

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 13:18:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695916.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_SRR1695916 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695916_1.fastq.gz SRR1695916_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 13:18:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,187,584
Mapped reads	2,180,236 / 99.66%
Unmapped reads	7,348 / 0.34%
Mapped paired reads	2,180,236 / 99.66%
Mapped reads, first in pair	1,091,410 / 49.89%
Mapped reads, second in pair	1,088,826 / 49.77%
Mapped reads, both in pair	2,176,120 / 99.48%
Mapped reads, singletons	4,116 / 0.19%
Secondary alignments	0
Supplementary alignments	57,198 / 2.61%
Read min/max/mean length	30 / 150 / 151.38
Duplicated reads (estimated)	7,304 / 0.33%
Duplication rate	0.25%
Clipped reads	203,293 / 9.29%

2.2. ACGT Content

Number/percentage of A's	95,769,655 / 29.5%
Number/percentage of C's	66,387,399 / 20.45%
Number/percentage of T's	95,126,745 / 29.3%
Number/percentage of G's	67,327,178 / 20.74%
Number/percentage of N's	43,858 / 0.01%

GC Percentage	41.19%
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2.3. Coverage

Mean	0.1049
Standard Deviation	0.3545

2.4. Mapping Quality

Mean Mapping Quality	54.75
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2.5. Insert size

Mean	71,295.59
Standard Deviation	2,566,488.15
P25/Median/P75	300 / 309 / 318

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	1,270,648
Insertions	38,209
Mapped reads with at least one insertion	1.69%
Deletions	37,745
Mapped reads with at least one deletion	1.67%
Homopolymer indels	46.83%

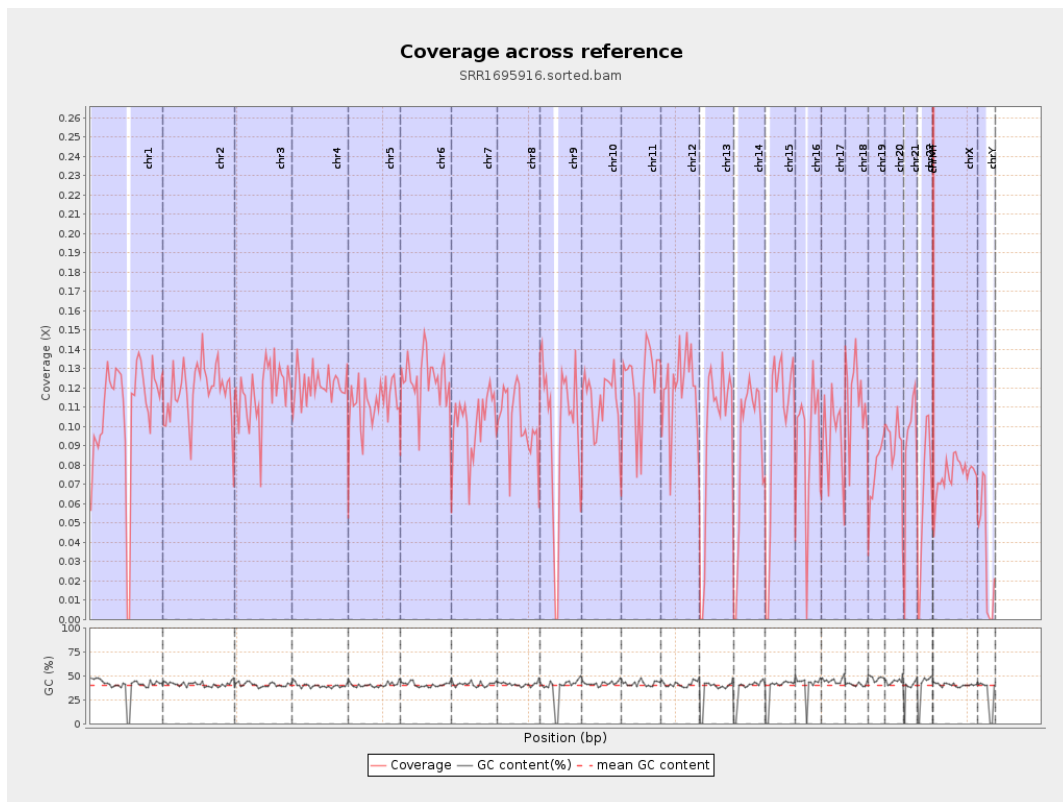
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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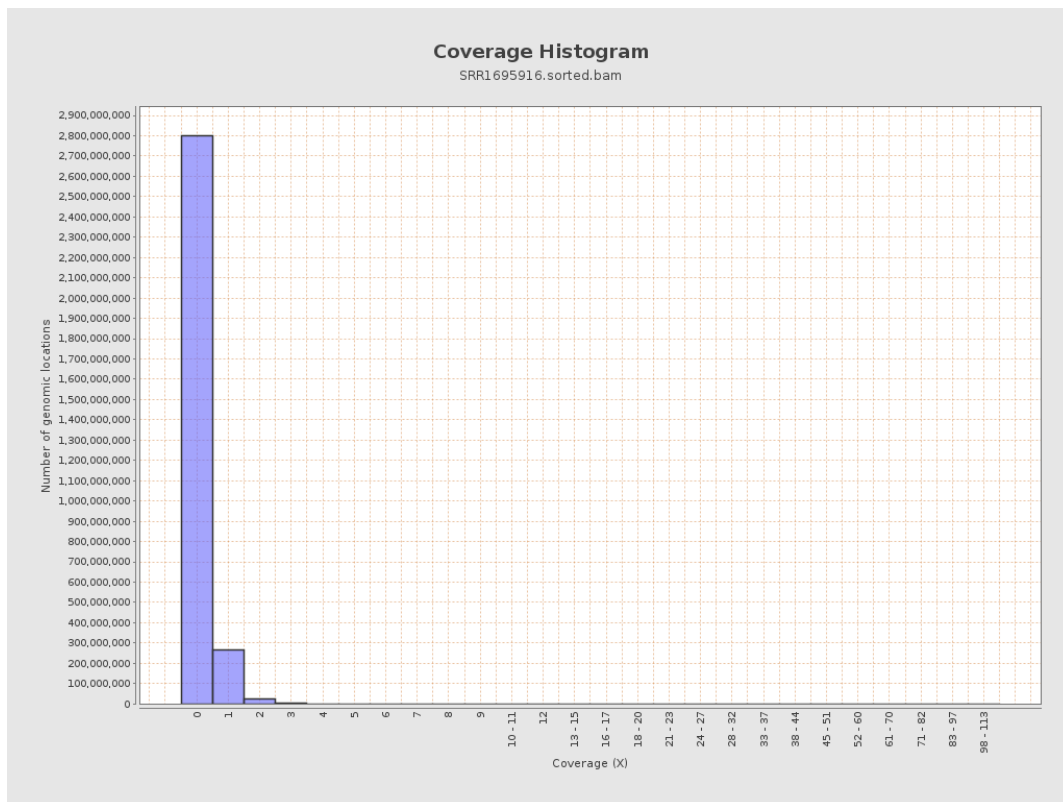
		bases	coverage	deviation
chr1	249250621	26812000	0.1076	0.3597
chr2	243199373	28836749	0.1186	0.3985
chr3	198022430	23295881	0.1176	0.3562
chr4	191154276	23291887	0.1218	0.3726
chr5	180915260	20288167	0.1121	0.3474
chr6	171115067	21294515	0.1244	0.3735
chr7	159138663	16211897	0.1019	0.3346
chr8	146364022	14860542	0.1015	0.3312
chr9	141213431	13805522	0.0978	0.3435
chr10	135534747	15442611	0.1139	0.3755
chr11	135006516	16560433	0.1227	0.3696
chr12	133851895	15998650	0.1195	0.3607
chr13	115169878	11135714	0.0967	0.3272
chr14	107349540	9770119	0.091	0.3169
chr15	102531392	10246002	0.0999	0.3326
chr16	90354753	8160461	0.0903	0.3495
chr17	81195210	7687949	0.0947	0.3353
chr18	78077248	8990899	0.1152	0.3756
chr19	59128983	4596606	0.0777	0.2994
chr20	63025520	5778228	0.0917	0.3186
chr21	48129895	4398974	0.0914	0.368
chr22	51304566	3282350	0.064	0.2706
chrMT	16571	410325	24.7616	8.1355
chrX	155270560	11572334	0.0745	0.2828

chrY	59373566	2024607	0.0341	0.2321
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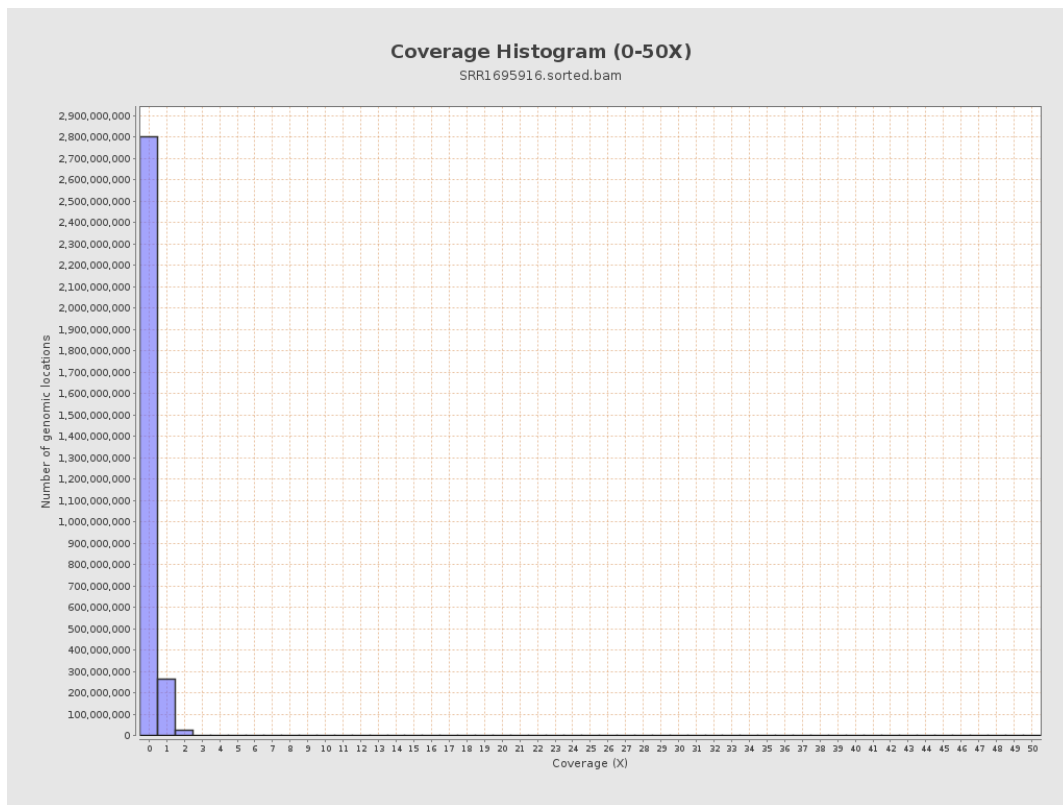
3. Results : Coverage across reference



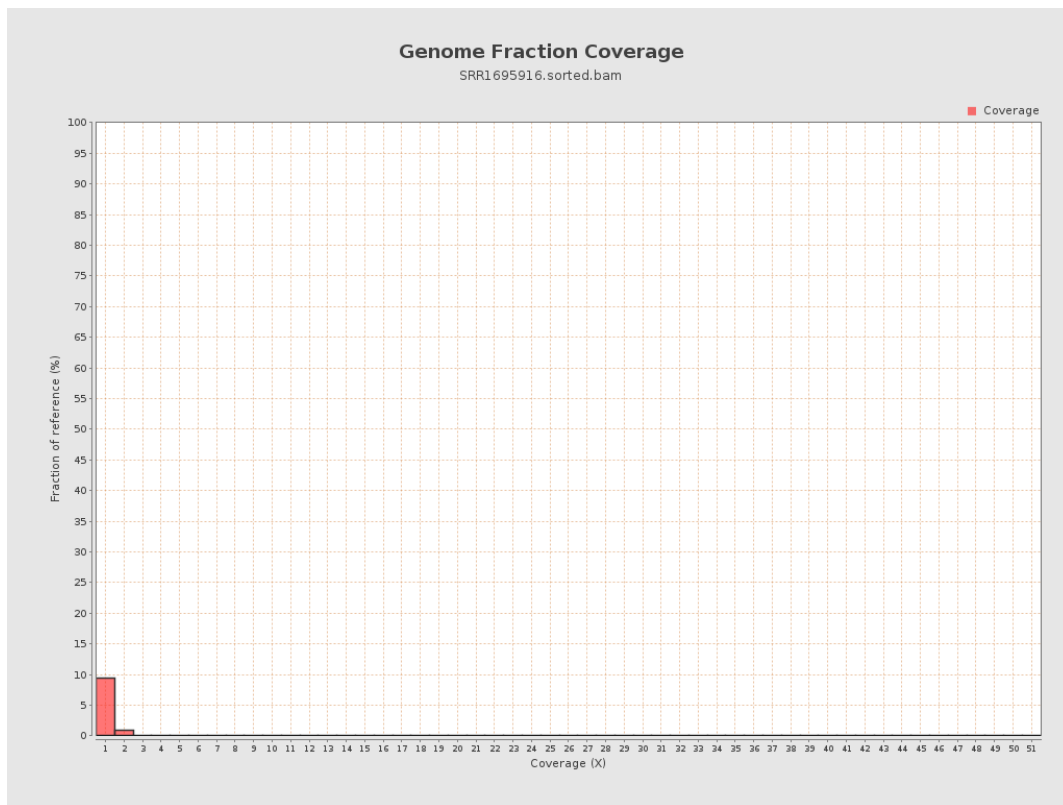
4. Results : Coverage Histogram



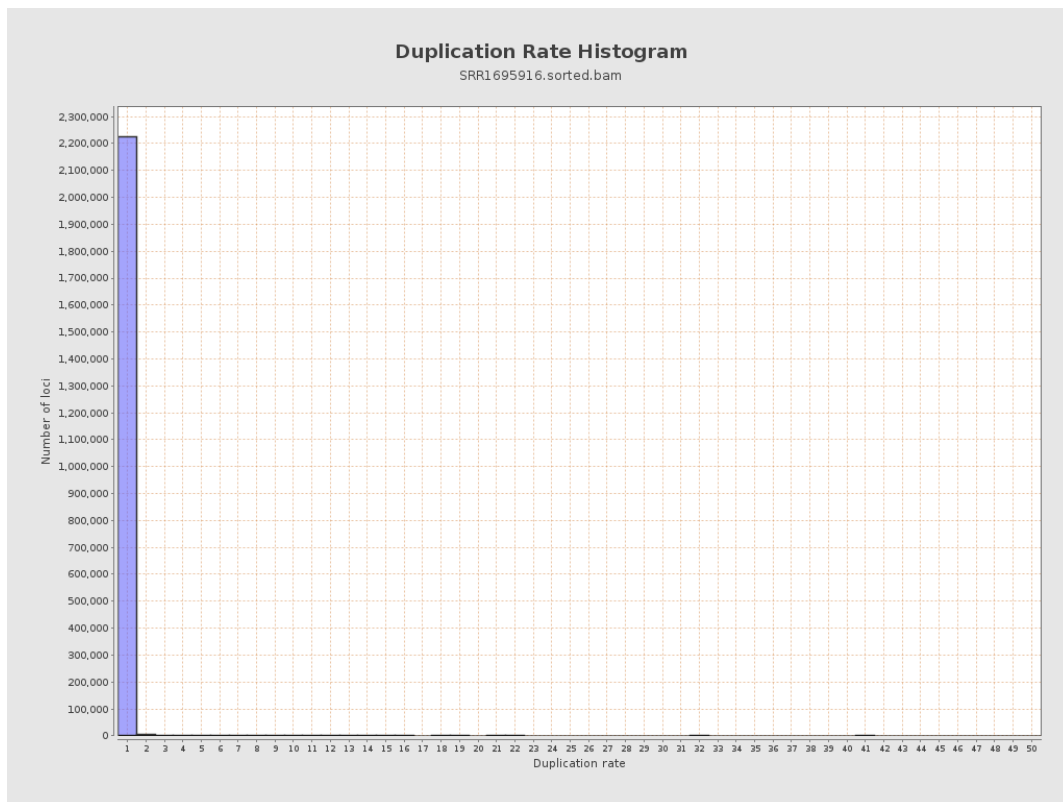
5. Results : Coverage Histogram (0-50X)



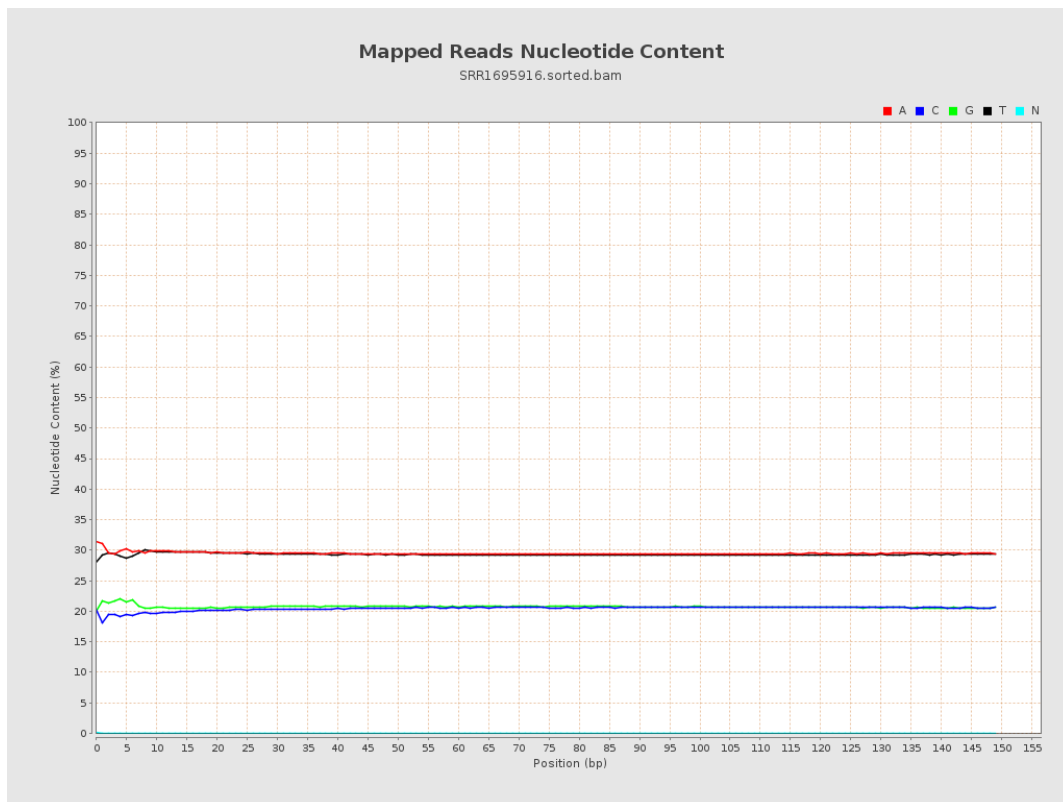
6. Results : Genome Fraction Coverage



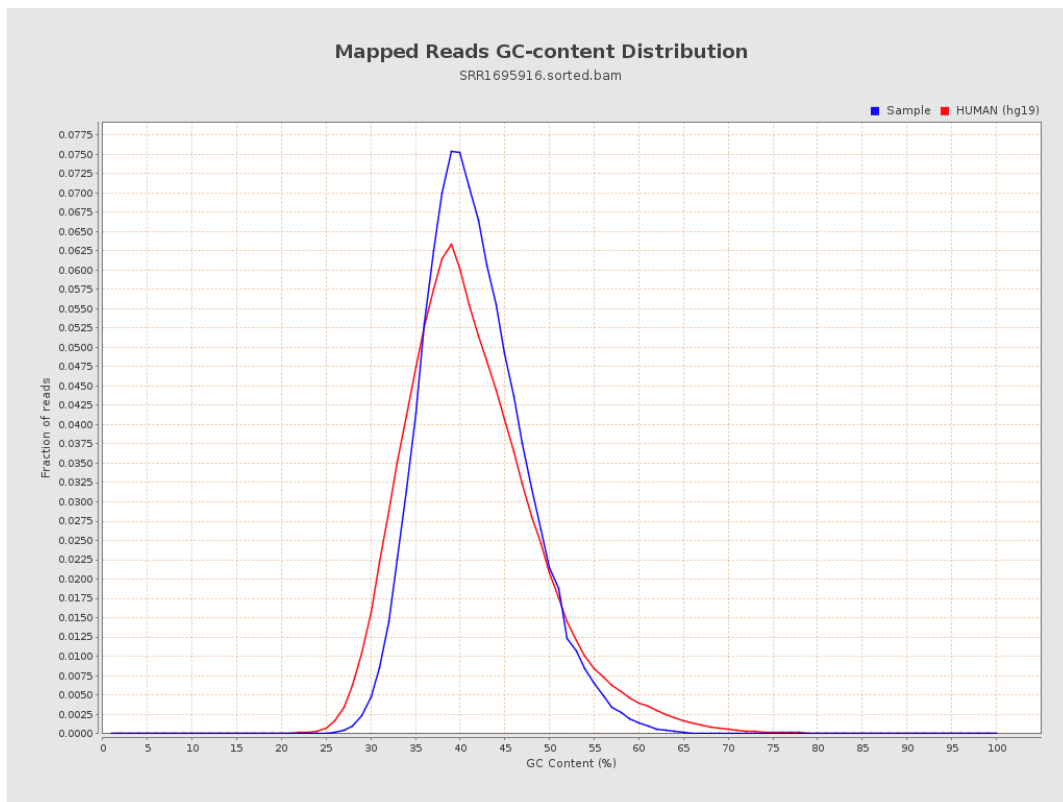
7. Results : Duplication Rate Histogram



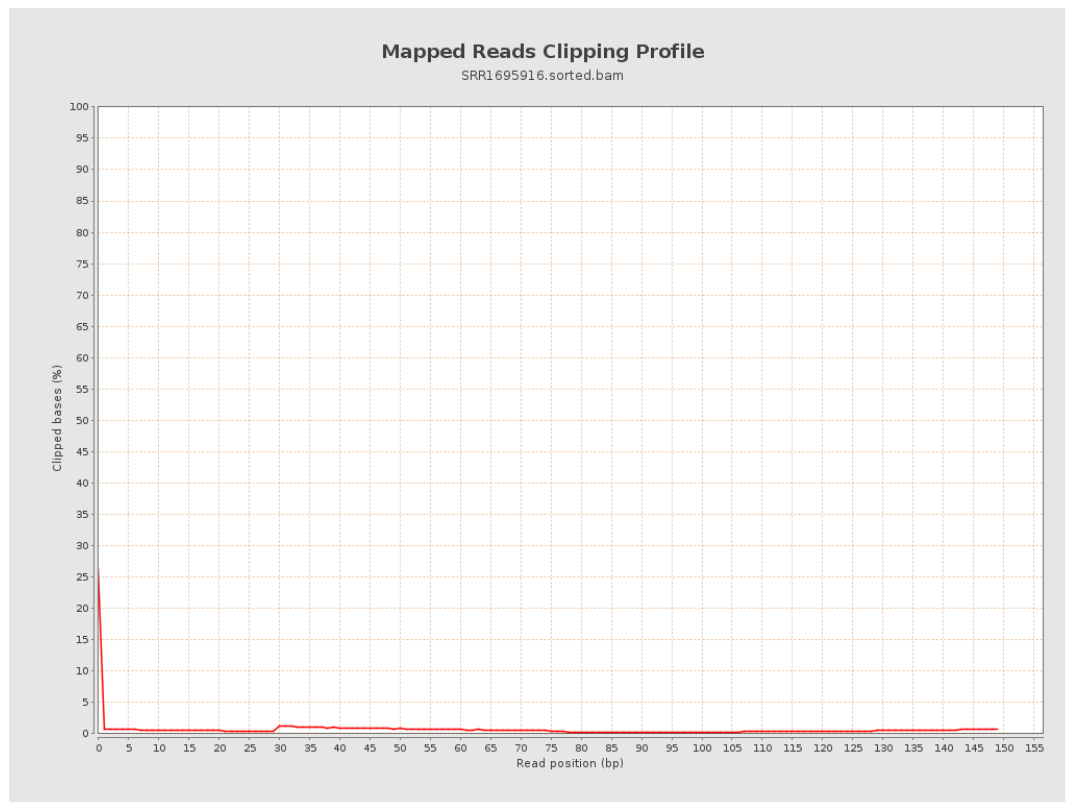
8. Results : Mapped Reads Nucleotide Content



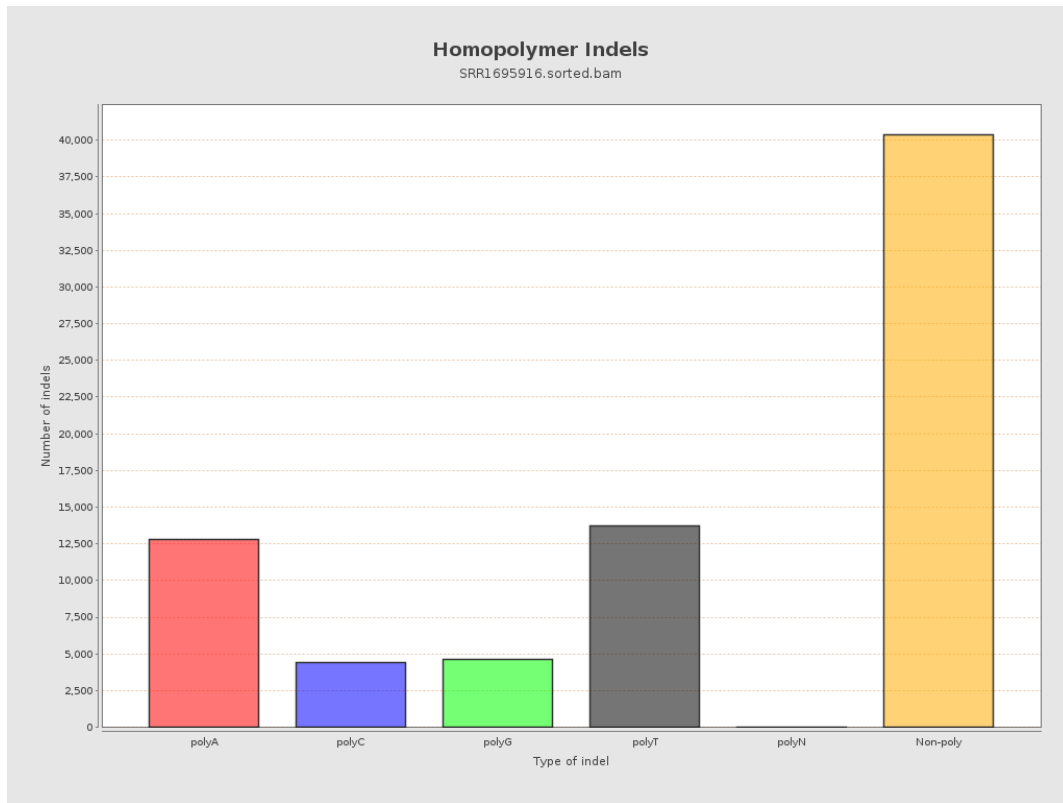
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



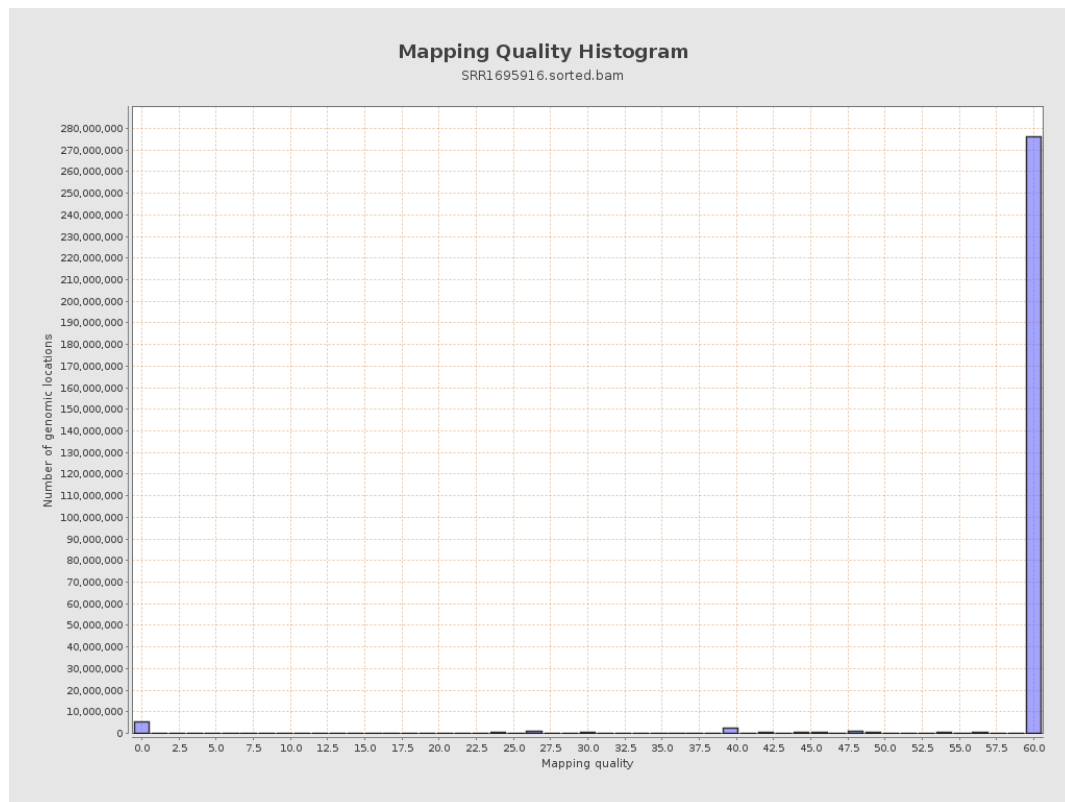
11. Results : Homopolymer Indels



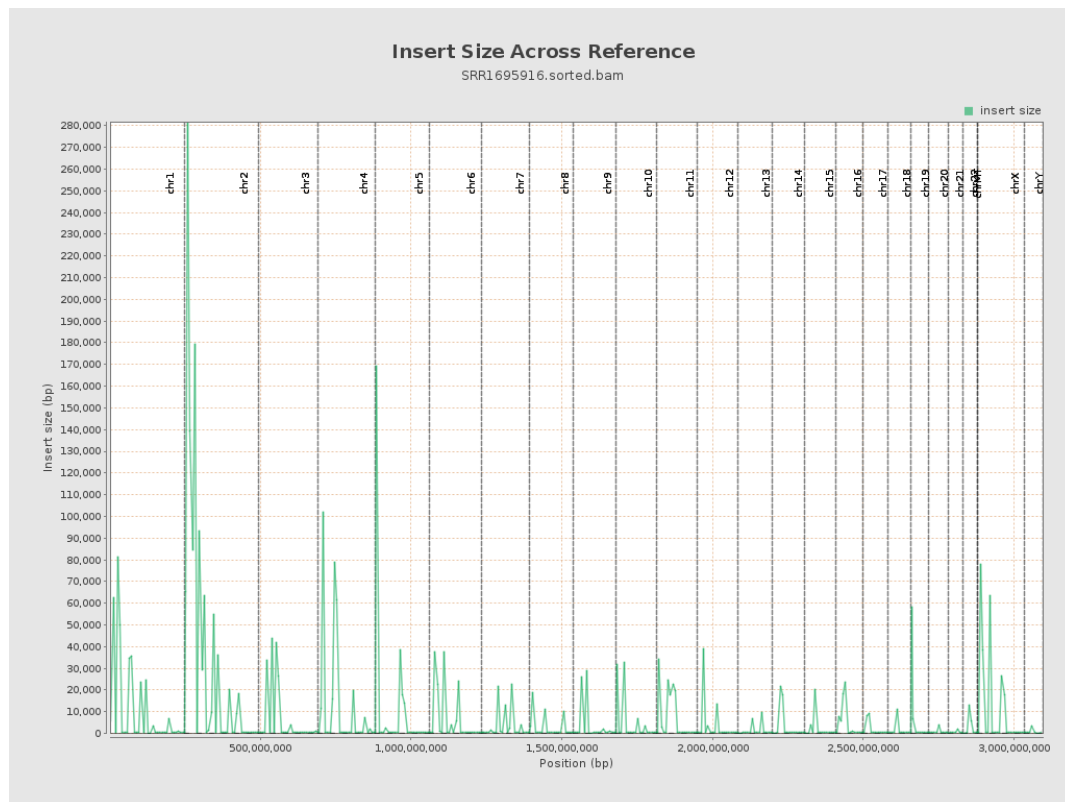
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

