586
chr21	48129895	6739142	0.14	0.6755
chr22	51304566	4478806	0.0873	0.4144
chrMT	16571	147210	8.8836	6.082
chrX	155270560	16433486	0.1058	0.8788

chrY	59373566	7672679	0.1292	2.9318
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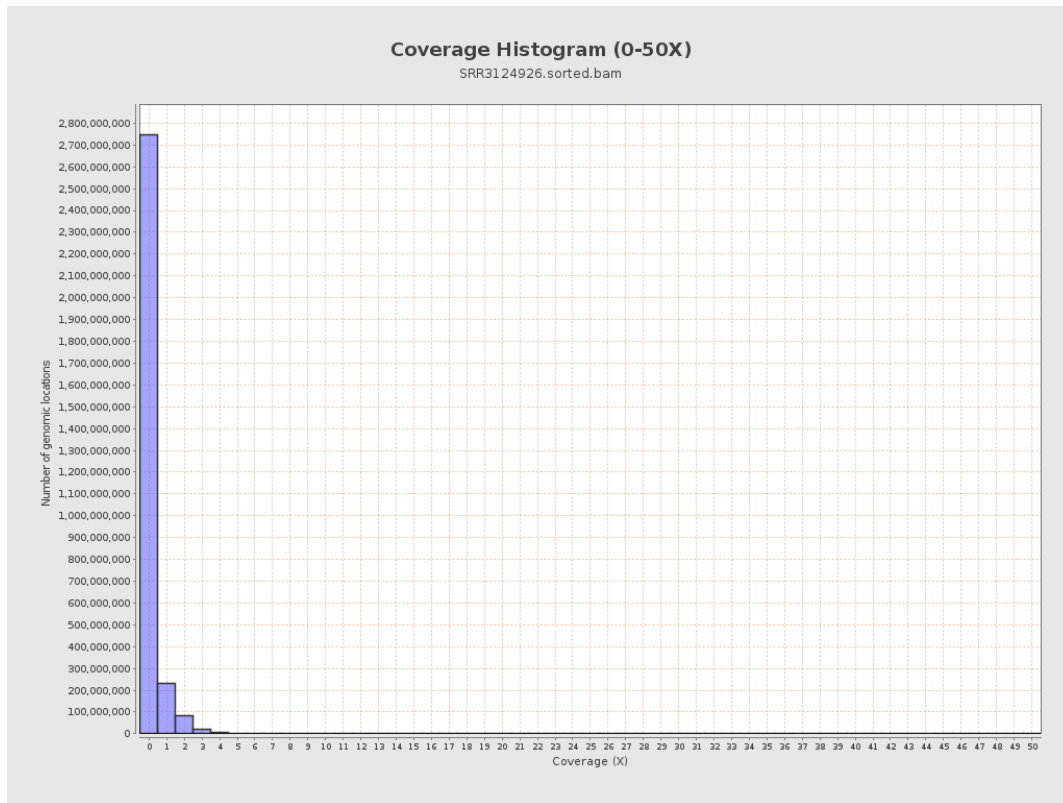
3. Results : Coverage across reference



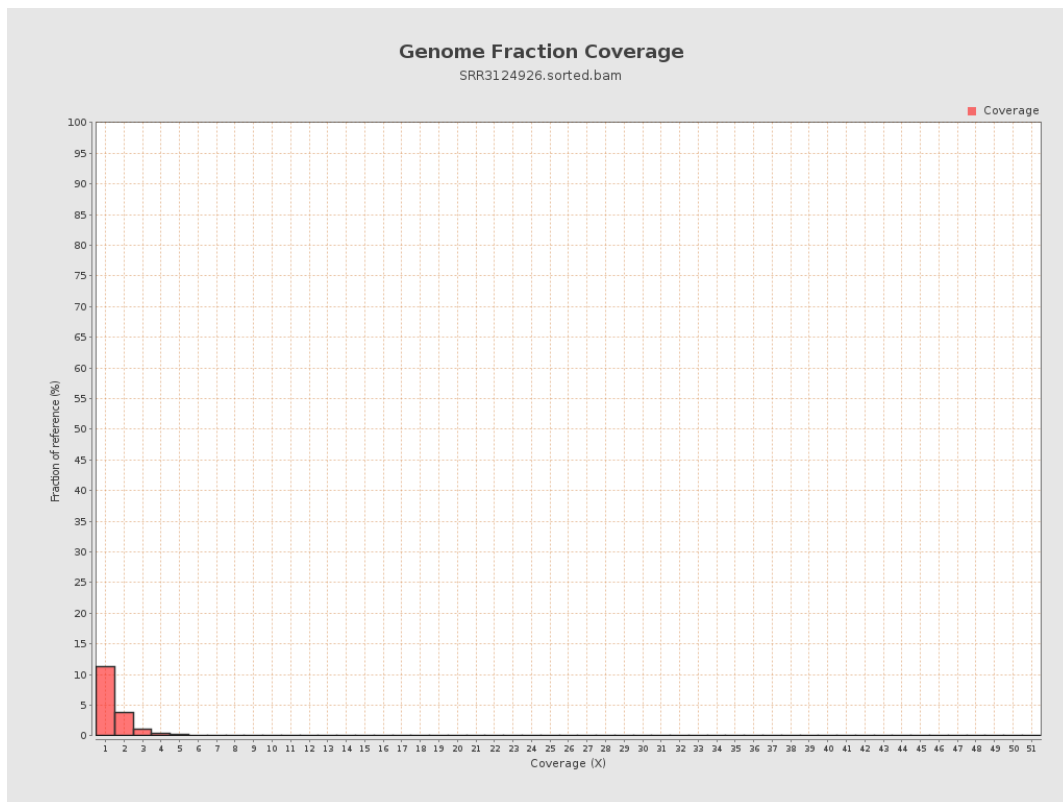
4. Results : Coverage Histogram



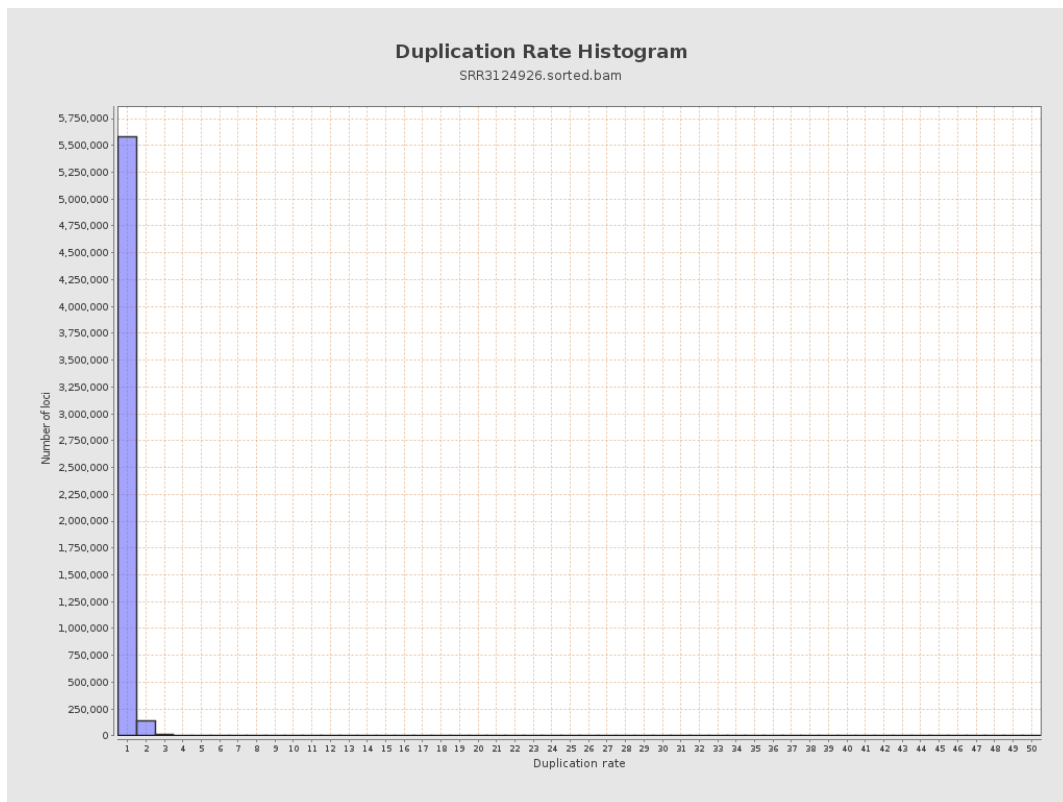
5. Results : Coverage Histogram (0-50X)



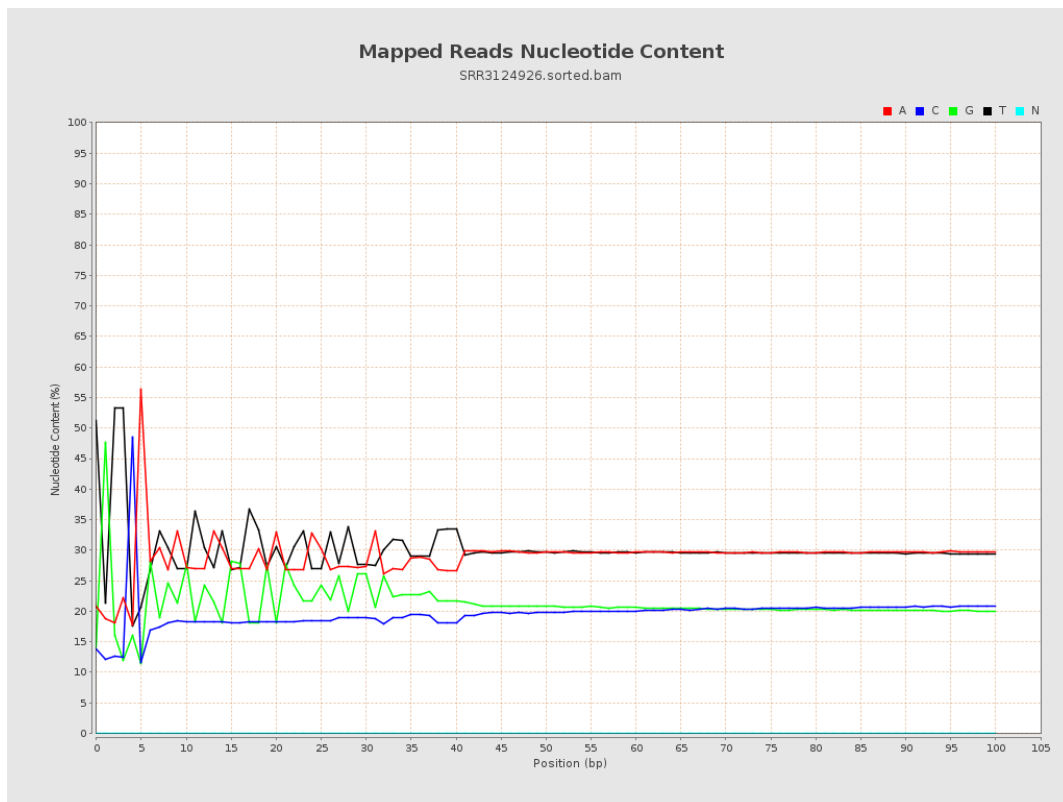
6. Results : Genome Fraction Coverage



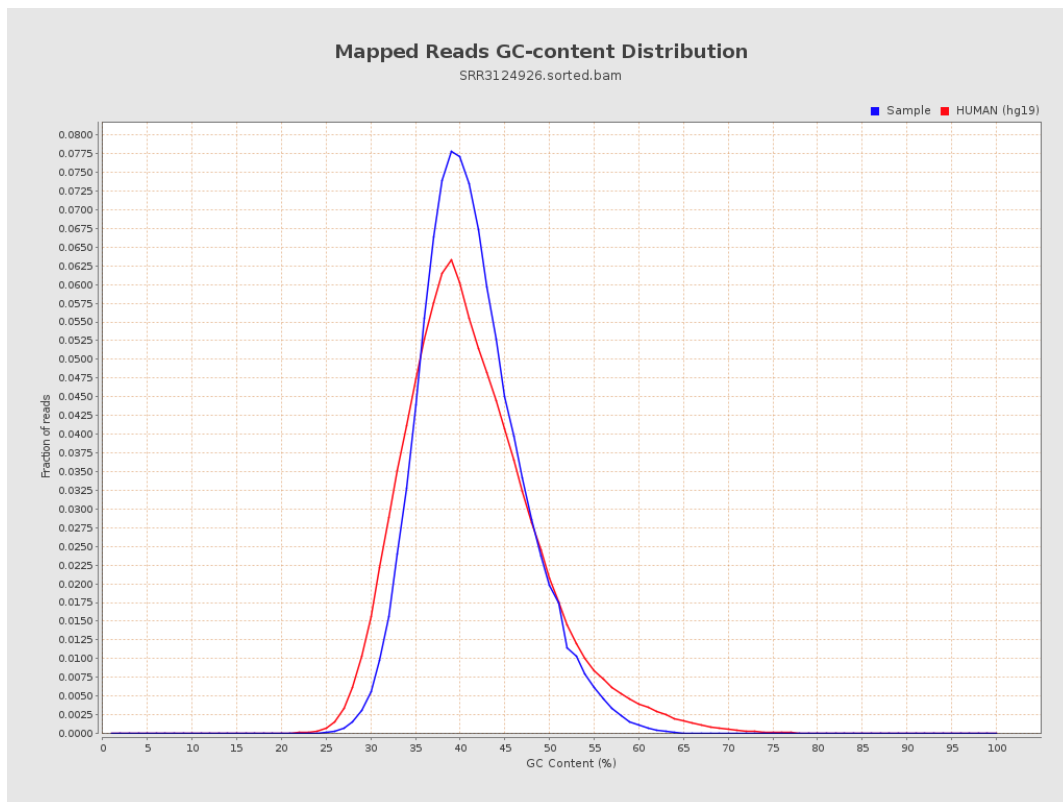
7. Results : Duplication Rate Histogram



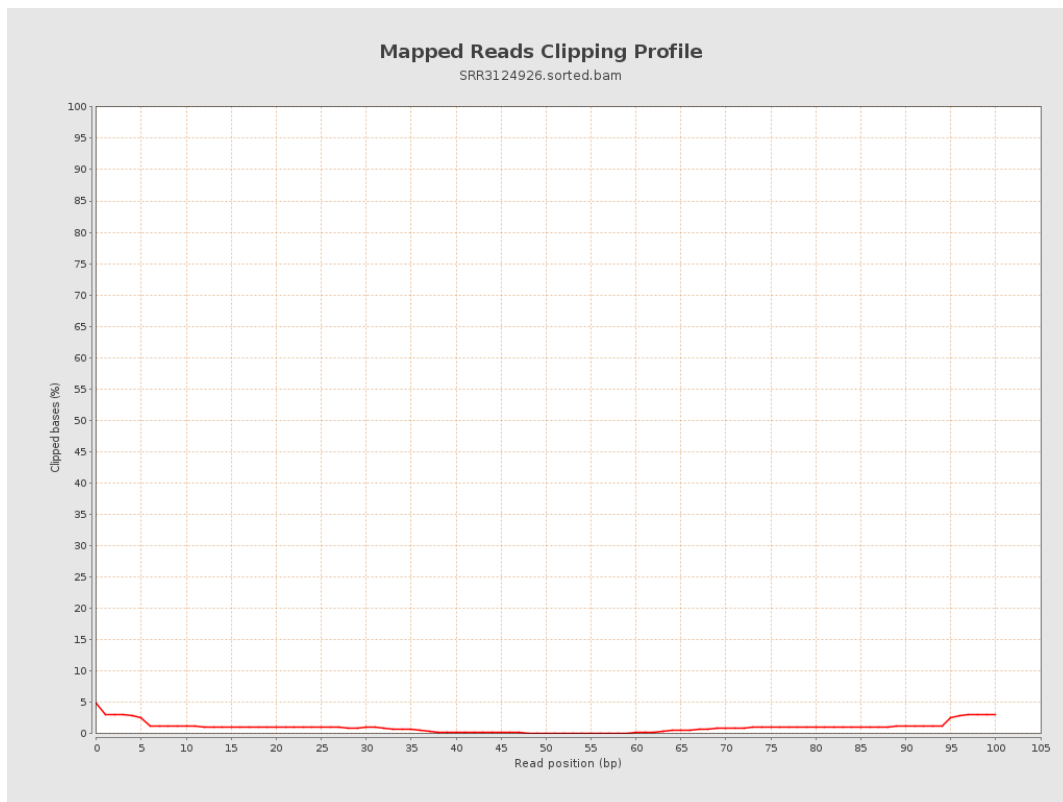
8. Results : Mapped Reads Nucleotide Content



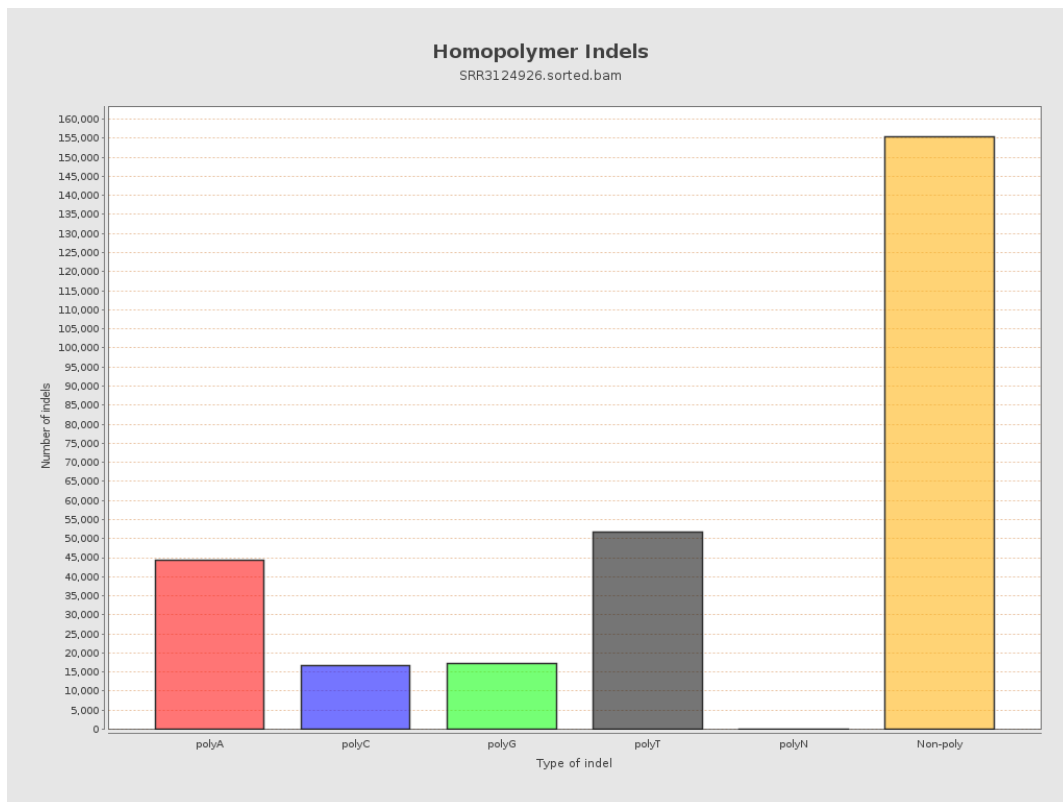
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



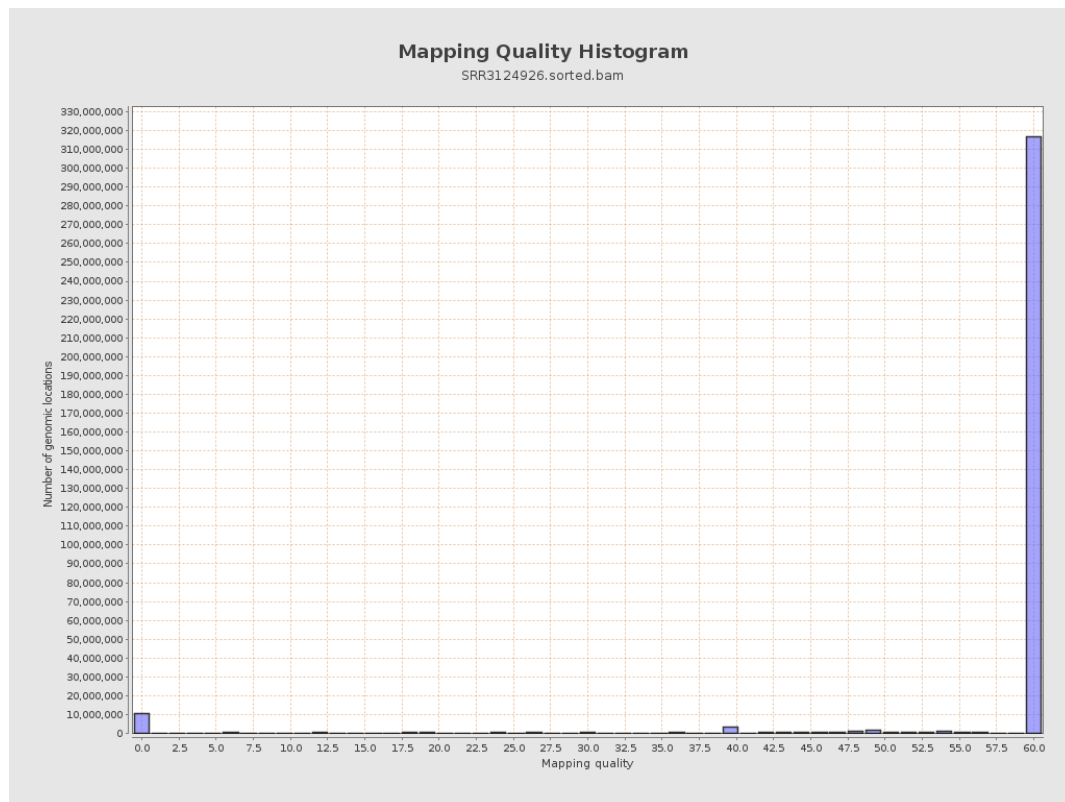
11. Results : Homopolymer Indels



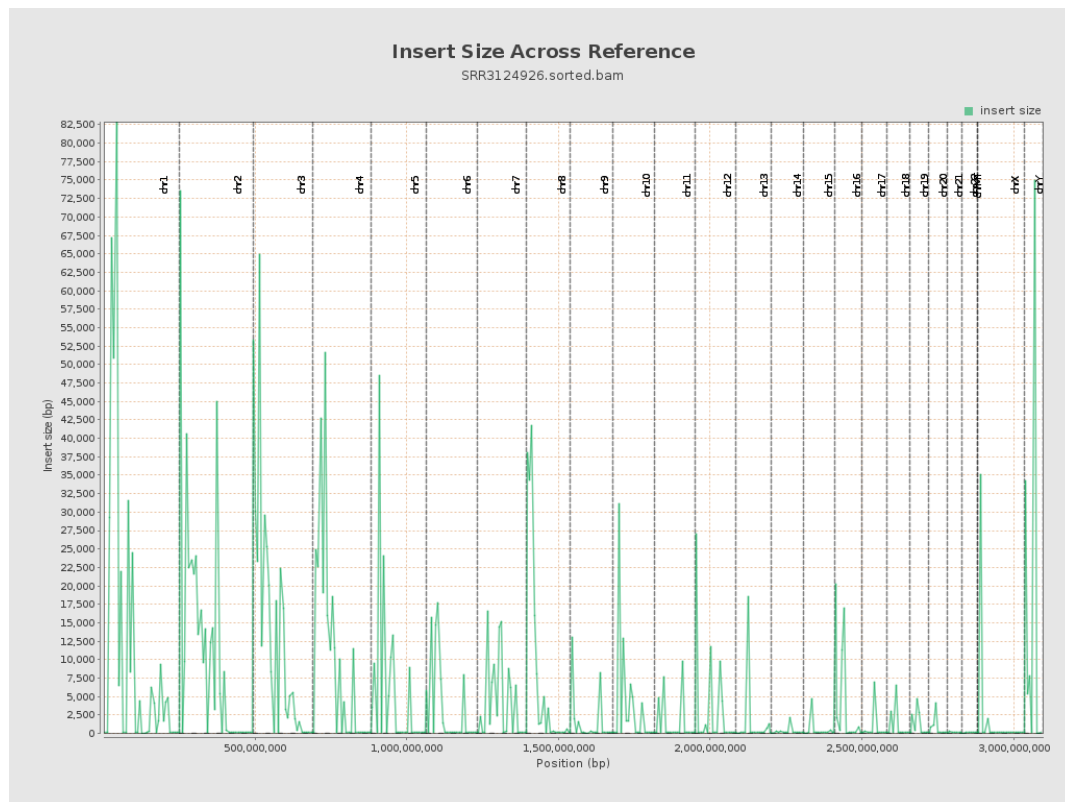
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

