

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 00:31:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695968.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695968 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695968_1.fastq.gz SRR1695968_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 00:31:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695968.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	409,059,110
Mapped reads	406,496,086 / 99.37%
Unmapped reads	2,563,024 / 0.63%
Mapped paired reads	406,496,086 / 99.37%
Mapped reads, first in pair	203,873,996 / 49.84%
Mapped reads, second in pair	202,622,090 / 49.53%
Mapped reads, both in pair	404,648,054 / 98.92%
Mapped reads, singletons	1,848,032 / 0.45%
Secondary alignments	0
Supplementary alignments	4,073,954 / 1%
Read min/max/mean length	30 / 100 / 100.41
Duplicated reads (estimated)	51,549,067 / 12.6%
Duplication rate	11.85%
Clipped reads	25,727,345 / 6.29%

2.2. ACGT Content

Number/percentage of A's	11,924,847,962 / 29.56%
Number/percentage of C's	8,160,889,998 / 20.23%
Number/percentage of T's	11,826,954,067 / 29.32%
Number/percentage of G's	8,414,081,474 / 20.86%
Number/percentage of N's	9,030,498 / 0.02%

GC Percentage	41.09%
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2.3. Coverage

Mean	13.0326
Standard Deviation	16.8487

2.4. Mapping Quality

Mean Mapping Quality	53.93
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2.5. Insert size

Mean	72,497.38
Standard Deviation	2,587,660.78
P25/Median/P75	315 / 325 / 335

2.6. Mismatches and indels

General error rate	0.49%
Mismatches	189,474,348
Insertions	3,843,676
Mapped reads with at least one insertion	0.93%
Deletions	3,905,946
Mapped reads with at least one deletion	0.94%
Homopolymer indels	45.46%

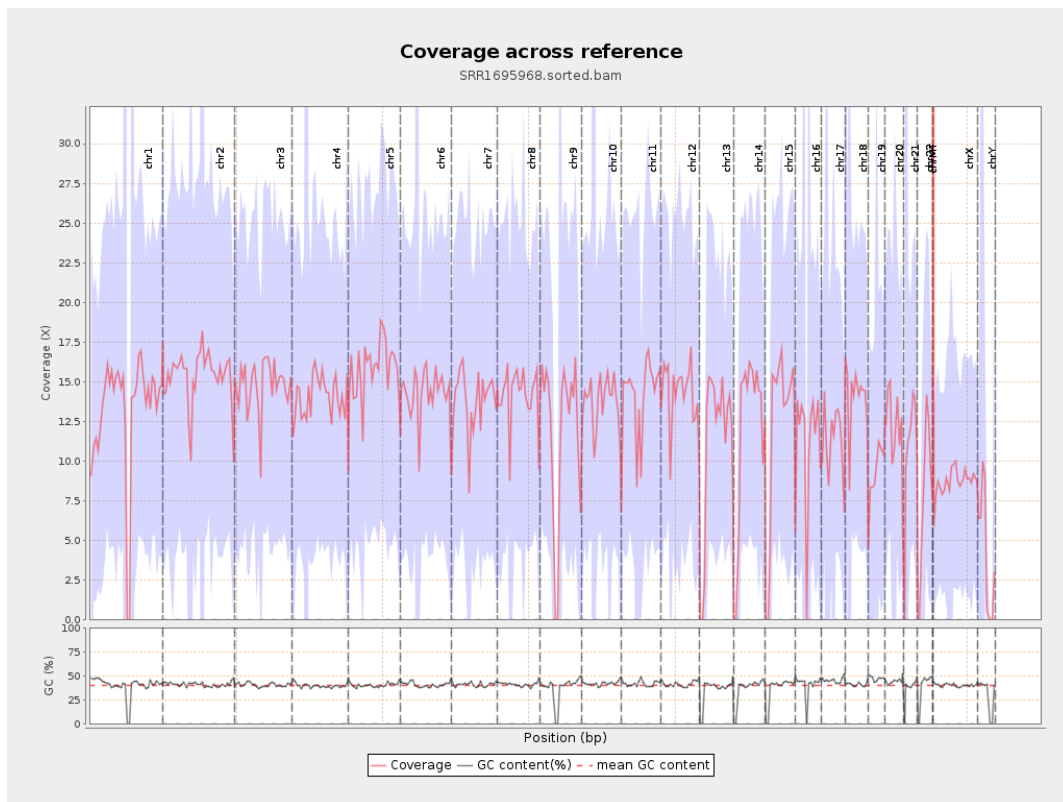
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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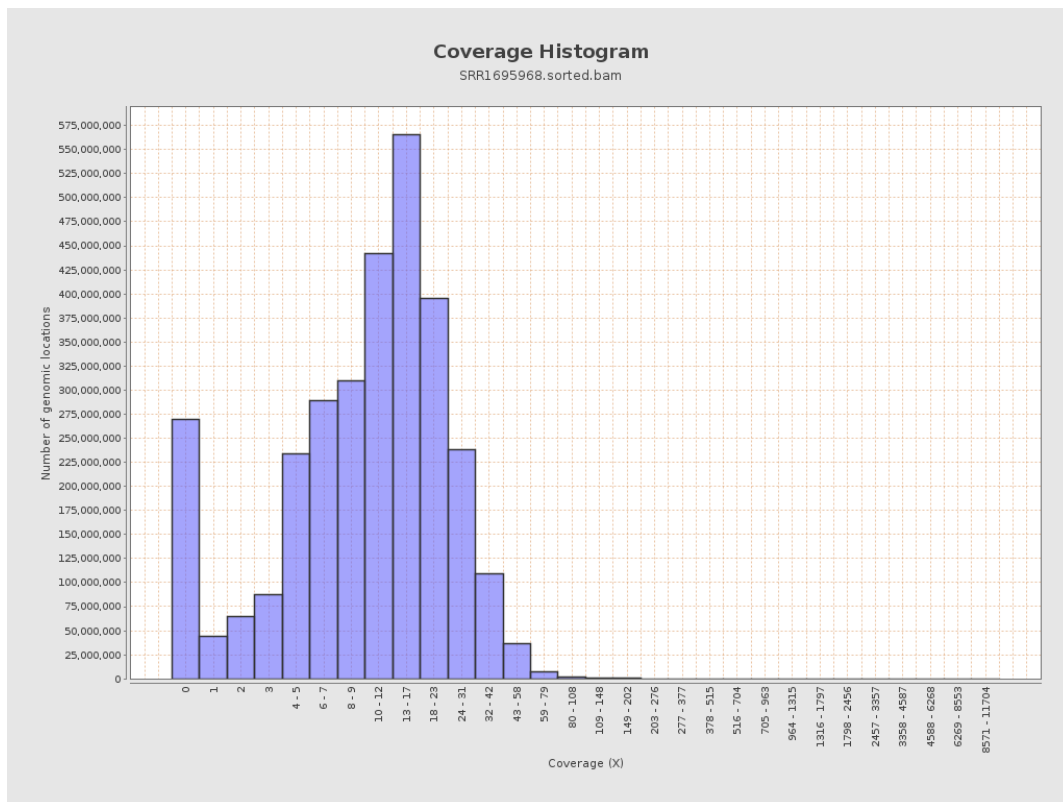
		bases	coverage	deviation
chr1	249250621	3295725784	13.2225	17.467
chr2	243199373	3731249909	15.3424	15.8084
chr3	198022430	2918421044	14.7378	10.0976
chr4	191154276	2691514297	14.0803	14.516
chr5	180915260	2851974715	15.7641	10.7336
chr6	171115067	2446713501	14.2986	12.7048
chr7	159138663	2182638552	13.7153	10.8652
chr8	146364022	2067568423	14.1262	10.572
chr9	141213431	1678954436	11.8895	13.4134
chr10	135534747	1869357008	13.7925	18.7712
chr11	135006516	1908984837	14.1399	11.181
chr12	133851895	1919403538	14.3398	10.4713
chr13	115169878	1302925587	11.3131	9.9303
chr14	107349540	1296316537	12.0757	10.9566
chr15	102531392	1244937471	12.142	11.4795
chr16	90354753	991985434	10.9788	16.2169
chr17	81195210	926541793	11.4113	13.6807
chr18	78077248	1092783979	13.9962	18.0363
chr19	59128983	560157097	9.4735	12.1546
chr20	63025520	767925953	12.1844	11.5324
chr21	48129895	520477360	10.814	21.2775
chr22	51304566	405037295	7.8948	10.129
chrMT	16571	69294768	4,181.689	1,065.8269
chrX	155270560	1347027345	8.6754	7.0619

chrY	59373566	256901895	4.3269	16.8143
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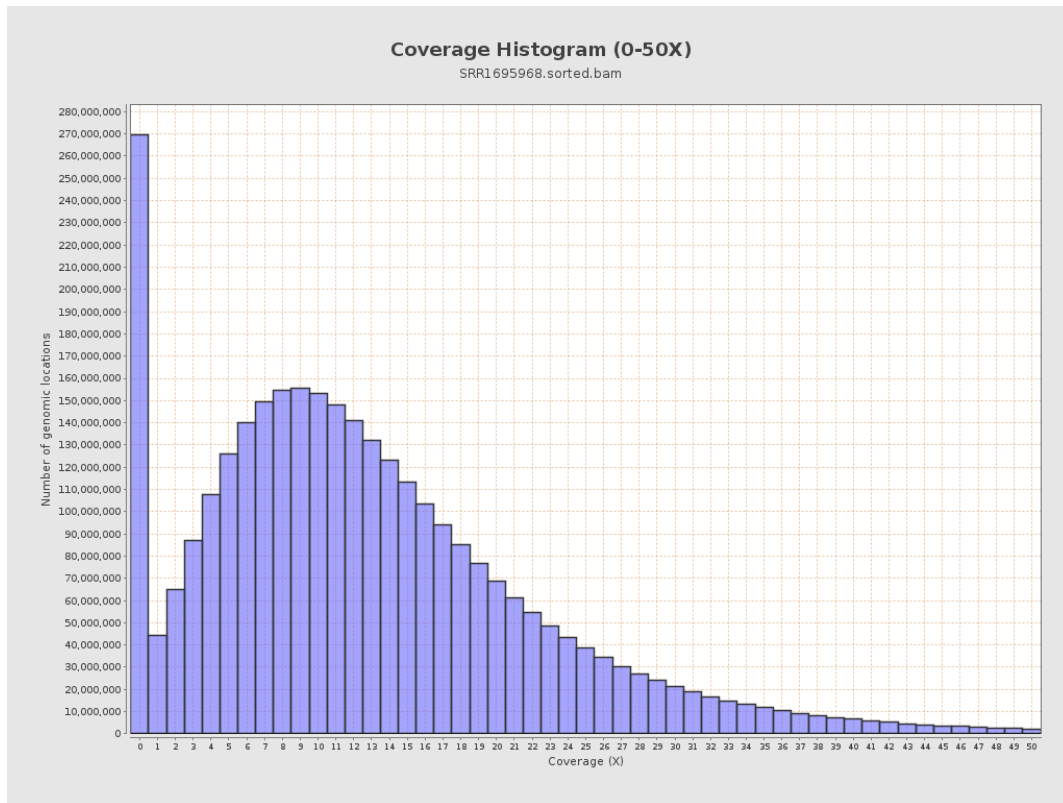
3. Results : Coverage across reference



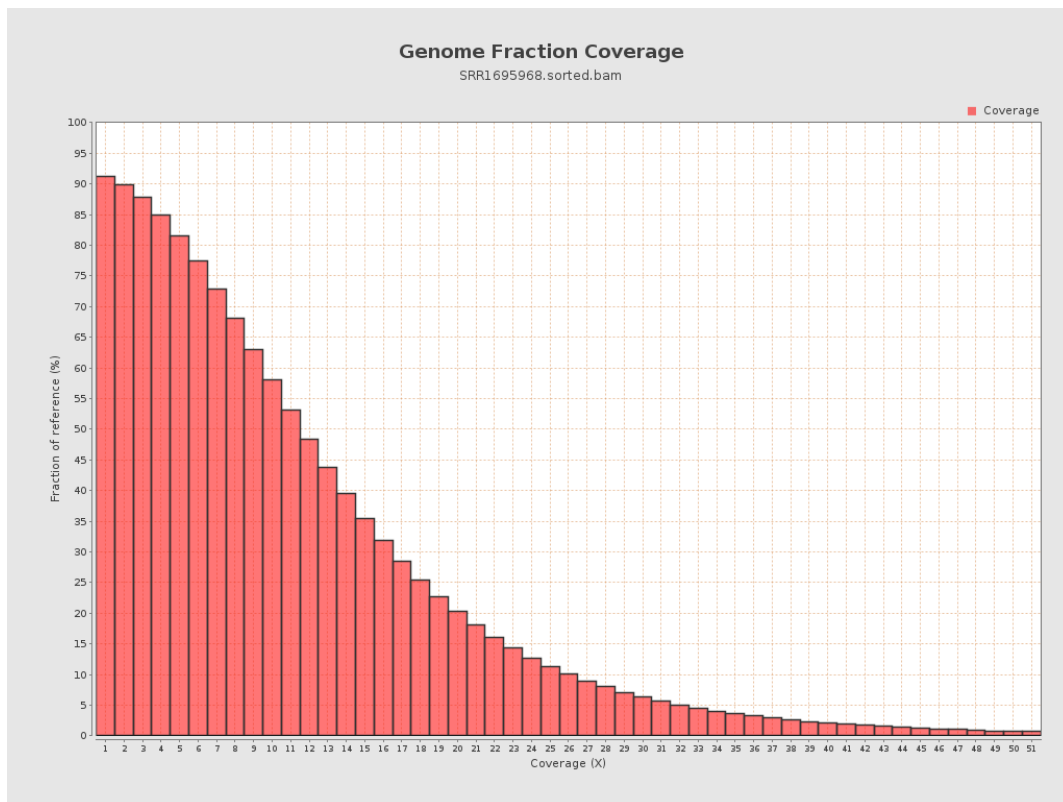
4. Results : Coverage Histogram



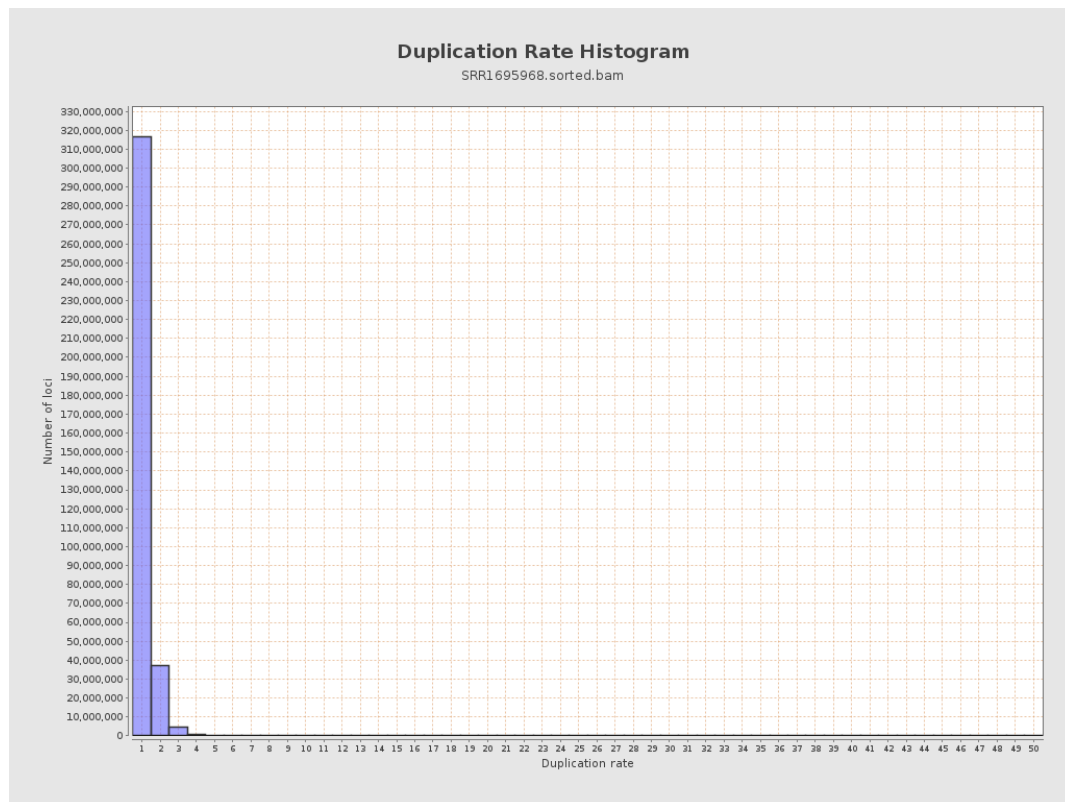
5. Results : Coverage Histogram (0-50X)



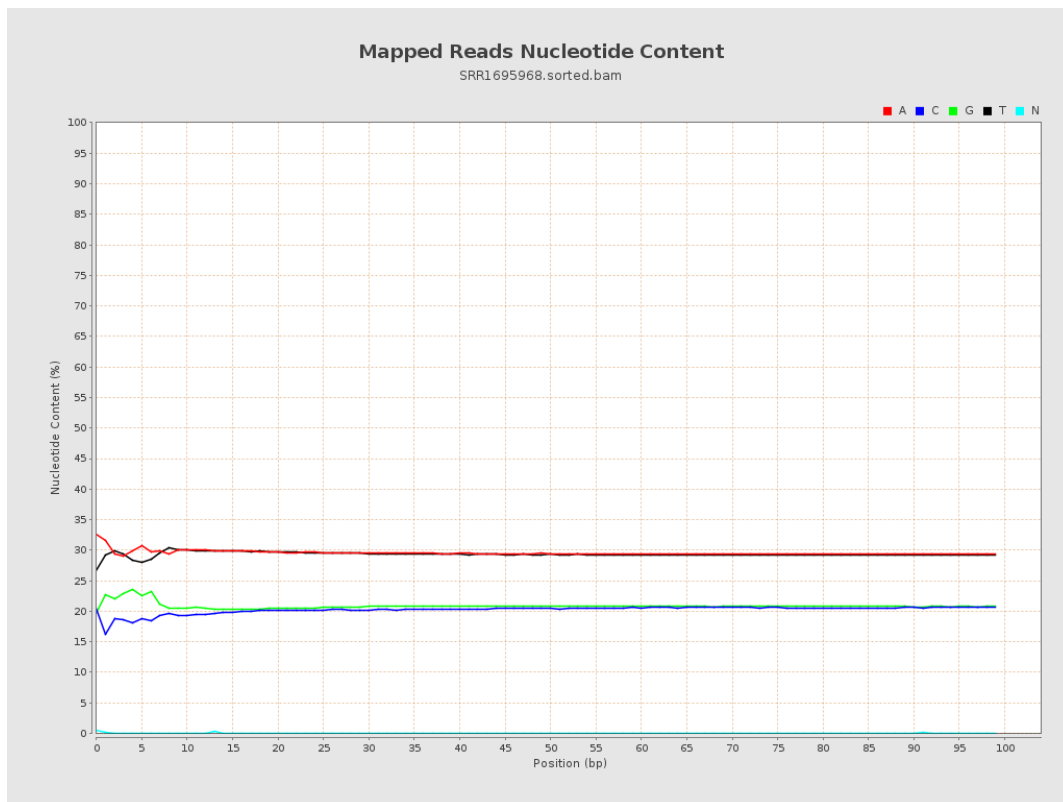
6. Results : Genome Fraction Coverage



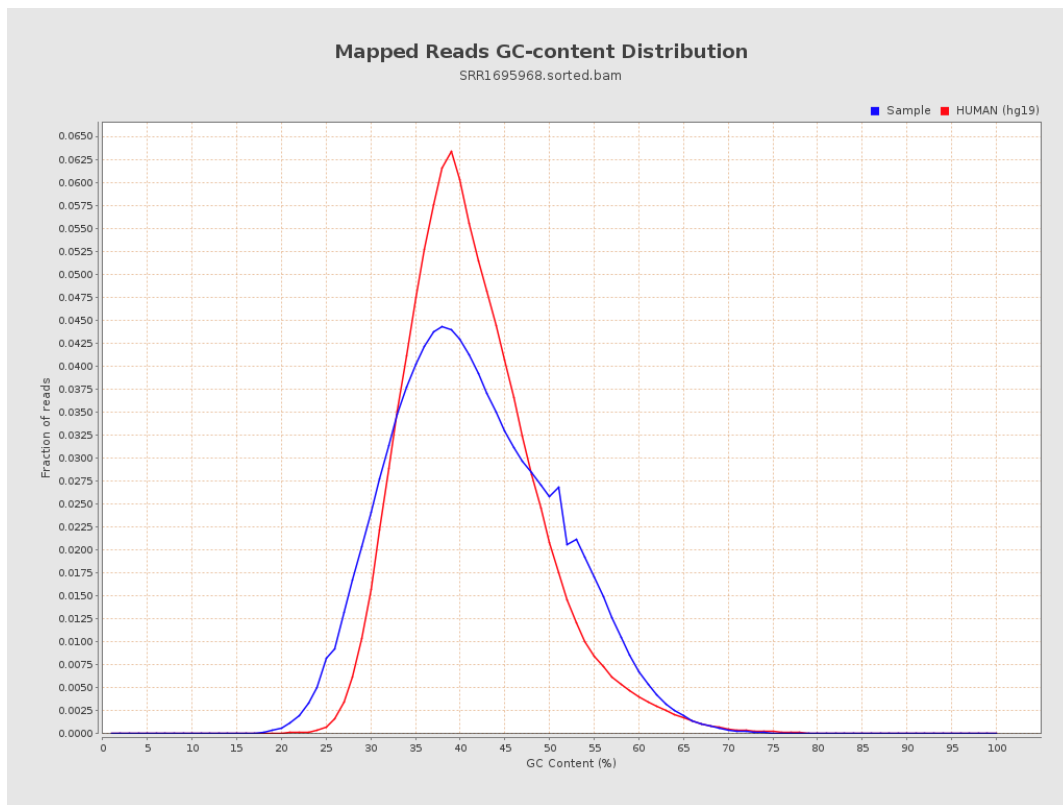
7. Results : Duplication Rate Histogram



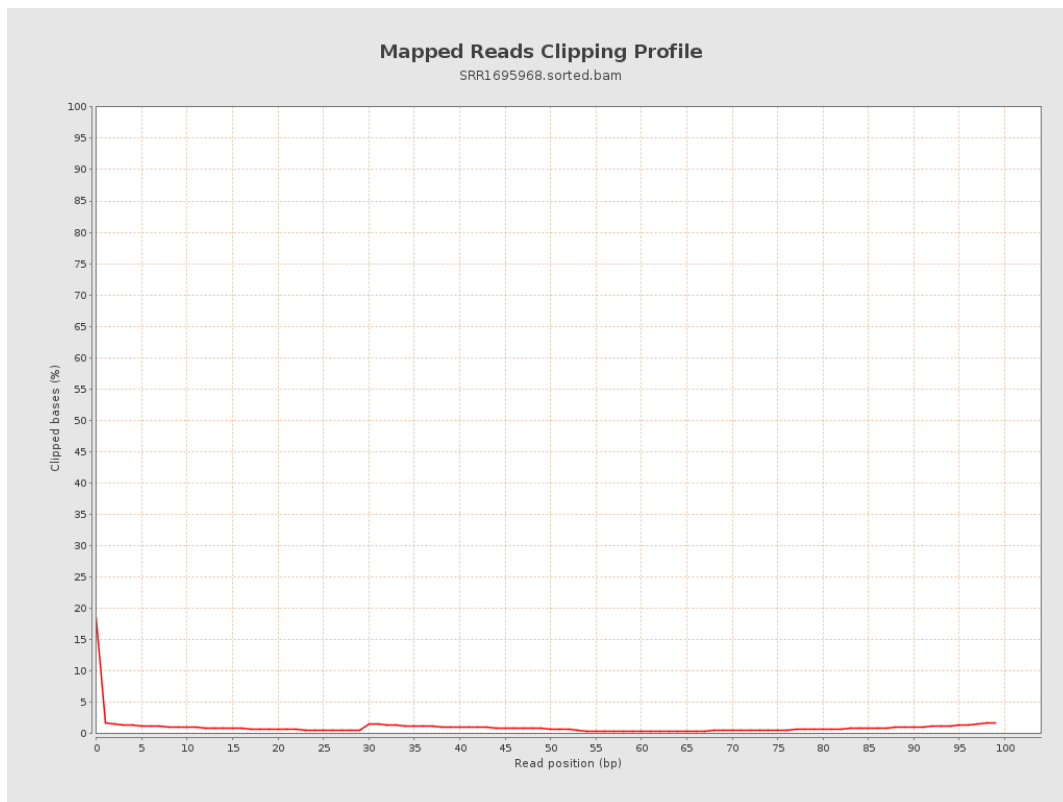
8. Results : Mapped Reads Nucleotide Content



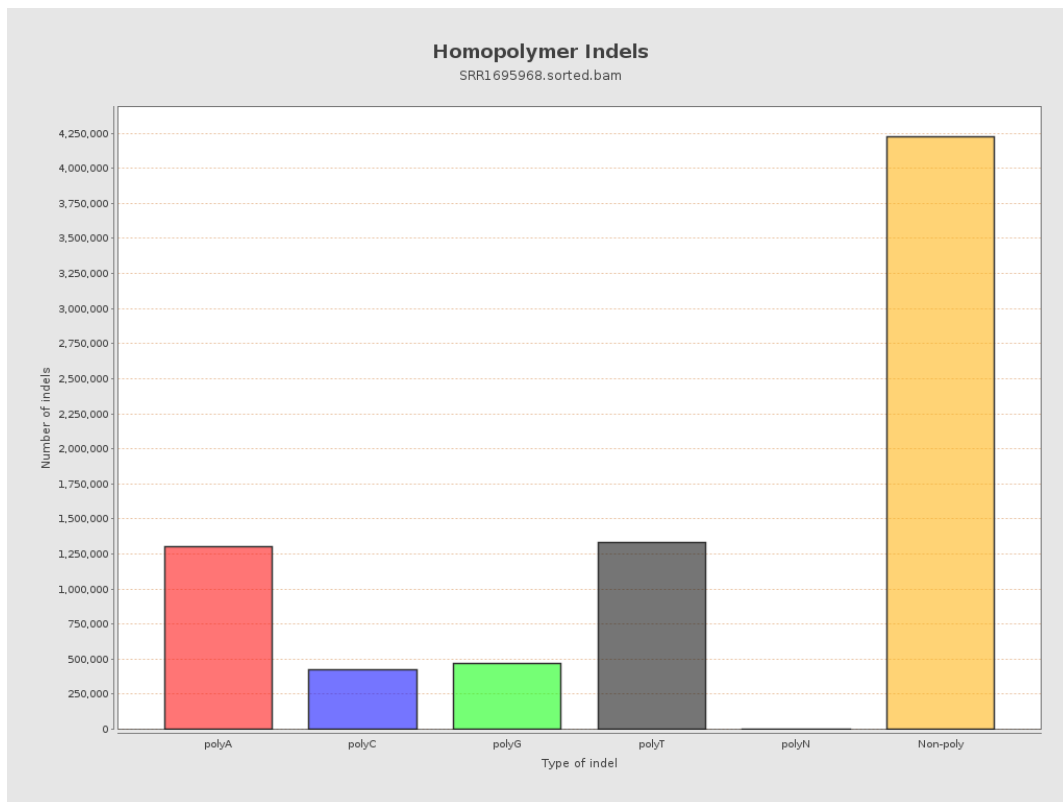
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



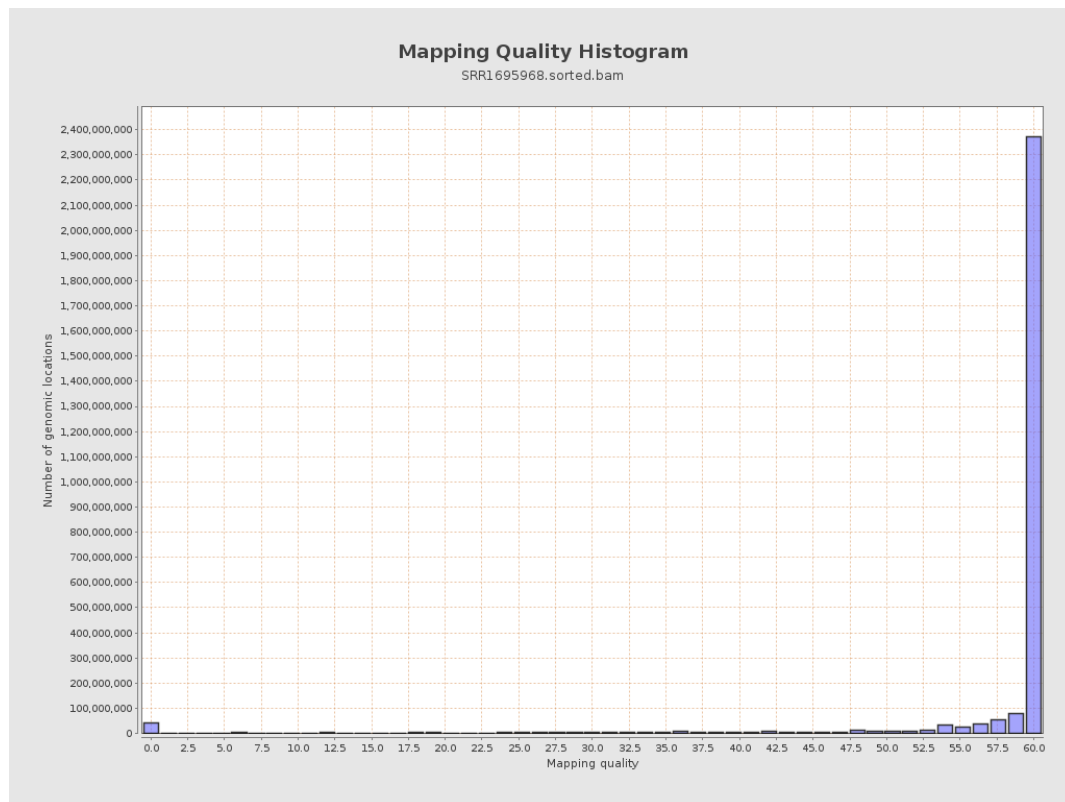
11. Results : Homopolymer Indels



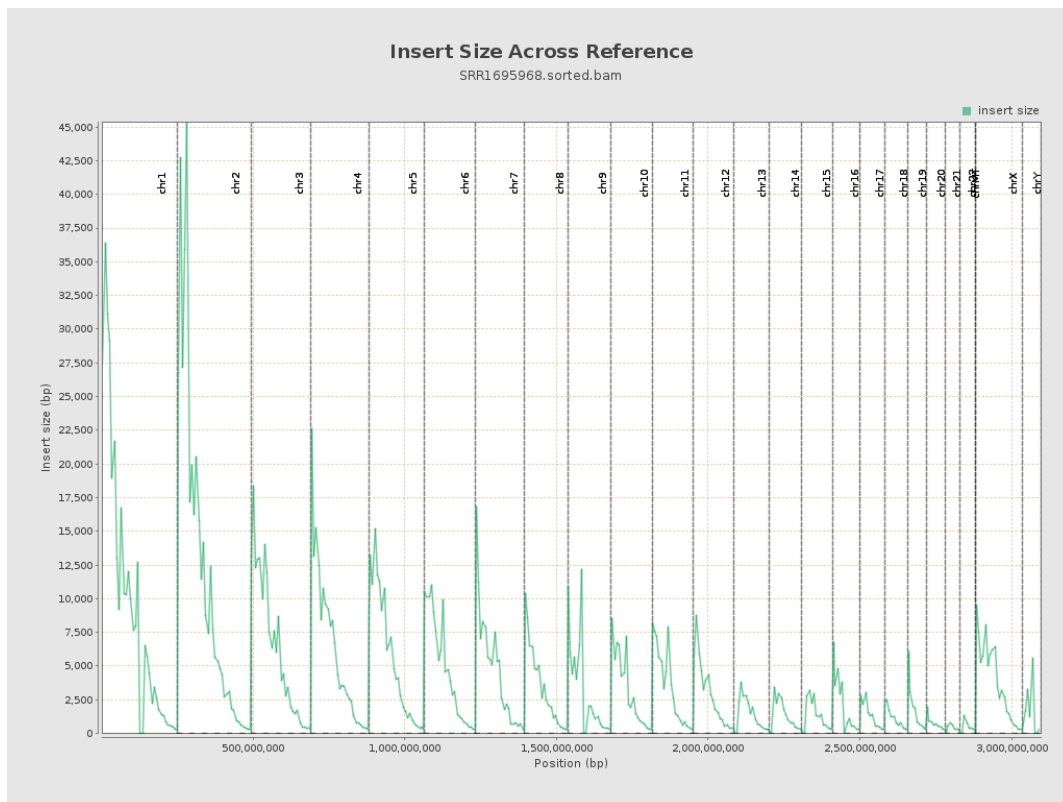
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

