

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 14:30:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695949.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_SRR1695949 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695949_1.fastq.gz SRR1695949_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Fri Sep 13 14:30:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695949.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	338,325,590
Mapped reads	336,520,034 / 99.47%
Unmapped reads	1,805,556 / 0.53%
Mapped paired reads	336,520,034 / 99.47%
Mapped reads, first in pair	168,553,952 / 49.82%
Mapped reads, second in pair	167,966,082 / 49.65%
Mapped reads, both in pair	335,430,696 / 99.14%
Mapped reads, singletons	1,089,338 / 0.32%
Secondary alignments	0
Supplementary alignments	2,923,418 / 0.86%
Read min/max/mean length	30 / 100 / 100.36
Duplicated reads (estimated)	36,658,003 / 10.84%
Duplication rate	10%
Clipped reads	17,988,548 / 5.32%

2.2. ACGT Content

Number/percentage of A's	9,623,005,973 / 28.8%
Number/percentage of C's	7,000,633,293 / 20.95%
Number/percentage of T's	9,576,965,304 / 28.67%
Number/percentage of G's	7,200,569,540 / 21.55%
Number/percentage of N's	7,783,296 / 0.02%

GC Percentage	42.51%
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2.3. Coverage

Mean	10.7946
Standard Deviation	15.4698

2.4. Mapping Quality

Mean Mapping Quality	54.13
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2.5. Insert size

Mean	58,428.48
Standard Deviation	2,334,406.6
P25/Median/P75	314 / 321 / 328

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	137,656,952
Insertions	3,335,040
Mapped reads with at least one insertion	0.97%
Deletions	3,307,882
Mapped reads with at least one deletion	0.96%
Homopolymer indels	45.17%

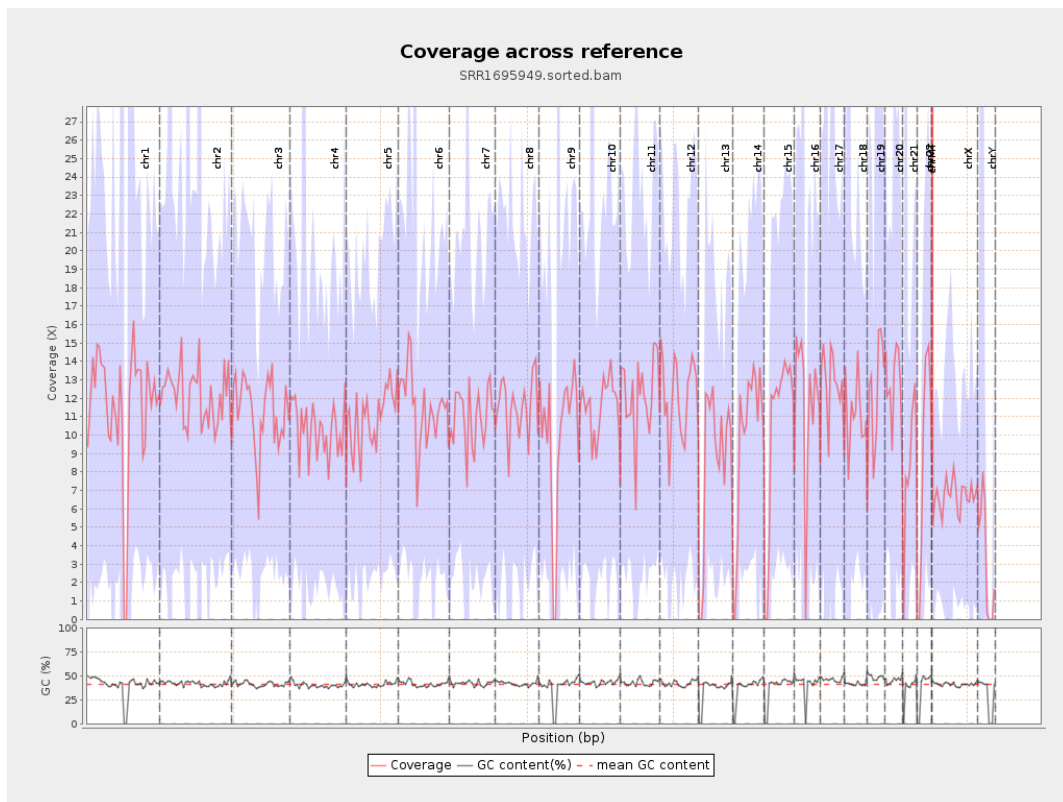
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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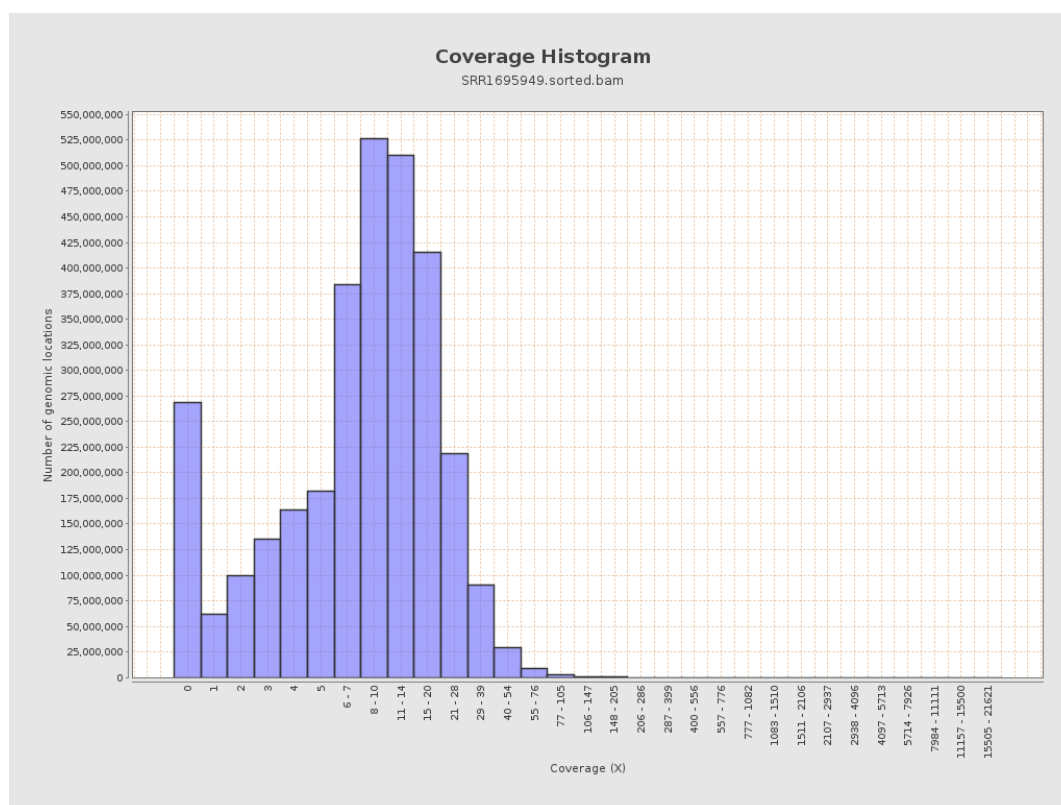
		bases	coverage	deviation
chr1	249250621	2886939169	11.5825	22.1027
chr2	243199373	2956649966	12.1573	22.4601
chr3	198022430	2235631915	11.2898	8.5253
chr4	191154276	1970952543	10.3108	14.0793
chr5	180915260	1986888906	10.9824	8.4359
chr6	171115067	1968061354	11.5014	11.5816
chr7	159138663	1741249033	10.9417	10.3794
chr8	146364022	1690141098	11.5475	10.0965
chr9	141213431	1393768506	9.8699	13.7536
chr10	135534747	1574960223	11.6203	17.596
chr11	135006516	1643368984	12.1725	11.0234
chr12	133851895	1623318305	12.1277	10.0513
chr13	115169878	1001309206	8.6942	8.5907
chr14	107349540	1057642975	9.8523	9.7387
chr15	102531392	1061727808	10.3551	10.0196
chr16	90354753	1041450547	11.5262	14.6645
chr17	81195210	1036226932	12.7622	17.4923
chr18	78077248	876089538	11.2208	24.3807
chr19	59128983	743436443	12.5731	17.7321
chr20	63025520	799761719	12.6895	11.5131
chr21	48129895	415912553	8.6415	21.0719
chr22	51304566	448474666	8.7414	10.7951
chrMT	16571	32302299	1,949.3271	597.0846
chrX	155270560	1033468572	6.6559	6.4807

chrY	59373566	196945326	3.3171	18.1476
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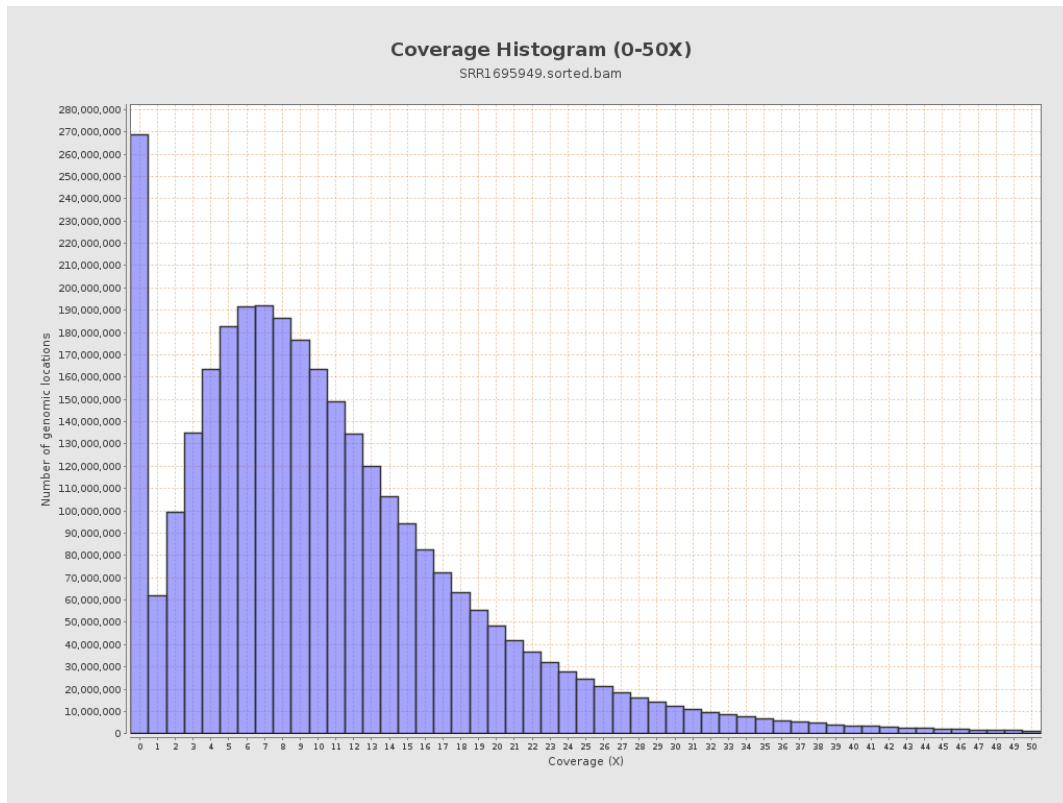
3. Results : Coverage across reference



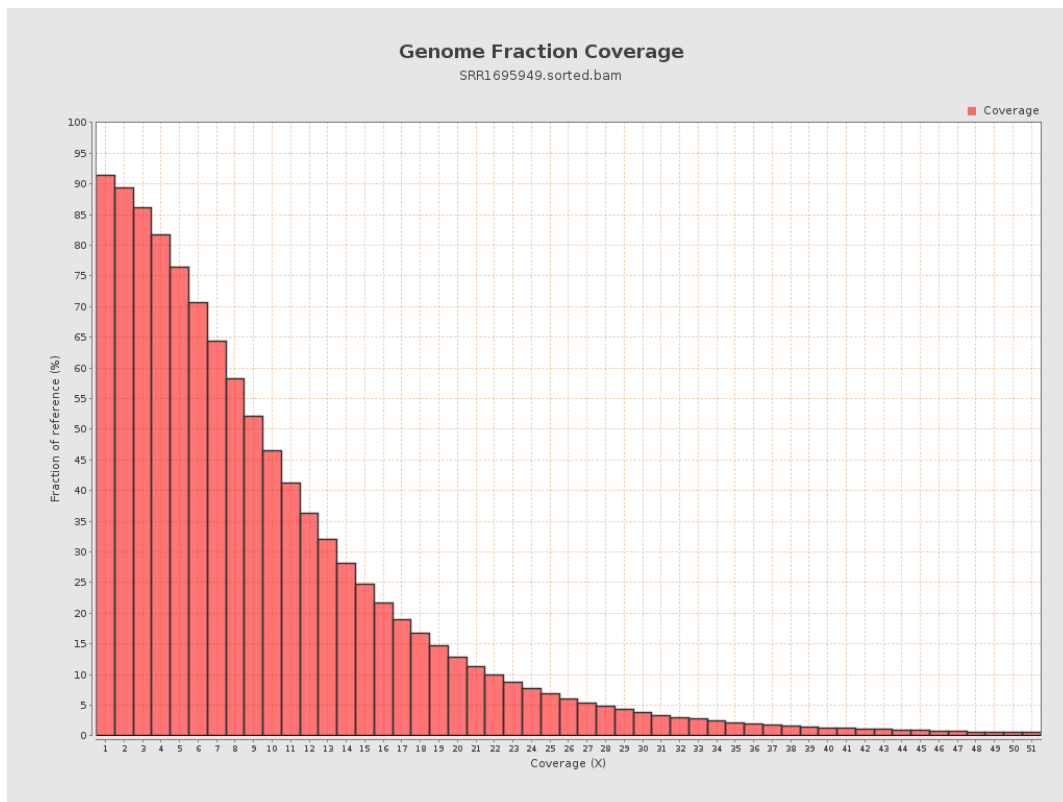
4. Results : Coverage Histogram



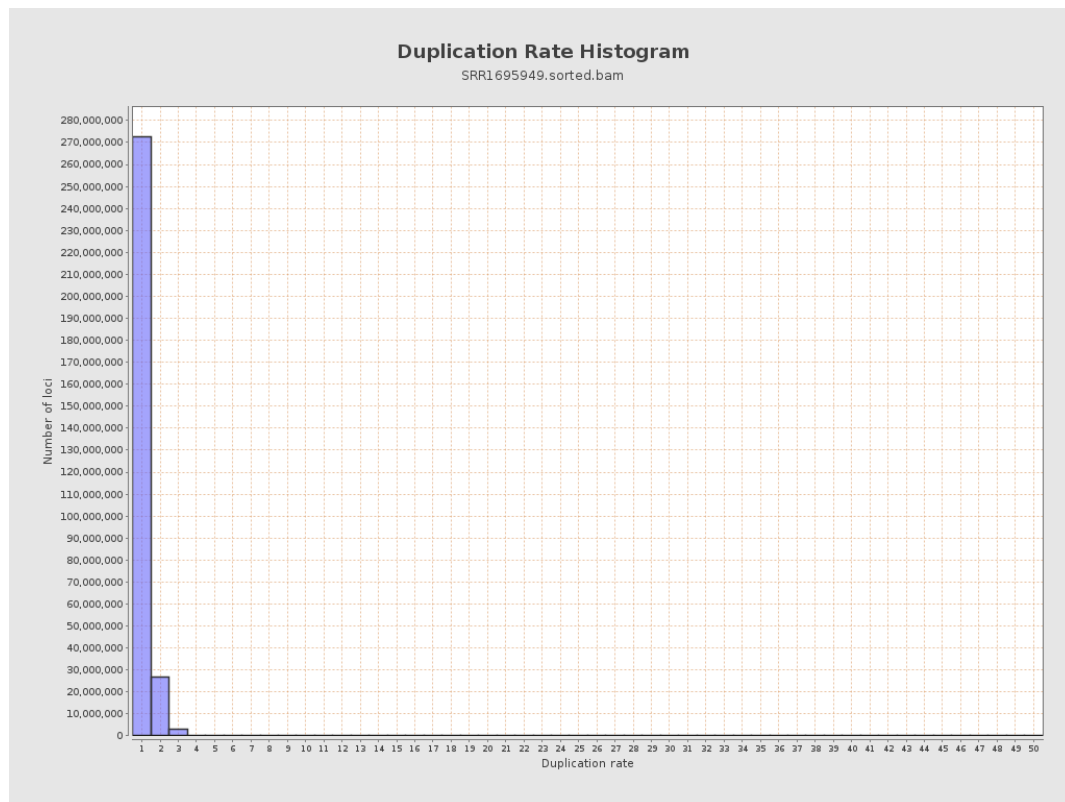
5. Results : Coverage Histogram (0-50X)



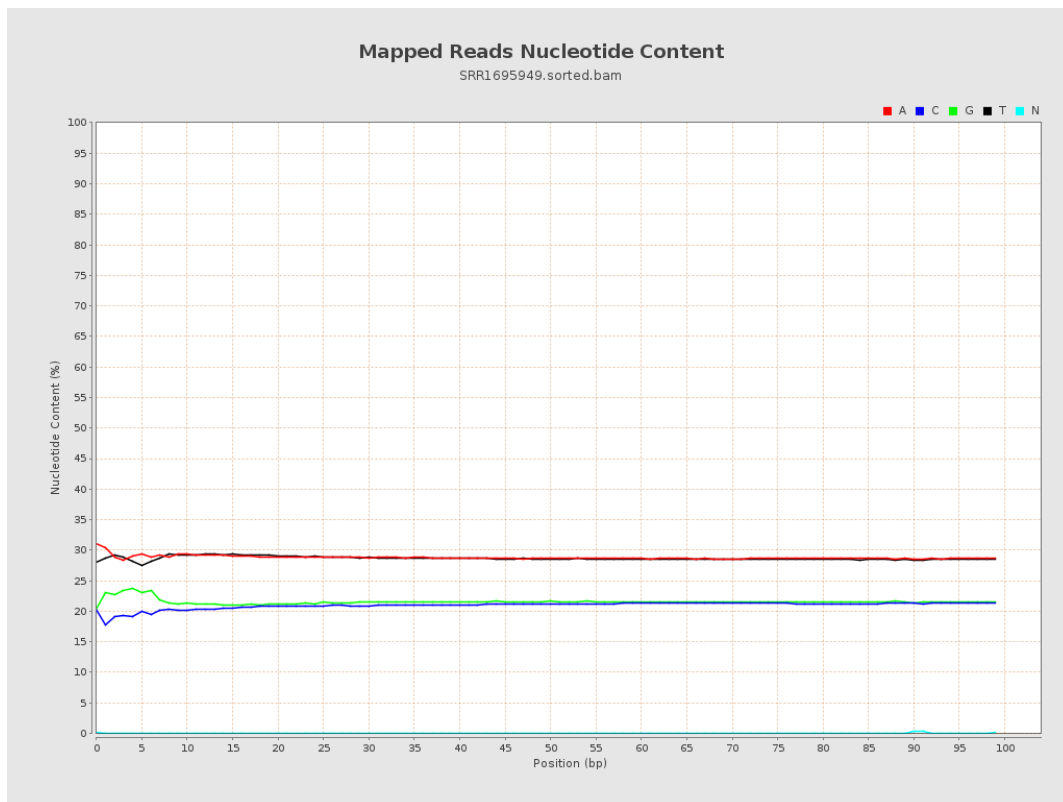
6. Results : Genome Fraction Coverage



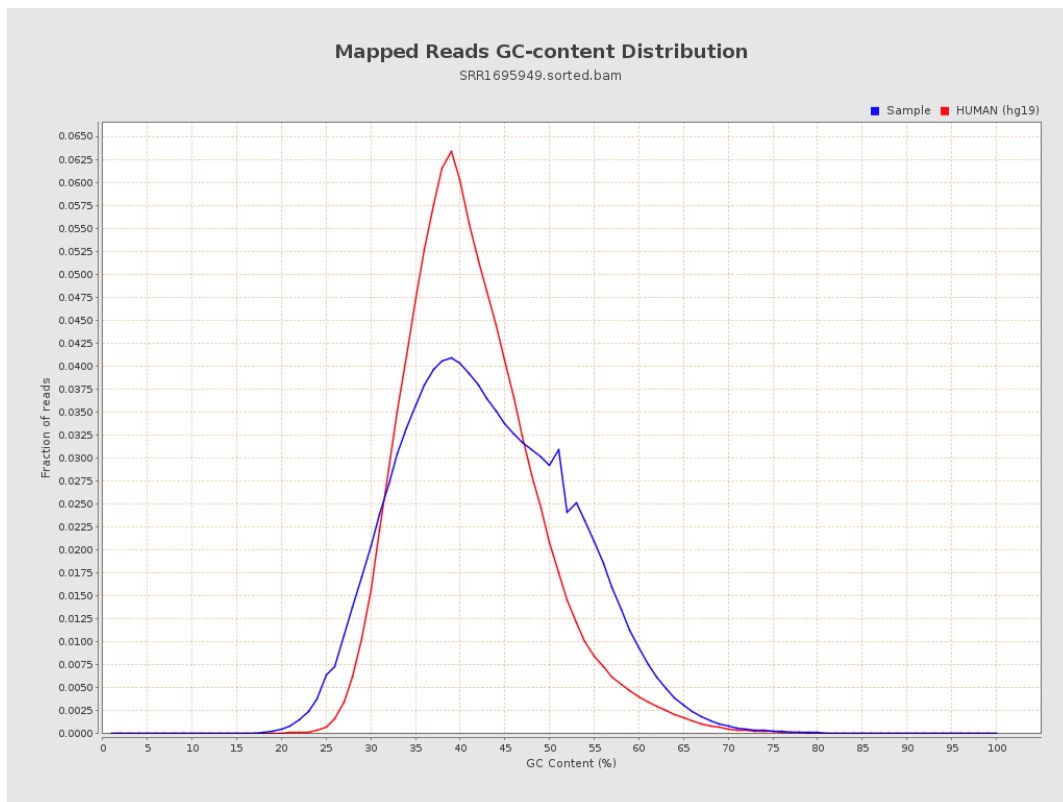
7. Results : Duplication Rate Histogram



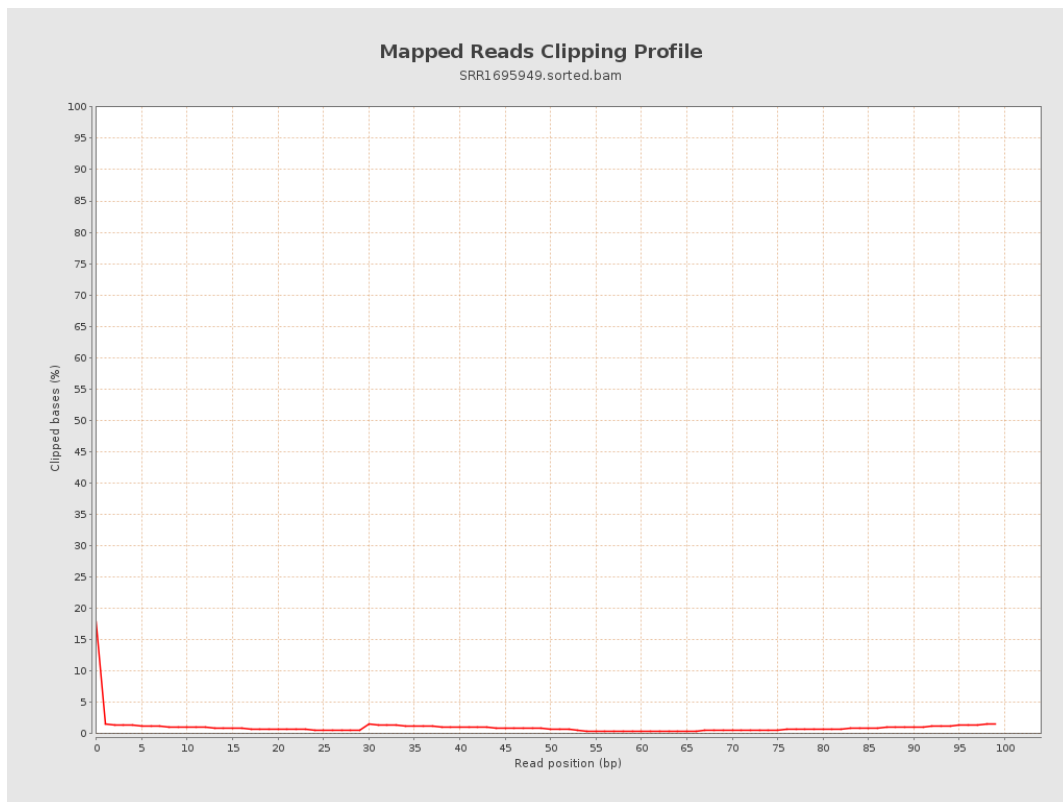
8. Results : Mapped Reads Nucleotide Content



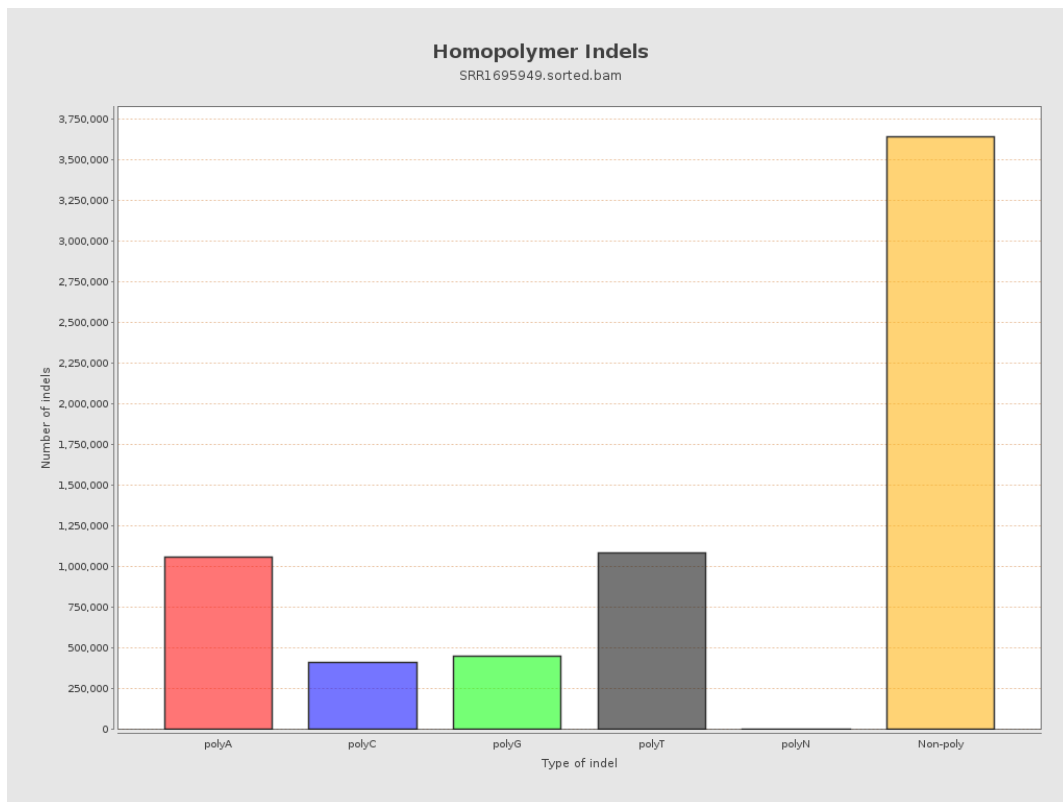
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



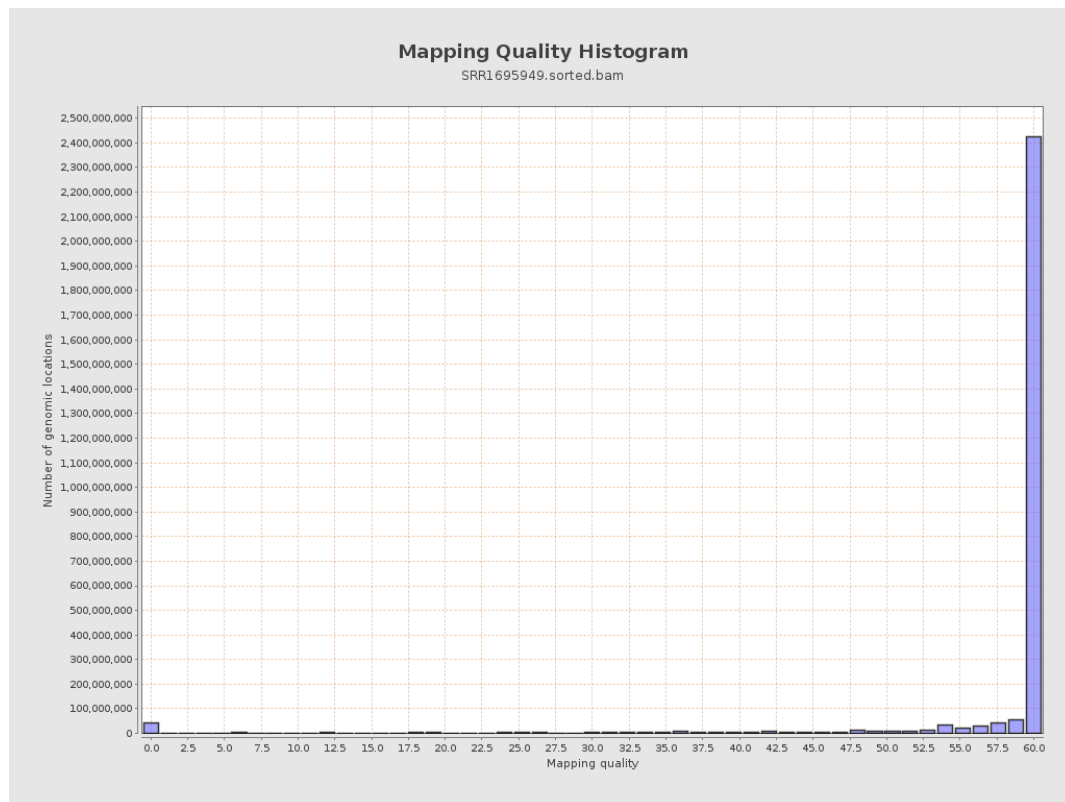
11. Results : Homopolymer Indels



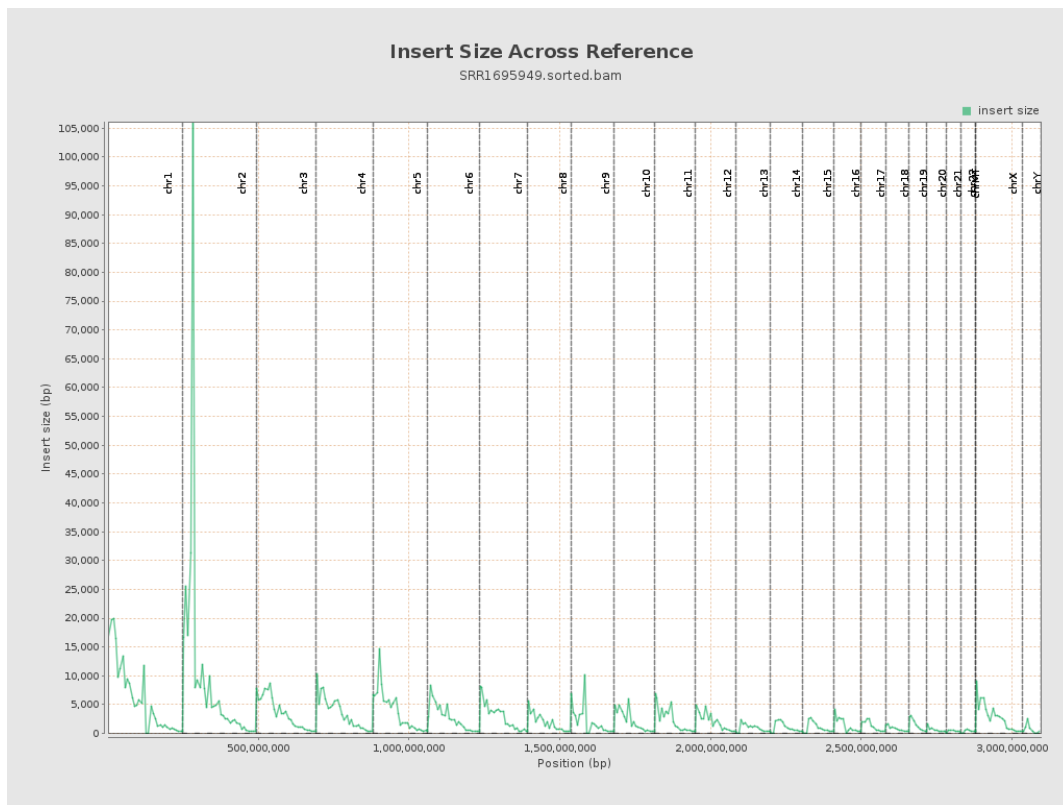
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

