

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 02:47:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695940.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 940 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695940_1.fastq.gz SRR1695940_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 02:47:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,319,318
Mapped reads	20,161,142 / 99.22%
Unmapped reads	158,176 / 0.78%
Mapped paired reads	20,161,142 / 99.22%
Mapped reads, first in pair	10,128,022 / 49.84%
Mapped reads, second in pair	10,033,120 / 49.38%
Mapped reads, both in pair	20,048,872 / 98.67%
Mapped reads, singletons	112,270 / 0.55%
Secondary alignments	0
Supplementary alignments	52,717 / 0.26%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	1,866,643 / 9.19%
Duplication rate	8.67%
Clipped reads	855,130 / 4.21%

2.2. ACGT Content

Number/percentage of A's	593,928,540 / 29.7%
Number/percentage of C's	404,316,421 / 20.22%
Number/percentage of T's	594,131,034 / 29.71%
Number/percentage of G's	406,719,405 / 20.34%
Number/percentage of N's	882,384 / 0.04%

GC Percentage	40.55%
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2.3. Coverage

Mean	0.6462
Standard Deviation	3.5438

2.4. Mapping Quality

Mean Mapping Quality	49.98
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2.5. Insert size

Mean	37,345.24
Standard Deviation	1,893,924.4
P25/Median/P75	319 / 326 / 333

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	12,932,452
Insertions	127,470
Mapped reads with at least one insertion	0.62%
Deletions	163,013
Mapped reads with at least one deletion	0.79%
Homopolymer indels	44.66%

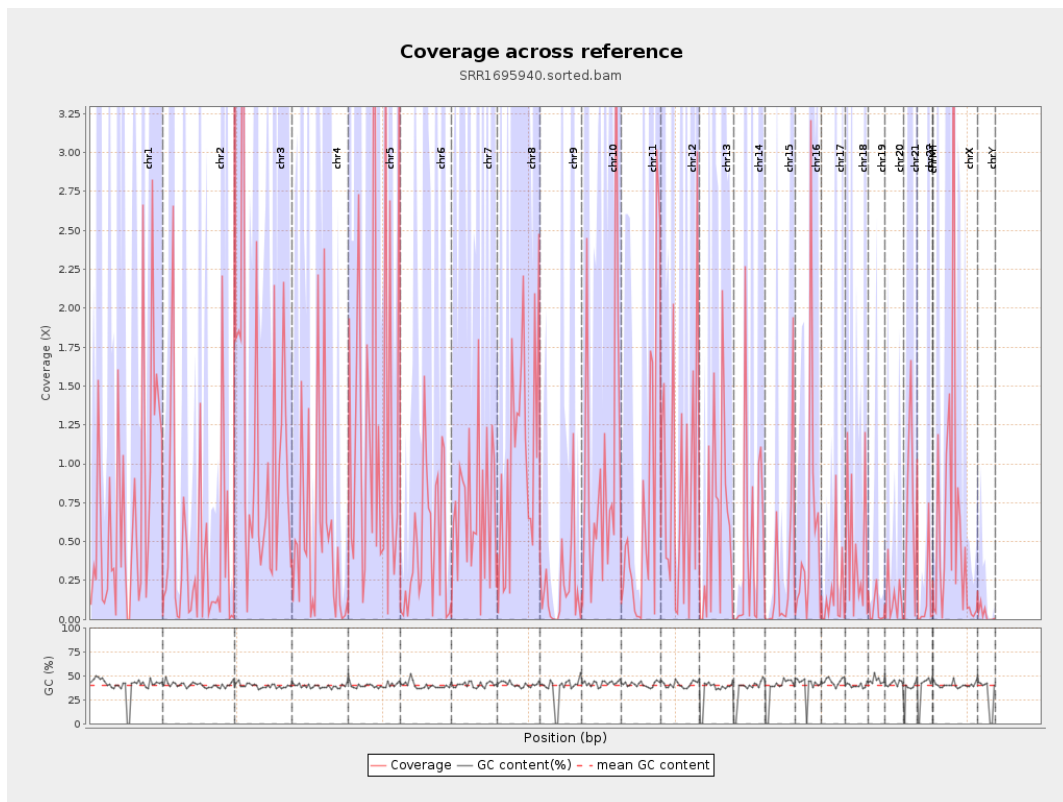
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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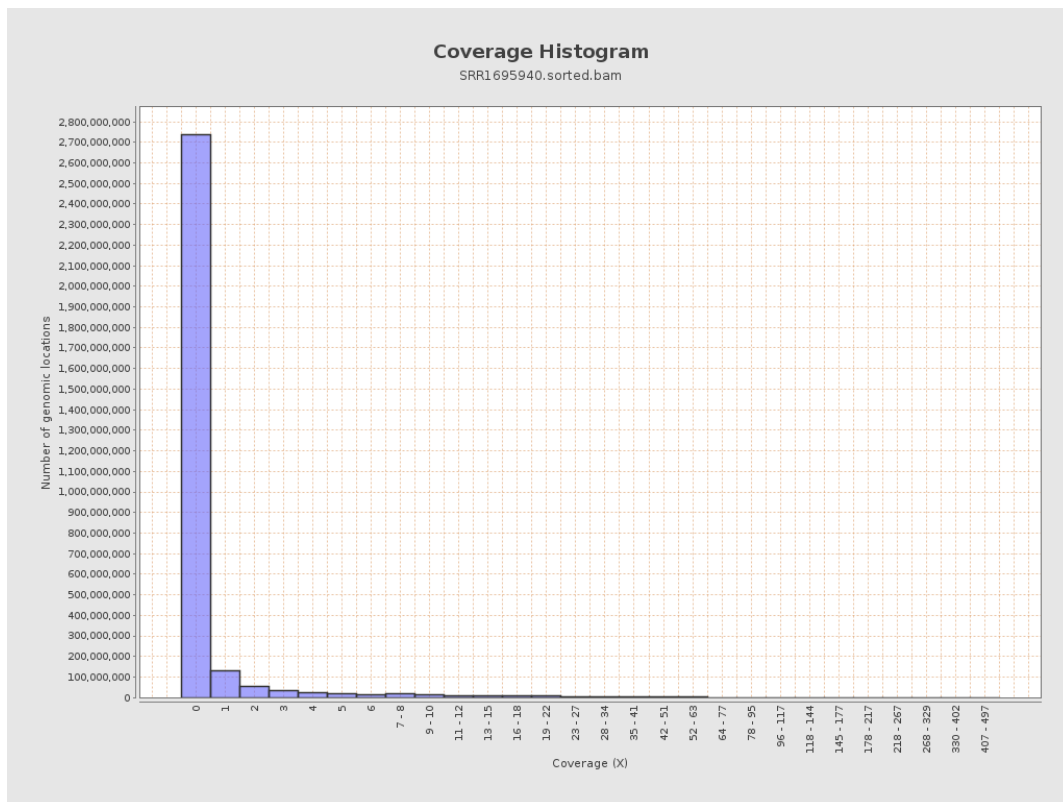
		bases	coverage	deviation
chr1	249250621	177814568	0.7134	3.5299
chr2	243199373	100647707	0.4138	3.1836
chr3	198022430	241477510	1.2194	4.5407
chr4	191154276	103554908	0.5417	3.1254
chr5	180915260	253986942	1.4039	6.2294
chr6	171115067	82863888	0.4843	2.1436
chr7	159138663	111421715	0.7002	2.9609
chr8	146364022	156392501	1.0685	4.4278
chr9	141213431	29297777	0.2075	1.8759
chr10	135534747	132520036	0.9778	4.2708
chr11	135006516	97168546	0.7197	3.71
chr12	133851895	115994710	0.8666	4.0029
chr13	115169878	70905398	0.6157	2.9727
chr14	107349540	51094632	0.476	2.4984
chr15	102531392	29469026	0.2874	2.2987
chr16	90354753	51697216	0.5722	3.0008
chr17	81195210	14746587	0.1816	1.8882
chr18	78077248	34733643	0.4449	2.4703
chr19	59128983	4112599	0.0696	0.9358
chr20	63025520	8534651	0.1354	0.9505
chr21	48129895	32449942	0.6742	2.8976
chr22	51304566	6930671	0.1351	2.2569
chrMT	16571	4187	0.2527	0.5862
chrX	155270560	90660686	0.5839	4.6426

chrY	59373566	1870073	0.0315	0.3607
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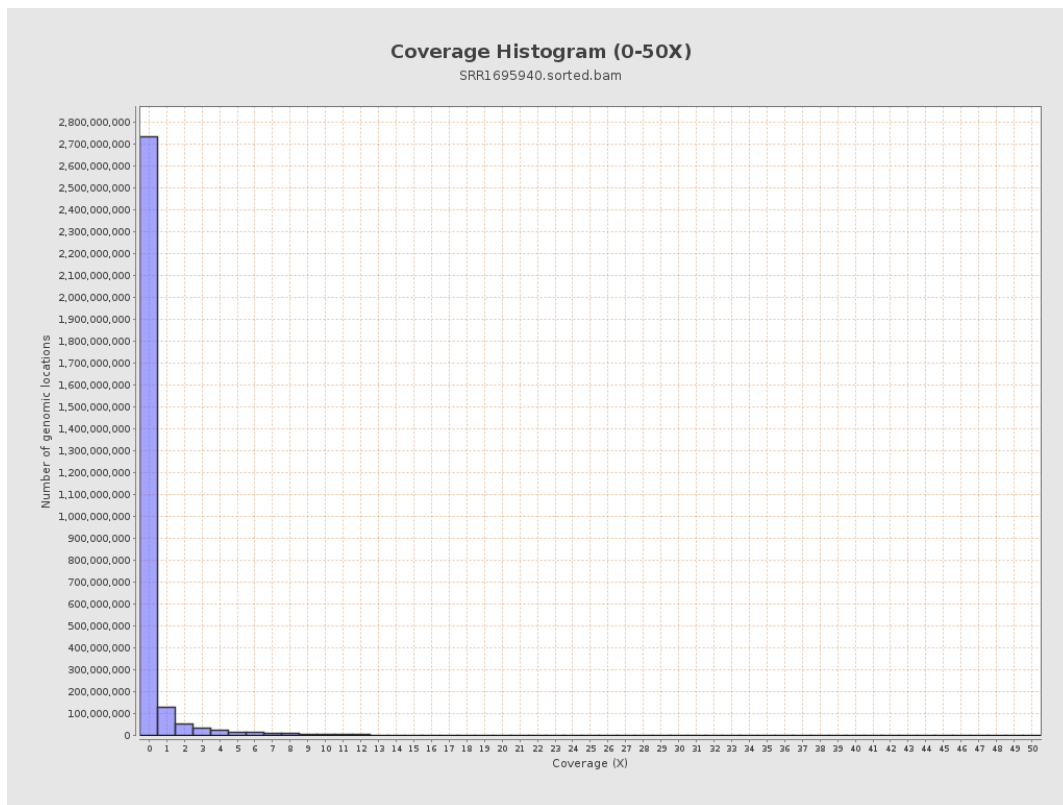
3. Results : Coverage across reference



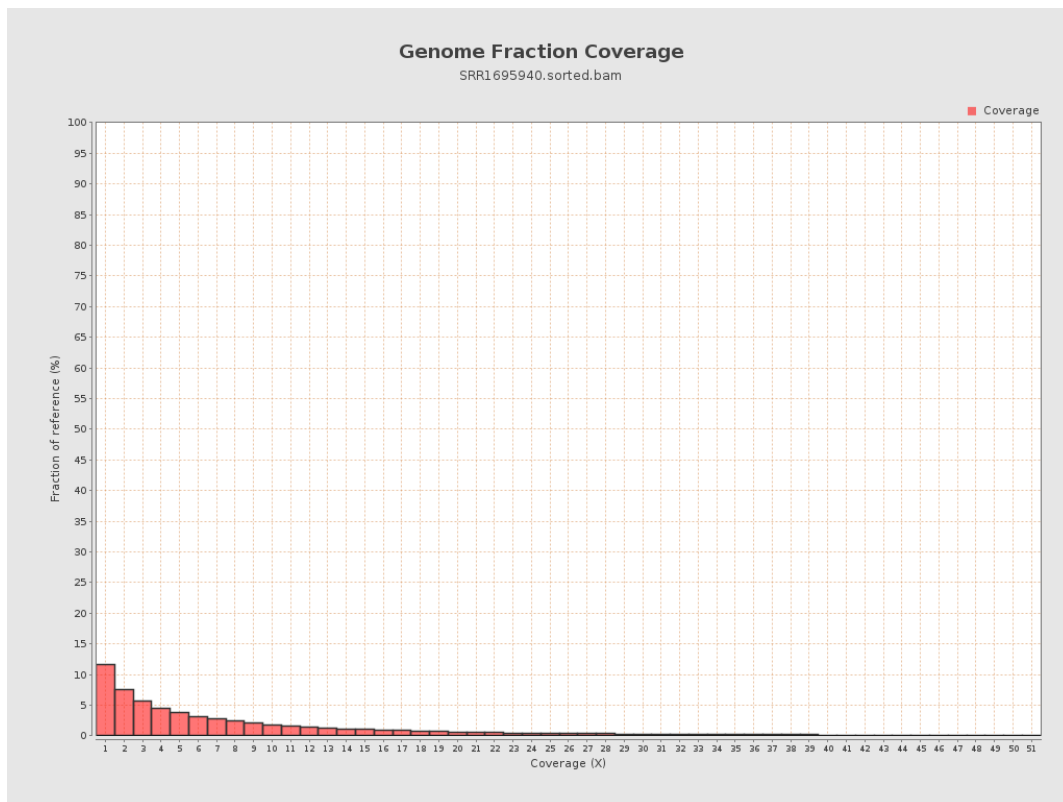
4. Results : Coverage Histogram



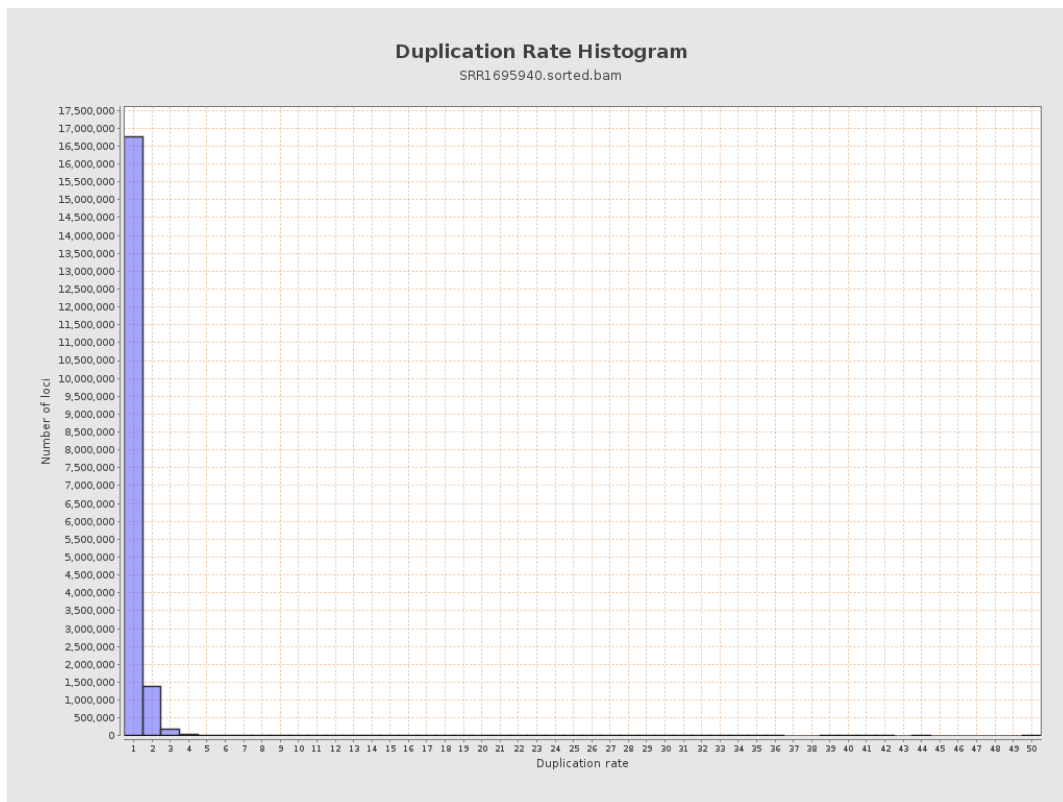
5. Results : Coverage Histogram (0-50X)



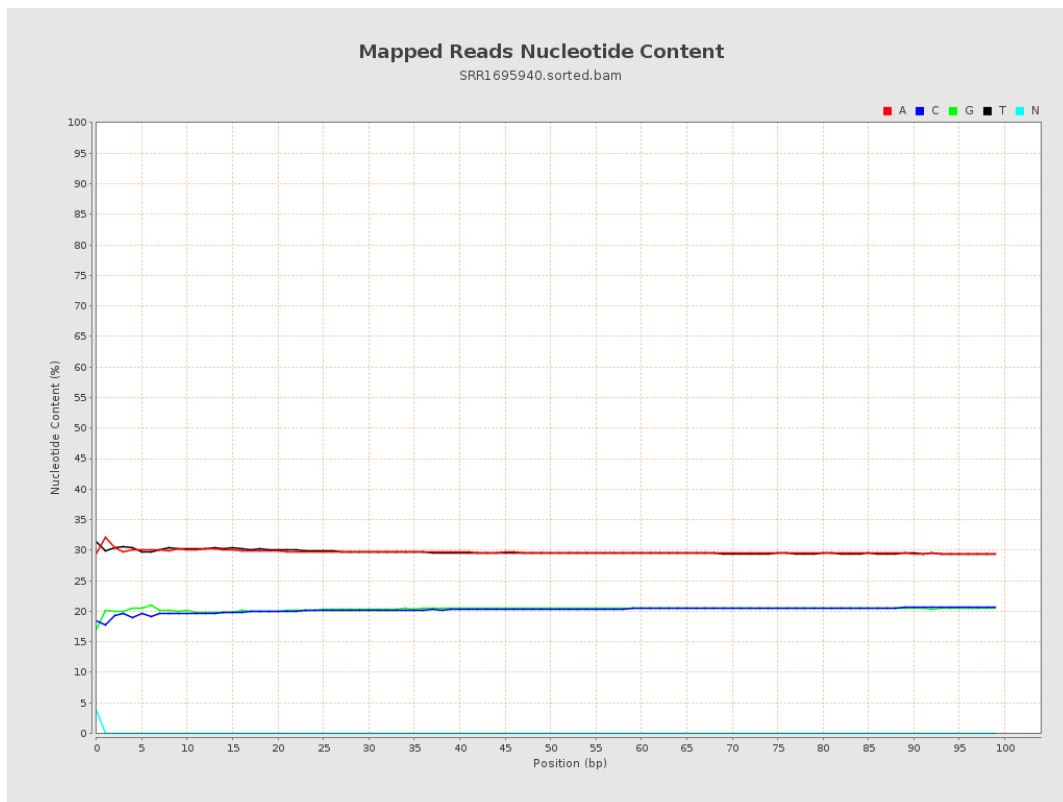
6. Results : Genome Fraction Coverage



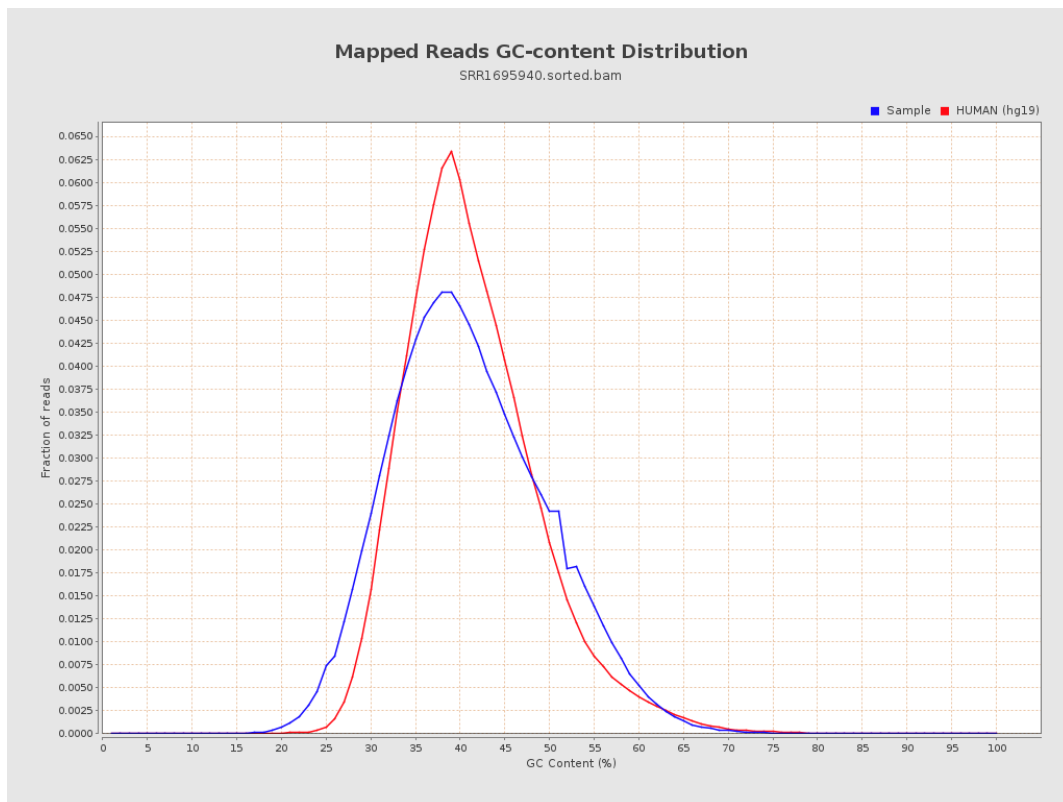
7. Results : Duplication Rate Histogram



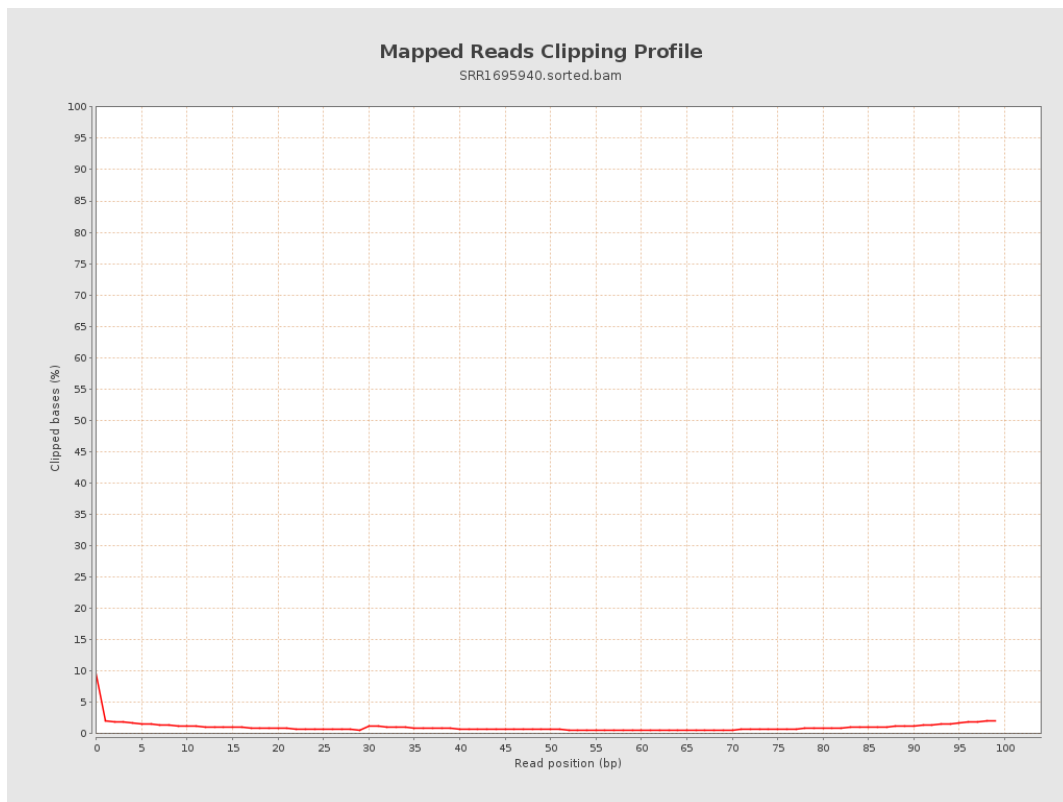
8. Results : Mapped Reads Nucleotide Content



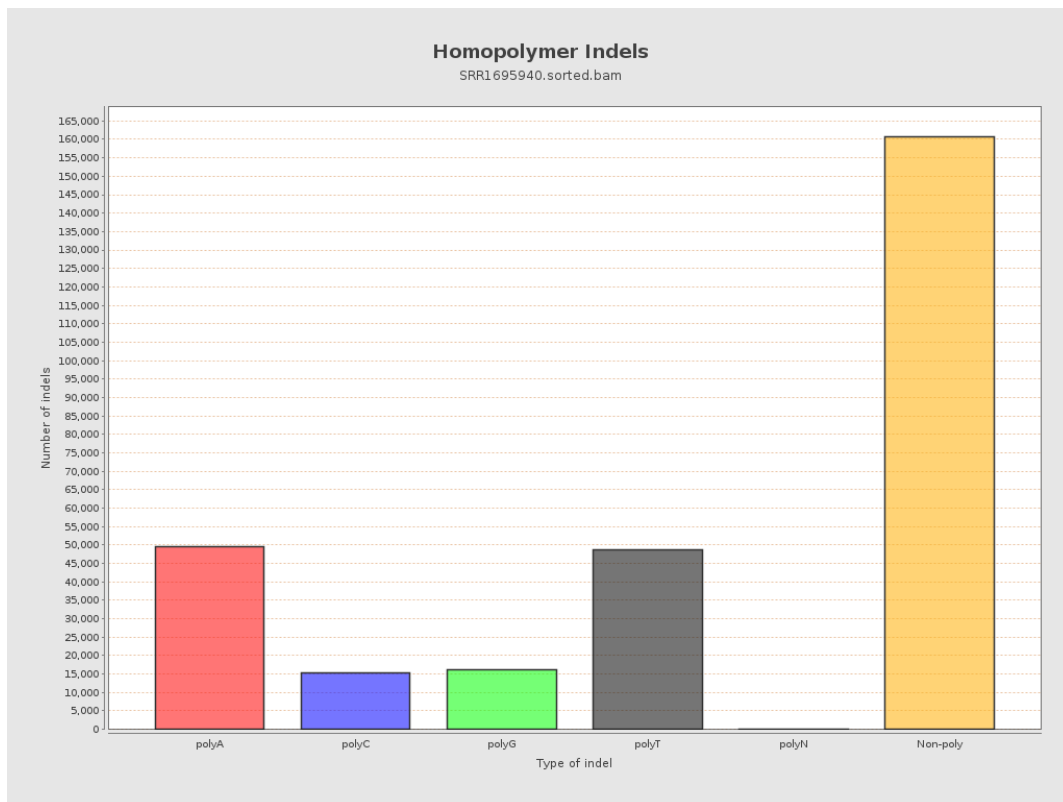
9. Results : Mapped Reads GC-content Distribution



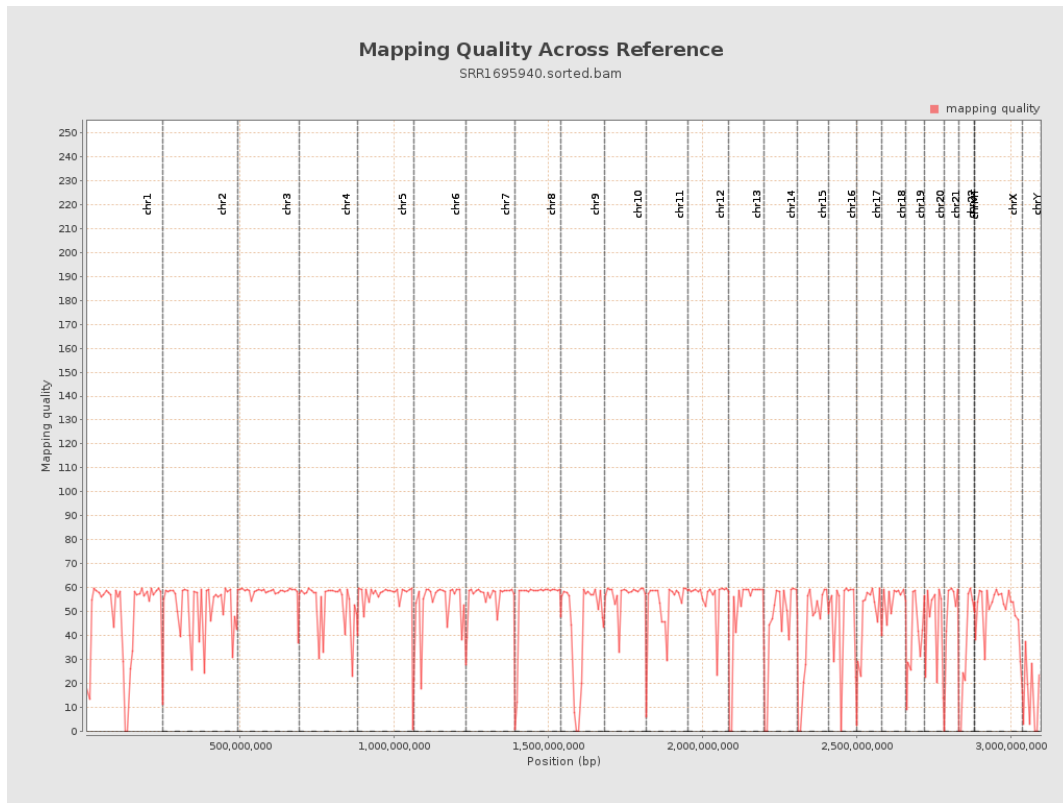
10. Results : Mapped Reads Clipping Profile



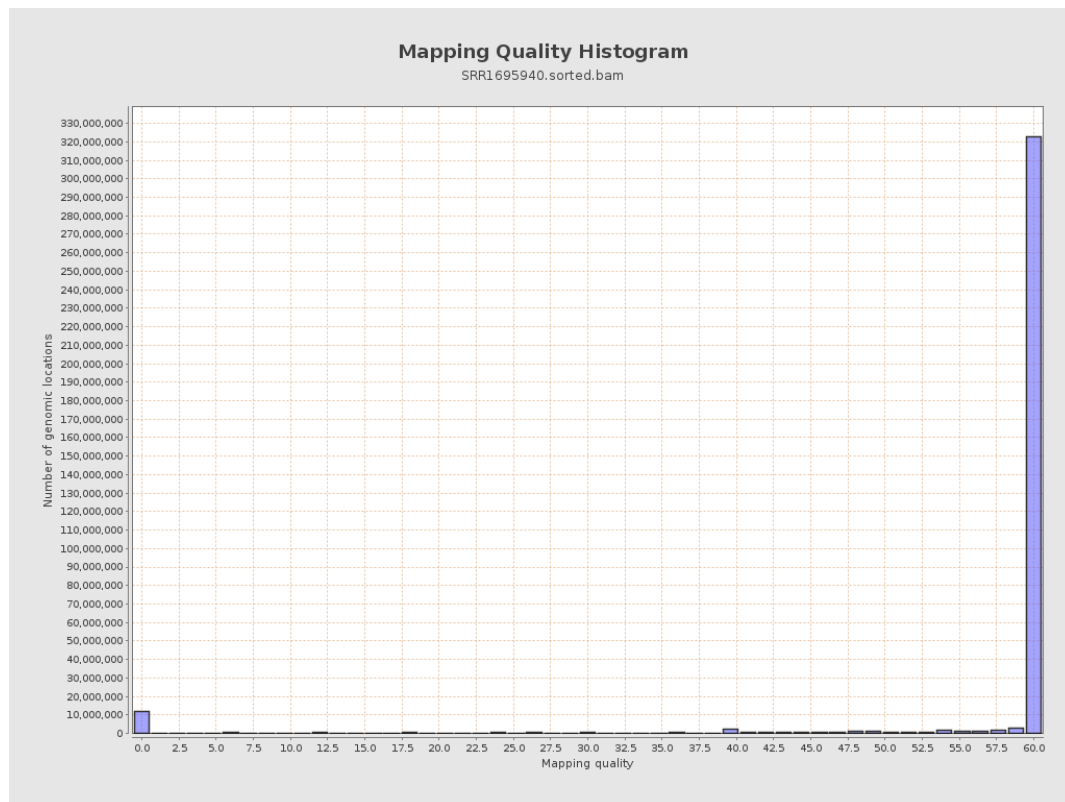
11. Results : Homopolymer Indels



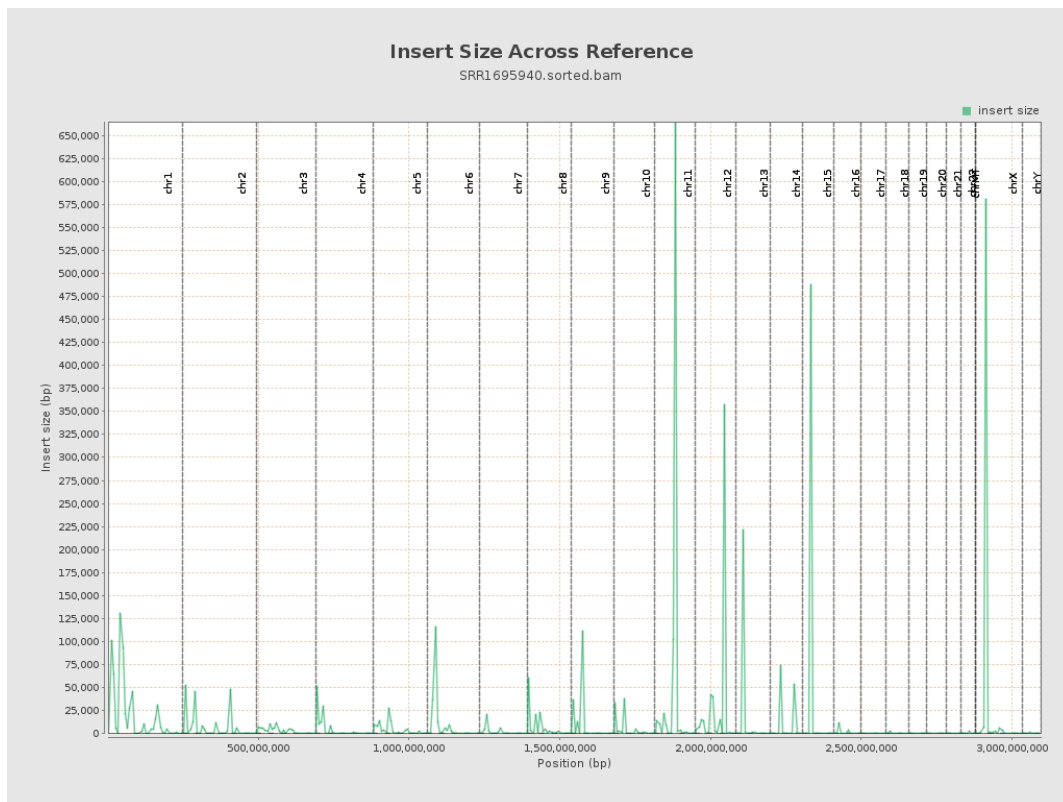
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

