

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 04:45:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695943.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_SRR1695943 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695943_1.fastq.gz SRR1695943_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 04:45:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695943.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	418,477,858
Mapped reads	414,116,976 / 98.96%
Unmapped reads	4,360,882 / 1.04%
Mapped paired reads	414,116,976 / 98.96%
Mapped reads, first in pair	208,171,523 / 49.74%
Mapped reads, second in pair	205,945,453 / 49.21%
Mapped reads, both in pair	411,015,684 / 98.22%
Mapped reads, singletons	3,101,292 / 0.74%
Secondary alignments	0
Supplementary alignments	5,425,976 / 1.3%
Read min/max/mean length	30 / 100 / 100.53
Duplicated reads (estimated)	88,726,043 / 21.2%
Duplication rate	18.3%
Clipped reads	32,343,132 / 7.73%

2.2. ACGT Content

Number/percentage of A's	11,545,502,915 / 28.19%
Number/percentage of C's	8,838,644,225 / 21.58%
Number/percentage of T's	11,464,777,017 / 28%
Number/percentage of G's	9,097,840,046 / 22.22%
Number/percentage of N's	2,663,512 / 0.01%

GC Percentage	43.8%
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2.3. Coverage

Mean	13.2314
Standard Deviation	31.8117

2.4. Mapping Quality

Mean Mapping Quality	54.02
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2.5. Insert size

Mean	73,238.13
Standard Deviation	2,663,826.08
P25/Median/P75	305 / 314 / 322

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	212,457,095
Insertions	5,281,676
Mapped reads with at least one insertion	1.24%
Deletions	4,530,411
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.39%

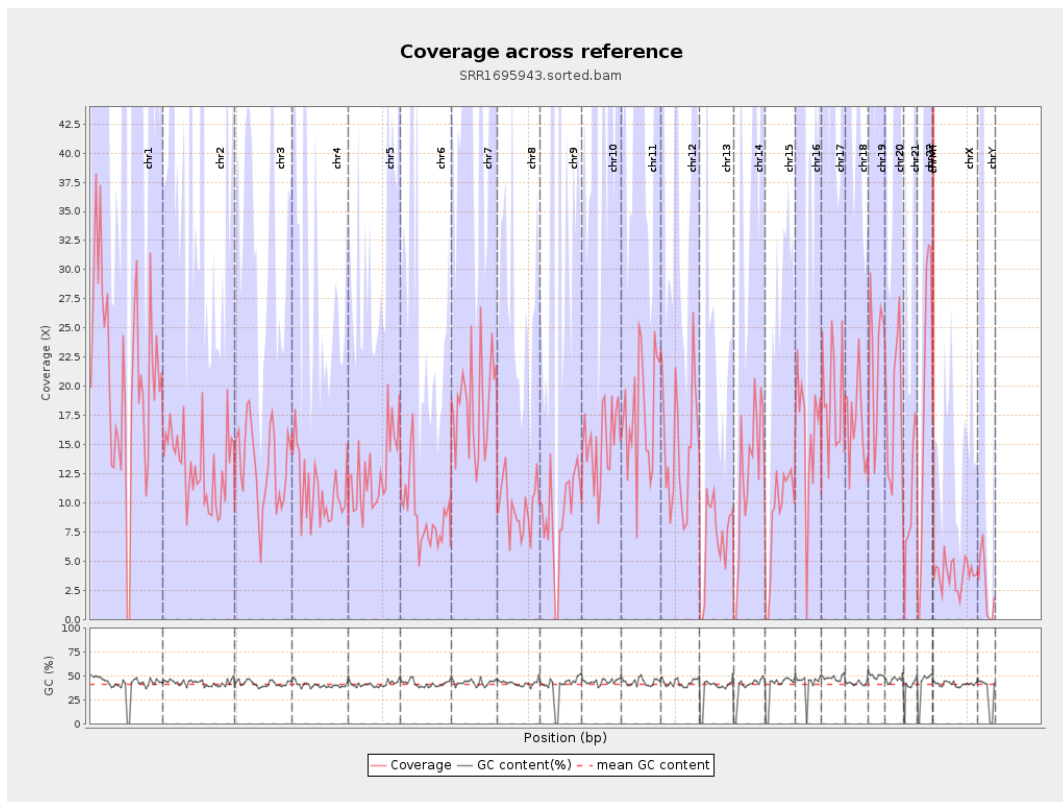
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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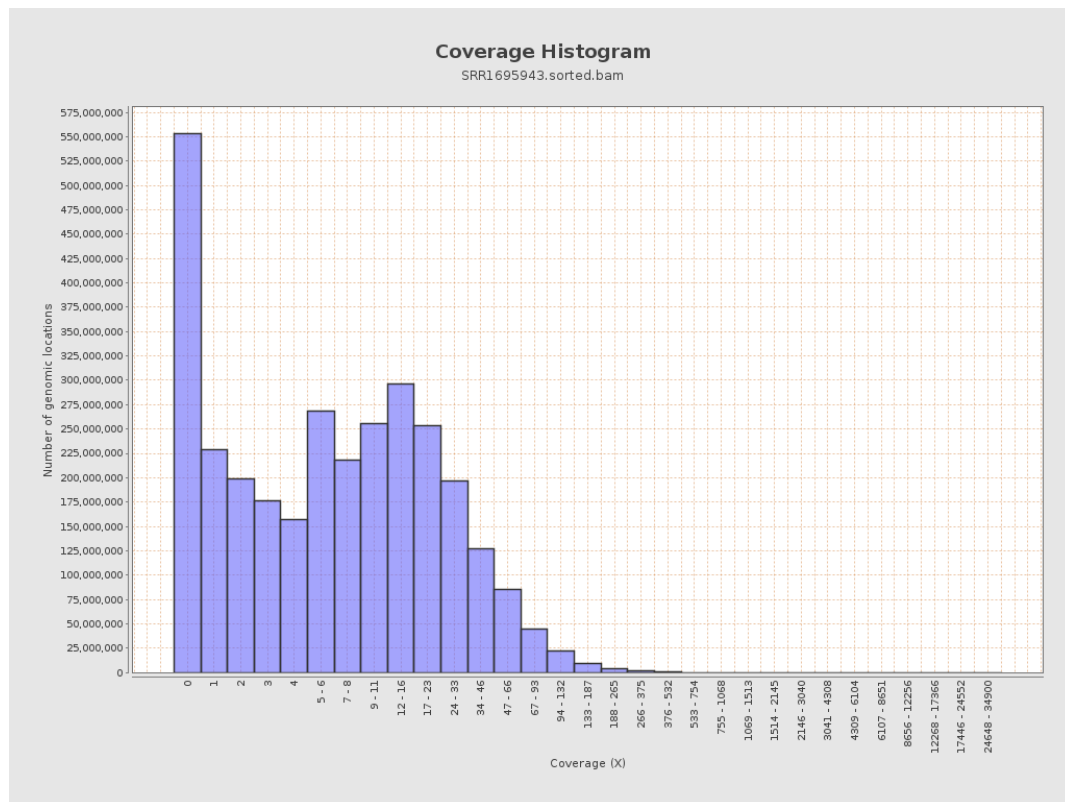
		bases	coverage	deviation
chr1	249250621	5175481599	20.7642	45.205
chr2	243199373	3179562592	13.0739	43.8833
chr3	198022430	2598352406	13.1215	19.6807
chr4	191154276	2118703950	11.0837	20.1483
chr5	180915260	2299846301	12.7123	19.5056
chr6	171115067	1514060599	8.8482	19.5536
chr7	159138663	2954884683	18.568	27.9897
chr8	146364022	1409764245	9.6319	18.4642
chr9	141213431	1270899942	8.9999	38.657
chr10	135534747	2051450561	15.136	43.7129
chr11	135006516	2388511269	17.6918	29.0756
chr12	133851895	1988505477	14.856	24.638
chr13	115169878	792780196	6.8836	16.5348
chr14	107349540	1336046892	12.4458	26.4924
chr15	102531392	910762747	8.8828	17.2777
chr16	90354753	1434421409	15.8754	39.9112
chr17	81195210	1543934686	19.0151	36.7485
chr18	78077248	1311797698	16.8013	47.853
chr19	59128983	1313361190	22.2118	42.6199
chr20	63025520	1107924514	17.579	28.6794
chr21	48129895	501568600	10.4211	24.1169
chr22	51304566	971546058	18.9368	43.0201
chrMT	16571	6347726	383.0623	131.6058
chrX	155270560	609795675	3.9273	11.9399

chrY	59373566	170084041	2.8646	36.769
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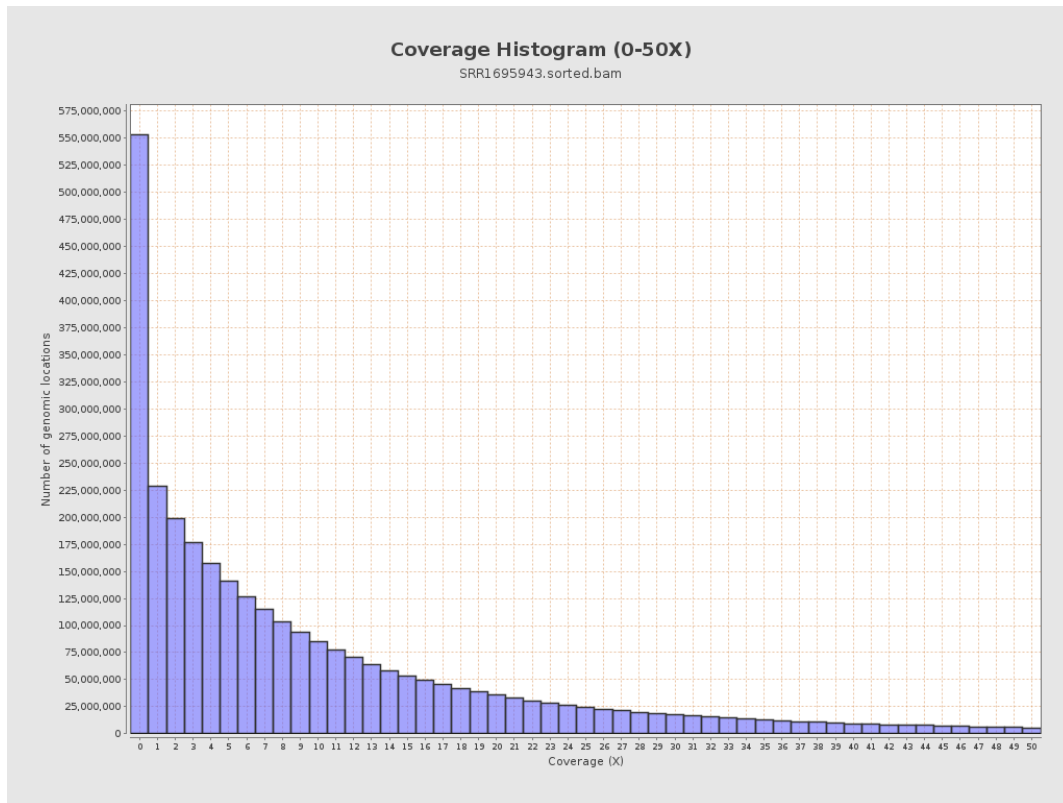
3. Results : Coverage across reference



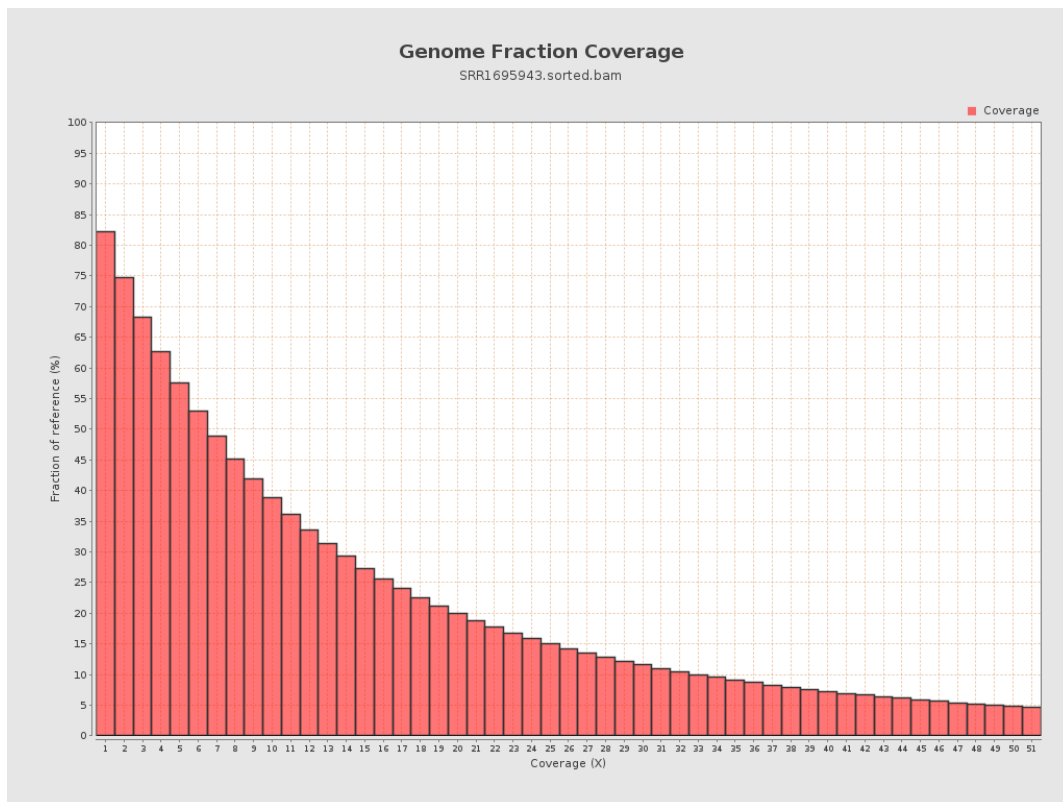
4. Results : Coverage Histogram



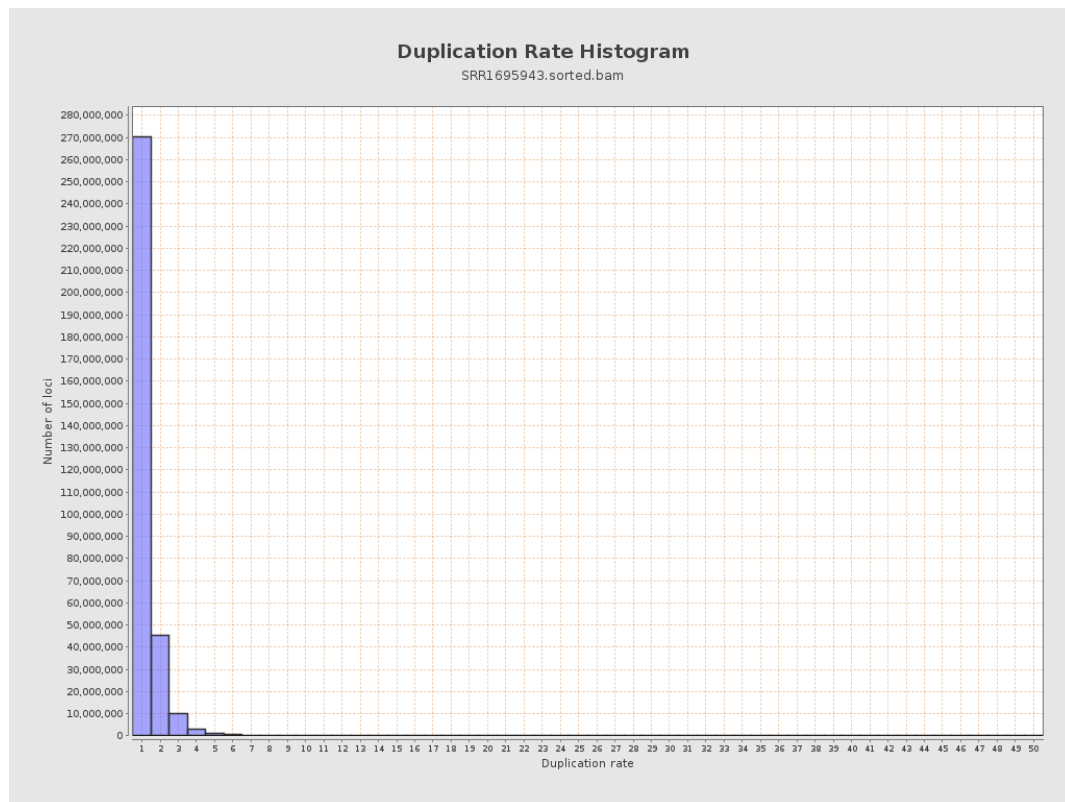
5. Results : Coverage Histogram (0-50X)



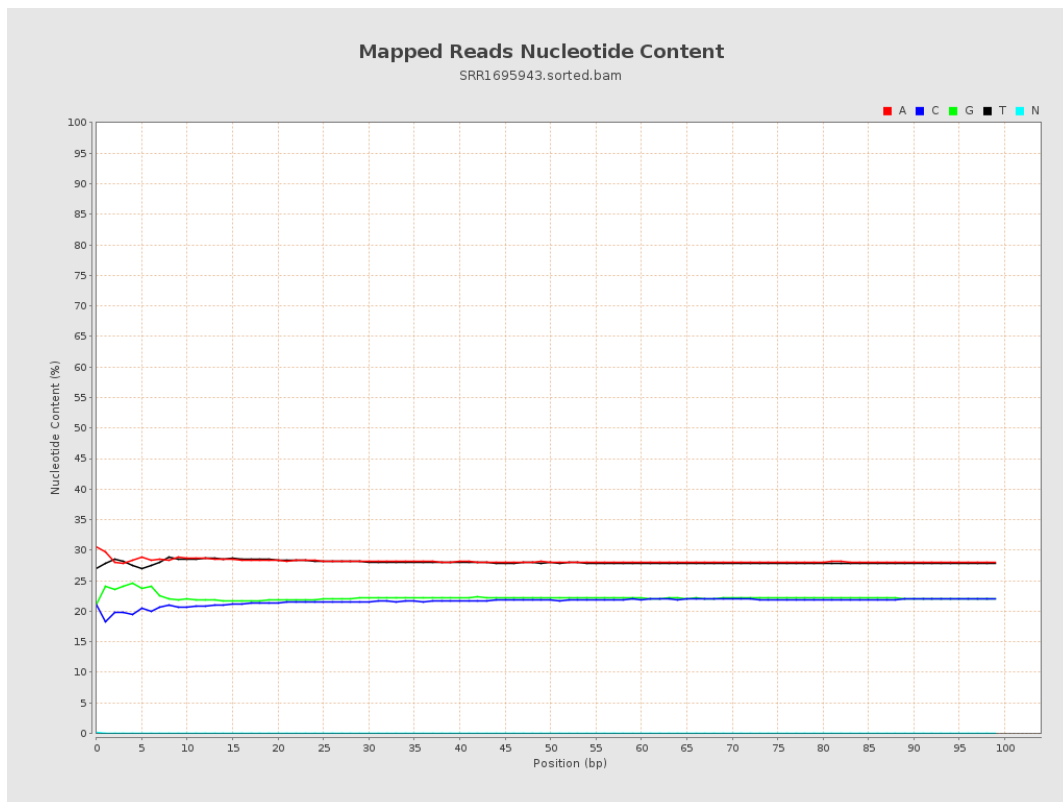
6. Results : Genome Fraction Coverage



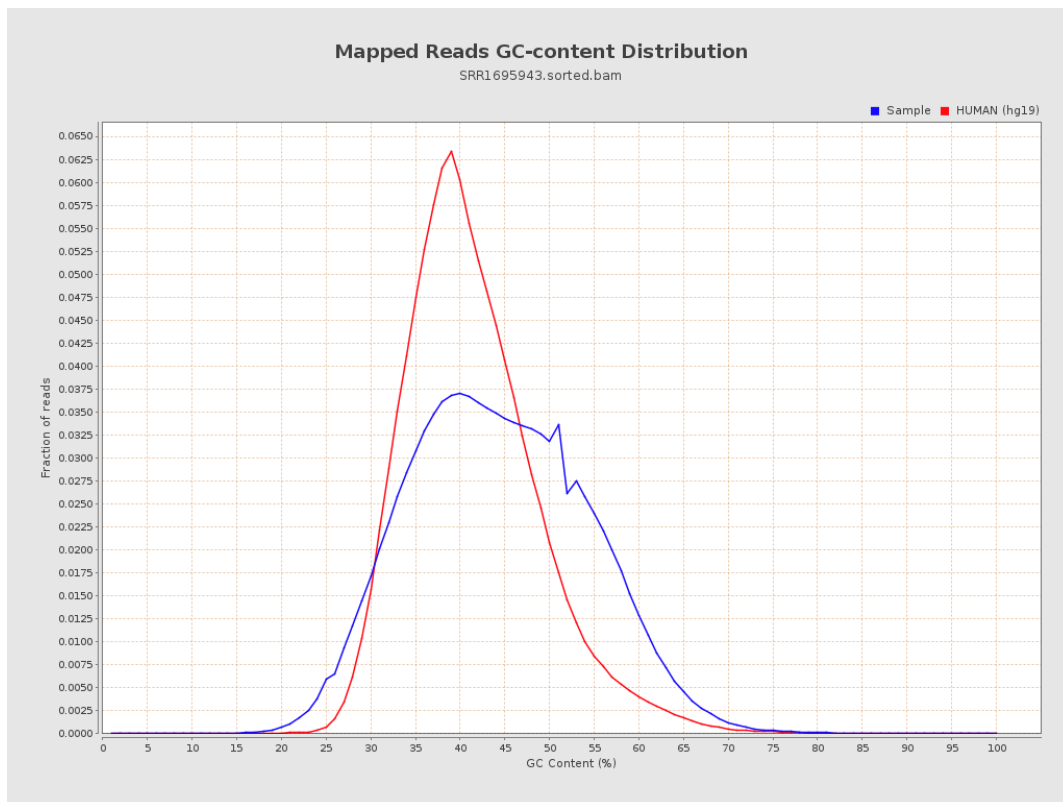
7. Results : Duplication Rate Histogram



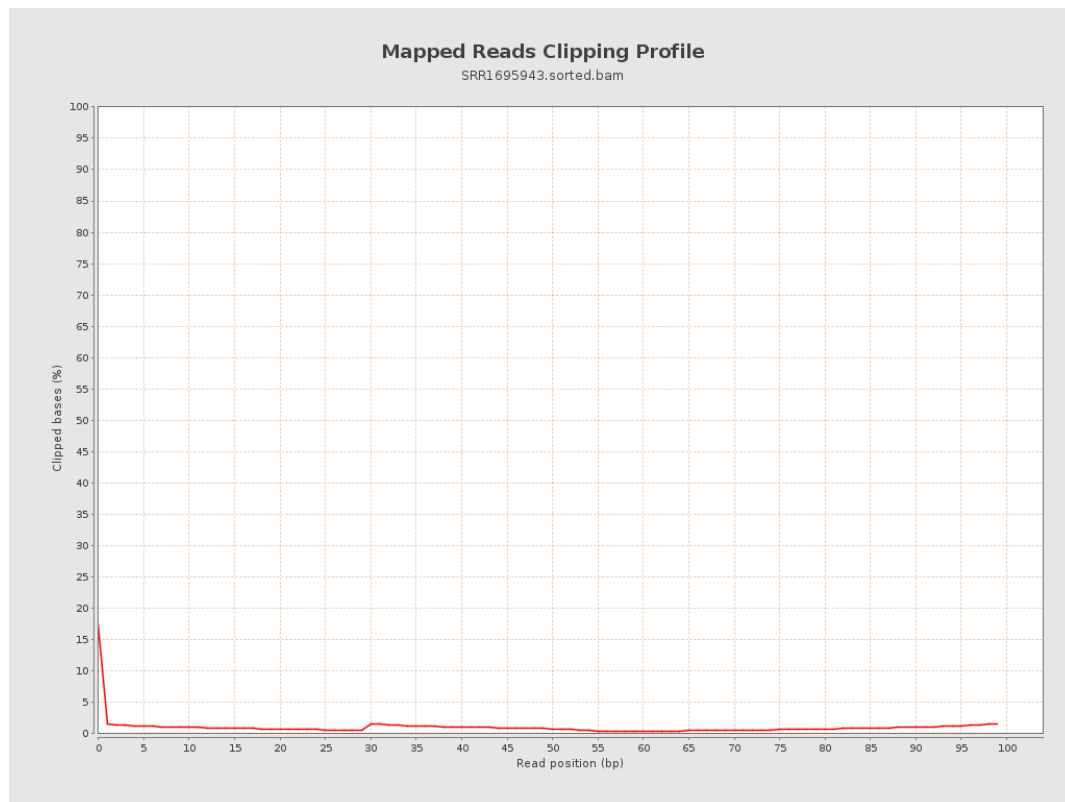
8. Results : Mapped Reads Nucleotide Content



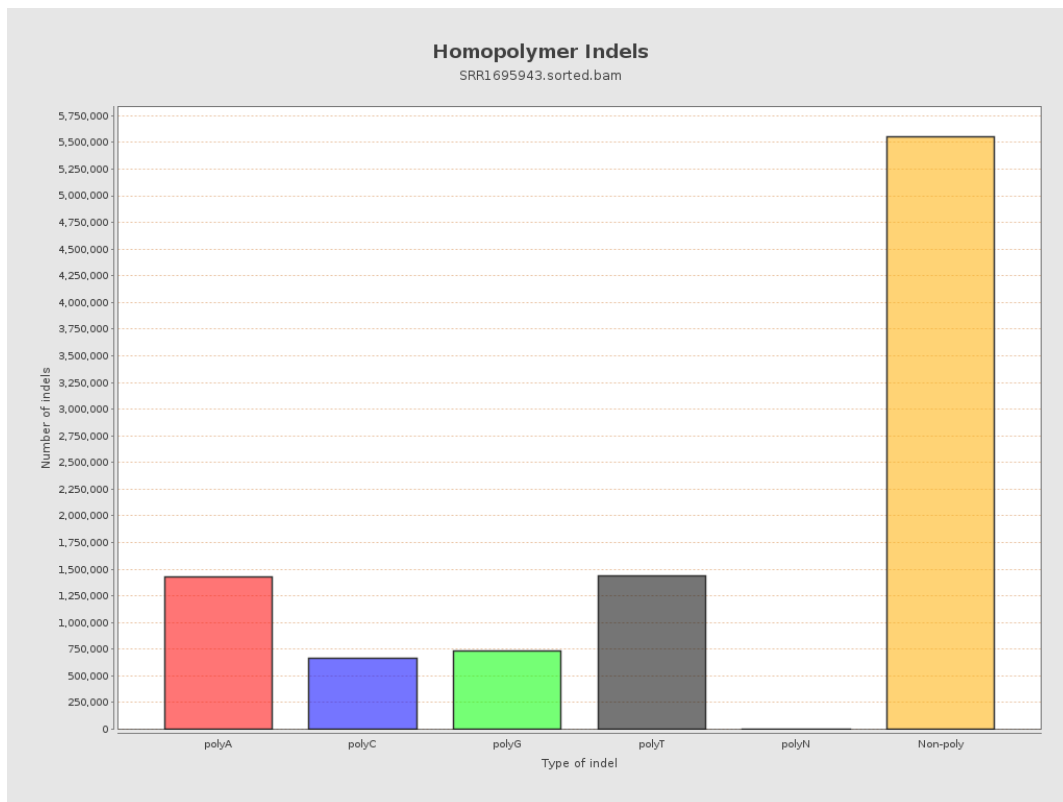
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



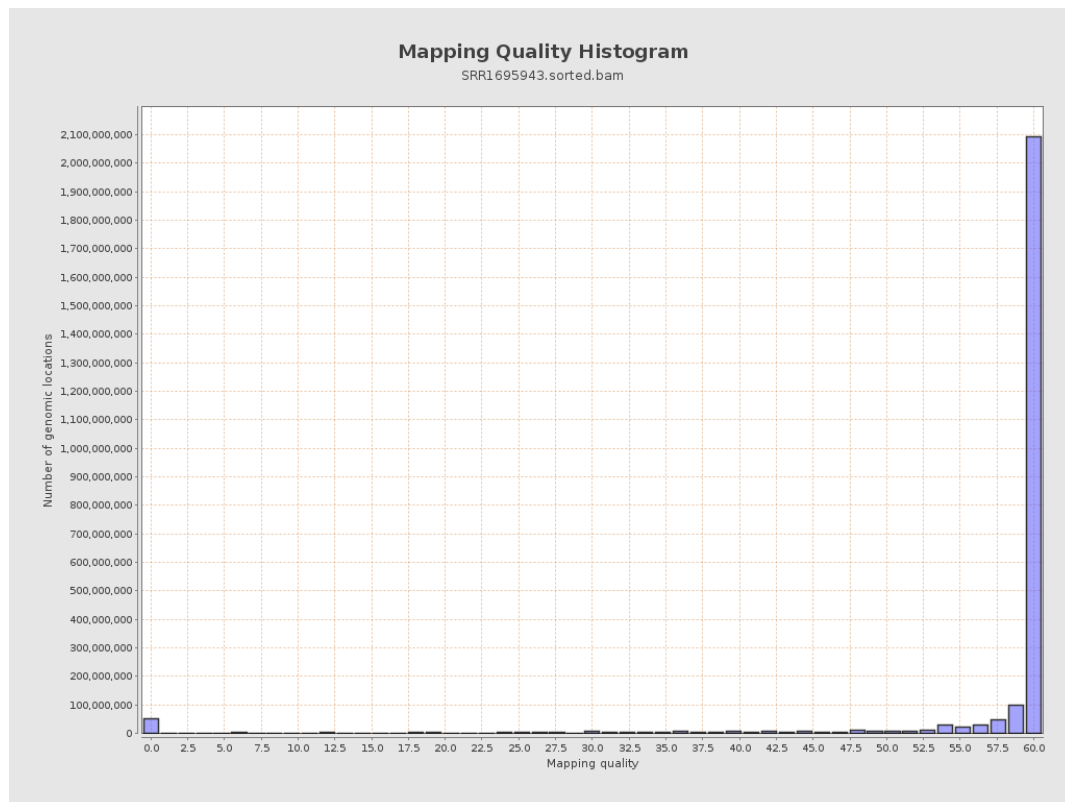
11. Results : Homopolymer Indels



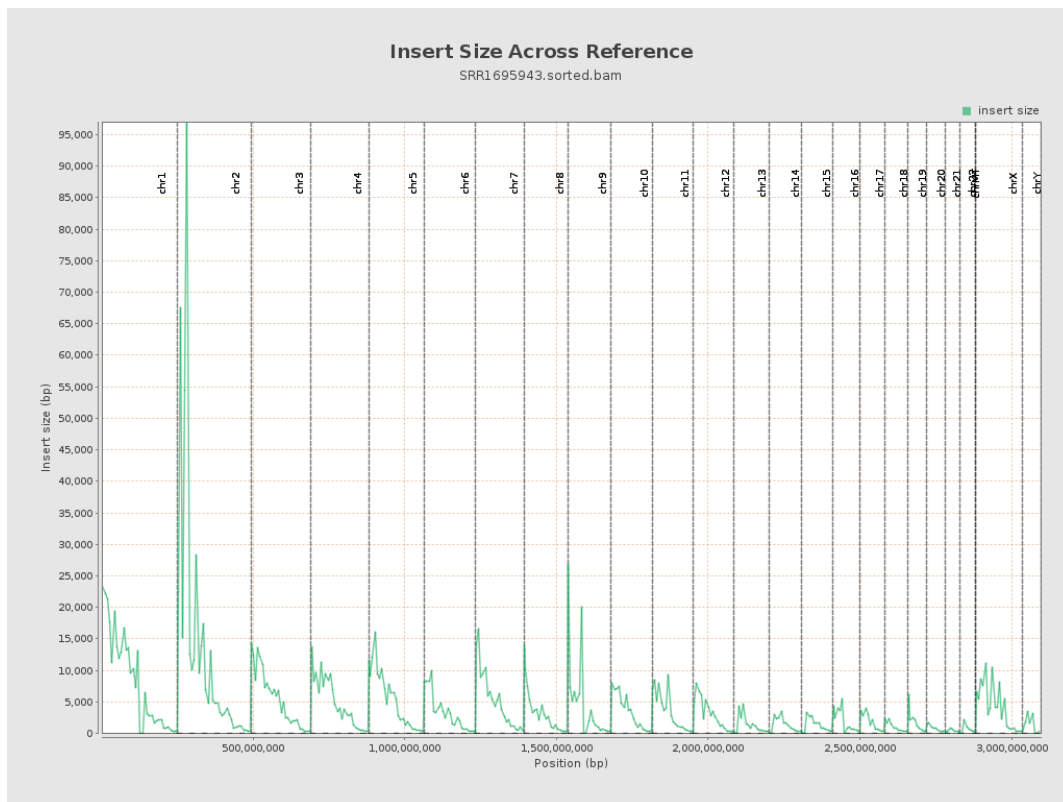
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

