

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 19:55:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695919.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/s oftware/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\t PL:ILLUMINA\tSM:sample_SRR1695 919 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695919_1.fastq.gz SRR1695919_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 19:55:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	106,940,708
Mapped reads	106,290,261 / 99.39%
Unmapped reads	650,447 / 0.61%
Mapped paired reads	106,290,261 / 99.39%
Mapped reads, first in pair	53,305,103 / 49.85%
Mapped reads, second in pair	52,985,158 / 49.55%
Mapped reads, both in pair	105,844,242 / 98.97%
Mapped reads, singletons	446,019 / 0.42%
Secondary alignments	0
Supplementary alignments	1,361,499 / 1.27%
Read min/max/mean length	30 / 100 / 100.52
Duplicated reads (estimated)	5,089,603 / 4.76%
Duplication rate	4.27%
Clipped reads	7,986,480 / 7.47%

2.2. ACGT Content

Number/percentage of A's	3,131,999,626 / 29.7%
Number/percentage of C's	2,110,579,616 / 20.01%
Number/percentage of T's	3,112,071,958 / 29.51%
Number/percentage of G's	2,176,036,064 / 20.64%
Number/percentage of N's	14,638,419 / 0.14%

GC Percentage	40.65%
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2.3. Coverage

Mean	3.4072
Standard Deviation	4.526

2.4. Mapping Quality

Mean Mapping Quality	53.85
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2.5. Insert size

Mean	82,096.47
Standard Deviation	2,735,353.76
P25/Median/P75	317 / 325 / 333

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	68,748,201
Insertions	1,055,608
Mapped reads with at least one insertion	0.98%
Deletions	1,022,878
Mapped reads with at least one deletion	0.94%
Homopolymer indels	45.88%

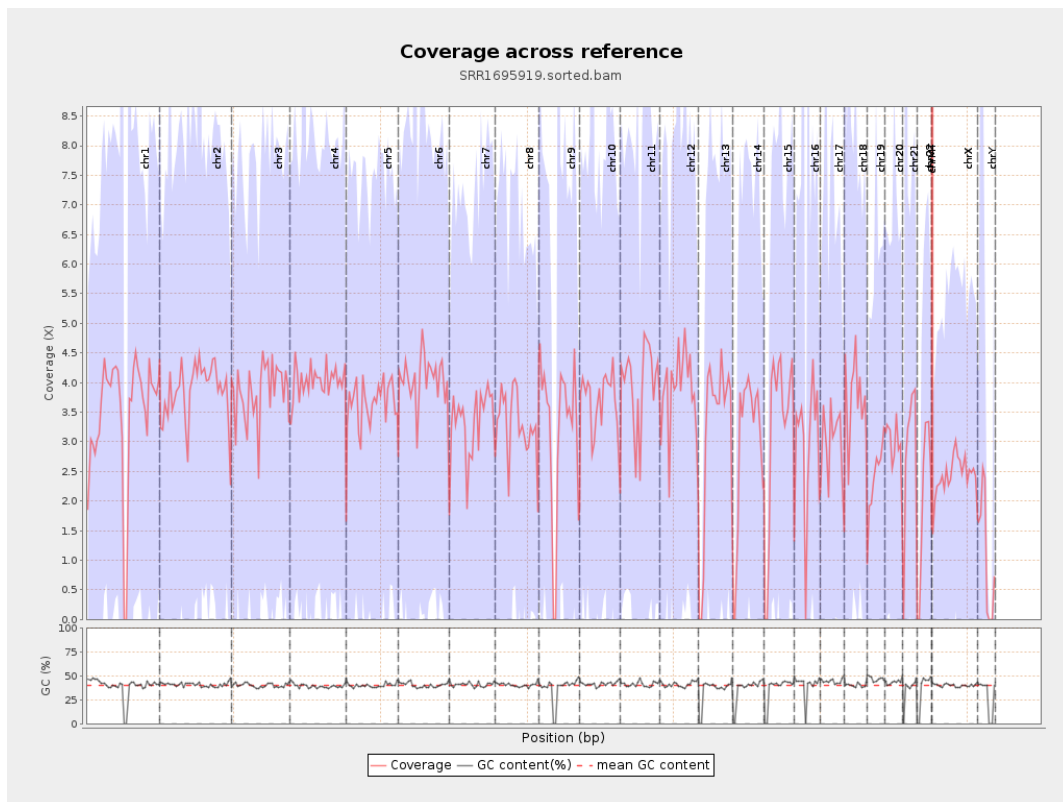
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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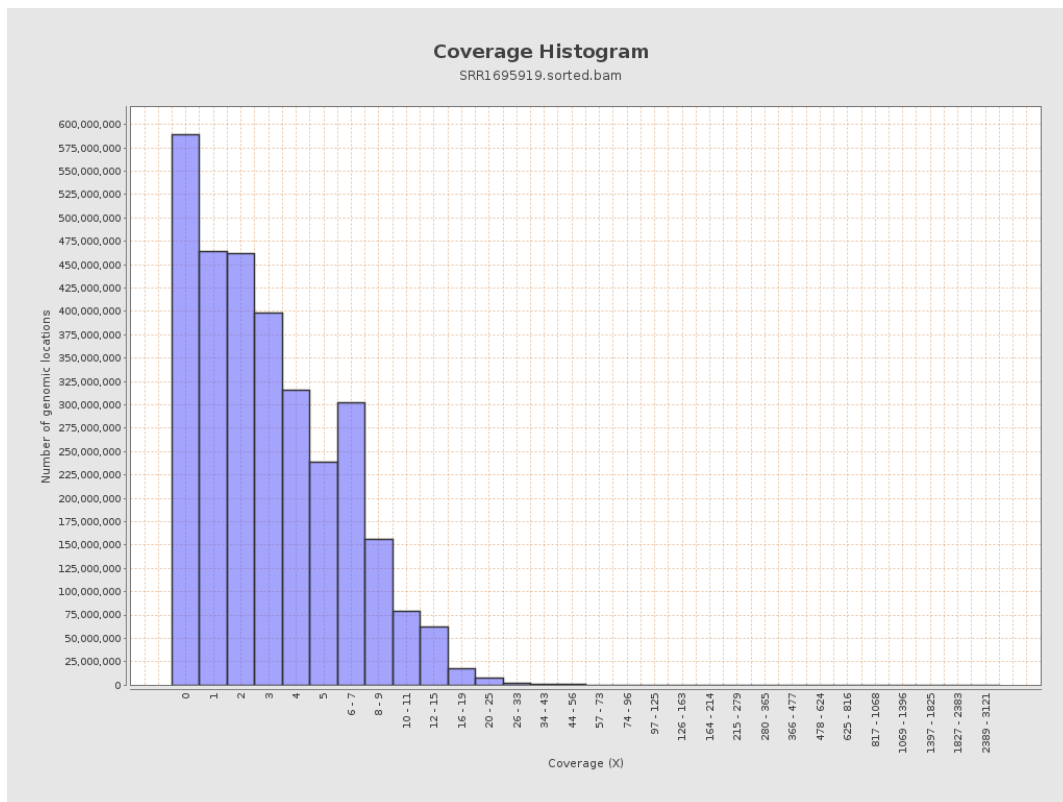
		bases	coverage	deviation
chr1	249250621	869062309	3.4867	4.6691
chr2	243199373	936923031	3.8525	5.2411
chr3	198022430	760979389	3.8429	3.4911
chr4	191154276	771111554	4.034	4.4621
chr5	180915260	661271778	3.6551	3.3243
chr6	171115067	695924552	4.067	4.0946
chr7	159138663	530474186	3.3334	3.4258
chr8	146364022	483016426	3.3001	3.2468
chr9	141213431	445948849	3.158	4.0919
chr10	135534747	501465912	3.6999	5.0855
chr11	135006516	535411512	3.9658	3.955
chr12	133851895	515631609	3.8523	3.7151
chr13	115169878	368287333	3.1978	3.4886
chr14	107349540	317966938	2.962	3.4104
chr15	102531392	329426998	3.2129	3.7032
chr16	90354753	259584551	2.8729	5.1414
chr17	81195210	239497313	2.9496	4.019
chr18	78077248	293976746	3.7652	4.8534
chr19	59128983	143136653	2.4208	3.4736
chr20	63025520	185051609	2.9361	3.5505
chr21	48129895	142324999	2.9571	6.0535
chr22	51304566	104180547	2.0306	3.1296
chrMT	16571	12550414	757.3722	203.6317
chrX	155270560	377631065	2.4321	2.6622

chrY	59373566	66854745	1.126	4.7507
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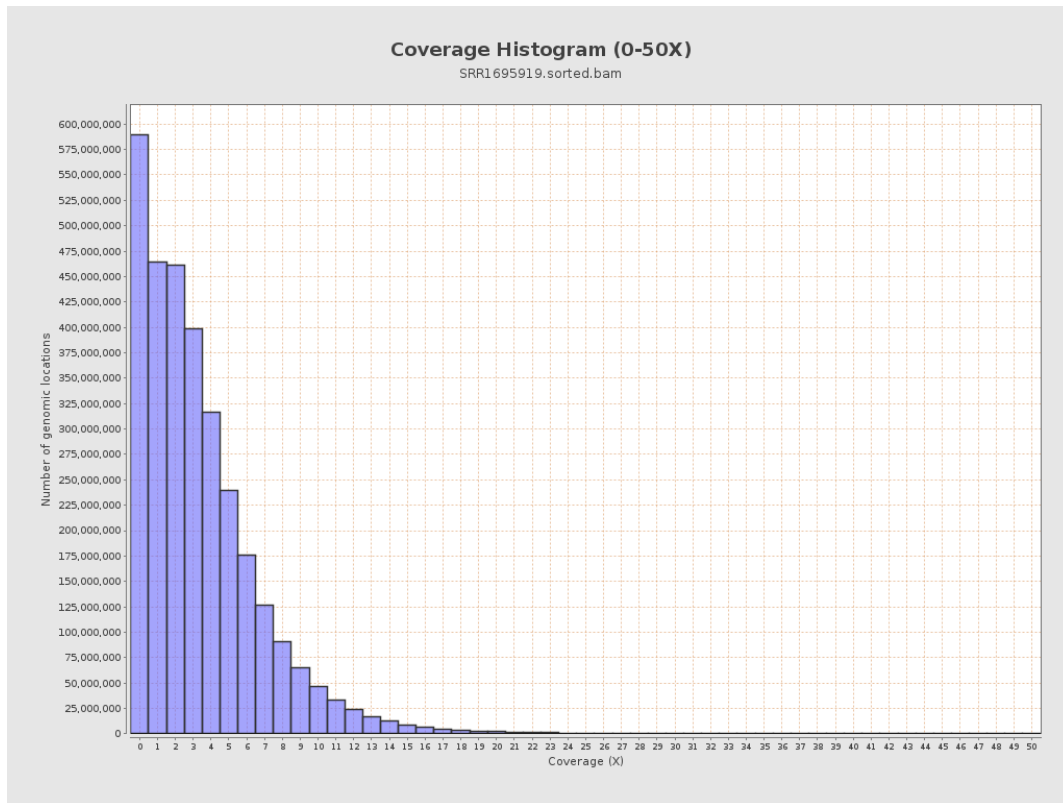
3. Results : Coverage across reference



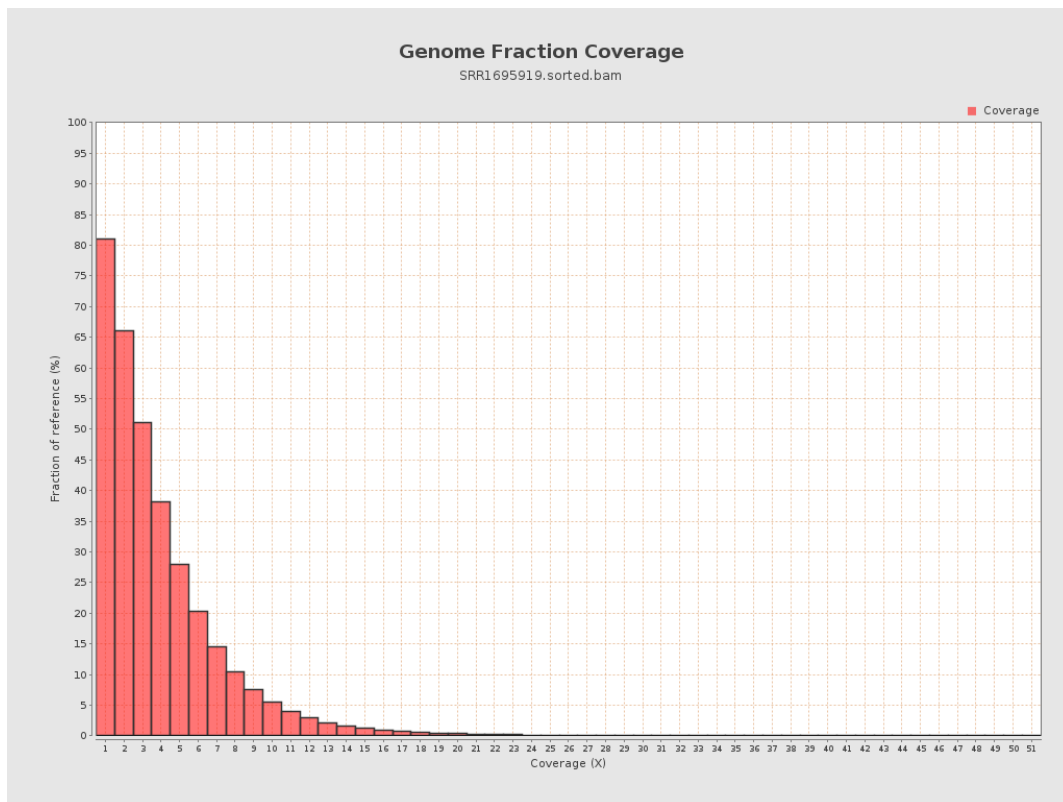
4. Results : Coverage Histogram



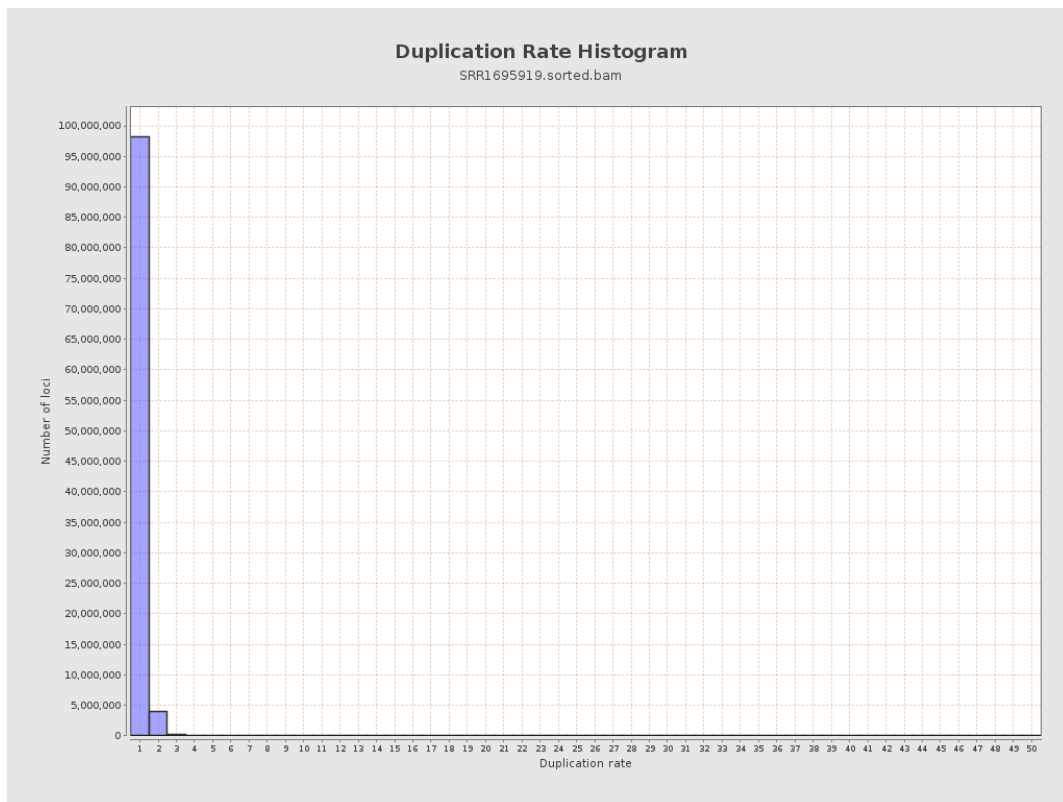
5. Results : Coverage Histogram (0-50X)



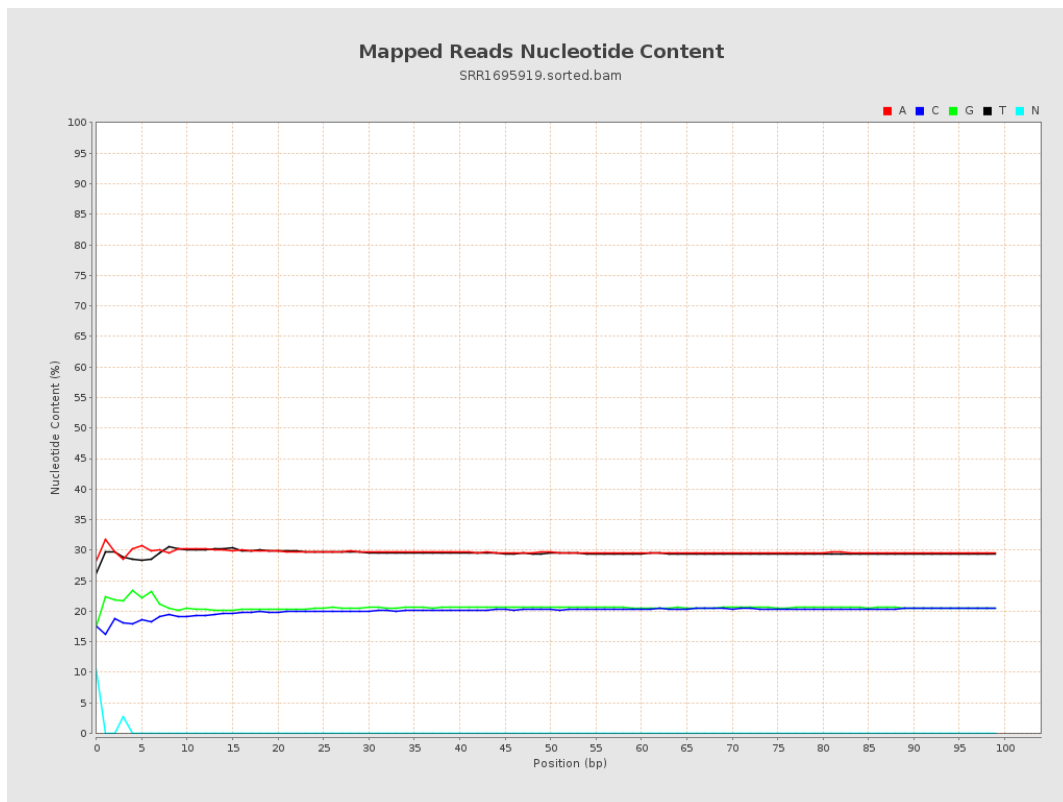
6. Results : Genome Fraction Coverage



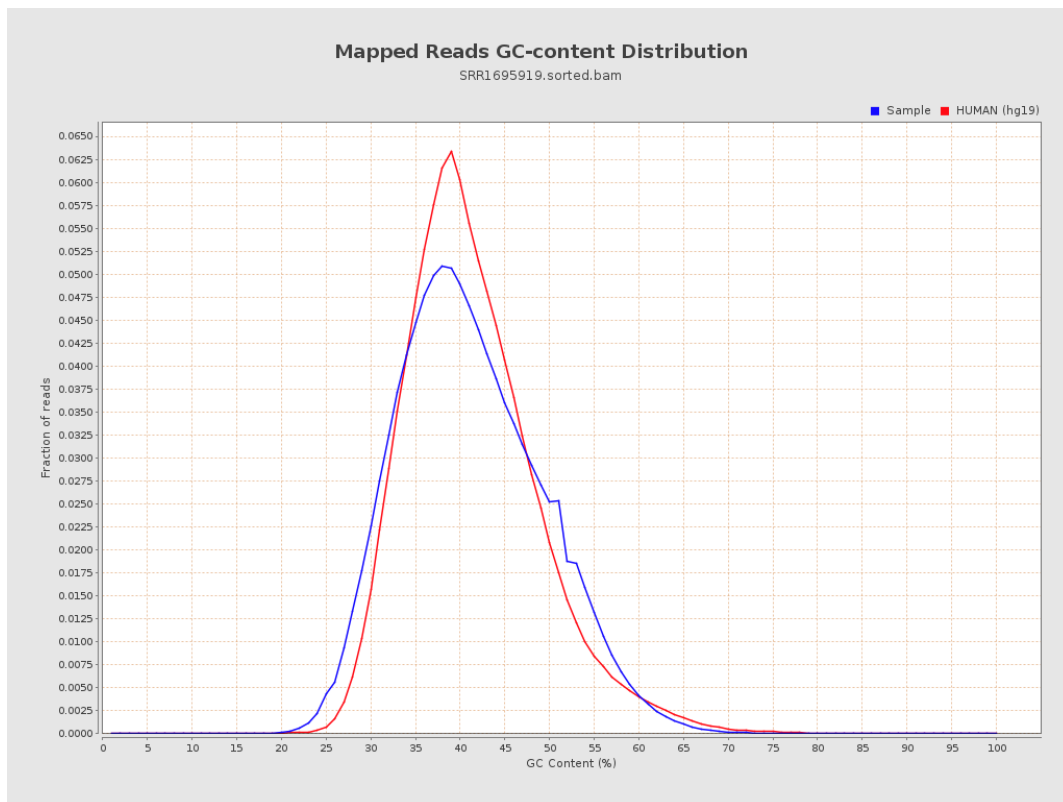
7. Results : Duplication Rate Histogram



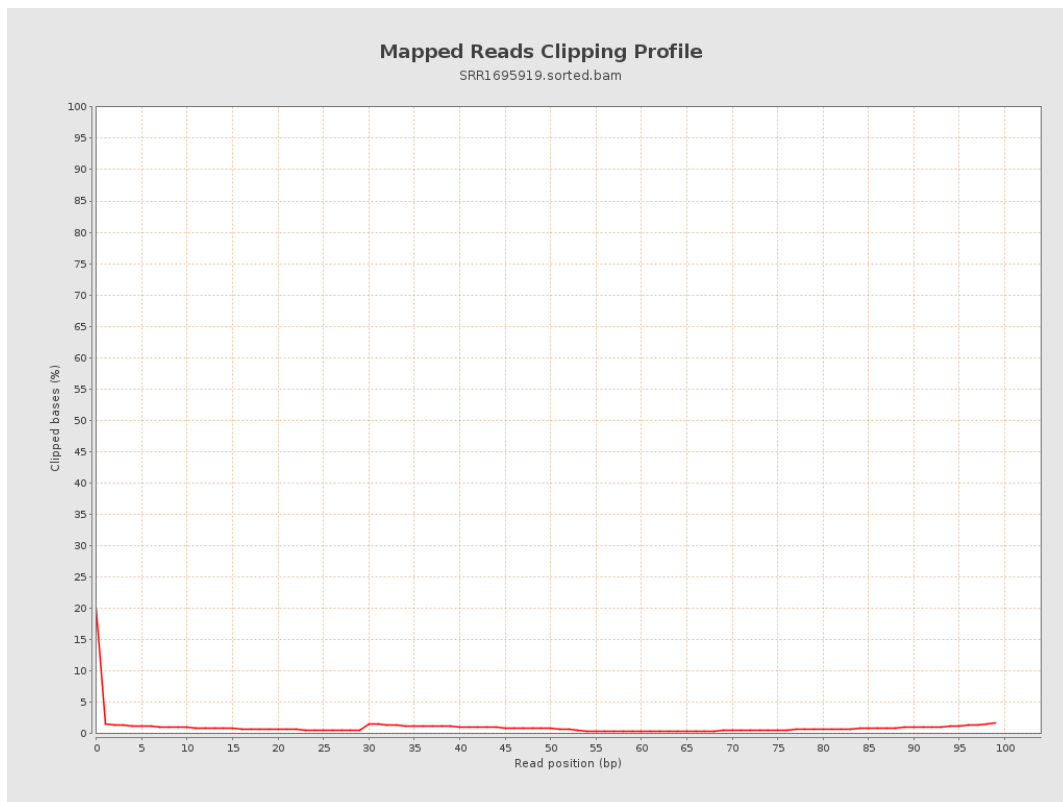
8. Results : Mapped Reads Nucleotide Content



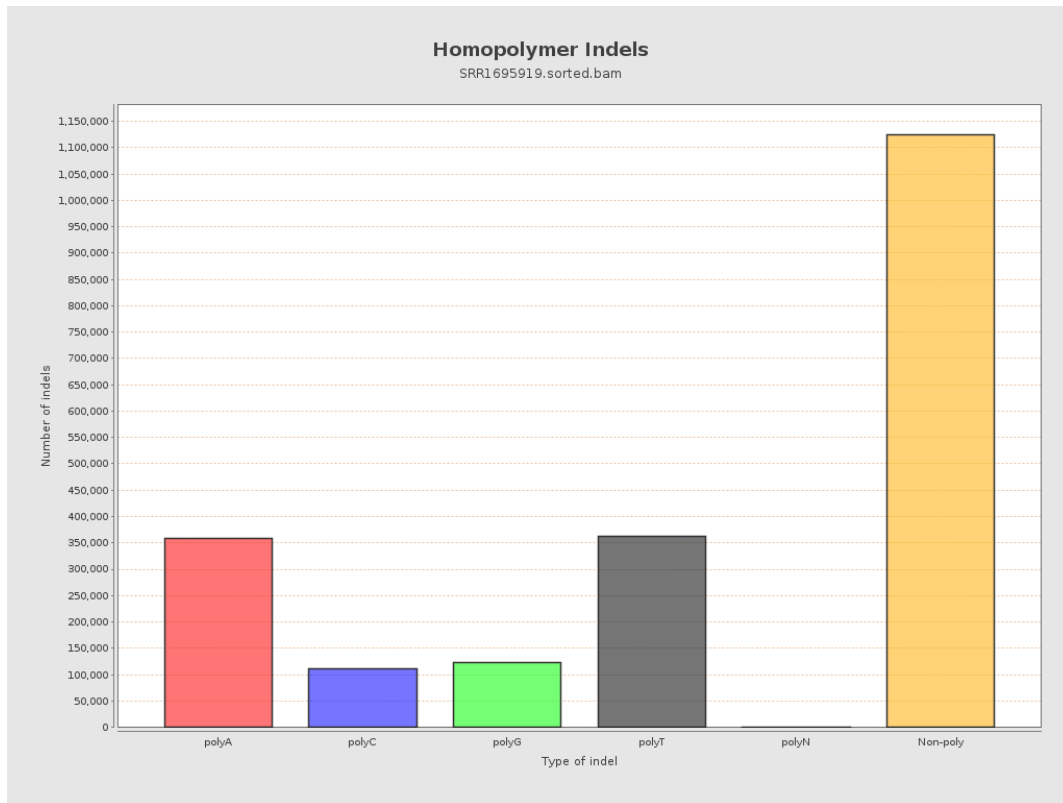
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



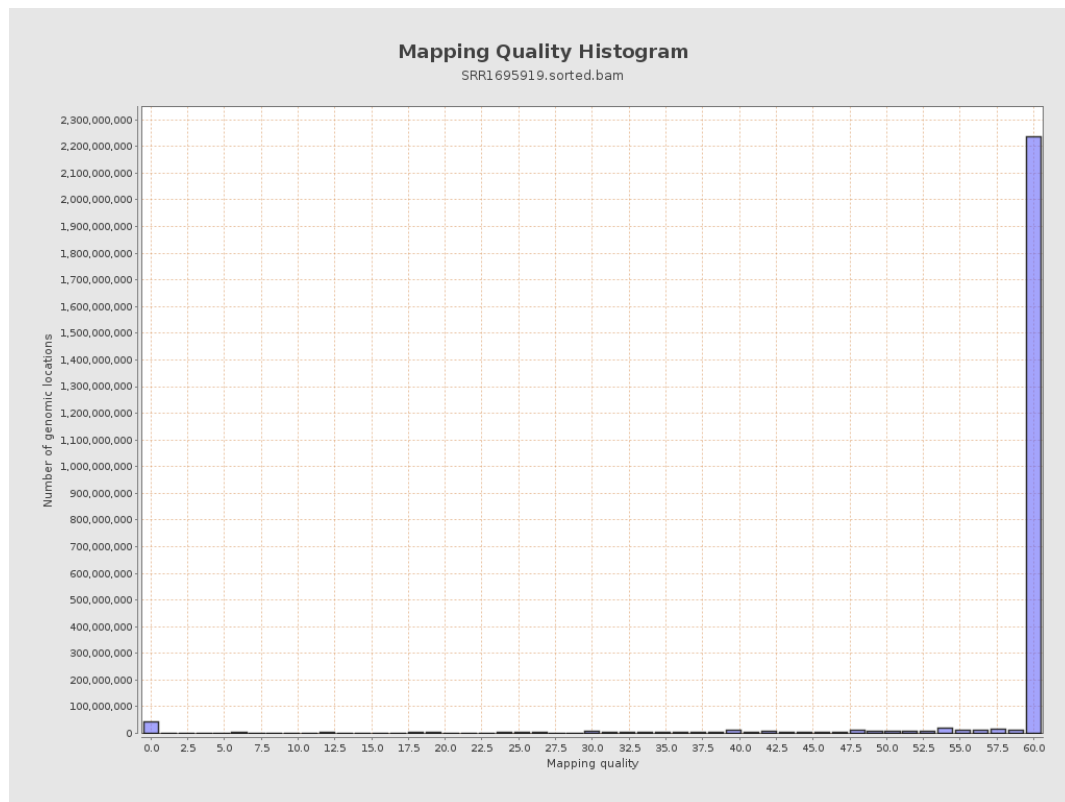
11. Results : Homopolymer Indels



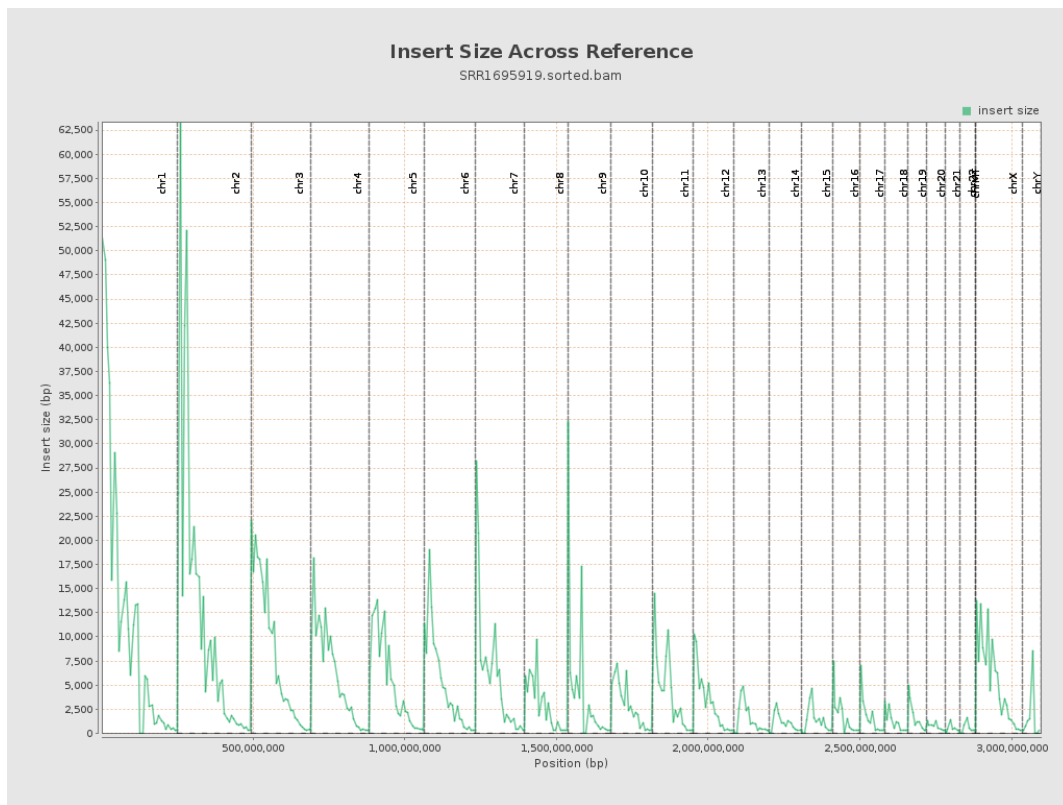
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

