

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 21:41:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695924.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 924 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695924_1.fastq.gz SRR1695924_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 21:41:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695924.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	162,038,866
Mapped reads	160,605,890 / 99.12%
Unmapped reads	1,432,976 / 0.88%
Mapped paired reads	160,605,890 / 99.12%
Mapped reads, first in pair	80,764,543 / 49.84%
Mapped reads, second in pair	79,841,347 / 49.27%
Mapped reads, both in pair	159,557,492 / 98.47%
Mapped reads, singletons	1,048,398 / 0.65%
Secondary alignments	0
Supplementary alignments	1,395,278 / 0.86%
Read min/max/mean length	30 / 100 / 100.35
Duplicated reads (estimated)	13,453,351 / 8.3%
Duplication rate	7.91%
Clipped reads	8,278,681 / 5.11%

2.2. ACGT Content

Number/percentage of A's	4,829,065,582 / 30.27%
Number/percentage of C's	3,131,011,872 / 19.63%
Number/percentage of T's	4,824,081,047 / 30.24%
Number/percentage of G's	3,166,156,024 / 19.85%
Number/percentage of N's	2,693,800 / 0.02%

GC Percentage	39.47%
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2.3. Coverage

Mean	5.1543
Standard Deviation	7.2235

2.4. Mapping Quality

Mean Mapping Quality	54.48
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2.5. Insert size

Mean	39,842.14
Standard Deviation	1,912,265.38
P25/Median/P75	300 / 310 / 319

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	70,435,404
Insertions	1,079,819
Mapped reads with at least one insertion	0.66%
Deletions	1,440,595
Mapped reads with at least one deletion	0.88%
Homopolymer indels	46.15%

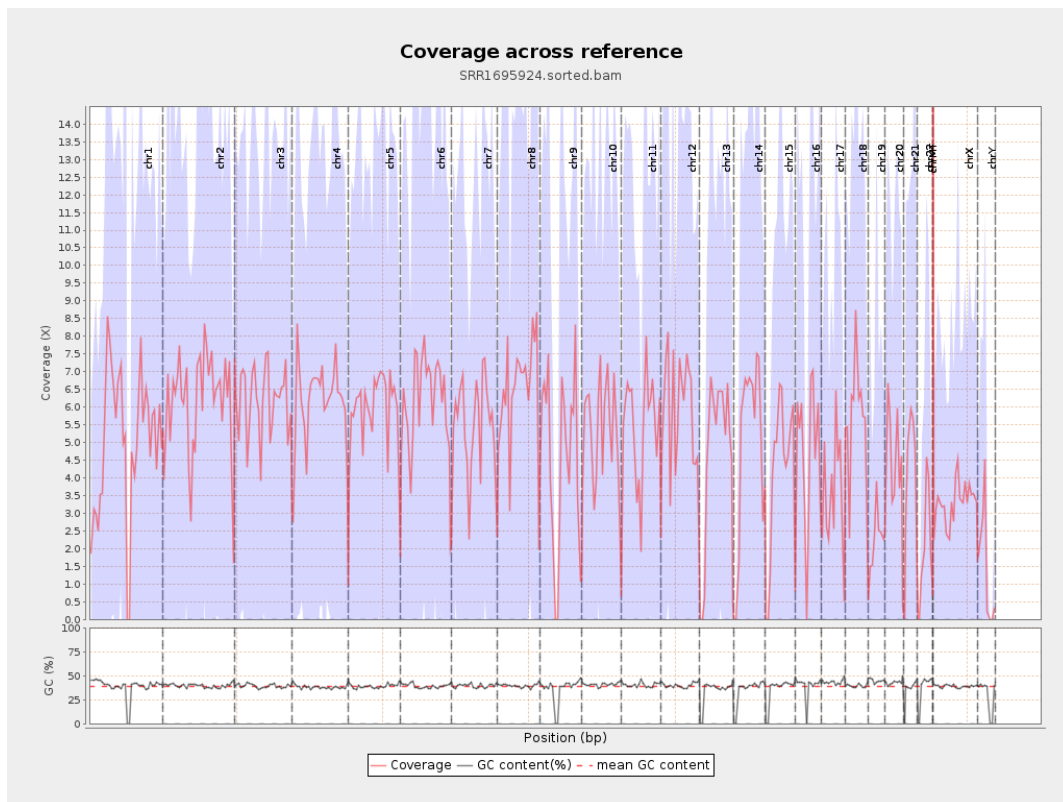
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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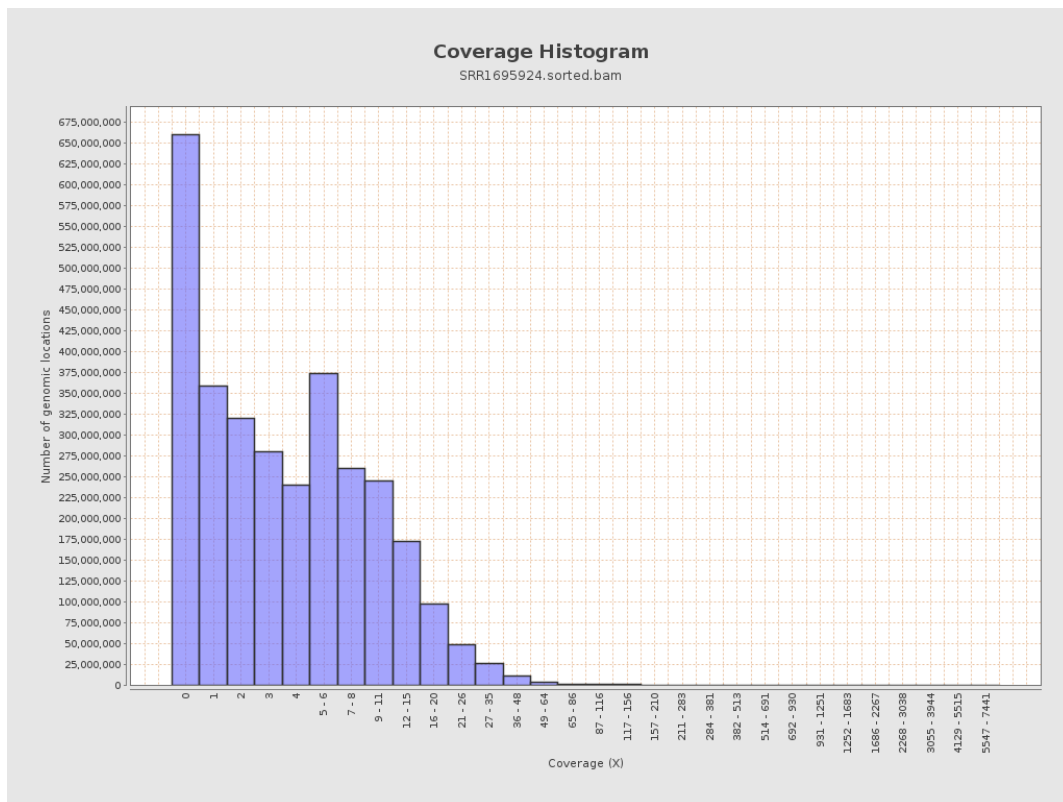
		bases	coverage	deviation
chr1	249250621	1250058579	5.0153	8.0656
chr2	243199373	1495507593	6.1493	8.9422
chr3	198022430	1221005727	6.166	6.9406
chr4	191154276	1184890478	6.1986	6.6916
chr5	180915260	1065754021	5.8909	6.7695
chr6	171115067	1067804848	6.2403	7.8425
chr7	159138663	858636968	5.3955	6.5903
chr8	146364022	950747860	6.4958	8.2035
chr9	141213431	643866516	4.5595	6.8953
chr10	135534747	727849483	5.3702	7.271
chr11	135006516	731930293	5.4214	6.6859
chr12	133851895	788408000	5.8902	7.4407
chr13	115169878	541568317	4.7023	6.4447
chr14	107349540	540520722	5.0351	7.0838
chr15	102531392	426214253	4.1569	6.1258
chr16	90354753	406138878	4.4949	7.6597
chr17	81195210	293490943	3.6146	6.2463
chr18	78077248	442230637	5.664	7.2239
chr19	59128983	135027210	2.2836	5.8071
chr20	63025520	282478161	4.482	6.441
chr21	48129895	193506857	4.0205	8.4026
chr22	51304566	107174149	2.089	4.7983
chrMT	16571	727761	43.9177	19.2818
chrX	155270560	511305865	3.293	5.0365

chrY	59373566	89315971	1.5043	4.1323
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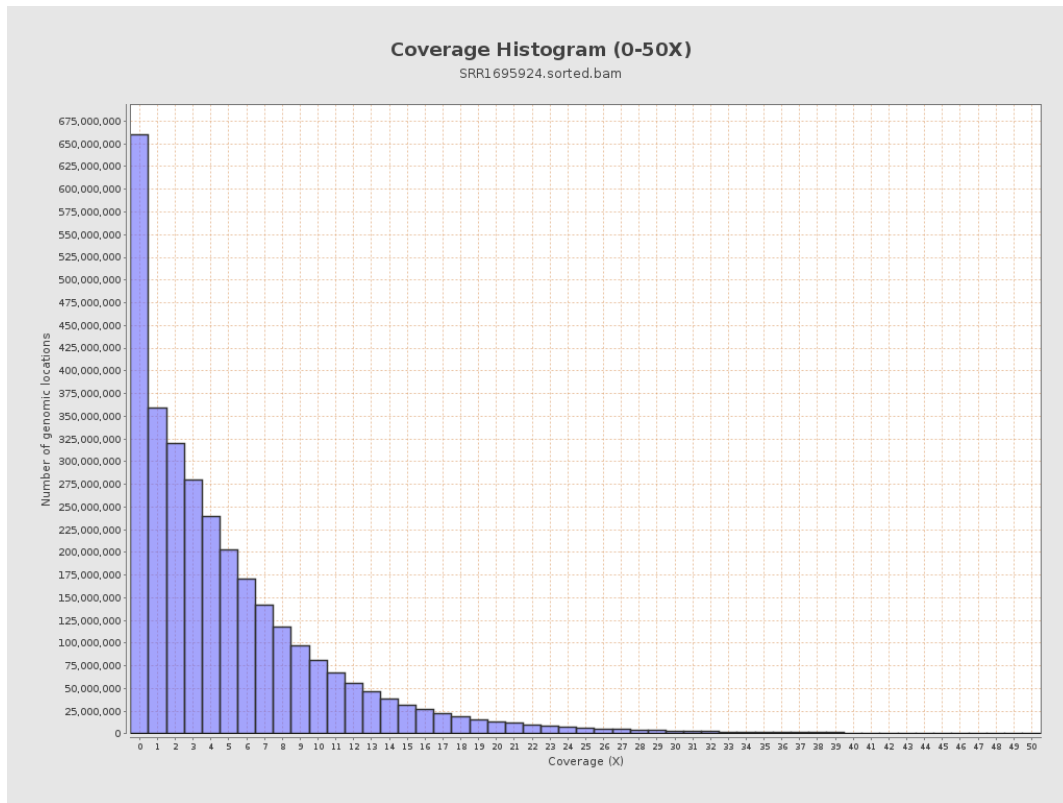
3. Results : Coverage across reference



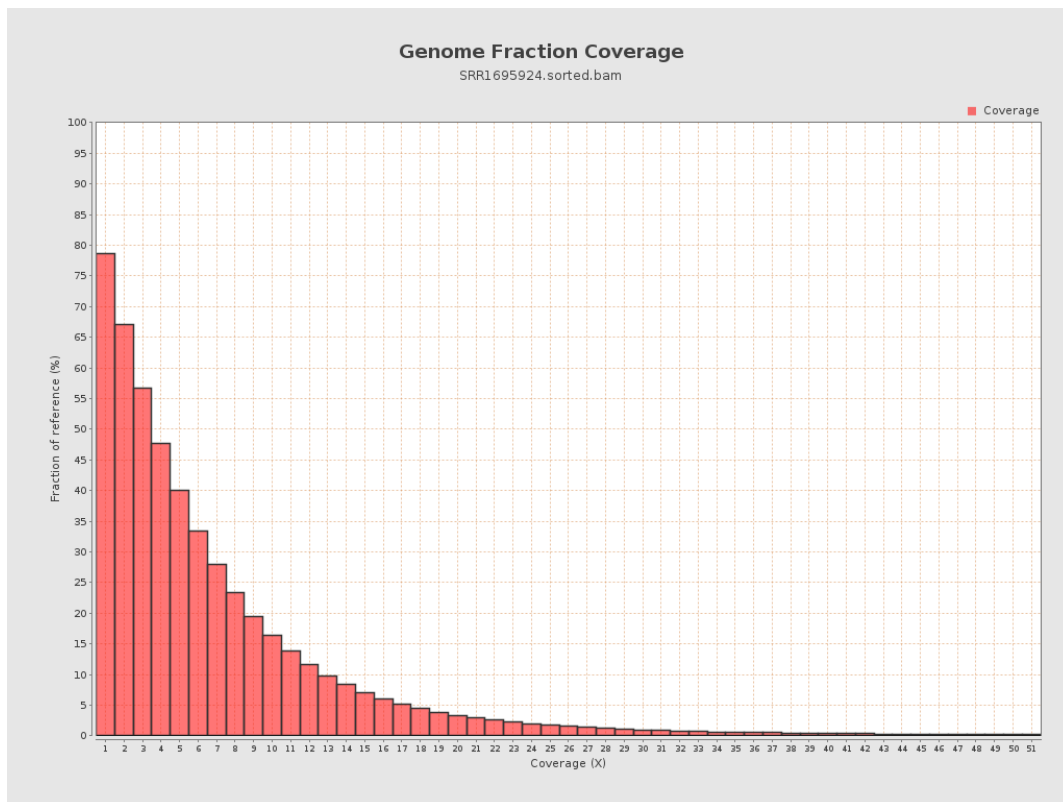
4. Results : Coverage Histogram



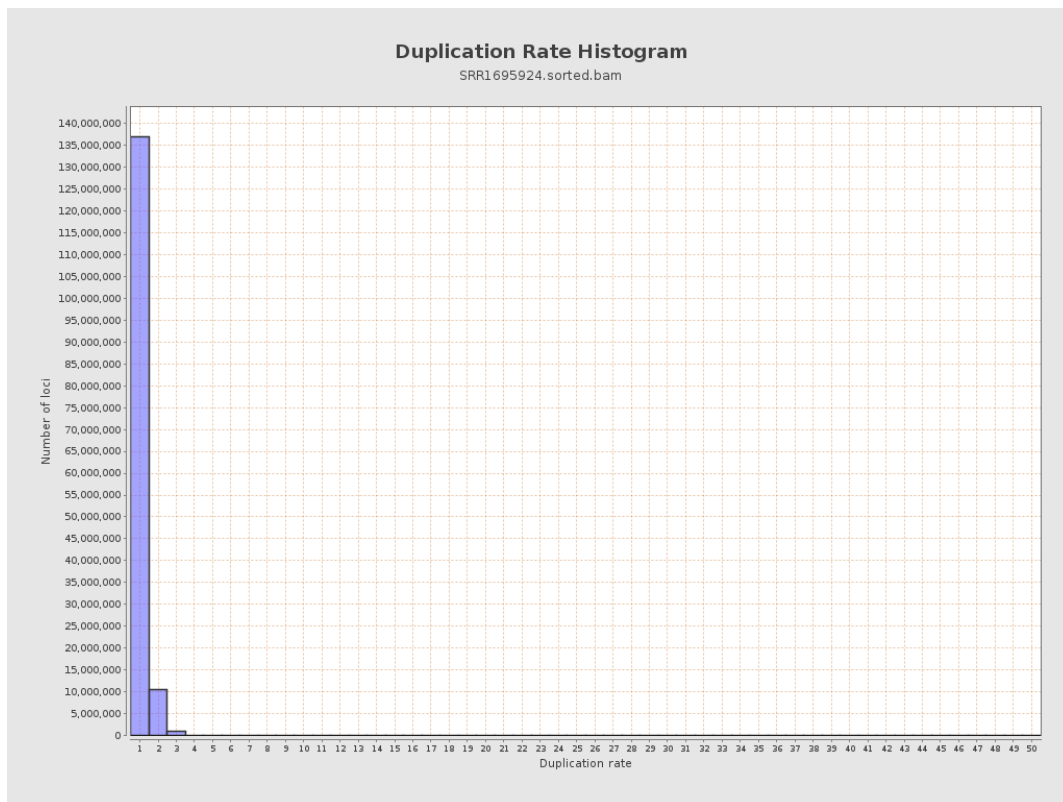
5. Results : Coverage Histogram (0-50X)



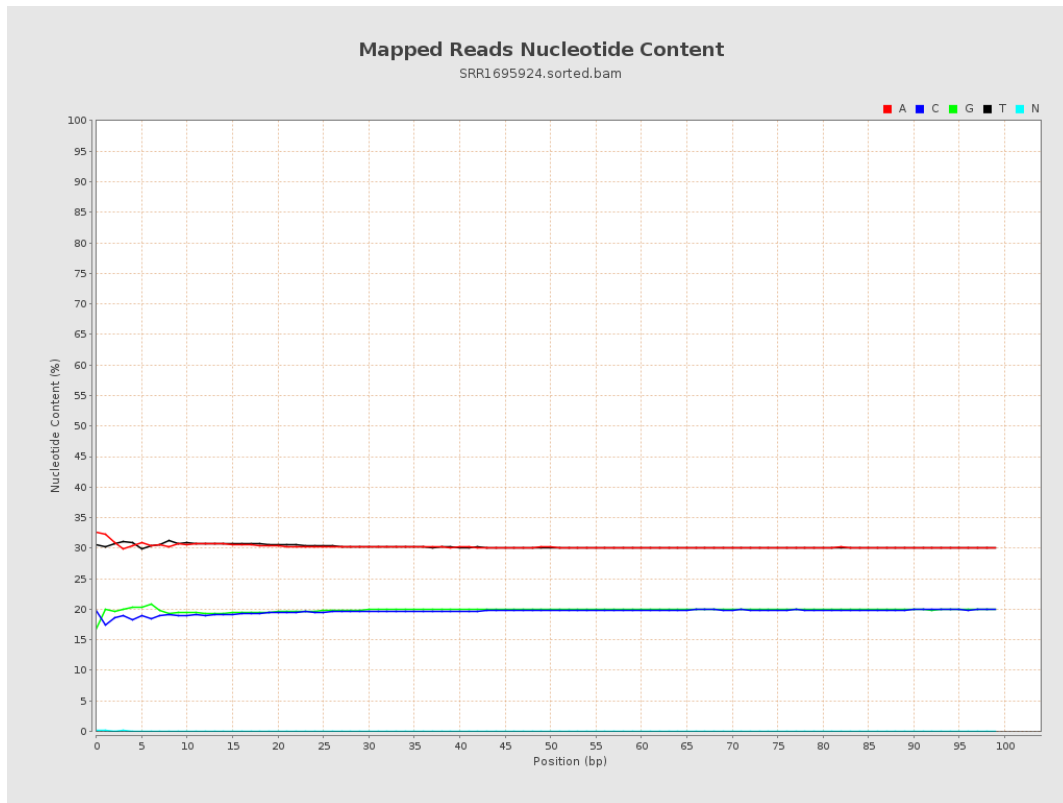
6. Results : Genome Fraction Coverage



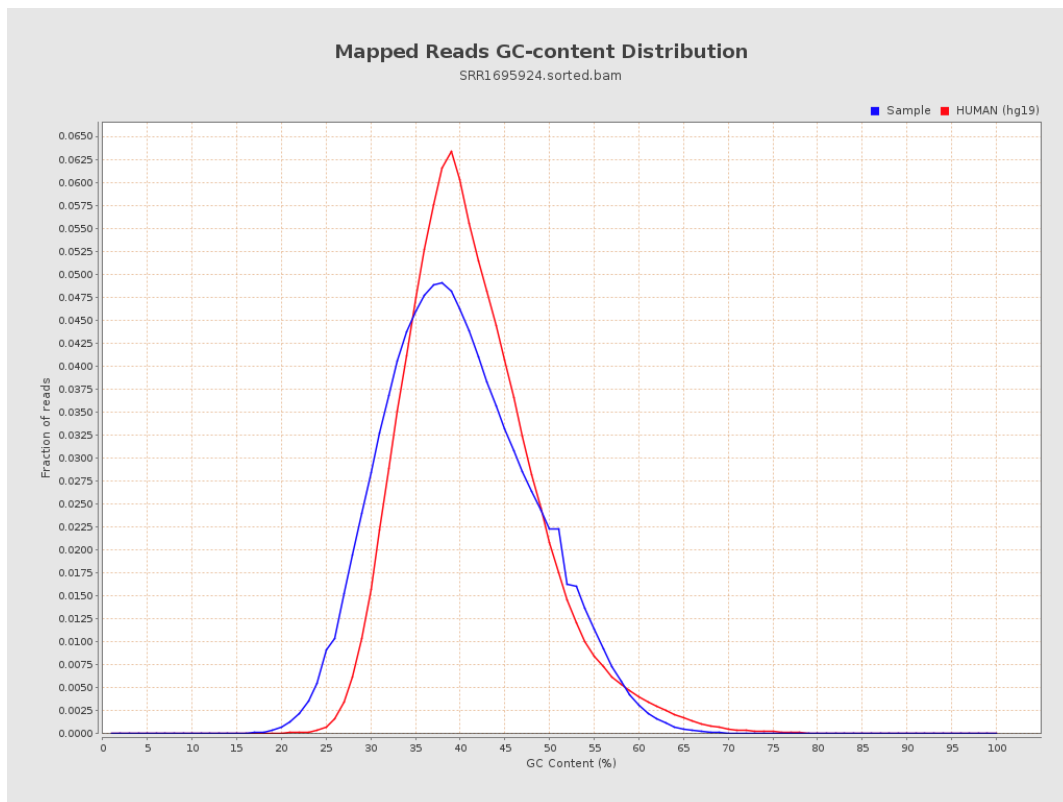
7. Results : Duplication Rate Histogram



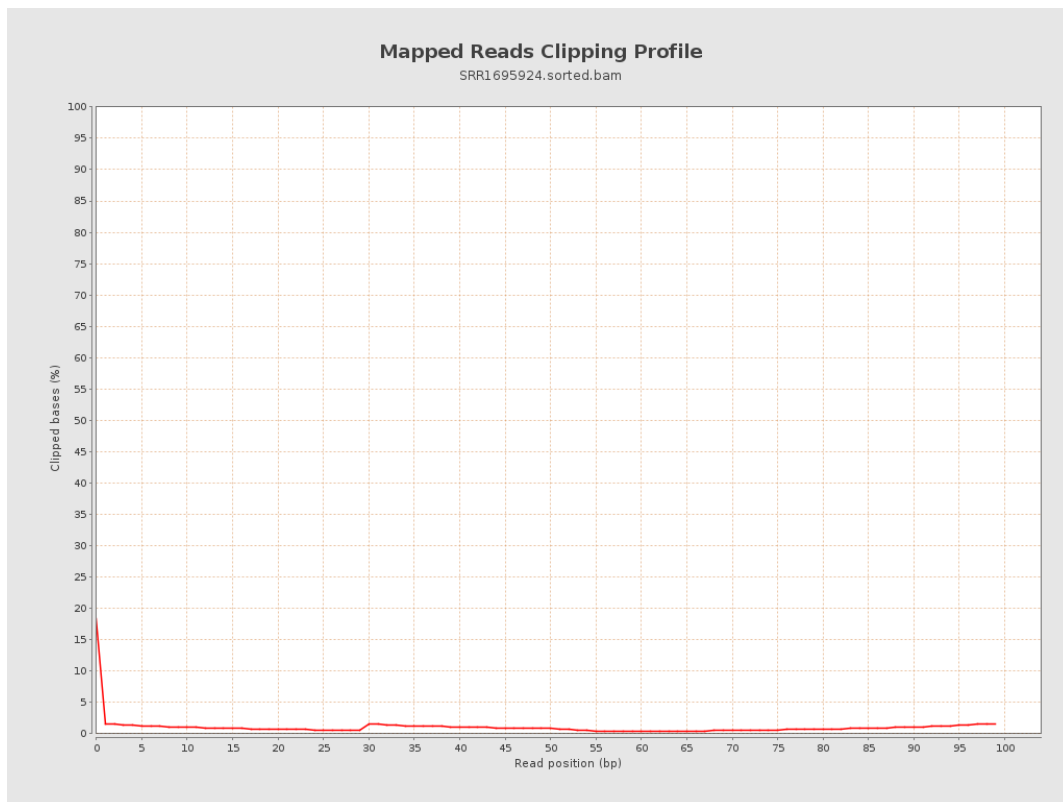
8. Results : Mapped Reads Nucleotide Content



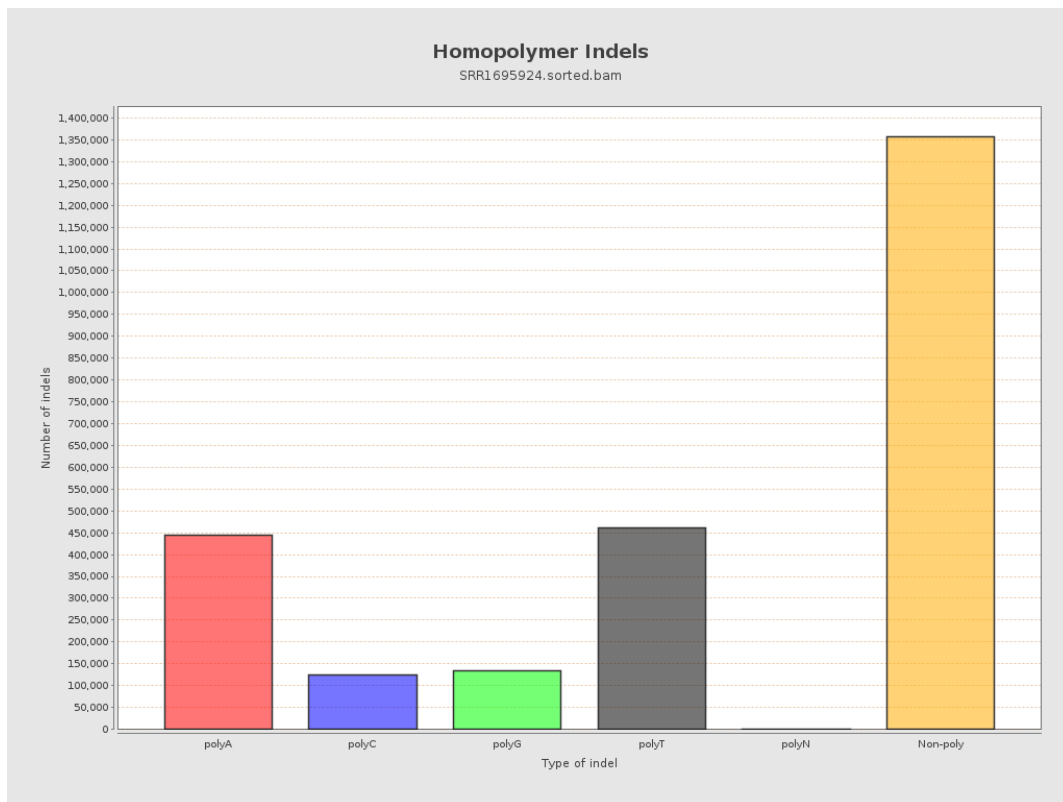
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



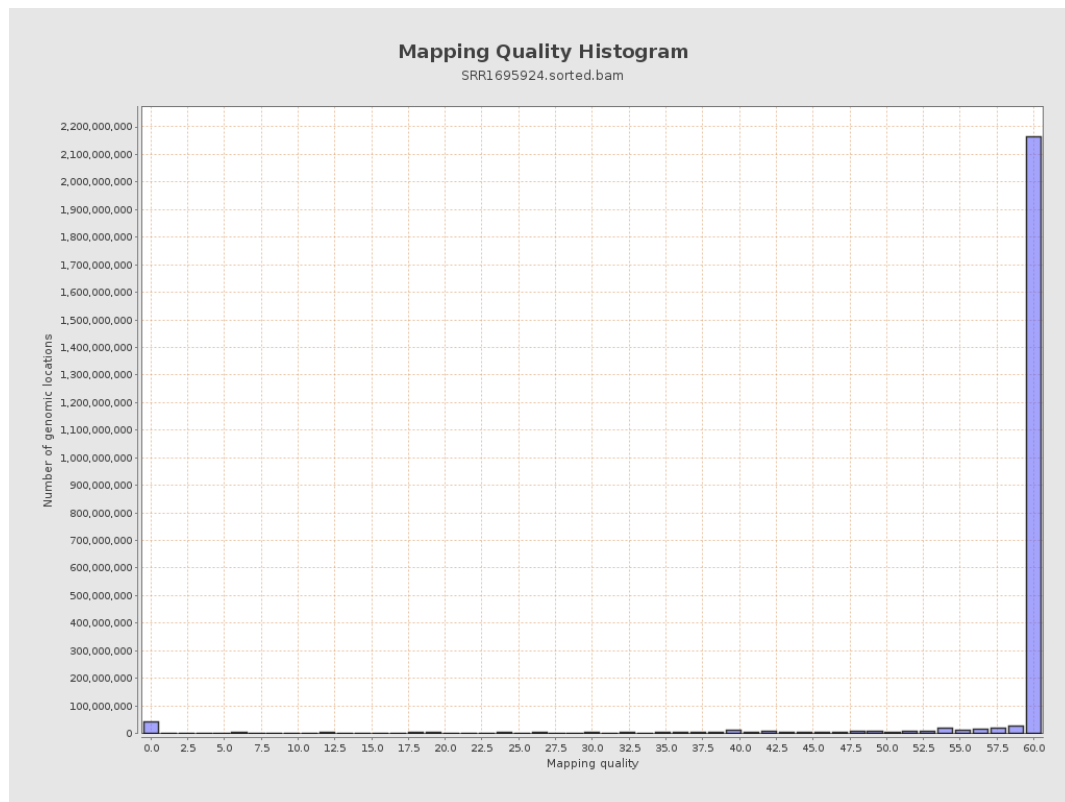
11. Results : Homopolymer Indels



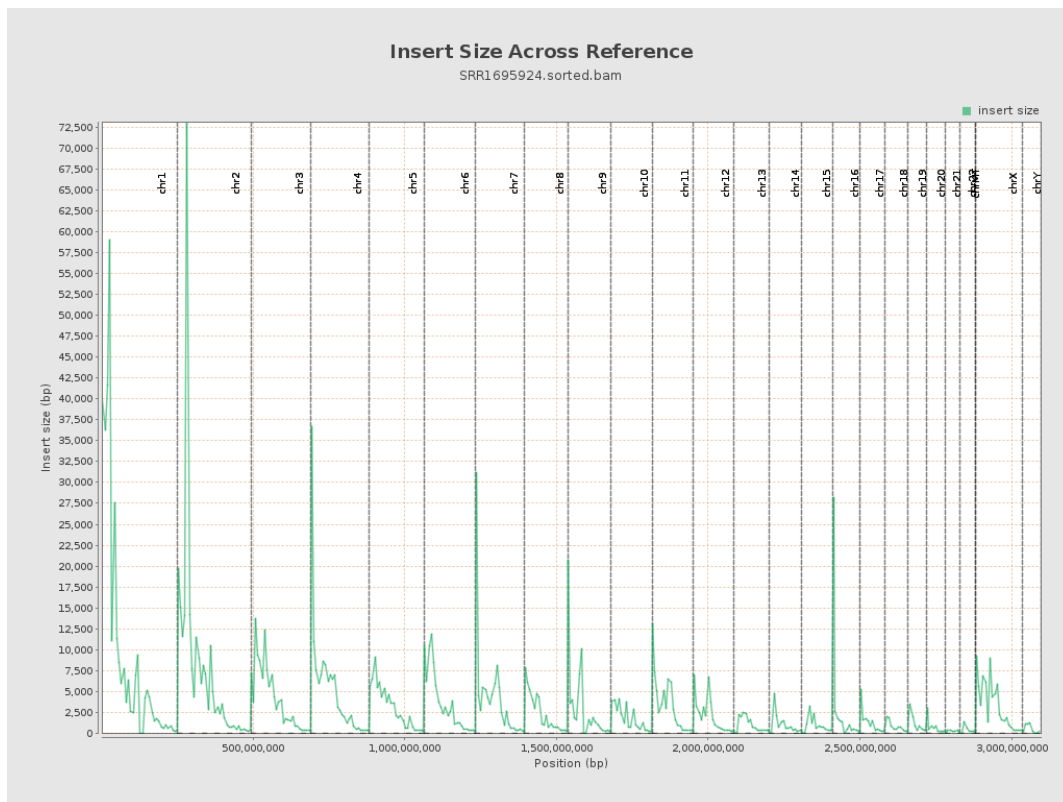
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

